NCBI/ BLAST/ blastp suite/ Formatting Results - BF49E19P015

Your search parameters were adjusted to search for a short input sequence.

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How to read this page | Blast report description

APMAP_KLLLSSETPIEGKDMSFVNDLTVTQDGRK_Mod

RID BF49E19P015 (Expires on 01-16 17:06 pm)

Query ID lcl|78059
Description None
Molecule type amino acid
Query Length 29

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

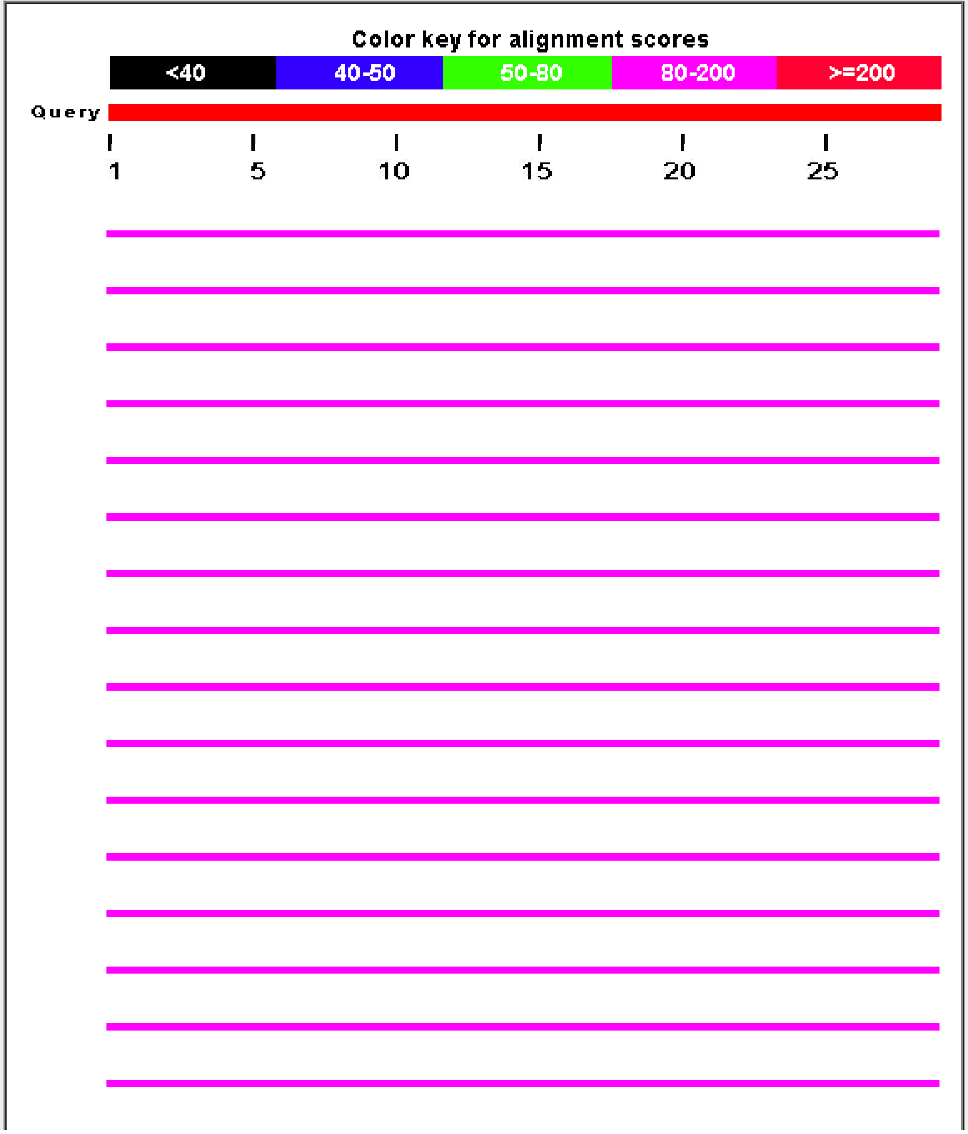
Graphic Summary

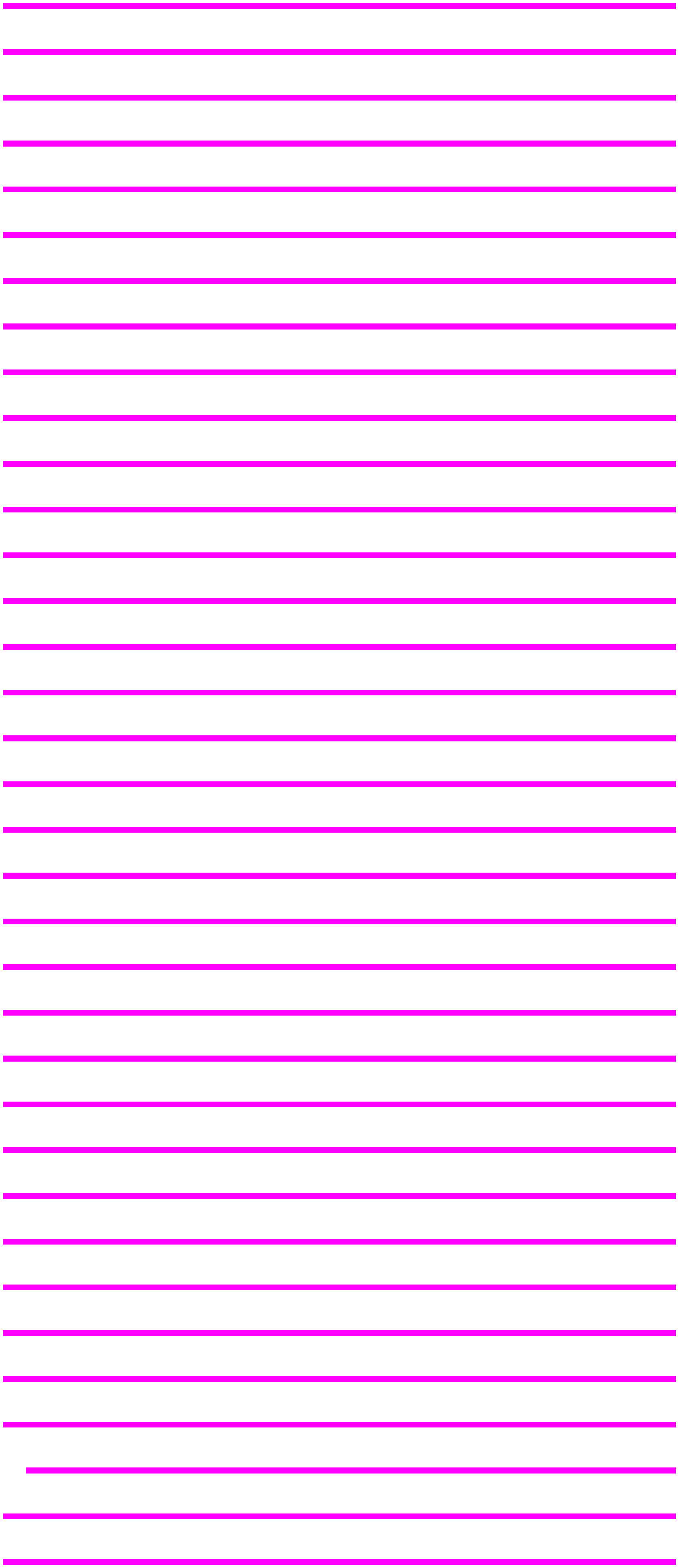
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	91.4	91.4	100%	4e-19	97%	gi|194378020|BAG63373.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	91.4	91.4	100%	4e-19	97%	gi|530425819|XP_005260820.1
☐	C20orf3 [Homo sapiens]	91.4	91.4	100%	4e-19	97%	gi|37183270|AAQ89435.1
☐	chromosome 20 open reading frame 3, isoform CRA_b [Homo sapi	91.4	91.4	100%	4e-19	97%	gi|119630519|EAX10114.1
☐	adipocyte plasma membrane-associated protein [Homo sapiens]	91.4	91.4	100%	4e-19	97%	gi|24308201|NP_065392.1
☐	unnamed protein product [Homo sapiens]	91.4	91.4	100%	4e-19	97%	gi|158255694|BAF83818.1
☐	BSCv [Homo sapiens]	91.4	91.4	100%	4e-19	97%	gi|9836652|BAB11885.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	88.9	88.9	100%	3e-18	97%	gi|675656498|XP_008994116.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	88.9	88.9	100%	3e-18	97%	gi|675656496|XP_008994115.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Gor	88.9	88.9	100%	3e-18	97%	gi|426391191|XP_004061964.1
☐	Protein BSCv [Macaca fascicularis]	88.9	88.9	100%	3e-18	97%	gi|355784761|EHH65612.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Nor	88.9	88.9	100%	3e-18	97%	gi|332258942|XP_003278549.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pan	88.9	88.9	100%	3e-18	97%	gi|114681318|XP_514556.2
☐	adipocyte plasma membrane-associated protein [Macaca mulatta]	88.9	88.9	100%	3e-18	97%	gi|388453189|NP_001252979.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pon	88.9	88.9	100%	3e-18	97%	gi|686761455|XP_009231655.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	88.9	88.9	100%	3e-18	97%	gi|544463778|XP_005568209.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	88.9	88.9	100%	3e-18	97%	gi|544463776|XP_005568208.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	88.9	88.9	100%	4e-18	97%	gi|544463774|XP_005568207.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	88.9	88.9	100%	4e-18	97%	gi|544463772|XP_005568206.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ory	86.7	86.7	100%	2e-17	93%	gi|634885477|XP_007952365.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Oto	86.7	86.7	100%	2e-17	93%	gi|395857507|XP_003801133.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Sair	86.3	86.3	100%	2e-17	93%	gi|403304837|XP_003942992.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ele	86.3	86.3	100%	2e-17	93%	gi|585720265|XP_006902530.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pan	85.9	85.9	100%	3e-17	93%	gi|591342488|XP_007096642.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Feli	85.9	85.9	100%	3e-17	93%	gi|586981414|XP_006930067.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	85.5	85.5	100%	4e-17	93%	gi|724797097|XP_010359957.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	85.5	85.5	100%	5e-17	93%	gi|724797100|XP_010359965.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	84.6	84.6	100%	9e-17	93%	gi|568918452|XP_006500262.1
☐							

	PREDICTED: adipocyte plasma membrane-associated protein isofo	84.6	84.6	100%	9e-17	93%	gi|568918450|XP_006500261.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pero	84.6	84.6	100%	9e-17	93%	gi|589945824|XP_006985593.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Micr	84.6	84.6	100%	9e-17	93%	gi|532057169|XP_005371288.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Mes	84.6	84.6	100%	9e-17	93%	gi|524942103|XP_005072608.1
☐	adipocyte plasma membrane-associated protein [Mus musculus]	84.6	84.6	100%	9e-17	93%	gi|21313668|NP_082253.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Chr	84.2	84.2	100%	1e-16	90%	gi|586460140|XP_006860728.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	83.8	83.8	100%	2e-16	93%	gi|675792202|XP_008952974.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	83.8	83.8	100%	2e-16	93%	gi|675792200|XP_008952973.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Tars	83.3	83.3	100%	3e-16	93%	gi|640819801|XP_008066807.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ech	83.3	83.3	100%	3e-16	90%	gi|507712042|XP_004717841.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	82.5	82.5	100%	5e-16	90%	gi|564343542|XP_006235279.1
☐	adipocyte plasma membrane-associated protein precursor [Rattus n	82.5	82.5	100%	5e-16	90%	gi|77735352|NP_001029175.1
☐	Ab2-305 [Rattus norvegicus]	82.5	82.5	100%	5e-16	90%	gi|33086580|AAP92602.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Cor	82.5	82.5	100%	5e-16	90%	gi|507961028|XP_004687183.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	82.5	82.5	100%	5e-16	90%	gi|564343538|XP_006235277.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Lipo	81.7	81.7	100%	1e-15	90%	gi|602732221|XP_007451508.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Bala	81.7	81.7	100%	1e-15	90%	gi|594689044|XP_007191923.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Phy	81.7	81.7	100%	1e-15	90%	gi|593717611|XP_007105230.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Orc	81.7	81.7	100%	1e-15	90%	gi|466012177|XP_004270482.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Nar	81.2	81.2	100%	1e-15	90%	gi|674106802|XP_008824690.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Cer	80.8	80.8	96%	2e-15	89%	gi|478535723|XP_004441986.1
☐	hypothetical protein PANDA_019520 [Ailuropoda melanoleuca]	80.4	80.4	100%	3e-15	86%	gi|281351396|EFB26980.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Urs	80.4	80.4	100%	3e-15	86%	gi|671025584|XP_008703615.1
☐	PREDICTED: adipocyte plasma membrane-associated protein-like	80.4	80.4	100%	3e-15	86%	gi|301787895|XP_002929365.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Odo	80.4	80.4	100%	3e-15	86%	gi|472357692|XP_004398472.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Lep	80.4	80.4	100%	3e-15	86%	gi|585179120|XP_006741245.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Gal	80.0	80.0	100%	3e-15	90%	gi|667326556|XP_008589917.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Equ	80.0	80.0	100%	4e-15	86%	gi|664771366|XP_008504865.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	80.0	80.0	100%	4e-15	86%	gi|545199803|XP_005604486.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	80.0	80.0	100%	4e-15	86%	gi|545199801|XP_005604485.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ory	80.0	80.0	100%	4e-15	86%	gi|291410623|XP_002721586.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ictid	80.0	80.0	100%	4e-15	86%	gi|532097996|XP_005334647.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Jac	78.7	78.7	100%	1e-14	86%	gi|507568935|XP_004668094.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Lox	78.7	78.7	100%	1e-14	86%	gi|344279762|XP_003411656.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	78.7	78.7	100%	1e-14	86%	gi|611981959|XP_007476669.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	78.7	78.7	100%	1e-14	86%	gi|611981957|XP_001382089.2
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	78.3	78.3	100%	1e-14	90%	gi|625192556|XP_007638893.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	78.3	78.3	100%	1e-14	90%	gi|354475585|XP_003500008.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	78.3	78.3	100%	1e-14	90%	gi|625266624|XP_007624792.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Bos	77.8	77.8	100%	2e-14	86%	gi|555978143|XP_005901017.1
☐	Adipocyte plasma membrane-associated protein [Bos mutus]	77.8	77.8	100%	2e-14	86%	gi|440901758|ELR52645.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Bisc	77.8	77.8	100%	2e-14	86%	gi|742102975|XP_010834658.1
☐	adipocyte plasma membrane-associated protein [Bos taurus]	77.8	77.8	100%	2e-14	86%	gi|78369434|NP_001030490.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Bub	77.8	77.8	100%	2e-14	86%	gi|594034111|XP_006041771.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ovis	77.8	77.8	100%	2e-14	86%	gi|426240952|XP_004014356.1

☐	PREDICTED: adipocyte plasma membrane-associated protein [Cap	77.8	77.8	100%	2e-14	86%	gi|548489969|XP_005688183.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pan	77.8	77.8	100%	2e-14	86%	gi|556778497|XP_005984319.1
☐	PREDICTED: adipocyte plasma membrane-associated protein-like	77.4	77.4	100%	2e-14	86%	gi|545890060|XP_005658440.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Sus	77.4	77.4	100%	3e-14	86%	gi|350594715|XP_001927122.3
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	77.0	77.0	100%	4e-14	83%	gi|511864237|XP_004754143.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	77.0	77.0	100%	4e-14	83%	gi|511864235|XP_004754142.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	77.0	77.0	100%	4e-14	83%	gi|511864232|XP_004754141.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Fuk	76.1	76.1	100%	7e-14	83%	gi|731219302|XP_010623912.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	76.1	76.1	100%	7e-14	83%	gi|512880580|XP_004894998.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Chi	76.1	76.1	100%	7e-14	83%	gi|533132029|XP_005381039.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Oct	76.1	76.1	100%	7e-14	83%	gi|507661814|XP_004635630.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Sor	76.1	76.1	96%	7e-14	86%	gi|505845493|XP_004616227.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	76.1	76.1	100%	7e-14	83%	gi|512880576|XP_004894997.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	75.7	75.7	100%	1e-13	83%	gi|562871397|XP_006163663.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	75.7	75.7	100%	1e-13	83%	gi|562871395|XP_006163662.1
☐	Adipocyte plasma membrane-associated protein [Tupaia chinensis]	75.7	75.7	100%	1e-13	83%	gi|444520420|ELV12972.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Tric	74.9	74.9	100%	2e-13	83%	gi|471377312|XP_004376468.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Cav	74.9	74.9	100%	2e-13	83%	gi|348581358|XP_003476444.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Das	74.9	74.9	100%	2e-13	83%	gi|488570200|XP_004474706.1
☐	Adipocyte plasma membrane-associated protein [Myotis davidii]	74.4	74.4	100%	3e-13	79%	gi|432114788|ELK36543.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ept	74.4	74.4	100%	3e-13	79%	gi|641701525|XP_008139374.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Myc	74.4	74.4	100%	3e-13	79%	gi|584069940|XP_006755306.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Myc	73.2	73.2	100%	7e-13	79%	gi|554543332|XP_005866279.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Myc	73.2	73.2	100%	7e-13	79%	gi|558166297|XP_006098004.1
☐	Adipocyte plasma membrane-associated protein [Myotis brandtii]	73.2	73.2	100%	8e-13	79%	gi|521026002|EPQ07790.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Car	72.7	72.7	100%	1e-12	79%	gi|345789049|XP_850086.2
☐	PREDICTED: adipocyte plasma membrane-associated protein-like	70.2	70.2	93%	5e-12	81%	gi|620953601|XP_007656154.1

Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194378020|dbj|BAG63373.1| **Length:** 289 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 183 to 211 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
91.4 bits(208)	4e-19	28/29(97%)	29/29(100%)	0/29(0%)

```
Query  1    KLLLSSETPIEGKDMSFVNDLTVTQDGRK  29
            KLLLSSETPIEGK+MSFVNDLTVTQDGRK
Sbjct  183  KLLLSSETPIEGKNMSFVNDLTVTQDGRK  211
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: adipocyte plasma membrane-associated protein isoform X1 [Homo sapiens]

Sequence ID: gi|530425819|ref|XP_005260820.1| **Length:** 289 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 183 to 211 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
91.4 bits(208)	4e-19	28/29(97%)	29/29(100%)	0/29(0%)

```
Query  1    KLLLSSETPIEGKDMSFVNDLTVTQDGRK  29
```

```
            KLLLSSETPIEGK+MSFVNDLTVTQDGRK
Sbjct  183  KLLLSSETPIEGKNMSFVNDLTVTQDGRK  211
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

C20orf3 [Homo sapiens]

Sequence ID: gi|37183270|gb|AAQ89435.1| **Length:** 372 **Number of Matches:** 1

Range 1: 139 to 167 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
91.4 bits(208)	4e-19	28/29(97%)	29/29(100%)	0/29(0%)

```
Query  1    KLLLSSETPIEGKDMSFVNDLTVTQDGRK  29
            KLLLSSETPIEGK+MSFVNDLTVTQDGRK
Sbjct  139  KLLLSSETPIEGKNMSFVNDLTVTQDGRK  167
```

Related Information

Gene - associated gene details

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

chromosome 20 open reading frame 3, isoform CRA_b [Homo sapiens]

Sequence ID: gi|119630519|gb|EAX10114.1| **Length:** 380 **Number of Matches:** 1

Range 1: 139 to 167 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
91.4 bits(208)	4e-19	28/29(97%)	29/29(100%)	0/29(0%)

```
Query  1    KLLLSSETPIEGKDMSFVNDLTVTQDGRK  29
            KLLLSSETPIEGK+MSFVNDLTVTQDGRK
Sbjct  139  KLLLSSETPIEGKNMSFVNDLTVTQDGRK  167
```

Related Information

Gene - associated gene details

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

adipocyte plasma membrane-associated protein [Homo sapiens]

Sequence ID: gi|24308201|ref|NP_065392.1| **Length:** 416 **Number of Matches:** 1

▸ See 4 more title(s)

Range 1: 183 to 211 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
91.4 bits(208)	4e-19	28/29(97%)	29/29(100%)	0/29(0%)

```
Query  1    KLLLSSETPIEGKDMSFVNDLTVTQDGRK  29
            KLLLSSETPIEGK+MSFVNDLTVTQDGRK
Sbjct  183  KLLLSSETPIEGKNMSFVNDLTVTQDGRK  211
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

APMAP_KLLLSSETPIEGKNMSFVNDLTVTQDGRK_NonMod

RID B90W5YEY01R (Expires on 01-14 09:31 am)

Query ID lcl|38621
Description None
Molecule type amino acid
Query Length 29

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

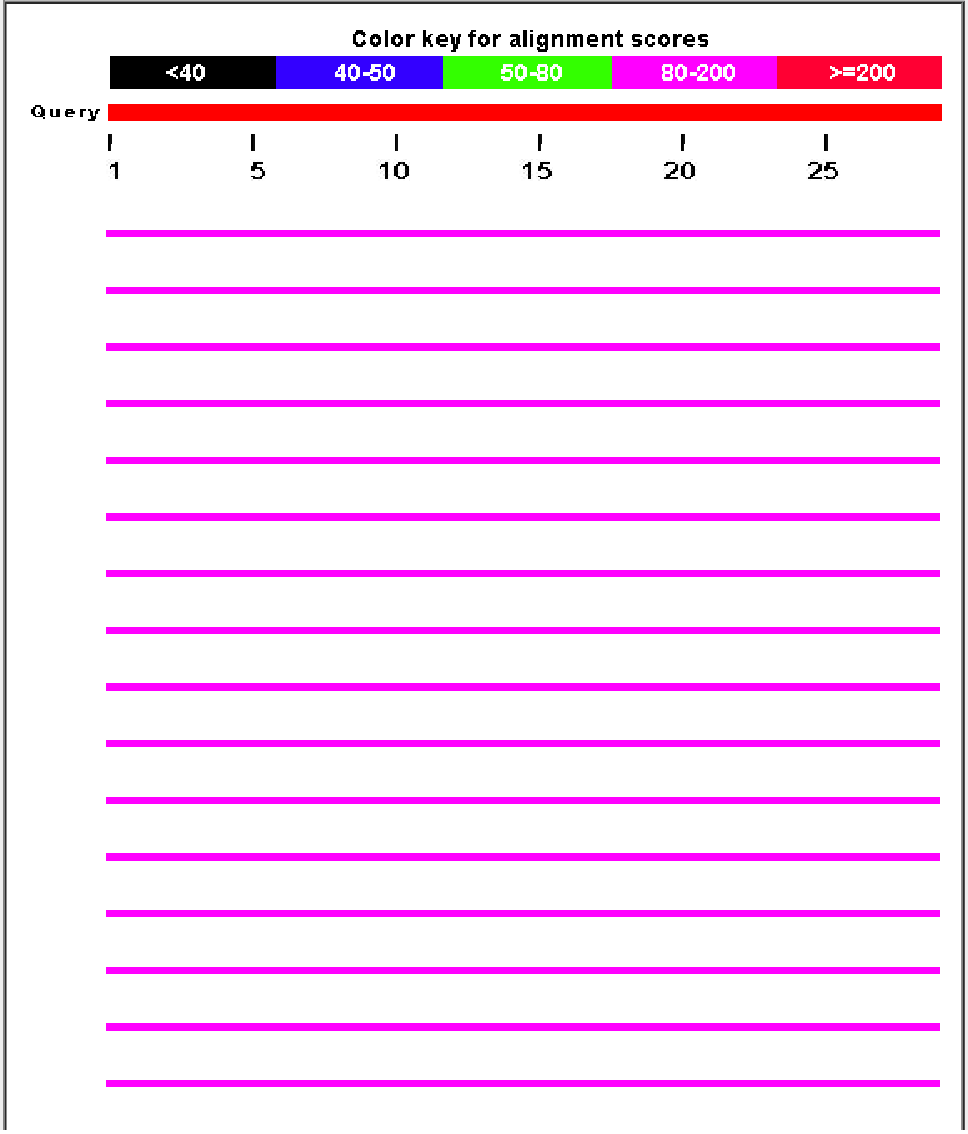
Graphic Summary

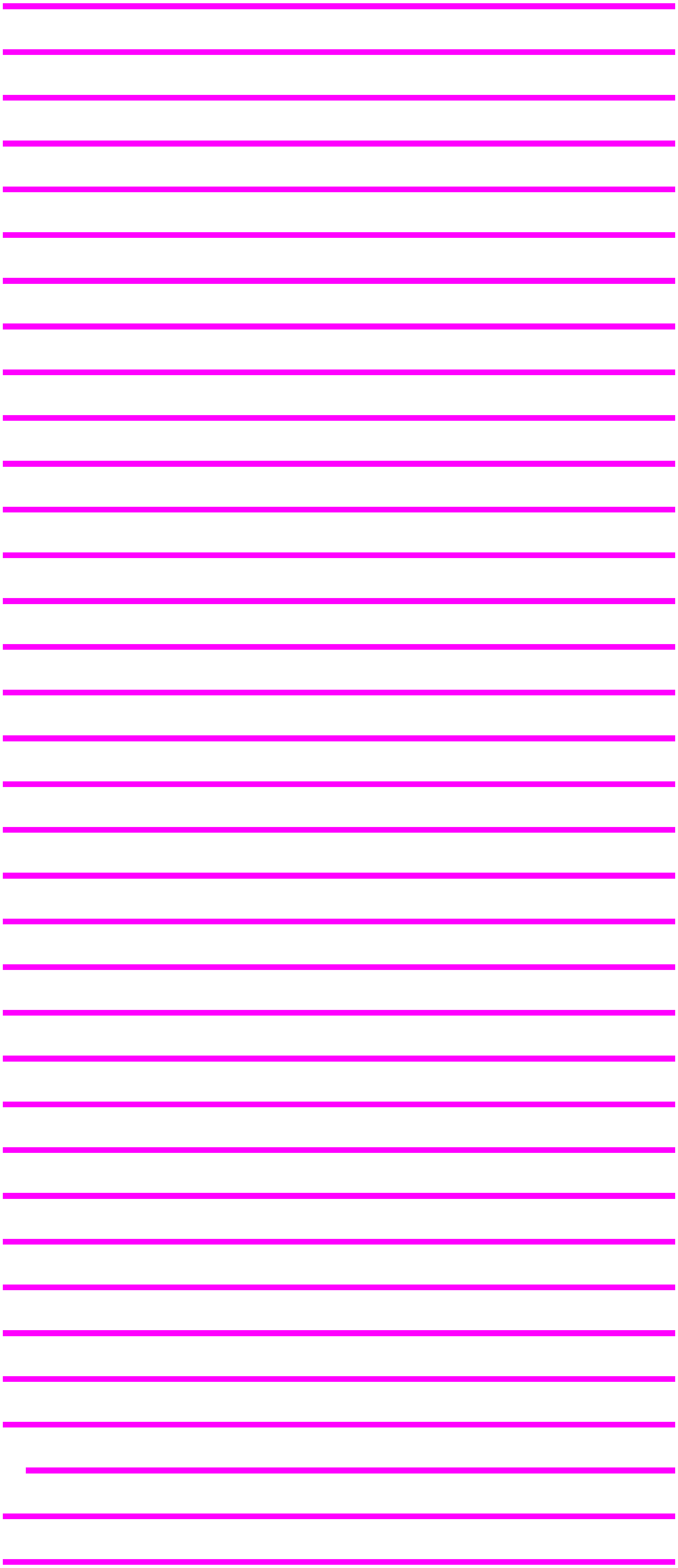
Show Conserved Domains

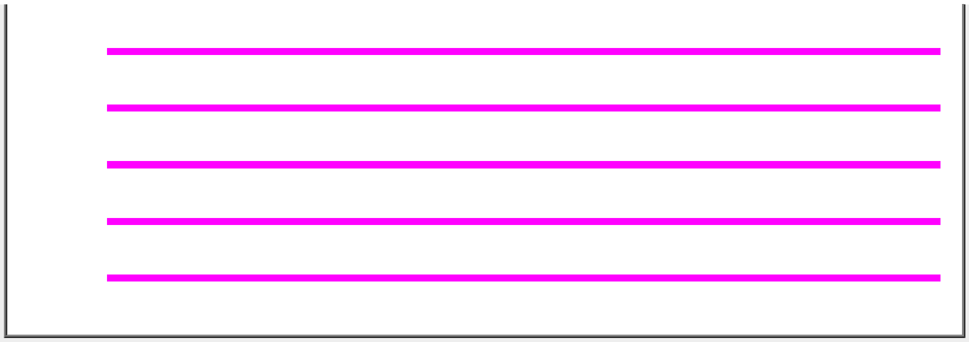
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	94.0	94.0	100%	5e-20	100%	gi|194378020|BAG63373.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	94.0	94.0	100%	5e-20	100%	gi|530425819|XP_005260820.1
☐	C20orf3 [Homo sapiens]	94.0	94.0	100%	5e-20	100%	gi|37183270|AAQ89435.1
☐	chromosome 20 open reading frame 3, isoform CRA_b [Homo sapi	94.0	94.0	100%	5e-20	100%	gi|119630519|EAX10114.1
☐	adipocyte plasma membrane-associated protein [Homo sapiens]	94.0	94.0	100%	6e-20	100%	gi|24308201|NP_065392.1
☐	unnamed protein product [Homo sapiens]	94.0	94.0	100%	6e-20	100%	gi|158255694|BAF83818.1
☐	BSCv [Homo sapiens]	94.0	94.0	100%	6e-20	100%	gi|9836652|BAB11885.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	90.1	90.1	100%	1e-18	97%	gi|675656498|XP_008994116.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	90.1	90.1	100%	1e-18	97%	gi|675656496|XP_008994115.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Gor	90.1	90.1	100%	1e-18	97%	gi|426391191|XP_004061964.1
☐	Protein BSCv [Macaca fascicularis]	90.1	90.1	100%	1e-18	97%	gi|355784761|EHH65612.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Nor	90.1	90.1	100%	1e-18	97%	gi|332258942|XP_003278549.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pan	90.1	90.1	100%	1e-18	97%	gi|114681318|XP_514556.2
☐	adipocyte plasma membrane-associated protein [Macaca mulatta]	90.1	90.1	100%	1e-18	97%	gi|388453189|NP_001252979.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pon	90.1	90.1	100%	1e-18	97%	gi|686761455|XP_009231655.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	90.1	90.1	100%	1e-18	97%	gi|544463778|XP_005568209.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	90.1	90.1	100%	1e-18	97%	gi|544463776|XP_005568208.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	90.1	90.1	100%	1e-18	97%	gi|544463774|XP_005568207.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	90.1	90.1	100%	1e-18	97%	gi|544463772|XP_005568206.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ory	88.0	88.0	100%	6e-18	93%	gi|634885477|XP_007952365.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Oto	88.0	88.0	100%	6e-18	93%	gi|395857507|XP_003801133.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Sai	87.6	87.6	100%	8e-18	93%	gi|403304837|XP_003942992.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ele	87.6	87.6	100%	9e-18	93%	gi|585720265|XP_006902530.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pan	87.2	87.2	100%	1e-17	93%	gi|591342488|XP_007096642.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Feli	87.2	87.2	100%	1e-17	93%	gi|586981414|XP_006930067.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	86.7	86.7	100%	2e-17	93%	gi|724797097|XP_010359957.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	86.7	86.7	100%	2e-17	93%	gi|724797100|XP_010359965.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	85.9	85.9	100%	3e-17	93%	gi|568918452|XP_006500262.1
☐							

PREDICTED: adipocyte plasma membrane-associated protein isofc	85.9	85.9	100%	3e-17	93%	gi|568918450|XP_006500261.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Per	85.9	85.9	100%	3e-17	93%	gi|589945824|XP_006985593.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Mic	85.9	85.9	100%	3e-17	93%	gi|532057169|XP_005371288.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Mes	85.9	85.9	100%	3e-17	93%	gi|524942103|XP_005072608.1
☐ adipocyte plasma membrane-associated protein [Mus musculus]	85.9	85.9	100%	3e-17	93%	gi|21313668|NP_082253.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Chr	85.5	85.5	100%	5e-17	90%	gi|586460140|XP_006860728.1
☐ PREDICTED: adipocyte plasma membrane-associated protein isofc	85.0	85.0	100%	6e-17	93%	gi|675792202|XP_008952974.1
☐ PREDICTED: adipocyte plasma membrane-associated protein isofc	85.0	85.0	100%	6e-17	93%	gi|675792200|XP_008952973.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Ech	84.6	84.6	100%	9e-17	90%	gi|507712042|XP_004717841.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Tars	84.2	84.2	100%	1e-16	93%	gi|640819801|XP_008066807.1
☐ PREDICTED: adipocyte plasma membrane-associated protein isofc	83.8	83.8	100%	2e-16	90%	gi|564343542|XP_006235279.1
☐ adipocyte plasma membrane-associated protein precursor [Rattus r	83.8	83.8	100%	2e-16	90%	gi|77735352|NP_001029175.1
☐ Ab2-305 [Rattus norvegicus]	83.8	83.8	100%	2e-16	90%	gi|33086580|AAP92602.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Cor	83.8	83.8	100%	2e-16	90%	gi|507961028|XP_004687183.1
☐ PREDICTED: adipocyte plasma membrane-associated protein isofc	83.8	83.8	100%	2e-16	90%	gi|564343538|XP_006235277.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Lipc	82.9	82.9	100%	3e-16	90%	gi|602732221|XP_007451508.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Bala	82.9	82.9	100%	3e-16	90%	gi|594689044|XP_007191923.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Phy	82.9	82.9	100%	3e-16	90%	gi|593717611|XP_007105230.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Orc	82.9	82.9	100%	3e-16	90%	gi|466012177|XP_004270482.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Nar	82.5	82.5	100%	4e-16	90%	gi|674106802|XP_008824690.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Cer	82.1	82.1	96%	7e-16	89%	gi|478535723|XP_004441986.1
☐ hypothetical protein PANDA_019520 [Ailuropoda melanoleuca]	81.7	81.7	100%	9e-16	86%	gi|281351396|EFB26980.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Urs	81.7	81.7	100%	9e-16	86%	gi|671025584|XP_008703615.1
☐ PREDICTED: adipocyte plasma membrane-associated protein-like	81.7	81.7	100%	9e-16	86%	gi|301787895|XP_002929365.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Odc	81.7	81.7	100%	9e-16	86%	gi|472357692|XP_004398472.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Lep	81.7	81.7	100%	9e-16	86%	gi|585179120|XP_006741245.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Gal	81.2	81.2	100%	1e-15	90%	gi|667326556|XP_008589917.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Equ	81.2	81.2	100%	1e-15	86%	gi|664771366|XP_008504865.1
☐ PREDICTED: adipocyte plasma membrane-associated protein isofc	81.2	81.2	100%	1e-15	86%	gi|545199803|XP_005604486.1
☐ PREDICTED: adipocyte plasma membrane-associated protein isofc	81.2	81.2	100%	1e-15	86%	gi|545199801|XP_005604485.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Ory	81.2	81.2	100%	1e-15	86%	gi|291410623|XP_002721586.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Ictic	81.2	81.2	100%	1e-15	86%	gi|532097996|XP_005334647.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Jac	80.0	80.0	100%	3e-15	86%	gi|507568935|XP_004668094.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Lox	80.0	80.0	100%	3e-15	86%	gi|344279762|XP_003411656.1
☐ PREDICTED: adipocyte plasma membrane-associated protein isofc	80.0	80.0	100%	4e-15	86%	gi|611981959|XP_007476669.1
☐ PREDICTED: adipocyte plasma membrane-associated protein isofc	80.0	80.0	100%	4e-15	86%	gi|611981957|XP_001382089.2
☐ PREDICTED: adipocyte plasma membrane-associated protein isofc	79.5	79.5	100%	5e-15	90%	gi|625192556|XP_007638893.1
☐ PREDICTED: adipocyte plasma membrane-associated protein isofc	79.5	79.5	100%	5e-15	90%	gi|354475585|XP_003500008.1
☐ PREDICTED: adipocyte plasma membrane-associated protein isofc	79.5	79.5	100%	5e-15	90%	gi|625266624|XP_007624792.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Bos	79.1	79.1	100%	6e-15	86%	gi|555978143|XP_005901017.1
☐ Adipocyte plasma membrane-associated protein [Bos mutus]	79.1	79.1	100%	6e-15	86%	gi|440901758|ELR52645.1
☐ adipocyte plasma membrane-associated protein [Bos taurus]	79.1	79.1	100%	7e-15	86%	gi|78369434|NP_001030490.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Bub	79.1	79.1	100%	7e-15	86%	gi|594034111|XP_006041771.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Ovis	79.1	79.1	100%	7e-15	86%	gi|426240952|XP_004014356.1
☐ PREDICTED: adipocyte plasma membrane-associated protein [Cap	79.1	79.1	100%	7e-15	86%	gi|548489969|XP_005688183.1

☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	79.1	79.1	100%	7e-15	86%	gi|528973115|XP_005214463.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pan	79.1	79.1	100%	7e-15	86%	gi|556778497|XP_005984319.1
☐	PREDICTED: adipocyte plasma membrane-associated protein-like	78.7	78.7	100%	8e-15	86%	gi|545890060|XP_005658440.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Sus	78.7	78.7	100%	9e-15	86%	gi|350594715|XP_001927122.3
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	78.3	78.3	100%	1e-14	83%	gi|511864237|XP_004754143.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	78.3	78.3	100%	1e-14	83%	gi|511864235|XP_004754142.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	78.3	78.3	100%	1e-14	83%	gi|511864232|XP_004754141.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Fuk	77.4	77.4	100%	3e-14	83%	gi|731219302|XP_010623912.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	77.4	77.4	100%	3e-14	83%	gi|512880580|XP_004894998.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Chi	77.4	77.4	100%	3e-14	83%	gi|533132029|XP_005381039.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Oct	77.4	77.4	100%	3e-14	83%	gi|507661814|XP_004635630.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Sor	77.4	77.4	96%	3e-14	86%	gi|505845493|XP_004616227.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	77.4	77.4	100%	3e-14	83%	gi|512880576|XP_004894997.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	77.0	77.0	100%	3e-14	83%	gi|562871397|XP_006163663.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	77.0	77.0	100%	4e-14	83%	gi|562871395|XP_006163662.1
☐	Adipocyte plasma membrane-associated protein [Tupaia chinensis]	77.0	77.0	100%	4e-14	83%	gi|444520420|ELV12972.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Tric	76.1	76.1	100%	7e-14	83%	gi|471377312|XP_004376468.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Cav	76.1	76.1	100%	7e-14	83%	gi|348581358|XP_003476444.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Das	76.1	76.1	100%	7e-14	83%	gi|488570200|XP_004474706.1
☐	Adipocyte plasma membrane-associated protein [Myotis davidii]	75.7	75.7	100%	1e-13	79%	gi|432114788|ELK36543.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ept	75.7	75.7	100%	1e-13	79%	gi|641701525|XP_008139374.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Myc	75.7	75.7	100%	1e-13	79%	gi|584069940|XP_006755306.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Myc	74.4	74.4	100%	3e-13	79%	gi|554543332|XP_005866279.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Myc	74.4	74.4	100%	3e-13	79%	gi|558166297|XP_006098004.1
☐	Adipocyte plasma membrane-associated protein [Myotis brandtii]	74.4	74.4	100%	3e-13	79%	gi|521026002|EPQ07790.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Car	74.0	74.0	100%	4e-13	79%	gi|345789049|XP_850086.2
☐	PREDICTED: adipocyte plasma membrane-associated protein-like	71.5	71.5	93%	2e-12	81%	gi|620953601|XP_007656154.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: gi|194378020|dbj|BAG63373.1| **Length:** 289 **Number of Matches:** 1

Range 1: 183 to 211 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.0 bits(214)	5e-20	29/29(100%)	29/29(100%)	0/29(0%)

```
Query  1    KLLLSSETPIEGKNMSFVNDLTVTQDGRK  29
            KLLLSSETPIEGKNMSFVNDLTVTQDGRK
Sbjct  183  KLLLSSETPIEGKNMSFVNDLTVTQDGRK  211
```

Related Information

Gene - associated gene details

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: adipocyte plasma membrane-associated protein isoform X1 [Homo sapiens]

Sequence ID: gi|530425819|ref|XP_005260820.1| **Length:** 289 **Number of Matches:** 1

Range 1: 183 to 211 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.0 bits(214)	5e-20	29/29(100%)	29/29(100%)	0/29(0%)

```
Query  1    KLLLSSETPIEGKNMSFVNDLTVTQDGRK  29
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

```
                KLLLSSETPIEGKNMSFVNDLTVTQDGRK
Sbjct  183  KLLLSSETPIEGKNMSFVNDLTVTQDGRK  211
```

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C20orf3 [Homo sapiens]

Sequence ID: gi|37183270|gb|AAQ89435.1| **Length:** 372 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 139 to 167 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.0 bits(214)	5e-20	29/29(100%)	29/29(100%)	0/29(0%)

```
Query  1    KLLLSSETPIEGKNMSFVNDLTVTQDGRK  29
            KLLLSSETPIEGKNMSFVNDLTVTQDGRK
Sbjct  139  KLLLSSETPIEGKNMSFVNDLTVTQDGRK  167
```

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chromosome 20 open reading frame 3, isoform CRA_b [Homo sapiens]

Sequence ID: gi|119630519|gb|EAX10114.1| **Length:** 380 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 139 to 167 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.0 bits(214)	5e-20	29/29(100%)	29/29(100%)	0/29(0%)

```
Query  1    KLLLSSETPIEGKNMSFVNDLTVTQDGRK  29
            KLLLSSETPIEGKNMSFVNDLTVTQDGRK
Sbjct  139  KLLLSSETPIEGKNMSFVNDLTVTQDGRK  167
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

adipocyte plasma membrane-associated protein [Homo sapiens]

Sequence ID: gi|24308201|ref|NP_065392.1| **Length:** 416 **Number of Matches:** 1

▶ See 4 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 183 to 211 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.0 bits(214)	6e-20	29/29(100%)	29/29(100%)	0/29(0%)

```
Query  1    KLLLSSETPIEGKNMSFVNDLTVTQDGRK  29
            KLLLSSETPIEGKNMSFVNDLTVTQDGRK
Sbjct  183  KLLLSSETPIEGKNMSFVNDLTVTQDGRK  211
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BGUJFG2N014

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   Formatting options   Download

How to read this page   Blast report description

APMAP_RAGPDGTLFVADAYKG_Mod

RID BGUJFG2N014 (Expires on 01-17 08:33 am)

Query ID lcl|83441

Description None

Molecule type amino acid

Query Length 16

Database Name nr

Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects

Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

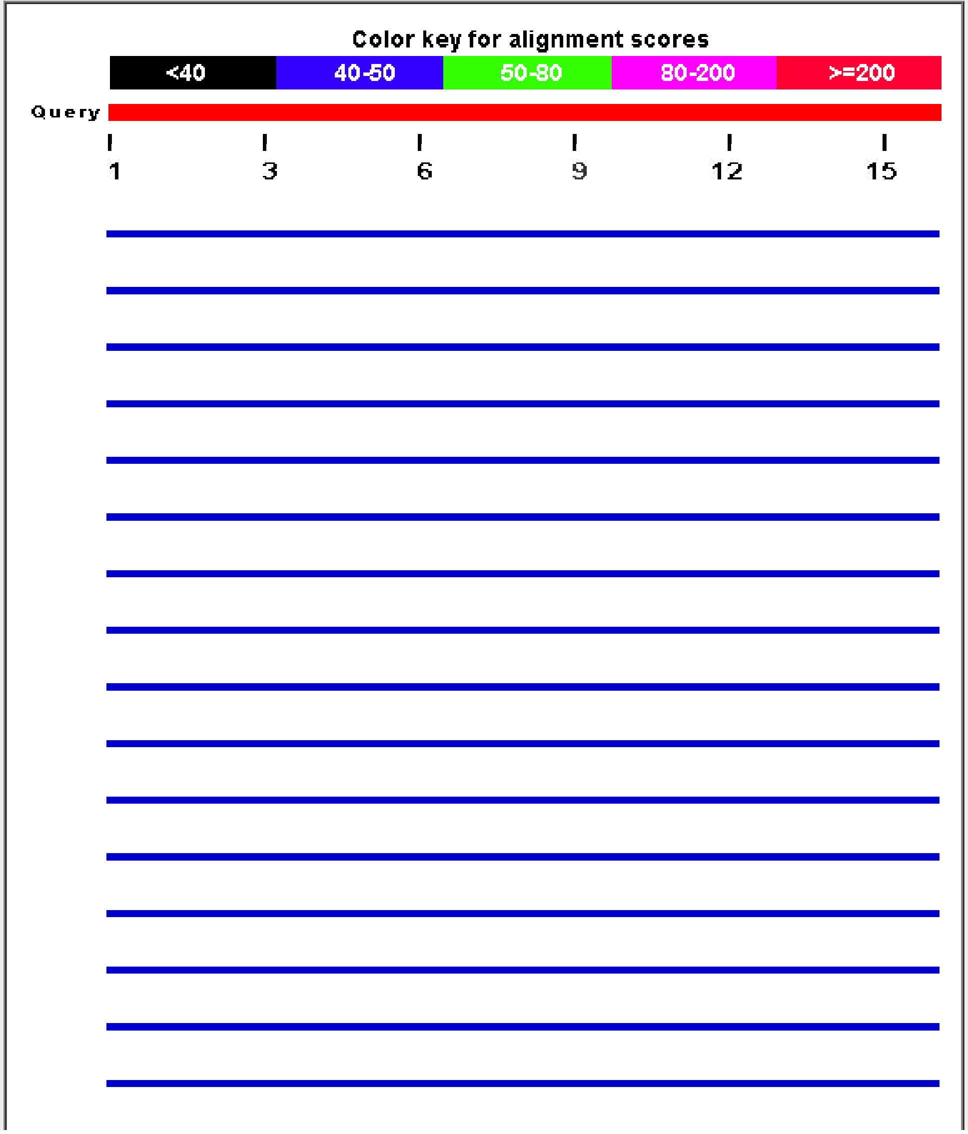
Graphic Summary

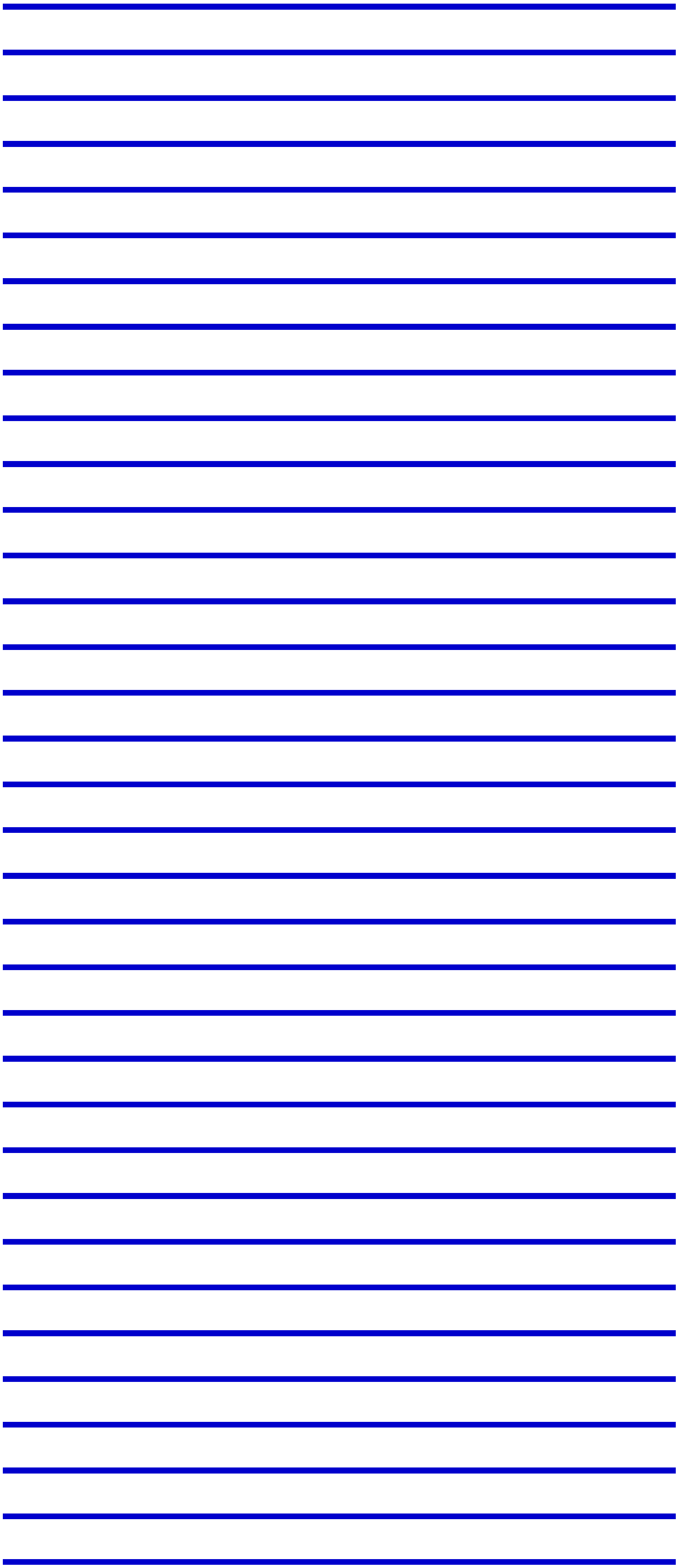
Show Conserved Domains

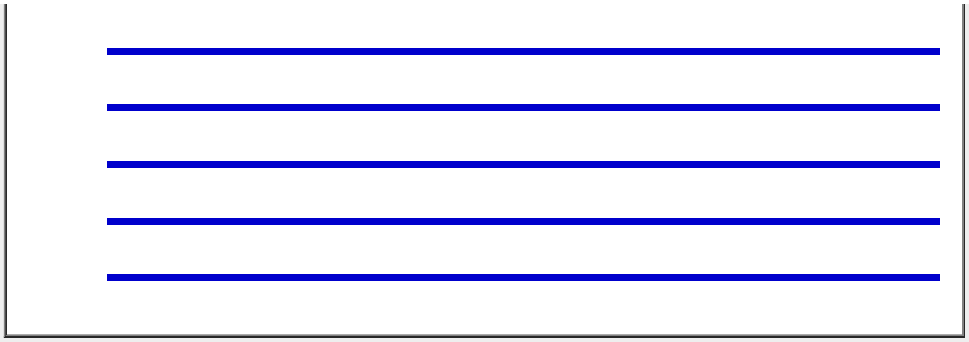
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	49.4	49.4	100%	2e-05	94%	gi|194378020|BAG63373.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	49.4	49.4	100%	2e-05	94%	gi|530425819|XP_005260820.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	49.4	49.4	100%	2e-05	94%	gi|724797097|XP_010359957.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Gal	49.4	49.4	100%	2e-05	94%	gi|667326556|XP_008589917.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	49.4	49.4	100%	2e-05	94%	gi|511864235|XP_004754142.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Can	49.4	49.4	100%	2e-05	94%	gi|743752696|XP_010971243.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	49.4	49.4	100%	2e-05	94%	gi|724797100|XP_010359965.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	49.4	49.4	100%	2e-05	94%	gi|675792202|XP_008952974.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	49.4	49.4	100%	2e-05	94%	gi|675656498|XP_008994116.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Vicu	49.4	49.4	100%	2e-05	94%	gi|560992411|XP_006218341.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Can	49.4	49.4	100%	2e-05	94%	gi|560894296|XP_006173641.1
☐	C20orf3 [Homo sapiens]	49.4	49.4	100%	2e-05	94%	gi|37183270|AAQ89435.1
☐	chromosome 20 open reading frame 3, isoform CRA_b [Homo sapi	49.4	49.4	100%	2e-05	94%	gi|119630519|EAX10114.1
☐	hypothetical protein PANDA_019520 [Ailuropoda melanoleuca]	49.4	49.4	100%	2e-05	94%	gi|281351396|EFB26980.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Equ	49.4	49.4	100%	2e-05	94%	gi|664771366|XP_008504865.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Urs	49.4	49.4	100%	2e-05	94%	gi|671025584|XP_008703615.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pan	49.4	49.4	100%	2e-05	94%	gi|591342488|XP_007096642.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	49.4	49.4	100%	2e-05	94%	gi|545199803|XP_005604486.1
☐	PREDICTED: adipocyte plasma membrane-associated protein-like	49.4	49.4	100%	2e-05	94%	gi|301787895|XP_002929365.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	49.4	49.4	100%	2e-05	94%	gi|545199801|XP_005604485.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Can	49.4	49.4	100%	2e-05	94%	gi|744602490|XP_010991040.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Tars	49.4	49.4	100%	2e-05	94%	gi|640819801|XP_008066807.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ory	49.4	49.4	100%	2e-05	94%	gi|291410623|XP_002721586.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Lipo	49.4	49.4	100%	2e-05	94%	gi|602732221|XP_007451508.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Bala	49.4	49.4	100%	2e-05	94%	gi|594689044|XP_007191923.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Phy	49.4	49.4	100%	2e-05	94%	gi|593717611|XP_007105230.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Feli	49.4	49.4	100%	2e-05	94%	gi|586981414|XP_006930067.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ictic	49.4	49.4	100%	2e-05	94%	gi|532097996|XP_005334647.1
☐							

	PREDICTED: adipocyte plasma membrane-associated protein isofc	49.4	49.4	100%	2e-05	94%	gi|511864232|XP_004754141.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Oct	49.4	49.4	100%	2e-05	94%	gi|507661814|XP_004635630.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Sor	49.4	49.4	100%	2e-05	94%	gi|505845493|XP_004616227.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Och	49.4	49.4	100%	2e-05	94%	gi|504167518|XP_004593426.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Cer	49.4	49.4	100%	2e-05	94%	gi|478535723|XP_004441986.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Tric	49.4	49.4	100%	2e-05	94%	gi|471377312|XP_004376468.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Orc	49.4	49.4	100%	2e-05	94%	gi|466012177|XP_004270482.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Oto	49.4	49.4	100%	2e-05	94%	gi|395857507|XP_003801133.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Car	49.4	49.4	100%	2e-05	94%	gi|345789049|XP_850086.2
☐	PREDICTED: adipocyte plasma membrane-associated protein [Lox	49.4	49.4	100%	2e-05	94%	gi|344279762|XP_003411656.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	49.4	49.4	100%	2e-05	94%	gi|675792200|XP_008952973.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	49.4	49.4	100%	2e-05	94%	gi|675656496|XP_008994115.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Gor	49.4	49.4	100%	2e-05	94%	gi|426391191|XP_004061964.1
☐	adipocyte plasma membrane-associated protein [Homo sapiens]	49.4	49.4	100%	2e-05	94%	gi|24308201|NP_065392.1
☐	Protein BSCv [Macaca fascicularis]	49.4	49.4	100%	2e-05	94%	gi|355784761|EHH65612.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Nor	49.4	49.4	100%	2e-05	94%	gi|332258942|XP_003278549.1
☐	unnamed protein product [Homo sapiens]	49.4	49.4	100%	2e-05	94%	gi|158255694|BAF83818.1
☐	adipocyte plasma membrane-associated protein [Macaca mulatta]	49.4	49.4	100%	2e-05	94%	gi|388453189|NP_001252979.1
☐	BSCv [Homo sapiens]	49.4	49.4	100%	2e-05	94%	gi|9836652|BAB11885.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pon	49.4	49.4	100%	2e-05	94%	gi|686761455|XP_009231655.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	49.4	49.4	100%	2e-05	94%	gi|544463778|XP_005568209.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	49.4	49.4	100%	2e-05	94%	gi|544463776|XP_005568208.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	49.4	49.4	100%	2e-05	94%	gi|544463774|XP_005568207.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	49.4	49.4	100%	2e-05	94%	gi|544463772|XP_005568206.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Bos	46.0	46.0	100%	2e-04	88%	gi|555978143|XP_005901017.1
☐	Adipocyte plasma membrane-associated protein [Bos mutus]	46.0	46.0	100%	2e-04	88%	gi|440901758|ELR52645.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Nar	46.0	46.0	100%	2e-04	88%	gi|674106802|XP_008824690.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	46.0	46.0	100%	2e-04	88%	gi|568918452|XP_006500262.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Bis	46.0	46.0	100%	2e-04	88%	gi|742102975|XP_010834658.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Fuk	46.0	46.0	100%	2e-04	88%	gi|731219302|XP_010623912.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	46.0	46.0	100%	2e-04	88%	gi|625192556|XP_007638893.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	46.0	46.0	100%	2e-04	88%	gi|568918450|XP_006500261.1
☐	adipocyte plasma membrane-associated protein [Bos taurus]	46.0	46.0	100%	2e-04	88%	gi|78369434|NP_001030490.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ovi	46.0	46.0	100%	2e-04	88%	gi|426240952|XP_004014356.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Per	46.0	46.0	100%	2e-04	88%	gi|589945824|XP_006985593.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Chi	46.0	46.0	100%	2e-04	88%	gi|533132029|XP_005381039.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Mes	46.0	46.0	100%	2e-04	88%	gi|524942103|XP_005072608.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Cor	46.0	46.0	100%	2e-04	88%	gi|507961028|XP_004687183.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Jac	46.0	46.0	100%	2e-04	88%	gi|507568935|XP_004668094.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Odc	46.0	46.0	100%	2e-04	88%	gi|472357692|XP_004398472.1
☐	adipocyte plasma membrane-associated protein [Mus musculus]	46.0	46.0	100%	2e-04	88%	gi|21313668|NP_082253.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Cav	46.0	46.0	100%	2e-04	88%	gi|348581358|XP_003476444.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	46.0	46.0	100%	2e-04	88%	gi|354475585|XP_003500008.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofc	46.0	46.0	100%	2e-04	88%	gi|625266624|XP_007624792.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Erin	46.0	46.0	100%	2e-04	88%	gi|617656120|XP_007535679.1

☐	PREDICTED: adipocyte plasma membrane-associated protein [Lep	46.0	46.0	100%	2e-04	88%	gi|585179120|XP_006741245.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Cap	46.0	46.0	100%	2e-04	88%	gi|548489969|XP_005688183.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pan	46.0	46.0	100%	2e-04	88%	gi|556778497|XP_005984319.1
☐	PREDICTED: adipocyte plasma membrane-associated protein-like	44.3	44.3	100%	8e-04	88%	gi|545890060|XP_005658440.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Sus	44.3	44.3	100%	8e-04	88%	gi|350594715|XP_001927122.3
☐	PREDICTED: adipocyte plasma membrane-associated protein [Not	43.9	43.9	87%	0.001	93%	gi|736191077|XP_010771427.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	43.9	43.9	87%	0.001	93%	gi|658891745|XP_008428753.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	43.9	43.9	87%	0.001	93%	gi|658891742|XP_008428752.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Poe	43.9	43.9	87%	0.001	93%	gi|617509077|XP_007542463.1
☐	PREDICTED: adipocyte plasma membrane-associated protein-like	43.9	43.9	87%	0.001	93%	gi|551525979|XP_005814467.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Mic	43.5	43.5	100%	0.002	81%	gi|532057169|XP_005371288.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	43.1	43.1	100%	0.002	88%	gi|562871397|XP_006163663.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	43.1	43.1	100%	0.002	88%	gi|562871395|XP_006163662.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ory	43.1	43.1	100%	0.002	88%	gi|634885477|XP_007952365.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Chr	43.1	43.1	100%	0.002	88%	gi|586460140|XP_006860728.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ele	43.1	43.1	100%	0.002	88%	gi|585720265|XP_006902530.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ech	43.1	43.1	100%	0.002	88%	gi|507712042|XP_004717841.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pan	43.1	43.1	100%	0.002	88%	gi|114681318|XP_514556.2
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	42.6	42.6	100%	0.003	81%	gi|564343542|XP_006235279.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Myo	42.6	42.6	100%	0.003	81%	gi|554543332|XP_005866279.1
☐	adipocyte plasma membrane-associated protein precursor [Rattus r	42.6	42.6	100%	0.003	81%	gi|77735352|NP_001029175.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	42.6	42.6	100%	0.003	81%	gi|512880580|XP_004894998.1
☐	Ab2-305 [Rattus norvegicus]	42.6	42.6	100%	0.003	81%	gi|33086580|AAP92602.1
☐	Adipocyte plasma membrane-associated protein [Myotis davidii]	42.6	42.6	100%	0.003	81%	gi|432114788|ELK36543.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ept	42.6	42.6	100%	0.003	81%	gi|641701525|XP_008139374.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Myo	42.6	42.6	100%	0.003	81%	gi|584069940|XP_006755306.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	42.6	42.6	100%	0.003	81%	gi|564343538|XP_006235277.1

Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194378020|dbj|BAG63373.1| **Length:** 289 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 156 to 171 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	2e-05	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RAGPDGTLFVADAYKG  16
            RAGP+GTLFVADAYKG
Sbjct  156  RAGPNGTLFVADAYKG  171
```

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PREDICTED: adipocyte plasma membrane-associated protein isoform X1 [Homo sapiens]

Sequence ID: gi|530425819|ref|XP_005260820.1| **Length:** 289 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 156 to 171 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	2e-05	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RAGPDGTLFVADAYKG  16
```

```
            RAGP+GTLFVADAYKG
Sbjct  156  RAGPNGTLFVADAYKG  171
```

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PREDICTED: adipocyte plasma membrane-associated protein isoform X1 [Rhinopithecus roxellana]

Sequence ID: gi|724797097|ref|XP_010359957.1| **Length:** 305 **Number of Matches:** 1

Range 1: 45 to 60 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	2e-05	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RAGPDGTLFVADAYKG  16
           RAGP+GTLFVADAYKG
Sbjct  45   RAGPNGTLFVADAYKG  60
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: adipocyte plasma membrane-associated protein, partial [Galeopterus variegatus]

Sequence ID: gi|667326556|ref|XP_008589917.1| **Length:** 345 **Number of Matches:** 1

Range 1: 85 to 100 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	2e-05	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RAGPDGTLFVADAYKG  16
           RAGP+GTLFVADAYKG
Sbjct  85   RAGPNGTLFVADAYKG  100
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: adipocyte plasma membrane-associated protein isoform X2 [Mustela putorius furo]

Sequence ID: gi|511864235|ref|XP_004754142.1| **Length:** 370 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 155 to 170 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	2e-05	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1     RAGPDGTLFVADAYKG  16
            RAGP+GTLFVADAYKG
Sbjct  155  RAGPNGTLFVADAYKG  170
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - B90WWHWV01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download

How to read this page   Blast report description

APMAP_RAGPNGTLFVADAYKG_NonMod

RID B90WWHWV01R (Expires on 01-14 09:31 am)

Query ID lcl|48851
Description None
Molecule type amino acid
Query Length 16

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

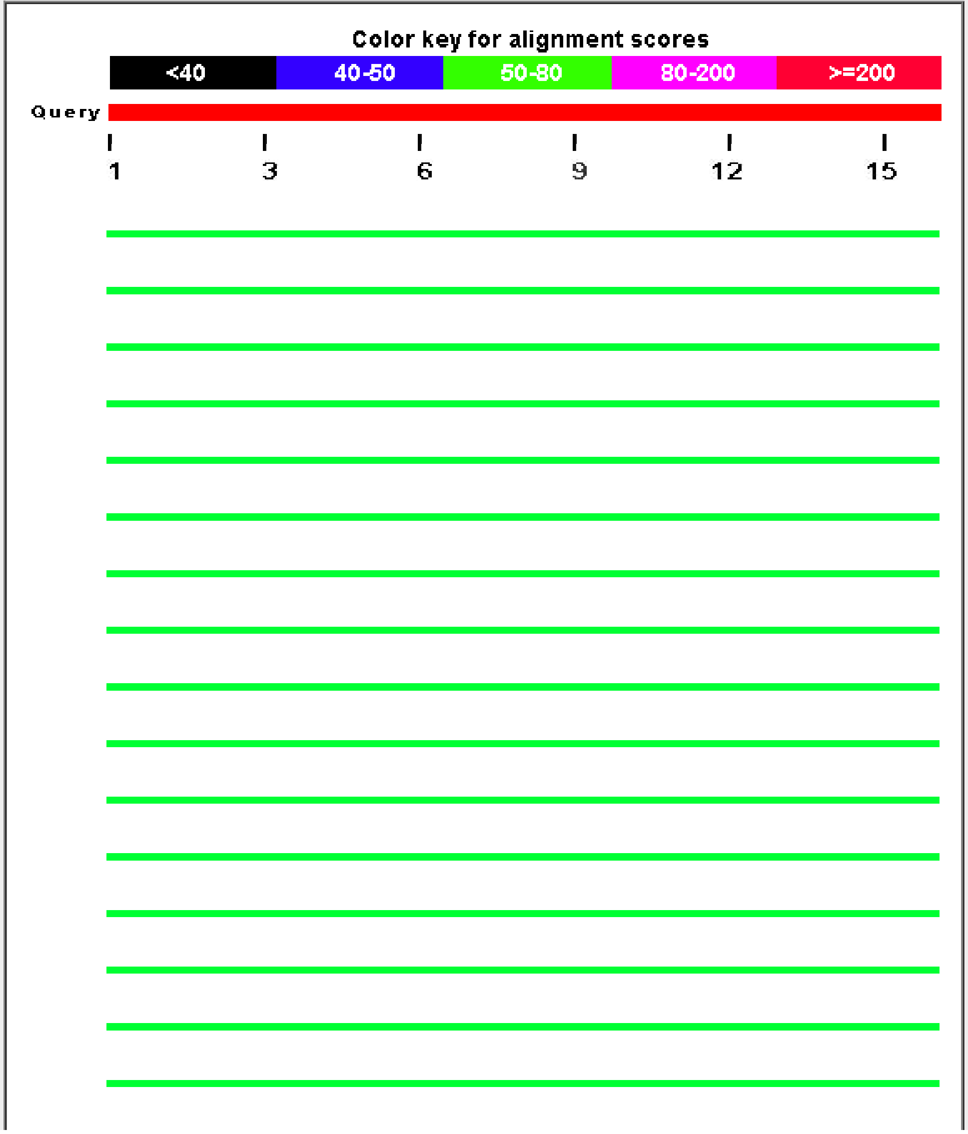
Graphic Summary

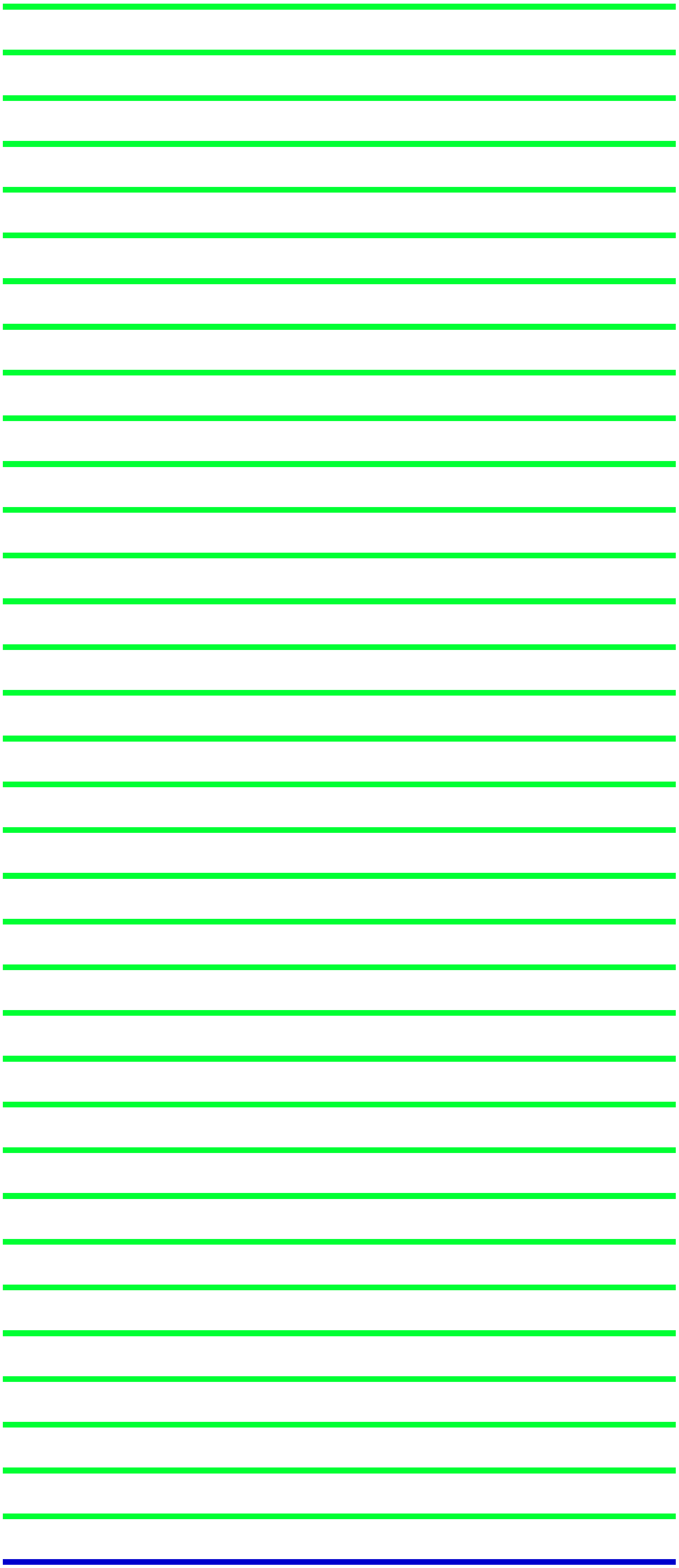
Show Conserved Domains

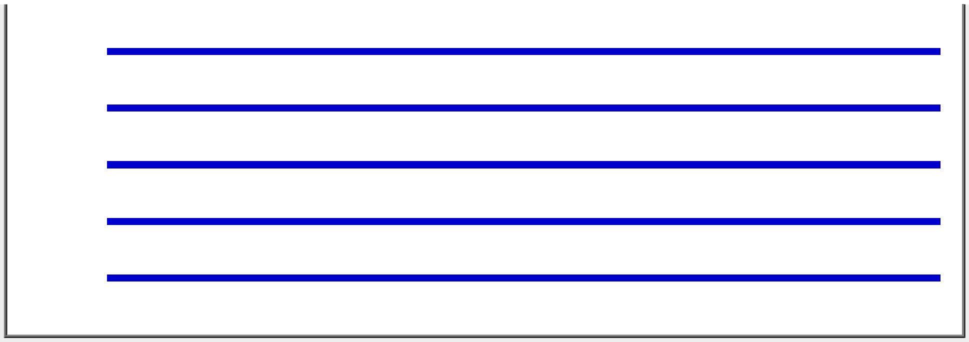
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	52.0	52.0	100%	2e-06	100%	gi|194378020|BAG63373.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|530425819|XP_005260820.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|724797097|XP_010359957.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Gal	52.0	52.0	100%	2e-06	100%	gi|667326556|XP_008589917.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|511864235|XP_004754142.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|724797100|XP_010359965.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|675792202|XP_008952974.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|675656498|XP_008994116.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Vicu	52.0	52.0	100%	2e-06	100%	gi|560992411|XP_006218341.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Car	52.0	52.0	100%	2e-06	100%	gi|560894296|XP_006173641.1
☐	C20orf3 [Homo sapiens]	52.0	52.0	100%	2e-06	100%	gi|37183270|AAQ89435.1
☐	chromosome 20 open reading frame 3, isoform CRA_b [Homo sapi	52.0	52.0	100%	2e-06	100%	gi|119630519|EAX10114.1
☐	hypothetical protein PANDA_019520 [Ailuropoda melanoleuca]	52.0	52.0	100%	2e-06	100%	gi|281351396|EFB26980.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Equ	52.0	52.0	100%	2e-06	100%	gi|664771366|XP_008504865.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Urs	52.0	52.0	100%	2e-06	100%	gi|671025584|XP_008703615.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pan	52.0	52.0	100%	2e-06	100%	gi|591342488|XP_007096642.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|545199803|XP_005604486.1
☐	PREDICTED: adipocyte plasma membrane-associated protein-like	52.0	52.0	100%	2e-06	100%	gi|301787895|XP_002929365.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|545199801|XP_005604485.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Tars	52.0	52.0	100%	2e-06	100%	gi|640819801|XP_008066807.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ory	52.0	52.0	100%	2e-06	100%	gi|291410623|XP_002721586.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Lipo	52.0	52.0	100%	2e-06	100%	gi|602732221|XP_007451508.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Bala	52.0	52.0	100%	2e-06	100%	gi|594689044|XP_007191923.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Phy	52.0	52.0	100%	2e-06	100%	gi|593717611|XP_007105230.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Feli	52.0	52.0	100%	2e-06	100%	gi|586981414|XP_006930067.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ictic	52.0	52.0	100%	2e-06	100%	gi|532097996|XP_005334647.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|511864232|XP_004754141.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Octo	52.0	52.0	100%	2e-06	100%	gi|507661814|XP_004635630.1
☐							

	PREDICTED: adipocyte plasma membrane-associated protein [Sor	52.0	52.0	100%	2e-06	100%	gi|505845493|XP_004616227.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Och	52.0	52.0	100%	2e-06	100%	gi|504167518|XP_004593426.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Cer	52.0	52.0	100%	2e-06	100%	gi|478535723|XP_004441986.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Tric	52.0	52.0	100%	2e-06	100%	gi|471377312|XP_004376468.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Orc	52.0	52.0	100%	2e-06	100%	gi|466012177|XP_004270482.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Oto	52.0	52.0	100%	2e-06	100%	gi|395857507|XP_003801133.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Car	52.0	52.0	100%	2e-06	100%	gi|345789049|XP_850086.2
☐	PREDICTED: adipocyte plasma membrane-associated protein [Lox	52.0	52.0	100%	2e-06	100%	gi|344279762|XP_003411656.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|675792200|XP_008952973.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|675656496|XP_008994115.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Gor	52.0	52.0	100%	2e-06	100%	gi|426391191|XP_004061964.1
☐	adipocyte plasma membrane-associated protein [Homo sapiens]	52.0	52.0	100%	2e-06	100%	gi|24308201|NP_065392.1
☐	Protein BSCv [Macaca fascicularis]	52.0	52.0	100%	2e-06	100%	gi|355784761|EHH65612.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Nor	52.0	52.0	100%	2e-06	100%	gi|332258942|XP_003278549.1
☐	unnamed protein product [Homo sapiens]	52.0	52.0	100%	2e-06	100%	gi|158255694|BAF83818.1
☐	adipocyte plasma membrane-associated protein [Macaca mulatta]	52.0	52.0	100%	2e-06	100%	gi|388453189|NP_001252979.1
☐	BSCv [Homo sapiens]	52.0	52.0	100%	2e-06	100%	gi|9836652|BAB11885.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pon	52.0	52.0	100%	2e-06	100%	gi|686761455|XP_009231655.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|544463778|XP_005568209.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|544463776|XP_005568208.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|544463774|XP_005568207.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	52.0	52.0	100%	2e-06	100%	gi|544463772|XP_005568206.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Bos	48.6	48.6	100%	3e-05	94%	gi|555978143|XP_005901017.1
☐	Adipocyte plasma membrane-associated protein [Bos mutus]	48.6	48.6	100%	3e-05	94%	gi|440901758|ELR52645.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Nar	48.6	48.6	100%	3e-05	94%	gi|674106802|XP_008824690.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	48.6	48.6	100%	3e-05	94%	gi|568918452|XP_006500262.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Fuk	48.6	48.6	100%	3e-05	94%	gi|731219302|XP_010623912.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	48.6	48.6	100%	3e-05	94%	gi|625192556|XP_007638893.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	48.6	48.6	100%	3e-05	94%	gi|568918450|XP_006500261.1
☐	adipocyte plasma membrane-associated protein [Bos taurus]	48.6	48.6	100%	3e-05	94%	gi|78369434|NP_001030490.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ovis	48.6	48.6	100%	3e-05	94%	gi|426240952|XP_004014356.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Per	48.6	48.6	100%	3e-05	94%	gi|589945824|XP_006985593.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Chi	48.6	48.6	100%	3e-05	94%	gi|533132029|XP_005381039.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Mes	48.6	48.6	100%	3e-05	94%	gi|524942103|XP_005072608.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Cor	48.6	48.6	100%	3e-05	94%	gi|507961028|XP_004687183.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Jac	48.6	48.6	100%	3e-05	94%	gi|507568935|XP_004668094.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Odo	48.6	48.6	100%	3e-05	94%	gi|472357692|XP_004398472.1
☐	adipocyte plasma membrane-associated protein [Mus musculus]	48.6	48.6	100%	3e-05	94%	gi|21313668|NP_082253.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Cav	48.6	48.6	100%	3e-05	94%	gi|348581358|XP_003476444.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	48.6	48.6	100%	3e-05	94%	gi|354475585|XP_003500008.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	48.6	48.6	100%	3e-05	94%	gi|625266624|XP_007624792.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Erin	48.6	48.6	100%	3e-05	94%	gi|617656120|XP_007535679.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Lep	48.6	48.6	100%	3e-05	94%	gi|585179120|XP_006741245.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Cap	48.6	48.6	100%	3e-05	94%	gi|548489969|XP_005688183.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	48.6	48.6	100%	3e-05	94%	gi|528973115|XP_005214463.1

☐	PREDICTED: adipocyte plasma membrane-associated protein [Pan	48.6	48.6	100%	3e-05	94%	gi|556778497|XP_005984319.1
☐	PREDICTED: adipocyte plasma membrane-associated protein-like	46.9	46.9	100%	1e-04	94%	gi|545890060|XP_005658440.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Sus	46.9	46.9	100%	1e-04	94%	gi|350594715|XP_001927122.3
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	46.4	46.4	87%	1e-04	100%	gi|658891745|XP_008428753.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	46.4	46.4	87%	2e-04	100%	gi|658891742|XP_008428752.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Poe	46.4	46.4	87%	2e-04	100%	gi|617509077|XP_007542463.1
☐	PREDICTED: adipocyte plasma membrane-associated protein-like	46.4	46.4	87%	2e-04	100%	gi|551525979|XP_005814467.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Mic	46.0	46.0	100%	2e-04	88%	gi|532057169|XP_005371288.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	45.6	45.6	100%	3e-04	94%	gi|562871397|XP_006163663.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	45.6	45.6	100%	3e-04	94%	gi|562871395|XP_006163662.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ory	45.6	45.6	100%	3e-04	94%	gi|634885477|XP_007952365.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Chr	45.6	45.6	100%	3e-04	94%	gi|586460140|XP_006860728.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ele	45.6	45.6	100%	3e-04	94%	gi|585720265|XP_006902530.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ech	45.6	45.6	100%	3e-04	94%	gi|507712042|XP_004717841.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Pan	45.6	45.6	100%	3e-04	94%	gi|114681318|XP_514556.2
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	45.2	45.2	100%	4e-04	88%	gi|564343542|XP_006235279.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Myo	45.2	45.2	100%	4e-04	88%	gi|554543332|XP_005866279.1
☐	adipocyte plasma membrane-associated protein precursor [Rattus r	45.2	45.2	100%	4e-04	88%	gi|77735352|NP_001029175.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	45.2	45.2	100%	4e-04	88%	gi|512880580|XP_004894998.1
☐	Ab2-305 [Rattus norvegicus]	45.2	45.2	100%	4e-04	88%	gi|33086580|AAP92602.1
☐	Adipocyte plasma membrane-associated protein [Myotis davidii]	45.2	45.2	100%	4e-04	88%	gi|432114788|ELK36543.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Ept	45.2	45.2	100%	4e-04	88%	gi|641701525|XP_008139374.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Myo	45.2	45.2	100%	4e-04	88%	gi|584069940|XP_006755306.1
☐	PREDICTED: adipocyte plasma membrane-associated protein [Myo	45.2	45.2	100%	4e-04	88%	gi|558166297|XP_006098004.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	45.2	45.2	100%	4e-04	88%	gi|512880576|XP_004894997.1
☐	PREDICTED: adipocyte plasma membrane-associated protein isofo	45.2	45.2	100%	4e-04	88%	gi|564343538|XP_006235277.1
☐	Adipocyte plasma membrane-associated protein [Myotis brandtii]	45.2	45.2	100%	4e-04	88%	gi|521026002|EPQ07790.1

⊟ Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194378020|dbj|BAG63373.1| **Length:** 289 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 156 to 171 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.0 bits(115)	2e-06	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RAGPNGTLFVADAYKG  16
            RAGPNGTLFVADAYKG
Sbjct  156  RAGPNGTLFVADAYKG  171
```

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PREDICTED: adipocyte plasma membrane-associated protein isoform X1 [Homo sapiens]

Sequence ID: gi|530425819|ref|XP_005260820.1| **Length:** 289 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 156 to 171 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.0 bits(115)	2e-06	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RAGPNGTLFVADAYKG  16
```

```
                 RAGPNGTLFVADAYKG
Sbjct  156  RAGPNGTLFVADAYKG  171
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: adipocyte plasma membrane-associated protein isoform X1 [Rhinopithecus roxellana]

Sequence ID: gi|724797097|ref|XP_010359957.1| **Length:** 305 **Number of Matches:** 1

Range 1: 45 to 60 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.0 bits(115)	2e-06	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RAGPNGTLFVADAYKG  16
            RAGPNGTLFVADAYKG
Sbjct  45   RAGPNGTLFVADAYKG  60
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: adipocyte plasma membrane-associated protein, partial [Galeopterus variegatus]

Sequence ID: gi|667326556|ref|XP_008589917.1| **Length:** 345 **Number of Matches:** 1

Range 1: 85 to 100 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.0 bits(115)	2e-06	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RAGPNGTLFVADAYKG  16
            RAGPNGTLFVADAYKG
Sbjct  85   RAGPNGTLFVADAYKG  100
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: adipocyte plasma membrane-associated protein isoform X2 [Mustela putorius furo]

Sequence ID: gi|511864235|ref|XP_004754142.1| **Length:** 370 **Number of Matches:** 1

▶ See 1 more title(s)

Range 1: 155 to 170 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.0 bits(115)	2e-06	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1     RAGPNGTLFVADAYKG  16
             RAGPNGTLFVADAYKG
Sbjct  155  RAGPNGTLFVADAYKG  170
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

ATRN_KAATCINPLDGSVCERPADHSAKQ_Mod

RID BGUS5DTZ014 (Expires on 01-17 08:36 am)

Query ID	lcl|50873	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	24		
		Program	BLASTP 2.2.30+ Citation

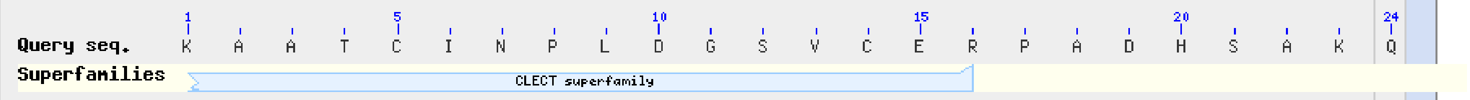
Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

New DELTA-BLAST a more sensitive protein-protein search Go

Graphic Summary

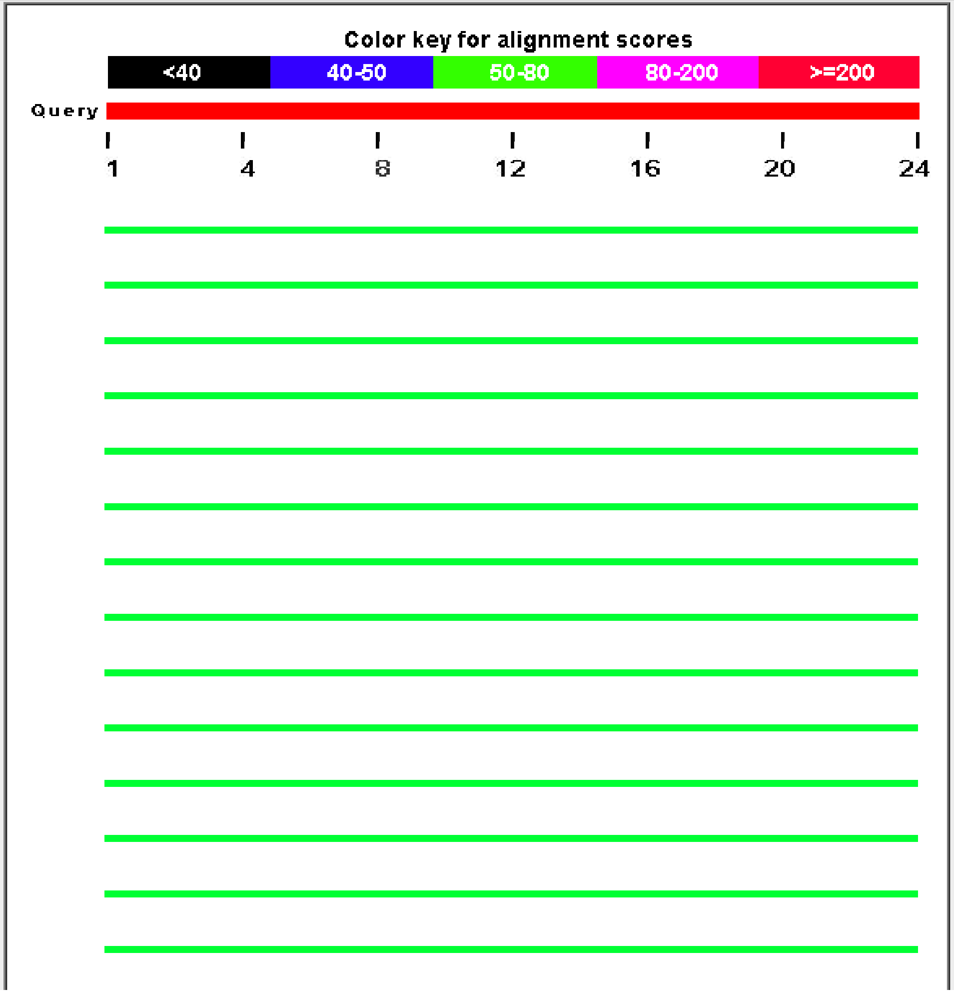
Show Conserved Domains

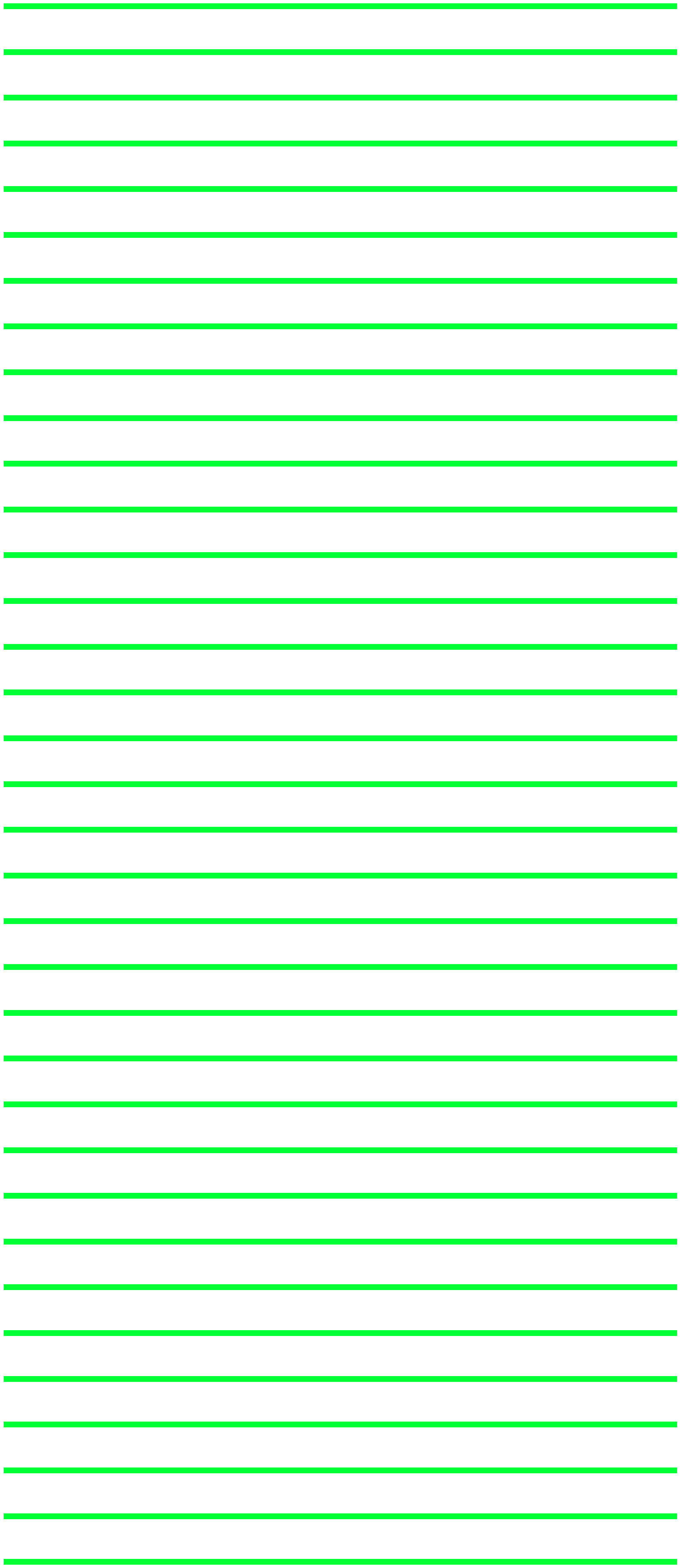
Putative conserved domains have been detected, click on the image below for detailed results.

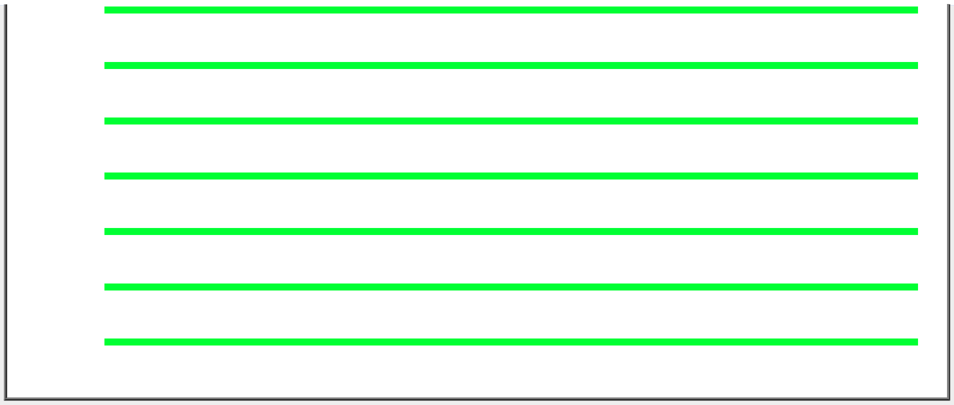


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: attractin-like [Galeopterus variegatus]	73.6	73.6	100%	2e-13	92%	gi|667345974|XP_008563464.1
☐	attractin [Bos taurus]	73.6	73.6	100%	3e-13	92%	gi|190683717|ACE82176.1
☐	Attractin [Tupaia chinensis]	73.6	73.6	100%	3e-13	92%	gi|444519420|ELV12829.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	73.6	73.6	100%	3e-13	92%	gi|585160208|XP_006732353.1
☐	PREDICTED: attractin isoform X2 [Papio anubis]	73.6	73.6	100%	3e-13	92%	gi|685567345|XP_009214752.1
☐	attractin [Canis lupus familiaris]	73.6	73.6	100%	3e-13	92%	gi|339892849|AEK21787.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	73.6	73.6	100%	3e-13	92%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin-like [Physeter catodon]	73.6	73.6	100%	3e-13	92%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin [Pongo abelii]	73.6	73.6	100%	3e-13	92%	gi|297706621|XP_002830129.1
☐	mKIAA0548 protein [Mus musculus]	73.6	73.6	100%	3e-13	92%	gi|26006173|BAC41429.1
☐	Attractin [Cricetulus griseus]	73.6	73.6	100%	3e-13	92%	gi|344236321|EGV92424.1
☐	attractin isoform 1 preproprotein [Camelus ferus]	73.6	73.6	100%	3e-13	92%	gi|528759526|EPY79185.1
☐	PREDICTED: attractin isoform X2 [Cricetulus griseus]	73.6	73.6	100%	3e-13	92%	gi|625260840|XP_007621856.1
☐	PREDICTED: attractin [Equus przewalskii]	73.6	73.6	100%	3e-13	92%	gi|664773944|XP_008506219.1
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	73.6	73.6	100%	3e-13	92%	gi|530426021|XP_005260918.1
☐	PREDICTED: attractin isoform X1 [Papio anubis]	73.6	73.6	100%	3e-13	92%	gi|685567343|XP_009214751.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	73.6	73.6	100%	3e-13	92%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	73.6	73.6	100%	3e-13	92%	gi|725600051|XP_010350111.1
☐	PREDICTED: attractin [Nannospalax galili]	73.6	73.6	100%	3e-13	92%	gi|674060132|XP_008836714.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	73.6	73.6	100%	3e-13	92%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin [Tarsius syrichta]	73.6	73.6	100%	3e-13	92%	gi|640796924|XP_008054571.1
☐	unnamed protein product [Homo sapiens]	73.6	73.6	100%	3e-13	92%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	73.6	73.6	100%	3e-13	92%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	73.6	73.6	100%	3e-13	92%	gi|332257827|XP_003278006.1
☐	PREDICTED: attractin isoform 2 [Dasypus novemcinctus]	73.6	73.6	100%	3e-13	92%	gi|488545593|XP_004464327.1
☐	attractin [Cricetulus griseus]	73.6	73.6	100%	3e-13	92%	gi|537146168|ERE69758.1
☐	Attractin [Fukomys damarensis]	73.6	73.6	100%	3e-13	92%	gi|676263950|KFO20529.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	73.6	73.6	100%	3e-13	92%	gi|556758951|XP_005974805.1

☐	PREDICTED: attractin [Sus scrofa]	73.6	73.6	100%	3e-13	92%	gi|545879723|XP_001927324.5
☐	PREDICTED: attractin isoform 2 [Ceratotherium simum simum]	73.6	73.6	100%	3e-13	92%	gi|478519276|XP_004433860.1
☐	PREDICTED: attractin isoform X2 [Condylura cristata]	73.6	73.6	100%	3e-13	92%	gi|507961710|XP_004687418.1
☐	PREDICTED: attractin [Gorilla gorilla gorilla]	73.6	73.6	100%	3e-13	92%	gi|426390844|XP_004061806.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	73.6	73.6	100%	3e-13	92%	gi|694977854|XP_009435012.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	73.6	73.6	100%	3e-13	92%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	73.6	73.6	100%	3e-13	92%	gi|4093196|AAD03057.1
☐	secreted attractin precursor [Homo sapiens]	73.6	73.6	100%	3e-13	92%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	73.6	73.6	100%	3e-13	92%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	73.6	73.6	100%	3e-13	92%	gi|21450863|NP_647538.1
☐	Mahogany-like protein [Macaca mulatta]	73.6	73.6	100%	3e-13	92%	gi|355563316|EHH19878.1
☐	attractin [Rattus norvegicus]	73.6	73.6	100%	3e-13	92%	gi|12275312|BAB21018.1
☐	attractin, isoform CRA_a [Rattus norvegicus]	73.6	73.6	100%	3e-13	92%	gi|149023319|EDL80213.1
☐	PREDICTED: attractin isoform X1 [Bos taurus]	73.6	73.6	100%	3e-13	92%	gi|741947708|XP_005214542.2
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	73.6	73.6	100%	3e-13	92%	gi|594099680|XP_006072965.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Pan paniscus]	73.6	73.6	100%	3e-13	92%	gi|675763672|XP_008973079.1
☐	PREDICTED: attractin isoform X2 [Canis lupus familiaris]	73.6	73.6	100%	3e-13	92%	gi|545540090|XP_005634905.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	73.6	73.6	100%	3e-13	92%	gi|694977852|XP_009435011.1
☐	attractin [Sus scrofa]	73.6	73.6	100%	3e-13	92%	gi|146741346|BAF62328.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	73.6	73.6	100%	3e-13	92%	gi|530426019|XP_005260917.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	73.6	73.6	100%	3e-13	92%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	73.6	73.6	100%	3e-13	92%	gi|635021368|XP_008017720.1
☐	PREDICTED: attractin isoform X2 [Mustela putorius furo]	73.6	73.6	100%	3e-13	92%	gi|511906947|XP_004772933.1
☐	Mahogany-like protein [Macaca fascicularis]	73.6	73.6	100%	3e-13	92%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin [Panthera tigris altaica]	73.6	73.6	100%	3e-13	92%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	73.6	73.6	100%	3e-13	92%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	73.6	73.6	100%	3e-13	92%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	73.6	73.6	100%	3e-13	92%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Capra hircus]	73.6	73.6	100%	3e-13	92%	gi|548490191|XP_005688293.1
☐	PREDICTED: attractin [Trichechus manatus latirostris]	73.6	73.6	100%	3e-13	92%	gi|471400634|XP_004383126.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	73.6	73.6	100%	3e-13	92%	gi|724902357|XP_010377335.1
☐	PREDICTED: attractin isoform 1 [Dasypus novemcinctus]	73.6	73.6	100%	3e-13	92%	gi|488545591|XP_004464326.1
☐	PREDICTED: attractin isoform X1 [Cricetulus griseus]	73.6	73.6	100%	3e-13	92%	gi|354473756|XP_003499099.1
☐	PREDICTED: attractin [Camelus ferus]	73.6	73.6	100%	3e-13	92%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Sorex araneus]	73.6	73.6	100%	3e-13	92%	gi|505831534|XP_004611050.1
☐	attractin [Cricetulus griseus]	73.6	73.6	100%	3e-13	92%	gi|537146167|ERE69757.1
☐	PREDICTED: attractin [Camelus dromedarius]	73.6	73.6	100%	3e-13	92%	gi|744589171|XP_010986570.1
☐	PREDICTED: attractin [Bos mutus]	73.6	73.6	100%	3e-13	92%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Ursus maritimus]	73.6	73.6	100%	3e-13	92%	gi|671021680|XP_008701660.1
☐	hypothetical protein PANDA_007354 [Ailuropoda melanoleuca]	73.6	73.6	100%	3e-13	92%	gi|281339872|EFB15456.1
☐	PREDICTED: attractin-like [Ailuropoda melanoleuca]	73.6	73.6	100%	3e-13	92%	gi|301766802|XP_002918837.1
☐	PREDICTED: attractin [Camelus bactrianus]	73.6	73.6	100%	3e-13	92%	gi|743752427|XP_010971103.1
☐	PREDICTED: attractin [Mustela putorius furo]	73.6	73.6	100%	3e-13	92%	gi|511947743|XP_004792355.1
☐	attractin, isoform CRA_b [Homo sapiens]	73.6	73.6	100%	3e-13	92%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	73.6	73.6	100%	3e-13	92%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin [Fukomys damarensis]	73.6	73.6	100%	3e-13	92%	gi|731281216|XP_010609356.1

☐	PREDICTED: attractin [Ovis aries]	73.6	73.6	100%	3e-13	92%	gi|426241795|XP_004014773.1
☐	PREDICTED: attractin [Peromyscus maniculatus bairdii]	73.6	73.6	100%	3e-13	92%	gi|589943852|XP_006984624.1
☐	PREDICTED: attractin [Felis catus]	73.6	73.6	100%	3e-13	92%	gi|586981105|XP_003983758.2
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	73.6	73.6	100%	3e-13	92%	gi|694977850|XP_009435010.1
☐	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	73.6	73.6	100%	3e-13	92%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin [Erinaceus europaeus]	73.6	73.6	100%	3e-13	92%	gi|617558695|XP_007539650.1
☐	PREDICTED: attractin [Vicugna pacos]	73.6	73.6	100%	3e-13	92%	gi|560970220|XP_006207473.1
☐	attractin [Bos taurus]	73.6	73.6	100%	3e-13	92%	gi|253560524|ACT32973.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	73.6	73.6	100%	3e-13	92%	gi|586533632|XP_006921705.1
☐	attractin [Bos taurus]	73.6	73.6	100%	3e-13	92%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	73.6	73.6	100%	3e-13	92%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin isoform X3 [Canis lupus familiaris]	73.6	73.6	100%	3e-13	92%	gi|73991942|XP_534360.2
☐	PREDICTED: attractin isoform 1 [Ceratotherium simum simum]	73.6	73.6	100%	3e-13	92%	gi|478519274|XP_004433859.1
☐	PREDICTED: attractin [Elephantulus edwardii]	73.6	73.6	100%	3e-13	92%	gi|585689645|XP_006894264.1
☐	PREDICTED: attractin [Orycteropus afer afer]	73.6	73.6	100%	3e-13	92%	gi|634830430|XP_007958185.1
☐	attractin [Mesocricetus auratus]	73.6	73.6	100%	3e-13	92%	gi|528078159|NP_001268565.1
☐	attractin isoform 1 preproprotein [Homo sapiens]	73.6	73.6	100%	3e-13	92%	gi|21450861|NP_647537.1
☐	PREDICTED: attractin [Macaca mulatta]	73.6	73.6	100%	3e-13	92%	gi|109092720|XP_001115192.1
☐	PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	73.6	73.6	100%	3e-13	92%	gi|635021360|XP_008017700.1
☐	attractin, isoform CRA_b [Mus musculus]	73.6	73.6	100%	3e-13	92%	gi|148696346|EDL28293.1
☐	PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	73.6	73.6	100%	3e-13	92%	gi|635021370|XP_008017729.1
☐	PREDICTED: attractin isoform X2 [Oryctolagus cuniculus]	73.6	73.6	100%	3e-13	92%	gi|655716500|XP_008254470.1
☐	PREDICTED: attractin [Tupaia chinensis]	73.6	73.6	100%	3e-13	92%	gi|562872246|XP_006164056.1
☐	PREDICTED: attractin isoform X2 [Pteropus alecto]	73.6	73.6	100%	3e-13	92%	gi|586533634|XP_006921706.1
☐	PREDICTED: attractin isoform X1 [Bubalus bubalis]	73.6	73.6	100%	3e-13	92%	gi|594099676|XP_006072963.1
☐	PREDICTED: attractin isoform X1 [Mus musculus]	73.6	73.6	100%	3e-13	92%	gi|568915132|XP_006498669.1

Alignments

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PREDICTED: attractin-like, partial [Galeopterus variegatus]

Sequence ID: gi|667345974|ref|XP_008563464.1| **Length:** 213 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 57 to 80 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.6 bits(166)	2e-13	22/24(92%)	24/24(100%)	0/24(0%)

```
Query  1    KAATCINPLDGSVCERPADHSAKQ  24
            KAATCINPL+GSVCERPA+HSAKQ
Sbjct  57   KAATCINPLNGSVCERPANHSAKQ  80
```

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attractin [Bos taurus]

Sequence ID: gi|190683717|gb|ACE82176.1| **Length:** 670 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 146 to 169 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.6 bits(166)	3e-13	22/24(92%)	24/24(100%)	0/24(0%)

```
Query  1    KAATCINPLDGSVCERPADHSAKQ  24
            KAATCINPL+GSVCERPA+HSAKQ
Sbjct  146  KAATCINPLNGSVCERPANHSAKQ  169
```

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Attractin [Tupaia chinensis]

Sequence ID: gi|444519420|gb|ELV12829.1| **Length:** 860 **Number of Matches:** 1

Related Information

Range 1: 552 to 575 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.6 bits(166)	3e-13	22/24(92%)	24/24(100%)	0/24(0%)

```
Query  1    KAATCINPLDGSVCERPADHSAKQ  24
            KAATCINPL+GSVCERPA+HSAKQ
Sbjct  552  KAATCINPLNGSVCERPANHSAKQ  575
```

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PREDICTED: attractin-like [Leptonychotes weddellii]

Sequence ID: gi|585160208|ref|XP_006732353.1| **Length:** 899 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 708 to 731 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.6 bits(166)	3e-13	22/24(92%)	24/24(100%)	0/24(0%)

```
Query  1    KAATCINPLDGSVCERPADHSAKQ  24
            KAATCINPL+GSVCERPA+HSAKQ
Sbjct  708  KAATCINPLNGSVCERPANHSAKQ  731
```

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PREDICTED: attractin isoform X2 [Papio anubis]

Sequence ID: gi|685567345|ref|XP_009214752.1| **Length:** 989 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 595 to 618 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.6 bits(166)	3e-13	22/24(92%)	24/24(100%)	0/24(0%)

```
Query  1    KAATCINPLDGSVCERPADHSAKQ  24
            KAATCINPL+GSVCERPA+HSAKQ
Sbjct  595  KAATCINPLNGSVCERPANHSAKQ  618
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - B90X7B8Y01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

ATRN_KAATCINPLNGSVCERPANHSAKQ_NonMod

RID	B90X7B8Y01R (Expires on 01-14 09:32 am)
Query ID	lcl|53405
Description	None
Molecule type	amino acid
Query Length	24

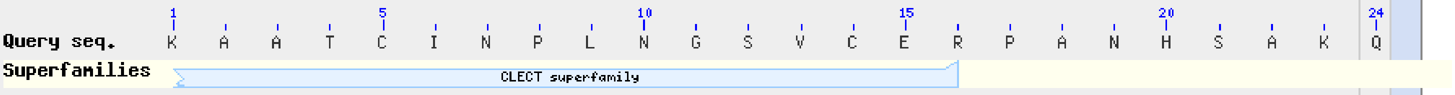
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

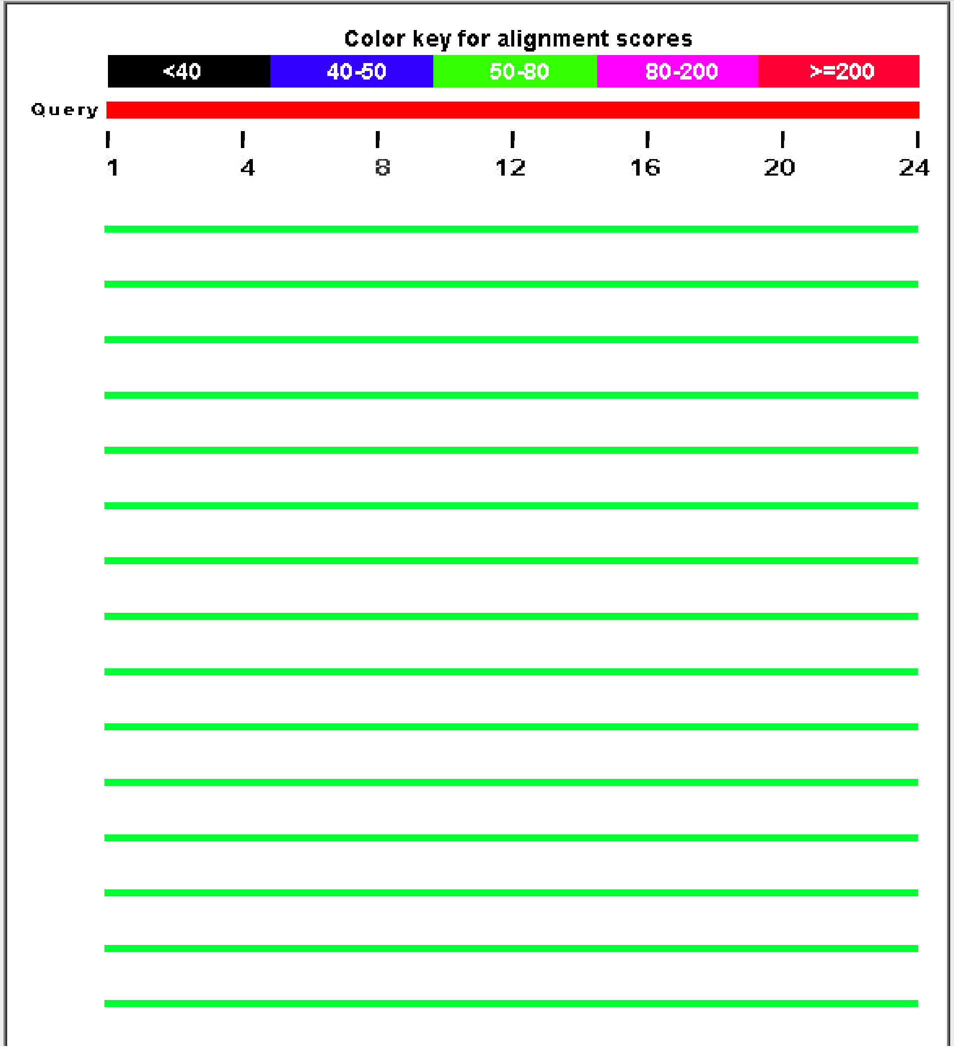
Show Conserved Domains

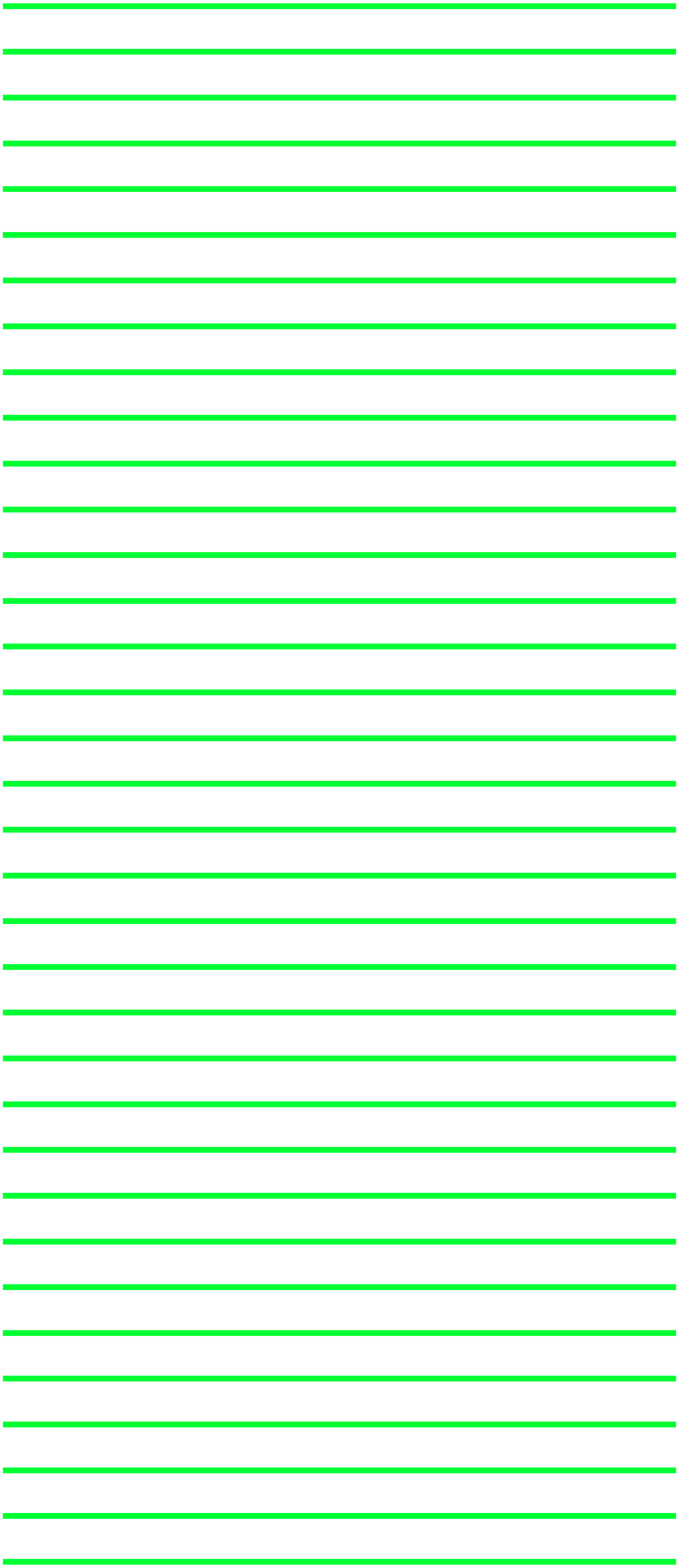
Putative conserved domains have been detected, click on the image below for detailed results.

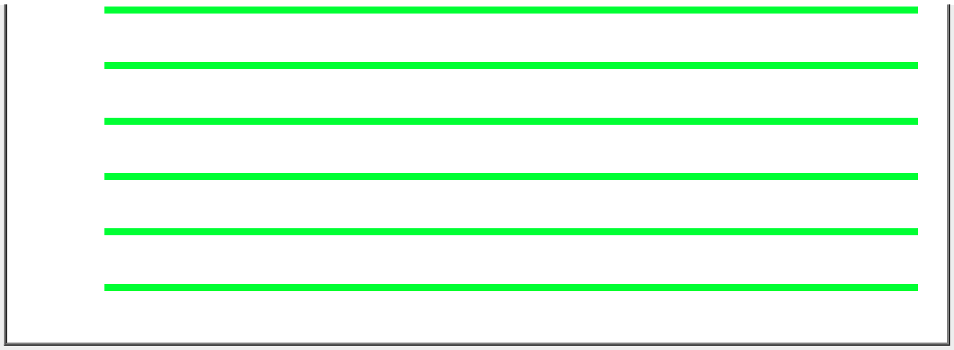


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: attractin-like [Galeopterus variegatus]	78.7	78.7	100%	4e-15	100%	gi|667345974|XP_008563464.1
☐	attractin [Bos taurus]	78.7	78.7	100%	5e-15	100%	gi|190683717|ACE82176.1
☐	Attractin [Tupaia chinensis]	78.7	78.7	100%	5e-15	100%	gi|444519420|ELV12829.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	78.7	78.7	100%	5e-15	100%	gi|585160208|XP_006732353.1
☐	PREDICTED: attractin isoform X2 [Papio anubis]	78.7	78.7	100%	6e-15	100%	gi|685567345|XP_009214752.1
☐	attractin [Canis lupus familiaris]	78.7	78.7	100%	6e-15	100%	gi|339892849|AEK21787.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	78.7	78.7	100%	6e-15	100%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin-like [Physeter catodon]	78.7	78.7	100%	6e-15	100%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin [Pongo abelii]	78.7	78.7	100%	6e-15	100%	gi|297706621|XP_002830129.1
☐	mKIAA0548 protein [Mus musculus]	78.7	78.7	100%	6e-15	100%	gi|26006173|BAC41429.1
☐	Attractin [Cricetulus griseus]	78.7	78.7	100%	6e-15	100%	gi|344236321|EGV92424.1
☐	attractin isoform 1 preproprotein [Camelus ferus]	78.7	78.7	100%	6e-15	100%	gi|528759526|EPY79185.1
☐	PREDICTED: attractin isoform X2 [Cricetulus griseus]	78.7	78.7	100%	6e-15	100%	gi|625260840|XP_007621856.1
☐	PREDICTED: attractin [Equus przewalskii]	78.7	78.7	100%	6e-15	100%	gi|664773944|XP_008506219.1
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	78.7	78.7	100%	6e-15	100%	gi|530426021|XP_005260918.1
☐	PREDICTED: attractin isoform X1 [Papio anubis]	78.7	78.7	100%	6e-15	100%	gi|685567343|XP_009214751.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	78.7	78.7	100%	6e-15	100%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	78.7	78.7	100%	6e-15	100%	gi|725600051|XP_010350111.1
☐	PREDICTED: attractin [Nannospalax galili]	78.7	78.7	100%	6e-15	100%	gi|674060132|XP_008836714.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	78.7	78.7	100%	6e-15	100%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin [Tarsius syrichta]	78.7	78.7	100%	6e-15	100%	gi|640796924|XP_008054571.1
☐	unnamed protein product [Homo sapiens]	78.7	78.7	100%	6e-15	100%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	78.7	78.7	100%	6e-15	100%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	78.7	78.7	100%	6e-15	100%	gi|332257827|XP_003278006.1
☐	PREDICTED: attractin isoform 2 [Dasypus novemcinctus]	78.7	78.7	100%	6e-15	100%	gi|488545593|XP_004464327.1
☐	attractin [Cricetulus griseus]	78.7	78.7	100%	6e-15	100%	gi|537146168|ERE69758.1
☐	Attractin [Fukomys damarensis]	78.7	78.7	100%	6e-15	100%	gi|676263950|KFO20529.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	78.7	78.7	100%	6e-15	100%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin [Sus scrofa]	78.7	78.7	100%	6e-15	100%	gi|545879723|XP_001927324.5

☐	PREDICTED: attractin isoform 2 [Ceratotherium simum simum]	78.7	78.7	100%	6e-15	100%	gi|478519276|XP_004433860.1
☐	PREDICTED: attractin isoform X2 [Condylura cristata]	78.7	78.7	100%	6e-15	100%	gi|507961710|XP_004687418.1
☐	PREDICTED: attractin [Gorilla gorilla gorilla]	78.7	78.7	100%	6e-15	100%	gi|426390844|XP_004061806.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	78.7	78.7	100%	6e-15	100%	gi|694977854|XP_009435012.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	78.7	78.7	100%	6e-15	100%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	78.7	78.7	100%	6e-15	100%	gi|4093196|AAD03057.1
☐	secreted attractin precursor [Homo sapiens]	78.7	78.7	100%	6e-15	100%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	78.7	78.7	100%	6e-15	100%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	78.7	78.7	100%	6e-15	100%	gi|21450863|NP_647538.1
☐	Mahogany-like protein [Macaca mulatta]	78.7	78.7	100%	6e-15	100%	gi|355563316|EHH19878.1
☐	attractin [Rattus norvegicus]	78.7	78.7	100%	6e-15	100%	gi|12275312|BAB21018.1
☐	attractin, isoform CRA_a [Rattus norvegicus]	78.7	78.7	100%	6e-15	100%	gi|149023319|EDL80213.1
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	78.7	78.7	100%	6e-15	100%	gi|594099680|XP_006072965.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Pan paniscus]	78.7	78.7	100%	6e-15	100%	gi|675763672|XP_008973079.1
☐	PREDICTED: attractin isoform X2 [Canis lupus familiaris]	78.7	78.7	100%	6e-15	100%	gi|545540090|XP_005634905.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	78.7	78.7	100%	6e-15	100%	gi|694977852|XP_009435011.1
☐	attractin [Sus scrofa]	78.7	78.7	100%	6e-15	100%	gi|146741346|BAF62328.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	78.7	78.7	100%	6e-15	100%	gi|530426019|XP_005260917.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	78.7	78.7	100%	6e-15	100%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	78.7	78.7	100%	6e-15	100%	gi|635021368|XP_008017720.1
☐	PREDICTED: attractin isoform X2 [Mustela putorius furo]	78.7	78.7	100%	6e-15	100%	gi|511906947|XP_004772933.1
☐	Mahogany-like protein [Macaca fascicularis]	78.7	78.7	100%	6e-15	100%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin [Panthera tigris altaica]	78.7	78.7	100%	6e-15	100%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	78.7	78.7	100%	6e-15	100%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	78.7	78.7	100%	6e-15	100%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	78.7	78.7	100%	6e-15	100%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Capra hircus]	78.7	78.7	100%	6e-15	100%	gi|548490191|XP_005688293.1
☐	PREDICTED: attractin [Trichechus manatus latirostris]	78.7	78.7	100%	6e-15	100%	gi|471400634|XP_004383126.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	78.7	78.7	100%	6e-15	100%	gi|724902357|XP_010377335.1
☐	PREDICTED: attractin isoform 1 [Dasypus novemcinctus]	78.7	78.7	100%	6e-15	100%	gi|488545591|XP_004464326.1
☐	PREDICTED: attractin isoform X1 [Cricetulus griseus]	78.7	78.7	100%	6e-15	100%	gi|354473756|XP_003499099.1
☐	PREDICTED: attractin [Camelus ferus]	78.7	78.7	100%	6e-15	100%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Sorex araneus]	78.7	78.7	100%	6e-15	100%	gi|505831534|XP_004611050.1
☐	attractin [Cricetulus griseus]	78.7	78.7	100%	6e-15	100%	gi|537146167|ERE69757.1
☐	PREDICTED: attractin [Bos mutus]	78.7	78.7	100%	6e-15	100%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Ursus maritimus]	78.7	78.7	100%	6e-15	100%	gi|671021680|XP_008701660.1
☐	hypothetical protein PANDA_007354 [Ailuropoda melanoleuca]	78.7	78.7	100%	6e-15	100%	gi|281339872|EFB15456.1
☐	PREDICTED: attractin-like [Ailuropoda melanoleuca]	78.7	78.7	100%	6e-15	100%	gi|301766802|XP_002918837.1
☐	PREDICTED: attractin [Mustela putorius furo]	78.7	78.7	100%	6e-15	100%	gi|511947743|XP_004792355.1
☐	attractin, isoform CRA_b [Homo sapiens]	78.7	78.7	100%	6e-15	100%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	78.7	78.7	100%	6e-15	100%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin [Fukomys damarensis]	78.7	78.7	100%	6e-15	100%	gi|731281216|XP_010609356.1
☐	PREDICTED: attractin [Ovis aries]	78.7	78.7	100%	6e-15	100%	gi|426241795|XP_004014773.1
☐	PREDICTED: attractin [Peromyscus maniculatus bairdii]	78.7	78.7	100%	6e-15	100%	gi|589943852|XP_006984624.1
☐	PREDICTED: attractin [Felis catus]	78.7	78.7	100%	6e-15	100%	gi|586981105|XP_003983758.2
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	78.7	78.7	100%	6e-15	100%	gi|694977850|XP_009435010.1

☐	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	78.7	78.7	100%	6e-15	100%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin [Erinaceus europaeus]	78.7	78.7	100%	6e-15	100%	gi|617558695|XP_007539650.1
☐	PREDICTED: attractin [Vicugna pacos]	78.7	78.7	100%	6e-15	100%	gi|560970220|XP_006207473.1
☐	attractin [Bos taurus]	78.7	78.7	100%	6e-15	100%	gi|253560524|ACT32973.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	78.7	78.7	100%	6e-15	100%	gi|586533632|XP_006921705.1
☐	attractin [Bos taurus]	78.7	78.7	100%	6e-15	100%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	78.7	78.7	100%	6e-15	100%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin isoform X3 [Canis lupus familiaris]	78.7	78.7	100%	6e-15	100%	gi|73991942|XP_534360.2
☐	PREDICTED: attractin isoform 1 [Ceratotherium simum simum]	78.7	78.7	100%	6e-15	100%	gi|478519274|XP_004433859.1
☐	PREDICTED: attractin [Orcinus orca]	78.7	78.7	100%	6e-15	100%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin [Lipotes vexillifer]	78.7	78.7	100%	6e-15	100%	gi|602710450|XP_007465469.1
☐	PREDICTED: attractin isoform X1 [Condylura cristata]	78.7	78.7	100%	6e-15	100%	gi|507961707|XP_004687417.1
☐	PREDICTED: attractin [Odobenus rosmarus divergens]	78.7	78.7	100%	6e-15	100%	gi|472357214|XP_004398236.1
☐	PREDICTED: attractin isoform X1 [Mustela putorius furo]	78.7	78.7	100%	6e-15	100%	gi|511906945|XP_004772932.1
☐	PREDICTED: attractin [Elephantulus edwardii]	78.7	78.7	100%	6e-15	100%	gi|585689645|XP_006894264.1
☐	PREDICTED: attractin [Orycteropus afer afer]	78.7	78.7	100%	6e-15	100%	gi|634830430|XP_007958185.1
☐	PREDICTED: attractin isoform X3 [Chinchilla lanigera]	78.7	78.7	100%	6e-15	100%	gi|533131617|XP_005380852.1
☐	PREDICTED: attractin-like [Octodon degus]	78.7	78.7	100%	6e-15	100%	gi|507657234|XP_004634315.1
☐	PREDICTED: attractin isoform X1 [Oryctolagus cuniculus]	78.7	78.7	100%	6e-15	100%	gi|291388868|XP_002710968.1
☐	PREDICTED: attractin [Ochotona princeps]	78.7	78.7	100%	6e-15	100%	gi|504146589|XP_004585711.1
☐	attractin [Mesocricetus auratus]	78.7	78.7	100%	6e-15	100%	gi|528078159|NP_001268565.1
☐	PREDICTED: attractin [Callithrix jacchus]	78.7	78.7	100%	6e-15	100%	gi|296200062|XP_002747358.1
☐	Attractin [Mus musculus]	78.7	78.7	100%	6e-15	100%	gi|223461387|AAI41055.1
☐	PREDICTED: attractin [Microtus ochrogaster]	78.7	78.7	100%	6e-15	100%	gi|532045699|XP_005365652.1
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	78.7	78.7	100%	6e-15	100%	gi|332857715|XP_003316827.1

⊟ Alignments

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PREDICTED: attractin-like, partial [Galeopterus variegatus]

Sequence ID: gi|667345974|ref|XP_008563464.1| **Length:** 213 **Number of Matches:** 1

Range 1: 57 to 80 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
78.7 bits(178)	4e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KAATCINPLNGSVCERPANHSAKQ  24
            KAATCINPLNGSVCERPANHSAKQ
Sbjct  57   KAATCINPLNGSVCERPANHSAKQ  80
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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attractin [Bos taurus]

Sequence ID: gi|190683717|gb|ACE82176.1| **Length:** 670 **Number of Matches:** 1

Range 1: 146 to 169 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
78.7 bits(178)	5e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KAATCINPLNGSVCERPANHSAKQ  24
            KAATCINPLNGSVCERPANHSAKQ
Sbjct  146  KAATCINPLNGSVCERPANHSAKQ  169
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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Attractin [Tupaia chinensis]

Sequence ID: gi|444519420|gb|ELV12829.1| **Length:** 860 **Number of Matches:** 1

Related Information

Range 1: 552 to 575 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
78.7 bits(178)	5e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KAATCINPLNGSVCERPANHSAKQ  24
            KAATCINPLNGSVCERPANHSAKQ
Sbjct  552  KAATCINPLNGSVCERPANHSAKQ  575
```

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PREDICTED: attractin-like [Leptonychotes weddellii]

Sequence ID: gi|585160208|ref|XP_006732353.1| **Length:** 899 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 708 to 731 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
78.7 bits(178)	5e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KAATCINPLNGSVCERPANHSAKQ  24
            KAATCINPLNGSVCERPANHSAKQ
Sbjct  708  KAATCINPLNGSVCERPANHSAKQ  731
```

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PREDICTED: attractin isoform X2 [Papio anubis]

Sequence ID: gi|685567345|ref|XP_009214752.1| **Length:** 989 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 595 to 618 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
78.7 bits(178)	6e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KAATCINPLNGSVCERPANHSAKQ  24
            KAATCINPLNGSVCERPANHSAKQ
Sbjct  595  KAATCINPLNGSVCERPANHSAKQ  618
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download

How to read this page | Blast report description

ATRN_KCEDLTTGKHCETCISGFYGDPTNGGKC_Mod

RID BH9CXYYD014 (Expires on 01-17 12:46 pm)

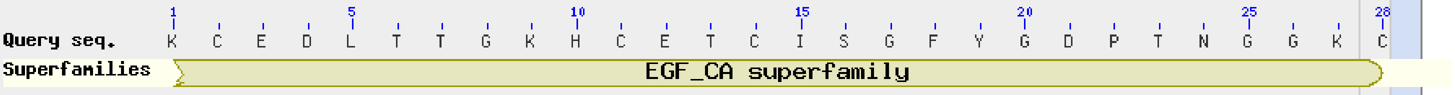
Query ID	lcl|31400	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	28		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

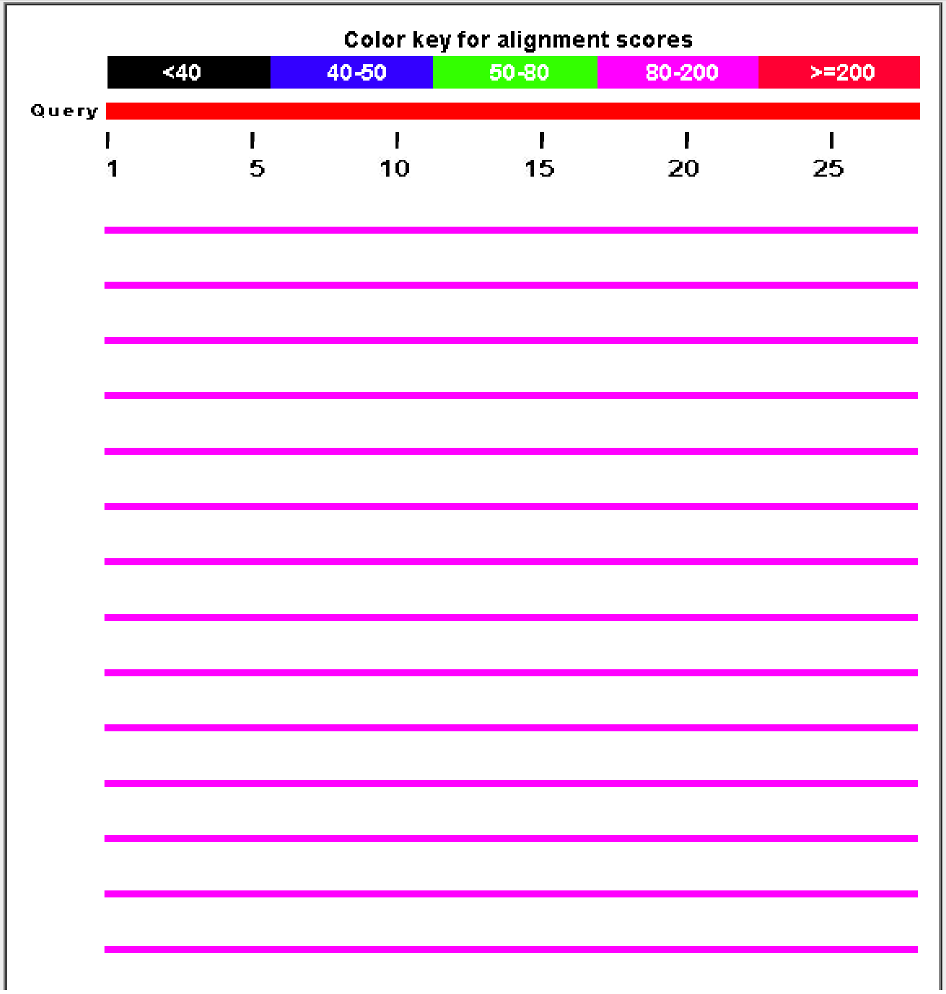
Show Conserved Domains

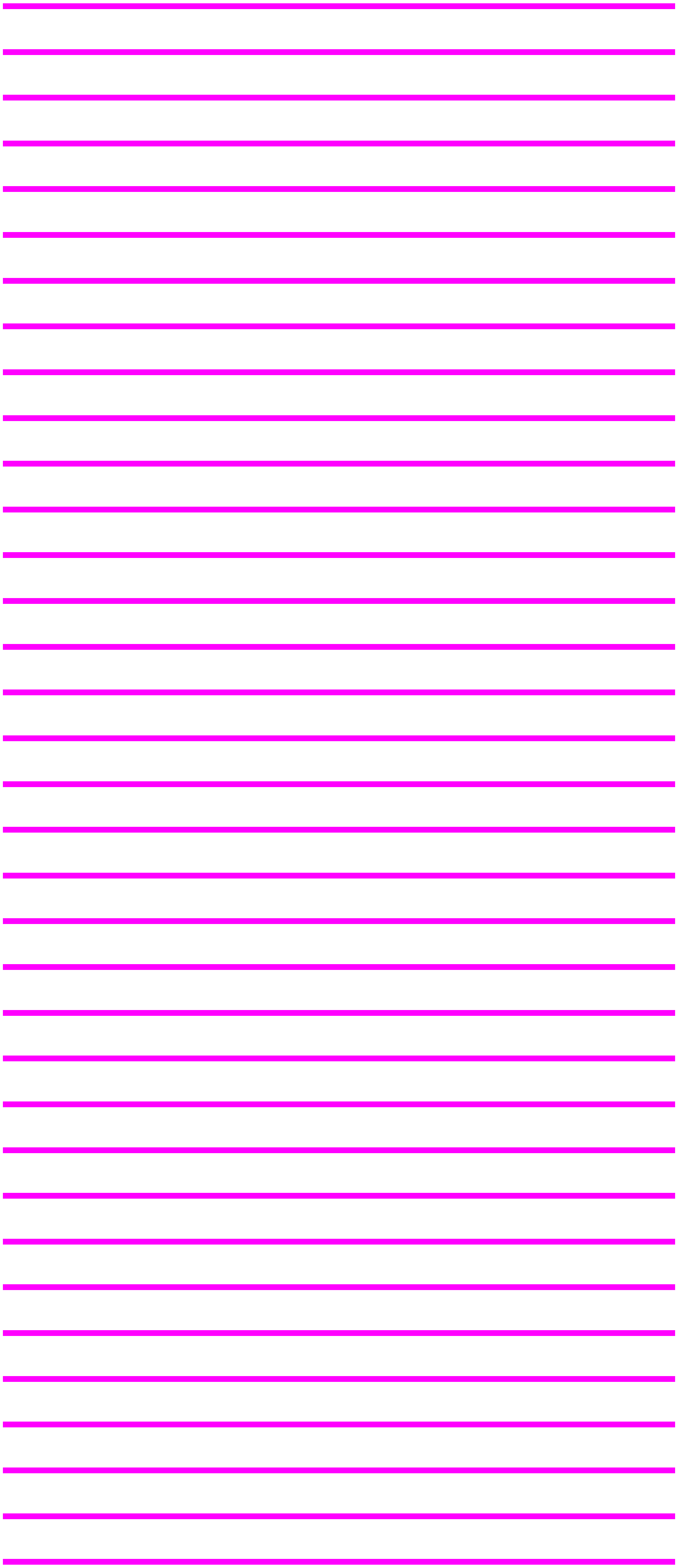
Putative conserved domains have been detected, click on the image below for detailed results.

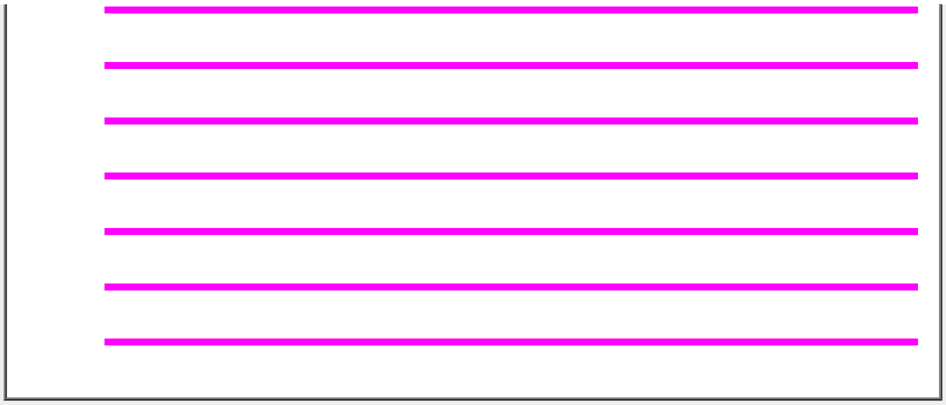


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	mKIAA0548 protein [Mus musculus]	94.8	94.8	100%	3e-20	100%	gi|26006173|BAC41429.1
☐	attractin [Rattus norvegicus]	94.8	94.8	100%	3e-20	100%	gi|12275312|BAB21018.1
☐	attractin, isoform CRA_a [Rattus norvegicus]	94.8	94.8	100%	3e-20	100%	gi|149023319|EDL80213.1
☐	Attractin [Mus musculus]	94.8	94.8	100%	3e-20	100%	gi|223461387|AAI41055.1
☐	attractin precursor [Mus musculus]	94.8	94.8	100%	3e-20	100%	gi|87299635|NP_033860.2
☐	attractin [Mus musculus]	94.8	94.8	100%	3e-20	100%	gi|4585307|AAD25372.1
☐	attractin precursor [Rattus norvegicus]	94.8	94.8	100%	3e-20	100%	gi|13786196|NP_112641.1
☐	attractin, isoform CRA_b [Mus musculus]	94.8	94.8	100%	3e-20	100%	gi|148696346|EDL28293.1
☐	mahogany protein [Mus musculus]	94.8	94.8	100%	3e-20	100%	gi|4454561|AAD20947.1
☐	PREDICTED: attractin isoform X1 [Mus musculus]	94.8	94.8	100%	3e-20	100%	gi|568915132|XP_006498669.1
☐	attractin [Ovis aries]	92.3	92.3	100%	2e-19	96%	gi|78499351|ABB45710.1
☐	KIAA0548 protein [Homo sapiens]	92.3	92.3	100%	2e-19	96%	gi|3043620|BAA25474.1
☐	attractin [Bos taurus]	92.3	92.3	100%	2e-19	96%	gi|190683717|ACE82176.1
☐	Attractin [Tupaia chinensis]	92.3	92.3	100%	2e-19	96%	gi|444519420|ELV12829.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	92.3	92.3	100%	2e-19	96%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin [Pongo abelii]	92.3	92.3	100%	2e-19	96%	gi|297706621|XP_002830129.1
☐	Attractin [Cricetulus griseus]	92.3	92.3	100%	2e-19	96%	gi|344236321|EGV92424.1
☐	attractin isoform 1 preproprotein [Camelus ferus]	92.3	92.3	100%	2e-19	96%	gi|528759526|EPY79185.1
☐	PREDICTED: attractin isoform X2 [Cricetulus griseus]	92.3	92.3	100%	2e-19	96%	gi|625260840|XP_007621856.1
☐	PREDICTED: attractin-like [Ictidomys tridecemlineatus]	92.3	92.3	100%	2e-19	96%	gi|532069682|XP_005320676.1
☐	PREDICTED: attractin [Equus przewalskii]	92.3	92.3	100%	2e-19	96%	gi|664773944|XP_008506219.1
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	92.3	92.3	100%	2e-19	96%	gi|530426021|XP_005260918.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	92.3	92.3	100%	2e-19	96%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	92.3	92.3	100%	2e-19	96%	gi|725600051|XP_010350111.1
☐	PREDICTED: attractin [Nannospalax galili]	92.3	92.3	100%	2e-19	96%	gi|674060132|XP_008836714.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	92.3	92.3	100%	2e-19	96%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin [Tarsius syrichta]	92.3	92.3	100%	2e-19	96%	gi|640796924|XP_008054571.1
☐	unnamed protein product [Homo sapiens]	92.3	92.3	100%	2e-19	96%	gi|194380362|BAG63948.1

☐	attractin isoform 4 [Homo sapiens]	92.3	92.3	100%	2e-19	96%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	92.3	92.3	100%	2e-19	96%	gi|332257827|XP_003278006.1
☐	attractin [Cricetulus griseus]	92.3	92.3	100%	2e-19	96%	gi|537146168|ERE69758.1
☐	Attractin [Myotis davidii]	92.3	92.3	100%	2e-19	96%	gi|432111133|ELK34519.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	92.3	92.3	100%	2e-19	96%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin isoform X2 [Condylura cristata]	92.3	92.3	100%	2e-19	96%	gi|507961710|XP_004687418.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	92.3	92.3	100%	2e-19	96%	gi|694977854|XP_009435012.1
☐	Attractin [Myotis brandtii]	92.3	92.3	100%	2e-19	96%	gi|521031210|EPQ12996.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	92.3	92.3	100%	2e-19	96%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	92.3	92.3	100%	2e-19	96%	gi|4093196|AAD03057.1
☐	secreted attractin precursor [Homo sapiens]	92.3	92.3	100%	2e-19	96%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	92.3	92.3	100%	2e-19	96%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	92.3	92.3	100%	2e-19	96%	gi|21450863|NP_647538.1
☐	Mahogany-like protein [Macaca mulatta]	92.3	92.3	100%	2e-19	96%	gi|355563316|EHH19878.1
☐	PREDICTED: attractin isoform X1 [Bos taurus]	92.3	92.3	100%	2e-19	96%	gi|741947708|XP_005214542.2
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	92.3	92.3	100%	2e-19	96%	gi|594099680|XP_006072965.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Pan paniscus]	92.3	92.3	100%	2e-19	96%	gi|675763672|XP_008973079.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	92.3	92.3	100%	2e-19	96%	gi|694977852|XP_009435011.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	92.3	92.3	100%	2e-19	96%	gi|530426019|XP_005260917.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	92.3	92.3	100%	2e-19	96%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	92.3	92.3	100%	2e-19	96%	gi|635021368|XP_008017720.1
☐	Mahogany-like protein [Macaca fascicularis]	92.3	92.3	100%	2e-19	96%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin [Myotis davidii]	92.3	92.3	100%	2e-19	96%	gi|584075971|XP_006758187.1
☐	PREDICTED: attractin [Myotis brandtii]	92.3	92.3	100%	2e-19	96%	gi|554560893|XP_005874816.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	92.3	92.3	100%	2e-19	96%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	92.3	92.3	100%	2e-19	96%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	92.3	92.3	100%	2e-19	96%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Capra hircus]	92.3	92.3	100%	2e-19	96%	gi|548490191|XP_005688293.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	92.3	92.3	100%	2e-19	96%	gi|724902357|XP_010377335.1
☐	PREDICTED: attractin isoform X1 [Cricetulus griseus]	92.3	92.3	100%	2e-19	96%	gi|354473756|XP_003499099.1
☐	PREDICTED: attractin [Camelus ferus]	92.3	92.3	100%	2e-19	96%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Myotis lucifugus]	92.3	92.3	100%	2e-19	96%	gi|558159591|XP_006096513.1
☐	attractin [Cricetulus griseus]	92.3	92.3	100%	2e-19	96%	gi|537146167|ERE69757.1
☐	PREDICTED: attractin [Camelus dromedarius]	92.3	92.3	100%	2e-19	96%	gi|744589171|XP_010986570.1
☐	PREDICTED: attractin [Bos mutus]	92.3	92.3	100%	2e-19	96%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Camelus bactrianus]	92.3	92.3	100%	2e-19	96%	gi|743752427|XP_010971103.1
☐	attractin, isoform CRA_b [Homo sapiens]	92.3	92.3	100%	2e-19	96%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	92.3	92.3	100%	2e-19	96%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin [Ovis aries]	92.3	92.3	100%	2e-19	96%	gi|426241795|XP_004014773.1
☐	PREDICTED: attractin [Peromyscus maniculatus bairdii]	92.3	92.3	100%	2e-19	96%	gi|589943852|XP_006984624.1
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	92.3	92.3	100%	2e-19	96%	gi|694977850|XP_009435010.1
☐	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	92.3	92.3	100%	2e-19	96%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin [Otolemur garnettii]	92.3	92.3	100%	2e-19	96%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin [Vicugna pacos]	92.3	92.3	100%	2e-19	96%	gi|560970220|XP_006207473.1
☐	PREDICTED: attractin [Echinops telfairi]	92.3	92.3	100%	2e-19	96%	gi|507626122|XP_004697922.1
☐	attractin [Bos taurus]	92.3	92.3	100%	2e-19	96%	gi|253560524|ACT32973.1

☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	92.3	92.3	100%	2e-19	96%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin [Eptesicus fuscus]	92.3	92.3	100%	2e-19	96%	gi|641701319|XP_008139256.1
☐	attractin [Bos taurus]	92.3	92.3	100%	2e-19	96%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	92.3	92.3	100%	2e-19	96%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin [Orcinus orca]	92.3	92.3	100%	2e-19	96%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin [Lipotes vexillifer]	92.3	92.3	100%	2e-19	96%	gi|602710450|XP_007465469.1
☐	PREDICTED: attractin isoform X1 [Condylura cristata]	92.3	92.3	100%	2e-19	96%	gi|507961707|XP_004687417.1
☐	PREDICTED: attractin [Chrysochloris asiatica]	92.3	92.3	100%	2e-19	96%	gi|586488825|XP_006874887.1
☐	PREDICTED: attractin [Elephantulus edwardii]	92.3	92.3	100%	2e-19	96%	gi|585689645|XP_006894264.1
☐	PREDICTED: attractin [Orycteropus afer afer]	92.3	92.3	100%	2e-19	96%	gi|634830430|XP_007958185.1
☐	PREDICTED: attractin isoform X1 [Oryctolagus cuniculus]	92.3	92.3	100%	2e-19	96%	gi|291388868|XP_002710968.1
☐	PREDICTED: attractin isoform X1 [Ictidomys tridecemlineatus]	92.3	92.3	100%	2e-19	96%	gi|532069484|XP_005320577.1
☐	PREDICTED: attractin [Ochotona princeps]	92.3	92.3	100%	2e-19	96%	gi|504146589|XP_004585711.1
☐	attractin [Mesocricetus auratus]	92.3	92.3	100%	2e-19	96%	gi|528078159|NP_001268565.1
☐	PREDICTED: attractin isoform X3 [Ictidomys tridecemlineatus]	92.3	92.3	100%	2e-19	96%	gi|532069488|XP_005320579.1
☐	PREDICTED: attractin [Callithrix jacchus]	92.3	92.3	100%	2e-19	96%	gi|296200062|XP_002747358.1
☐	PREDICTED: attractin [Microtus ochrogaster]	92.3	92.3	100%	2e-19	96%	gi|532045699|XP_005365652.1
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	92.3	92.3	100%	2e-19	96%	gi|332857715|XP_003316827.1
☐	membrane attractin precursor [Homo sapiens]	92.3	92.3	100%	2e-19	96%	gi|8118082|AAF72881.1
☐	attractin isoform 1 preproprotein [Homo sapiens]	92.3	92.3	100%	2e-19	96%	gi|21450861|NP_647537.1
☐	PREDICTED: attractin isoform X2 [Ictidomys tridecemlineatus]	92.3	92.3	100%	2e-19	96%	gi|532069486|XP_005320578.1
☐	PREDICTED: attractin [Jaculus jaculus]	92.3	92.3	100%	2e-19	96%	gi|507555530|XP_004661535.1
☐	PREDICTED: attractin isoform X2 [Macaca fascicularis]	92.3	92.3	100%	2e-19	96%	gi|544464512|XP_005568510.1
☐	PREDICTED: attractin [Macaca mulatta]	92.3	92.3	100%	2e-19	96%	gi|109092720|XP_001115192.1
☐	PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	92.3	92.3	100%	2e-19	96%	gi|635021360|XP_008017700.1
☐	PREDICTED: attractin isoform X1 [Macaca fascicularis]	92.3	92.3	100%	2e-19	96%	gi|544464510|XP_005568509.1

⊖ Alignments

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mKIAA0548 protein [Mus musculus]

Sequence ID: gi|26006173|dbj|BAC41429.1| **Length:** 1059 **Number of Matches:** 1

Range 1: 709 to 736 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.8 bits(216)	3e-20	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    KCEDLTTGKHCETCISGFYGDPTNGGKC  28
            KCEDLTTGKHCETCISGFYGDPTNGGKC
Sbjct  709  KCEDLTTGKHCETCISGFYGDPTNGGKC  736
```

Related Information

Gene - associated gene details

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attractin [Rattus norvegicus]

Sequence ID: gi|12275312|dbj|BAB21018.1| **Length:** 1275 **Number of Matches:** 1

Range 1: 1082 to 1109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.8 bits(216)	3e-20	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1     KCEDLTTGKHCETCISGFYGDPTNGGKC  28
             KCEDLTTGKHCETCISGFYGDPTNGGKC
Sbjct  1082  KCEDLTTGKHCETCISGFYGDPTNGGKC  1109
```

Related Information

Gene - associated gene details

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attractin, isoform CRA_a [Rattus norvegicus]

Sequence ID: gi|149023319|gb|EDL80213.1| **Length:** 1275 **Number of Matches:** 1

Range 1: 1082 to 1109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.8 bits(216)	3e-20	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1     KCEDLTTGKHCETCISGFYGDPTNGGKC  28
             KCEDLTTGKHCETCISGFYGDPTNGGKC
Sbjct  1082  KCEDLTTGKHCETCISGFYGDPTNGGKC  1109
```

Related Information

Gene - associated gene details

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Attractin [Mus musculus]

Sequence ID: gi|223461387|gb|AAI41055.1| **Length:** 1428 **Number of Matches:** 1

Range 1: 1078 to 1105 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.8 bits(216)	3e-20	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1     KCEDLTTGKHCETCISGFYGDPTNGGKC  28
             KCEDLTTGKHCETCISGFYGDPTNGGKC
Sbjct  1078  KCEDLTTGKHCETCISGFYGDPTNGGKC  1105
```

Related Information

Gene - associated gene details

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attractin precursor [Mus musculus]

Sequence ID: gi|87299635|ref|NP_033860.2| **Length:** 1428 **Number of Matches:** 1

▷ See 2 more title(s)

Range 1: 1078 to 1105 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.8 bits(216)	3e-20	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1     KCEDLTTGKHCETCISGFYGDPTNGGKC  28
             KCEDLTTGKHCETCISGFYGDPTNGGKC
Sbjct  1078  KCEDLTTGKHCETCISGFYGDPTNGGKC  1105
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

BLAST ®

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NCBI/ BLAST/ blastp suite/ **Formatting Results - B90XK6N701R**

Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

ATRN_KCENLTTGKHCETCISGFYGDPTNGGKC_NonMod

RID B90XK6N701R (Expires on 01-14 09:32 am)

Query ID lcl|59450
Description None
Molecule type amino acid
Query Length 28

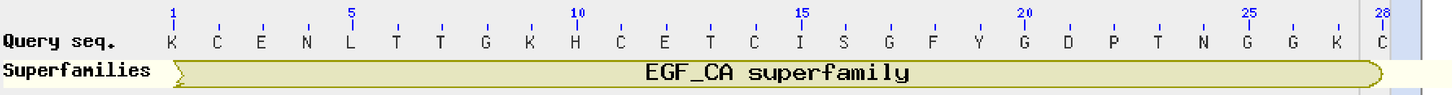
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

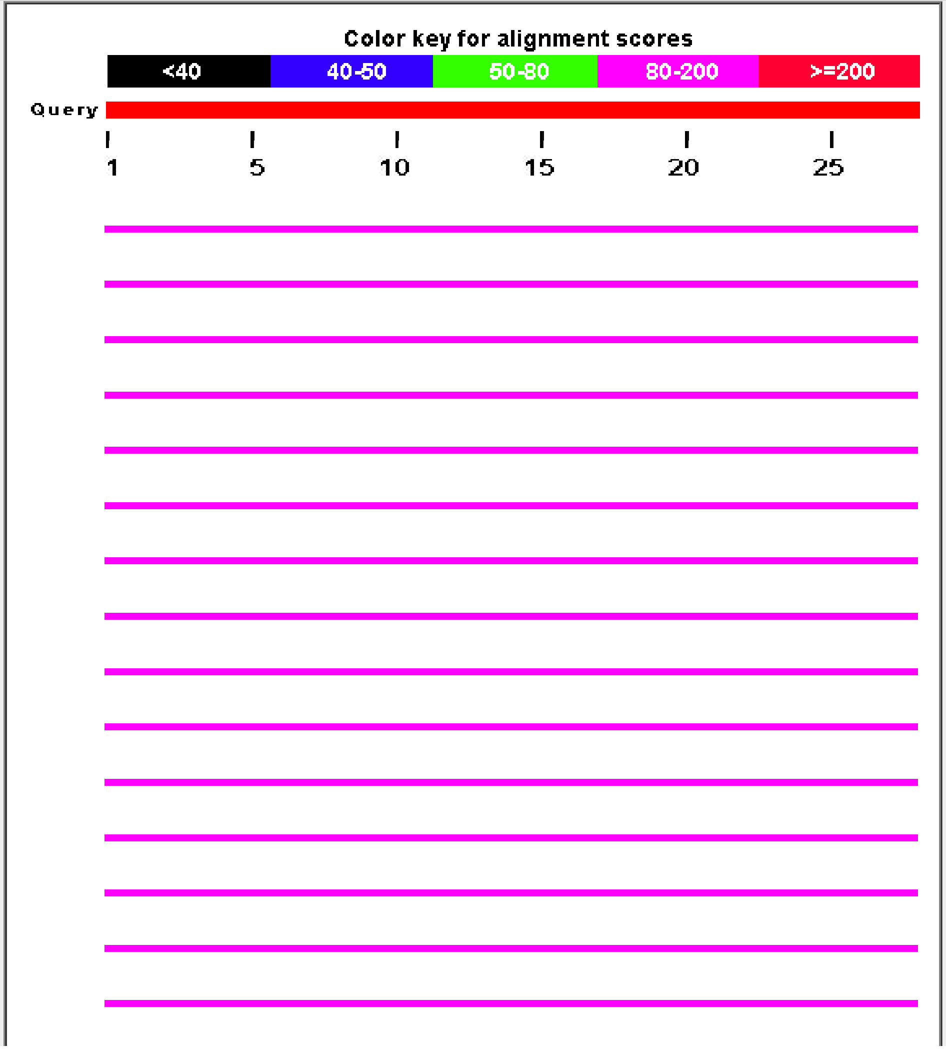
Show Conserved Domains

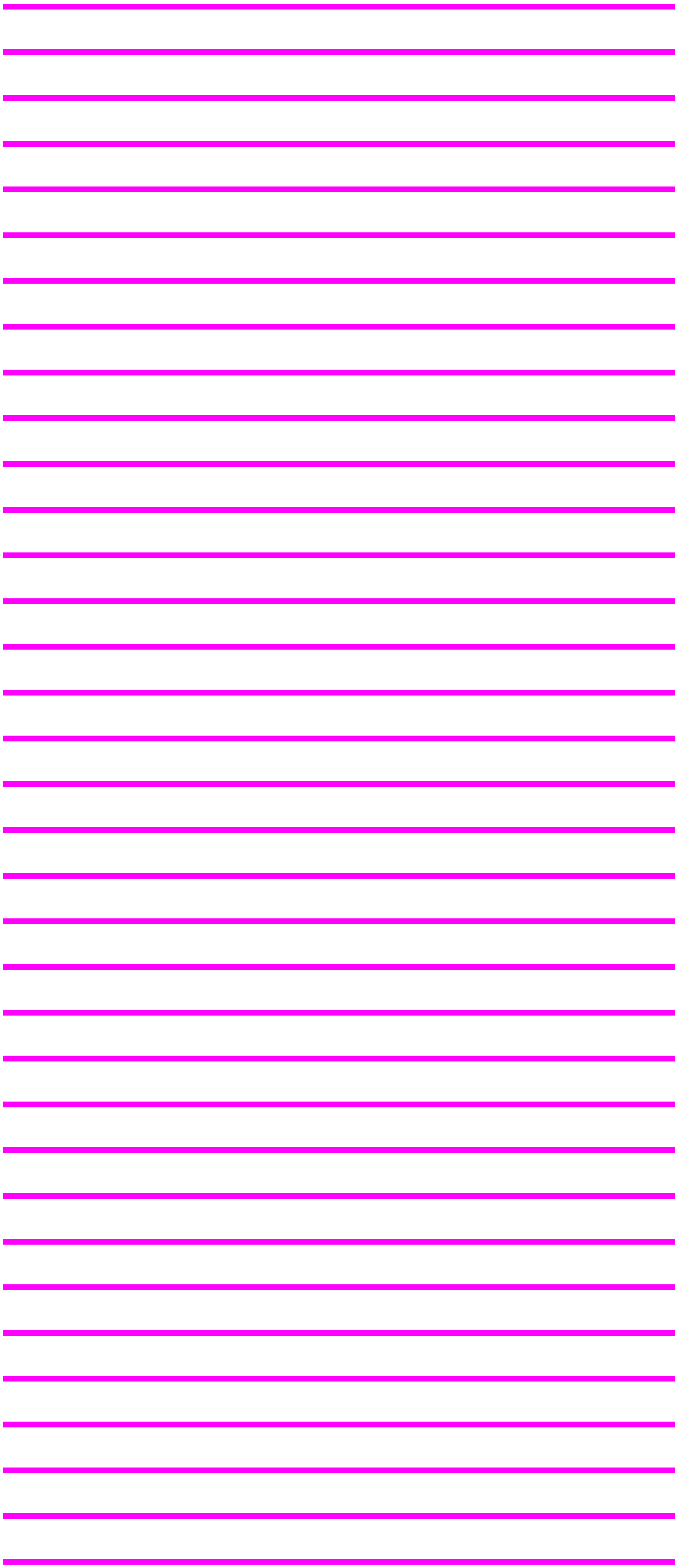
Putative conserved domains have been detected, click on the image below for detailed results.

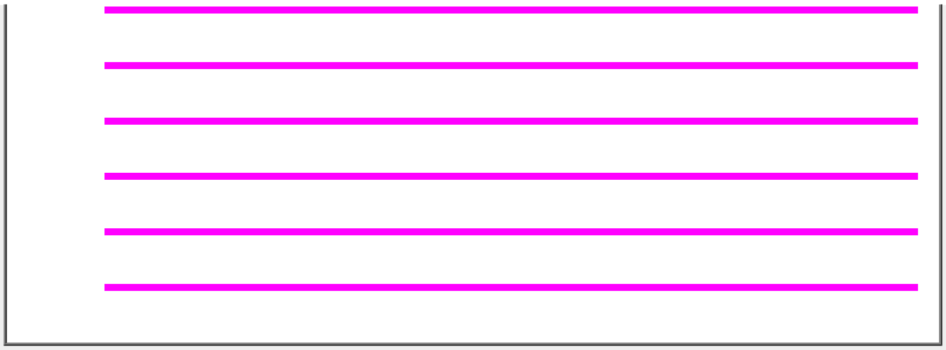


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	attractin [Ovis aries]	94.8	94.8	100%	2e-20	100%	gi|78499351|ABB45710.1
☐	KIAA0548 protein [Homo sapiens]	94.8	94.8	100%	3e-20	100%	gi|3043620|BAA25474.1
☐	attractin [Bos taurus]	94.8	94.8	100%	3e-20	100%	gi|190683717|ACE82176.1
☐	Attractin [Tupaia chinensis]	94.8	94.8	100%	3e-20	100%	gi|444519420|ELV12829.1
☐	PREDICTED: attractin isoform X2 [Papio anubis]	94.8	94.8	100%	3e-20	100%	gi|685567345|XP_009214752.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	94.8	94.8	100%	3e-20	100%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin [Pongo abelii]	94.8	94.8	100%	3e-20	100%	gi|297706621|XP_002830129.1
☐	Attractin [Cricetulus griseus]	94.8	94.8	100%	3e-20	100%	gi|344236321|EGV92424.1
☐	attractin isoform 1 preproprotein [Camelus ferus]	94.8	94.8	100%	3e-20	100%	gi|528759526|EPY79185.1
☐	PREDICTED: attractin isoform X2 [Cricetulus griseus]	94.8	94.8	100%	3e-20	100%	gi|625260840|XP_007621856.1
☐	PREDICTED: attractin-like [Ictidomys tridecemlineatus]	94.8	94.8	100%	3e-20	100%	gi|532069682|XP_005320676.1
☐	PREDICTED: attractin [Equus przewalskii]	94.8	94.8	100%	3e-20	100%	gi|664773944|XP_008506219.1
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	94.8	94.8	100%	3e-20	100%	gi|530426021|XP_005260918.1
☐	PREDICTED: attractin isoform X1 [Papio anubis]	94.8	94.8	100%	3e-20	100%	gi|685567343|XP_009214751.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	94.8	94.8	100%	3e-20	100%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	94.8	94.8	100%	3e-20	100%	gi|725600051|XP_010350111.1
☐	PREDICTED: attractin [Nannospalax galili]	94.8	94.8	100%	3e-20	100%	gi|674060132|XP_008836714.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	94.8	94.8	100%	3e-20	100%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin [Tarsius syrichta]	94.8	94.8	100%	3e-20	100%	gi|640796924|XP_008054571.1
☐	unnamed protein product [Homo sapiens]	94.8	94.8	100%	3e-20	100%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	94.8	94.8	100%	3e-20	100%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	94.8	94.8	100%	3e-20	100%	gi|332257827|XP_003278006.1
☐	attractin [Cricetulus griseus]	94.8	94.8	100%	3e-20	100%	gi|537146168|ERE69758.1
☐	Attractin [Myotis davidii]	94.8	94.8	100%	3e-20	100%	gi|432111133|ELK34519.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	94.8	94.8	100%	3e-20	100%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin isoform X2 [Condylura cristata]	94.8	94.8	100%	3e-20	100%	gi|507961710|XP_004687418.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	94.8	94.8	100%	3e-20	100%	gi|694977854|XP_009435012.1
☐	Attractin [Myotis brandtii]	94.8	94.8	100%	3e-20	100%	gi|521031210|EPQ12996.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	94.8	94.8	100%	3e-20	100%	gi|332257825|XP_003278005.1

☐ attractin-2 [Homo sapiens]	94.8	94.8	100%	3e-20	100%	gi|4093196|AAD03057.1
☐ secreted attractin precursor [Homo sapiens]	94.8	94.8	100%	3e-20	100%	gi|8118083|AAF72882.1
☐ unnamed protein product [Homo sapiens]	94.8	94.8	100%	3e-20	100%	gi|158259481|BAF85699.1
☐ attractin isoform 2 preproprotein [Homo sapiens]	94.8	94.8	100%	3e-20	100%	gi|21450863|NP_647538.1
☐ Mahogany-like protein [Macaca mulatta]	94.8	94.8	100%	3e-20	100%	gi|355563316|EHH19878.1
☐ PREDICTED: attractin isoform X3 [Bubalus bubalis]	94.8	94.8	100%	3e-20	100%	gi|594099680|XP_006072965.1
☐ PREDICTED: LOW QUALITY PROTEIN: attractin [Pan paniscus]	94.8	94.8	100%	3e-20	100%	gi|675763672|XP_008973079.1
☐ PREDICTED: attractin isoform X3 [Pan troglodytes]	94.8	94.8	100%	3e-20	100%	gi|694977852|XP_009435011.1
☐ PREDICTED: attractin isoform X1 [Homo sapiens]	94.8	94.8	100%	3e-20	100%	gi|530426019|XP_005260917.1
☐ PREDICTED: attractin isoform X4 [Macaca fascicularis]	94.8	94.8	100%	3e-20	100%	gi|544464516|XP_005568512.1
☐ PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	94.8	94.8	100%	3e-20	100%	gi|635021368|XP_008017720.1
☐ Mahogany-like protein [Macaca fascicularis]	94.8	94.8	100%	3e-20	100%	gi|355784657|EHH65508.1
☐ PREDICTED: attractin [Myotis davidii]	94.8	94.8	100%	3e-20	100%	gi|584075971|XP_006758187.1
☐ PREDICTED: attractin [Myotis brandtii]	94.8	94.8	100%	3e-20	100%	gi|554560893|XP_005874816.1
☐ PREDICTED: attractin isoform X3 [Macaca fascicularis]	94.8	94.8	100%	3e-20	100%	gi|544464514|XP_005568511.1
☐ PREDICTED: attractin-like [Galeopterus variegatus]	94.8	94.8	100%	3e-20	100%	gi|667324076|XP_008589101.1
☐ PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	94.8	94.8	100%	3e-20	100%	gi|635021366|XP_008017712.1
☐ PREDICTED: attractin [Capra hircus]	94.8	94.8	100%	3e-20	100%	gi|548490191|XP_005688293.1
☐ PREDICTED: attractin [Rhinopithecus roxellana]	94.8	94.8	100%	3e-20	100%	gi|724902357|XP_010377335.1
☐ PREDICTED: attractin isoform X1 [Cricetulus griseus]	94.8	94.8	100%	3e-20	100%	gi|354473756|XP_003499099.1
☐ PREDICTED: attractin [Camelus ferus]	94.8	94.8	100%	3e-20	100%	gi|560921992|XP_006187198.1
☐ PREDICTED: attractin [Myotis lucifugus]	94.8	94.8	100%	3e-20	100%	gi|558159591|XP_006096513.1
☐ attractin [Cricetulus griseus]	94.8	94.8	100%	3e-20	100%	gi|537146167|ERE69757.1
☐ PREDICTED: attractin [Bos mutus]	94.8	94.8	100%	3e-20	100%	gi|555963925|XP_005894036.1
☐ attractin, isoform CRA_b [Homo sapiens]	94.8	94.8	100%	3e-20	100%	gi|119630936|EAX10531.1
☐ PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	94.8	94.8	100%	3e-20	100%	gi|635021364|XP_008017707.1
☐ PREDICTED: attractin [Ovis aries]	94.8	94.8	100%	3e-20	100%	gi|426241795|XP_004014773.1
☐ PREDICTED: attractin [Peromyscus maniculatus bairdii]	94.8	94.8	100%	3e-20	100%	gi|589943852|XP_006984624.1
☐ PREDICTED: attractin isoform X2 [Pan troglodytes]	94.8	94.8	100%	3e-20	100%	gi|694977850|XP_009435010.1
☐ PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	94.8	94.8	100%	3e-20	100%	gi|635021362|XP_008017704.1
☐ PREDICTED: attractin [Otolemur garnettii]	94.8	94.8	100%	3e-20	100%	gi|395830288|XP_003788264.1
☐ PREDICTED: attractin [Vicugna pacos]	94.8	94.8	100%	3e-20	100%	gi|560970220|XP_006207473.1
☐ PREDICTED: attractin [Echinops telfairi]	94.8	94.8	100%	3e-20	100%	gi|507626122|XP_004697922.1
☐ attractin [Bos taurus]	94.8	94.8	100%	3e-20	100%	gi|253560524|ACT32973.1
☐ PREDICTED: attractin isoform X1 [Pteropus alecto]	94.8	94.8	100%	3e-20	100%	gi|586533632|XP_006921705.1
☐ PREDICTED: attractin [Eptesicus fuscus]	94.8	94.8	100%	3e-20	100%	gi|641701319|XP_008139256.1
☐ attractin [Bos taurus]	94.8	94.8	100%	3e-20	100%	gi|27806737|NP_776420.1
☐ PREDICTED: attractin isoform X2 [Bubalus bubalis]	94.8	94.8	100%	3e-20	100%	gi|594099678|XP_006072964.1
☐ PREDICTED: attractin [Orcinus orca]	94.8	94.8	100%	3e-20	100%	gi|466084723|XP_004285351.1
☐ PREDICTED: attractin [Lipotes vexillifer]	94.8	94.8	100%	3e-20	100%	gi|602710450|XP_007465469.1
☐ PREDICTED: attractin isoform X1 [Condylura cristata]	94.8	94.8	100%	3e-20	100%	gi|507961707|XP_004687417.1
☐ PREDICTED: attractin [Chrysochloris asiatica]	94.8	94.8	100%	3e-20	100%	gi|586488825|XP_006874887.1
☐ PREDICTED: attractin [Elephantulus edwardii]	94.8	94.8	100%	3e-20	100%	gi|585689645|XP_006894264.1
☐ PREDICTED: attractin [Orycteropus afer afer]	94.8	94.8	100%	3e-20	100%	gi|634830430|XP_007958185.1
☐ PREDICTED: attractin isoform X1 [Oryctolagus cuniculus]	94.8	94.8	100%	3e-20	100%	gi|291388868|XP_002710968.1
☐ PREDICTED: attractin isoform X1 [Ictidomys tridecemlineatus]	94.8	94.8	100%	3e-20	100%	gi|532069484|XP_005320577.1

☐	PREDICTED: attractin [Ochotona princeps]	94.8	94.8	100%	3e-20	100%	gi|504146589|XP_004585711.1
☐	attractin [Mesocricetus auratus]	94.8	94.8	100%	3e-20	100%	gi|528078159|NP_001268565.1
☐	PREDICTED: attractin isoform X3 [Ictidomys tridecemlineatus]	94.8	94.8	100%	3e-20	100%	gi|532069488|XP_005320579.1
☐	PREDICTED: attractin [Callithrix jacchus]	94.8	94.8	100%	3e-20	100%	gi|296200062|XP_002747358.1
☐	PREDICTED: attractin [Microtus ochrogaster]	94.8	94.8	100%	3e-20	100%	gi|532045699|XP_005365652.1
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	94.8	94.8	100%	3e-20	100%	gi|332857715|XP_003316827.1
☐	membrane attractin precursor [Homo sapiens]	94.8	94.8	100%	3e-20	100%	gi|8118082|AAF72881.1
☐	attractin isoform 1 preproprotein [Homo sapiens]	94.8	94.8	100%	3e-20	100%	gi|21450861|NP_647537.1
☐	PREDICTED: attractin isoform X2 [Ictidomys tridecemlineatus]	94.8	94.8	100%	3e-20	100%	gi|532069486|XP_005320578.1
☐	PREDICTED: attractin [Jaculus jaculus]	94.8	94.8	100%	3e-20	100%	gi|507555530|XP_004661535.1
☐	PREDICTED: attractin isoform X2 [Macaca fascicularis]	94.8	94.8	100%	3e-20	100%	gi|544464512|XP_005568510.1
☐	PREDICTED: attractin [Macaca mulatta]	94.8	94.8	100%	3e-20	100%	gi|109092720|XP_001115192.1
☐	PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	94.8	94.8	100%	3e-20	100%	gi|635021360|XP_008017700.1
☐	PREDICTED: attractin isoform X2 [Bos taurus]	94.8	94.8	100%	3e-20	100%	gi|528973313|XP_005214542.1
☐	PREDICTED: attractin isoform X1 [Macaca fascicularis]	94.8	94.8	100%	3e-20	100%	gi|544464510|XP_005568509.1
☐	PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	94.8	94.8	100%	3e-20	100%	gi|635021370|XP_008017729.1
☐	PREDICTED: attractin isoform X2 [Oryctolagus cuniculus]	94.8	94.8	100%	3e-20	100%	gi|655716500|XP_008254470.1
☐	PREDICTED: attractin [Tupaia chinensis]	94.8	94.8	100%	3e-20	100%	gi|562872246|XP_006164056.1
☐	PREDICTED: attractin isoform X2 [Pteropus alecto]	94.8	94.8	100%	3e-20	100%	gi|586533634|XP_006921706.1
☐	PREDICTED: attractin isoform X1 [Bubalus bubalis]	94.8	94.8	100%	3e-20	100%	gi|594099676|XP_006072963.1
☐	PREDICTED: attractin isoform X1 [Bos taurus]	94.8	94.8	100%	3e-20	100%	gi|528973311|XP_005214541.1
☐	mKIAA0548 protein [Mus musculus]	92.3	92.3	100%	2e-19	96%	gi|26006173|BAC41429.1
☐	attractin [Rattus norvegicus]	92.3	92.3	100%	2e-19	96%	gi|12275312|BAB21018.1
☐	attractin, isoform CRA_a [Rattus norvegicus]	92.3	92.3	100%	2e-19	96%	gi|149023319|EDL80213.1
☐	Attractin [Mus musculus]	92.3	92.3	100%	2e-19	96%	gi|223461387|AAI41055.1

Alignments

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attractin [Ovis aries]

Sequence ID: gi|78499351|gb|ABB45710.1| **Length:** 242 **Number of Matches:** 1

Range 1: 88 to 115 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.8 bits(216)	2e-20	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    KCENLTTGKHCETCISGFYGDPTNGGKC  28
            KCENLTTGKHCETCISGFYGDPTNGGKC
Sbjct  88   KCENLTTGKHCETCISGFYGDPTNGGKC  115
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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KIAA0548 protein [Homo sapiens]

Sequence ID: gi|3043620|dbj|BAA25474.1| **Length:** 452 **Number of Matches:** 1

Range 1: 102 to 129 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.8 bits(216)	3e-20	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    KCENLTTGKHCETCISGFYGDPTNGGKC  28
            KCENLTTGKHCETCISGFYGDPTNGGKC
Sbjct  102  KCENLTTGKHCETCISGFYGDPTNGGKC  129
```

Related Information

Gene - associated gene details

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attractin [Bos taurus]

Sequence ID: gi|190683717|gb|ACE82176.1| **Length:** 670 **Number of Matches:** 1

Range 1: 320 to 347 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.8 bits(216)	3e-20	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    KCENLTTGKHCETCISGFYGDPTNGGKC  28
            KCENLTTGKHCETCISGFYGDPTNGGKC
Sbjct  320  KCENLTTGKHCETCISGFYGDPTNGGKC  347
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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Attractin [Tupaia chinensis]

Sequence ID: gi|444519420|gb|ELV12829.1| **Length:** 860 **Number of Matches:** 1

Range 1: 648 to 675 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.8 bits(216)	3e-20	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    KCENLTTGKHCETCISGFYGDPTNGGKC  28
            KCENLTTGKHCETCISGFYGDPTNGGKC
Sbjct  648  KCENLTTGKHCETCISGFYGDPTNGGKC  675
```

Related Information

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: attractin isoform X2 [Papio anubis]

Sequence ID: gi|685567345|ref|XP_009214752.1| **Length:** 989 **Number of Matches:** 1

Range 1: 769 to 796 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.8 bits(216)	3e-20	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    KCENLTTGKHCETCISGFYGDPTNGGKC  28
            KCENLTTGKHCETCISGFYGDPTNGGKC
Sbjct  769  KCENLTTGKHCETCISGFYGDPTNGGKC  796
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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NCBI/ BLAST/ blastp suite/ Formatting Results - BHBPXXNG014

Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

ATRN_KCIDQSICEKC_Mod

RID BHBPXXNG014 (Expires on 01-17 13:25 pm)

Query ID	lcl|96533	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	11		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

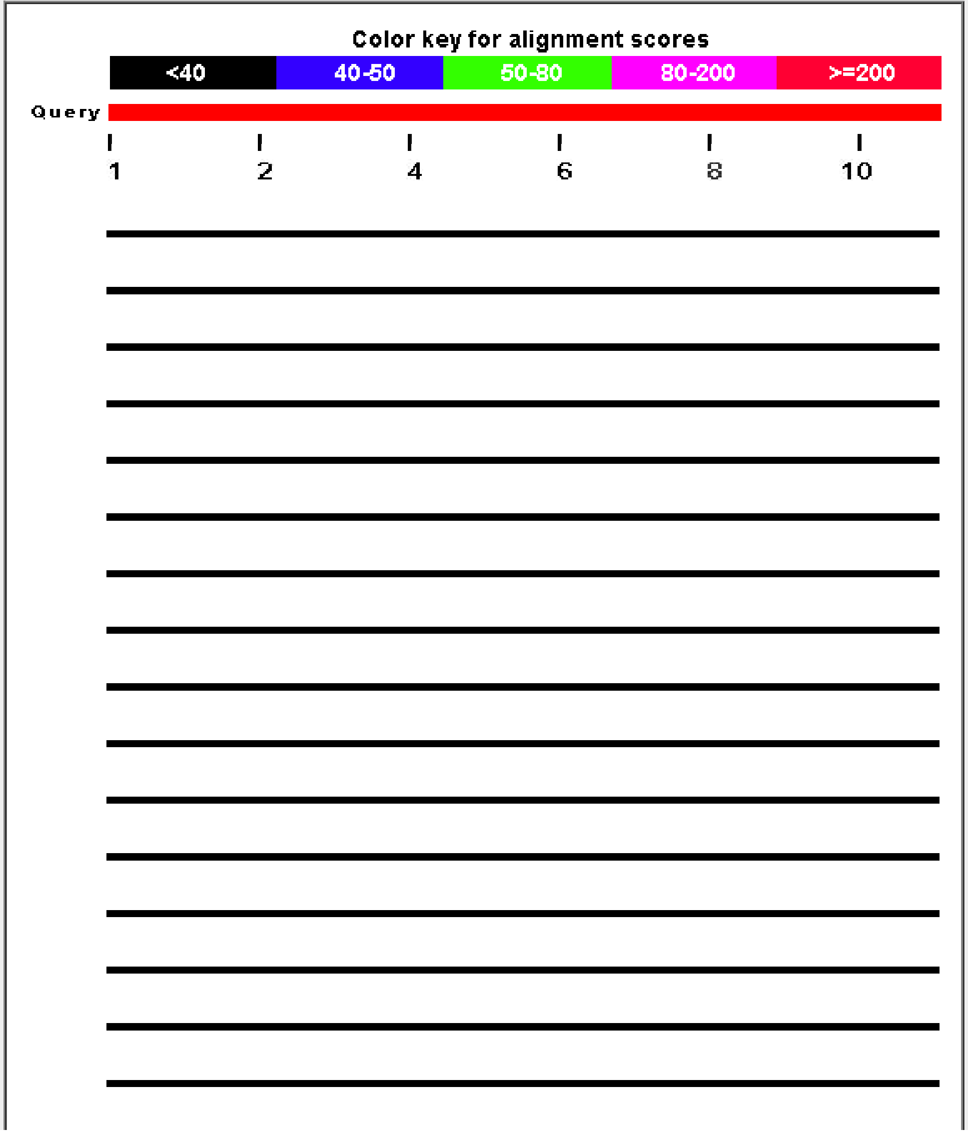
Graphic Summary

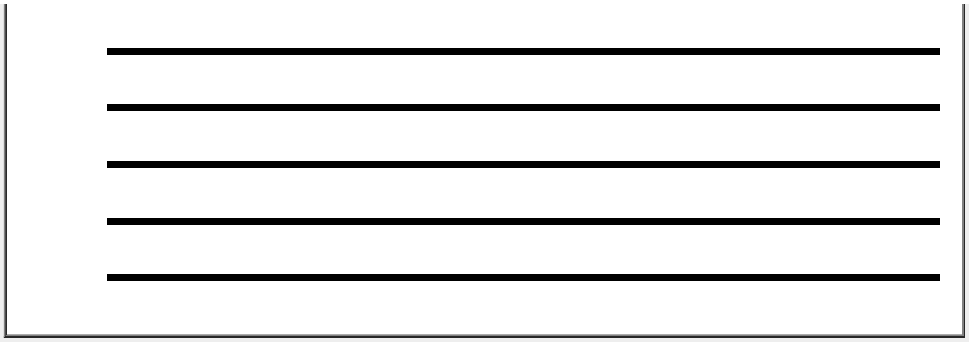
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 105 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	attractin [Ovis aries]	38.8	38.8	100%	0.029	91%	gi|78499351|ABB45710.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	38.8	38.8	100%	0.030	91%	gi|585182065|XP_006742666.1
☐	KIAA0548 protein [Homo sapiens]	38.8	38.8	100%	0.031	91%	gi|3043620|BAA25474.1
☐	attractin [Bos taurus]	38.8	38.8	100%	0.032	91%	gi|190683717|ACE82176.1
☐	Attractin [Tupaia chinensis]	38.8	38.8	100%	0.033	91%	gi|444519420|ELV12829.1
☐	PREDICTED: attractin isoform X2 [Papio anubis]	38.8	77.6	100%	0.033	91%	gi|685567345|XP_009214752.1
☐	attractin [Canis lupus familiaris]	38.8	38.8	100%	0.033	91%	gi|339892849|AEK21787.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	38.8	38.8	100%	0.033	91%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin-like [Physeter catodon]	38.8	38.8	100%	0.033	91%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin [Pongo abelii]	38.8	38.8	100%	0.033	91%	gi|297706621|XP_002830129.1
☐	attractin isoform 1 preproprotein [Camelus ferus]	38.8	38.8	100%	0.033	91%	gi|528759526|EPY79185.1
☐	PREDICTED: attractin-like [Ictidomys tridecemlineatus]	38.8	38.8	100%	0.033	91%	gi|532069682|XP_005320676.1
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	38.8	38.8	100%	0.033	91%	gi|530426021|XP_005260918.1
☐	PREDICTED: attractin isoform X1 [Papio anubis]	38.8	77.6	100%	0.033	91%	gi|685567343|XP_009214751.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	38.8	38.8	100%	0.033	91%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	38.8	38.8	100%	0.033	91%	gi|725600051|XP_010350111.1
☐	PREDICTED: attractin [Nannospalax galili]	38.8	38.8	100%	0.033	91%	gi|674060132|XP_008836714.1
☐	PREDICTED: attractin [Tarsius syrichta]	38.8	38.8	100%	0.033	91%	gi|640796924|XP_008054571.1
☐	unnamed protein product [Homo sapiens]	38.8	38.8	100%	0.033	91%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	38.8	38.8	100%	0.033	91%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	38.8	38.8	100%	0.033	91%	gi|332257827|XP_003278006.1
☐	Attractin [Fukomys damarensis]	38.8	38.8	100%	0.033	91%	gi|676263950|KFO20529.1
☐	Attractin [Myotis davidii]	38.8	58.1	100%	0.033	91%	gi|432111133|ELK34519.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	38.8	38.8	100%	0.033	91%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	38.8	38.8	100%	0.033	91%	gi|694977854|XP_009435012.1
☐	Attractin [Myotis brandtii]	38.8	58.1	100%	0.033	91%	gi|521031210|EPQ12996.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	38.8	38.8	100%	0.033	91%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	38.8	38.8	100%	0.033	91%	gi|4093196|AAD03057.1
☐							

	secreted attractin precursor [Homo sapiens]	38.8	38.8	100%	0.033	91%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	38.8	38.8	100%	0.033	91%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	38.8	38.8	100%	0.033	91%	gi|21450863|NP_647538.1
☐	Mahogany-like protein [Macaca mulatta]	38.8	38.8	100%	0.033	91%	gi|355563316|EHH19878.1
☐	attractin [Rattus norvegicus]	38.8	38.8	100%	0.033	91%	gi|12275312|BAB21018.1
☐	attractin, isoform CRA_a [Rattus norvegicus]	38.8	38.8	100%	0.033	91%	gi|149023319|EDL80213.1
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	38.8	38.8	100%	0.033	91%	gi|594099680|XP_006072965.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Pan paniscus]	38.8	38.8	100%	0.033	91%	gi|675763672|XP_008973079.1
☐	PREDICTED: attractin isoform X2 [Canis lupus familiaris]	38.8	38.8	100%	0.033	91%	gi|545540090|XP_005634905.1
☐	PREDICTED: attractin isoform X2 [Heterocephalus glaber]	38.8	38.8	100%	0.033	91%	gi|512956910|XP_004840783.1
☐	PREDICTED: attractin isoform X2 [Loxodonta africana]	38.8	38.8	100%	0.033	91%	gi|731487307|XP_010589860.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	38.8	38.8	100%	0.033	91%	gi|694977852|XP_009435011.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	38.8	38.8	100%	0.033	91%	gi|530426019|XP_005260917.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	38.8	38.8	100%	0.033	91%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	38.8	38.8	100%	0.033	91%	gi|635021368|XP_008017720.1
☐	Mahogany-like protein [Macaca fascicularis]	38.8	38.8	100%	0.033	91%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin [Myotis davidii]	38.8	58.1	100%	0.033	91%	gi|584075971|XP_006758187.1
☐	PREDICTED: attractin [Panthera tigris altaica]	38.8	38.8	100%	0.033	91%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin [Myotis brandtii]	38.8	58.1	100%	0.033	91%	gi|554560893|XP_005874816.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	38.8	38.8	100%	0.033	91%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	38.8	38.8	100%	0.033	91%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	38.8	38.8	100%	0.033	91%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Capra hircus]	38.8	38.8	100%	0.033	91%	gi|548490191|XP_005688293.1
☐	Attractin [Heterocephalus glaber]	38.8	38.8	100%	0.033	91%	gi|351701383|EHB04302.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	38.8	38.8	100%	0.033	91%	gi|724902357|XP_010377335.1
☐	PREDICTED: attractin [Camelus ferus]	38.8	38.8	100%	0.033	91%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Sorex araneus]	38.8	38.8	100%	0.033	91%	gi|505831534|XP_004611050.1
☐	PREDICTED: attractin [Myotis lucifugus]	38.8	58.1	100%	0.033	91%	gi|558159591|XP_006096513.1
☐	PREDICTED: attractin [Bos mutus]	38.8	38.8	100%	0.033	91%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Ursus maritimus]	38.8	38.8	100%	0.033	91%	gi|671021680|XP_008701660.1
☐	hypothetical protein PANDA_007354 [Ailuropoda melanoleuca]	38.8	38.8	100%	0.033	91%	gi|281339872|EFB15456.1
☐	PREDICTED: attractin-like [Ailuropoda melanoleuca]	38.8	38.8	100%	0.033	91%	gi|301766802|XP_002918837.1
☐	attractin, isoform CRA_b [Homo sapiens]	38.8	38.8	100%	0.033	91%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	38.8	38.8	100%	0.033	91%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin [Fukomys damarensis]	38.8	38.8	100%	0.033	91%	gi|731281216|XP_010609356.1
☐	PREDICTED: attractin [Heterocephalus glaber]	38.8	38.8	100%	0.033	91%	gi|512849696|XP_004886859.1
☐	PREDICTED: attractin [Ovis aries]	38.8	38.8	100%	0.033	91%	gi|426241795|XP_004014773.1
☐	PREDICTED: attractin [Peromyscus maniculatus bairdii]	38.8	38.8	100%	0.033	91%	gi|589943852|XP_006984624.1
☐	PREDICTED: attractin [Felis catus]	38.8	38.8	100%	0.033	91%	gi|586981105|XP_003983758.2
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	38.8	38.8	100%	0.033	91%	gi|694977850|XP_009435010.1
☐	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	38.8	38.8	100%	0.033	91%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin [Otolemur garnettii]	38.8	38.8	100%	0.033	91%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin [Erinaceus europaeus]	38.8	38.8	100%	0.033	91%	gi|617558695|XP_007539650.1
☐	PREDICTED: attractin [Vicugna pacos]	38.8	38.8	100%	0.033	91%	gi|560970220|XP_006207473.1
☐	PREDICTED: attractin [Echinops telfairi]	38.8	38.8	100%	0.033	91%	gi|507626122|XP_004697922.1

☐	attractin [Bos taurus]	38.8	38.8	100%	0.033	91%	gi|253560524|ACT32973.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	38.8	38.8	100%	0.033	91%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin [Eptesicus fuscus]	38.8	38.8	100%	0.033	91%	gi|641701319|XP_008139256.1
☐	attractin [Bos taurus]	38.8	38.8	100%	0.033	91%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	38.8	38.8	100%	0.033	91%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin isoform X3 [Canis lupus familiaris]	38.8	38.8	100%	0.033	91%	gi|73991942|XP_534360.2
☐	PREDICTED: attractin [Orcinus orca]	38.8	38.8	100%	0.033	91%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin [Lipotes vexillifer]	38.8	38.8	100%	0.033	91%	gi|602710450|XP_007465469.1
☐	PREDICTED: attractin [Odobenus rosmarus divergens]	38.8	38.8	100%	0.033	91%	gi|472357214|XP_004398236.1
☐	PREDICTED: attractin [Chrysochloris asiatica]	38.8	38.8	100%	0.033	91%	gi|586488825|XP_006874887.1
☐	PREDICTED: attractin [Elephantulus edwardii]	38.8	38.8	100%	0.033	91%	gi|585689645|XP_006894264.1
☐	PREDICTED: attractin isoform X1 [Heterocephalus glaber]	38.8	38.8	100%	0.033	91%	gi|512956908|XP_004840782.1
☐	PREDICTED: attractin [Orycteropus afer afer]	38.8	38.8	100%	0.033	91%	gi|634830430|XP_007958185.1
☐	PREDICTED: attractin isoform X3 [Chinchilla lanigera]	38.8	38.8	100%	0.033	91%	gi|533131617|XP_005380852.1
☐	PREDICTED: attractin isoform X1 [Oryctolagus cuniculus]	38.8	38.8	100%	0.033	91%	gi|291388868|XP_002710968.1
☐	PREDICTED: attractin isoform X1 [Ictidomys tridecemlineatus]	38.8	38.8	100%	0.033	91%	gi|532069484|XP_005320577.1
☐	PREDICTED: attractin [Ochotona princeps]	38.8	38.8	100%	0.033	91%	gi|504146589|XP_004585711.1
☐	PREDICTED: attractin isoform X1 [Loxodonta africana]	38.8	38.8	100%	0.033	91%	gi|344279766|XP_003411658.1
☐	attractin [Mesocricetus auratus]	38.8	38.8	100%	0.033	91%	gi|528078159|NP_001268565.1
☐	PREDICTED: attractin isoform X3 [Ictidomys tridecemlineatus]	38.8	38.8	100%	0.033	91%	gi|532069488|XP_005320579.1
☐	PREDICTED: attractin [Callithrix jacchus]	38.8	38.8	100%	0.033	91%	gi|296200062|XP_002747358.1
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	38.8	38.8	100%	0.033	91%	gi|332857715|XP_003316827.1
☐	PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	38.8	38.8	100%	0.033	91%	gi|635021360|XP_008017700.1
☐	PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	38.8	38.8	100%	0.033	91%	gi|635021370|XP_008017729.1
☐	PREDICTED: attractin isoform X2 [Oryctolagus cuniculus]	38.8	38.8	100%	0.033	91%	gi|655716500|XP_008254470.1

Alignments

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attractin [Ovis aries]

Sequence ID: gi|78499351|gb|ABB45710.1| **Length:** 242 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 79 to 89 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
38.8 bits(84)	0.029	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    KCIDQSICEKC  11
            KCI+QSICEKC
Sbjct  79   KCINQSICEKC  89
```

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PREDICTED: attractin-like [Leptonychotes weddellii]

Sequence ID: gi|585182065|ref|XP_006742666.1| **Length:** 290 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 14 to 24 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
38.8 bits(84)	0.030	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    KCIDQSICEKC  11
            KCI+QSICEKC
Sbjct  14   KCINQSICEKC  24
```

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KIAA0548 protein [Homo sapiens]

Sequence ID: gi|3043620|dbj|BAA25474.1| **Length:** 452 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 93 to 103 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
38.8 bits(84)	0.031	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    KCIDQSICEKC  11
            KCI+QSICEKC
Sbjct  93   KCINQSICEKC  103
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

attractin [Bos taurus]

Sequence ID: gi|190683717|gb|ACE82176.1| **Length:** 670 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 311 to 321 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
38.8 bits(84)	0.032	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    KCIDQSICEKC  11
            KCI+QSICEKC
Sbjct  311  KCINQSICEKC  321
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Attractin [Tupaia chinensis]

Sequence ID: gi|444519420|gb|ELV12829.1| **Length:** 860 **Number of Matches:** 1

Related Information

Range 1: 639 to 649 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
38.8 bits(84)	0.033	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    KCIDQSICEKC  11
            KCI+QSICEKC
Sbjct  639  KCINQSICEKC  649
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - B90YB87G01R

Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

ATRN_KCINQSICEKC_NonMod

RID B90YB87G01R (Expires on 01-14 09:32 am)

Query ID	lcl|70916	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	11		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

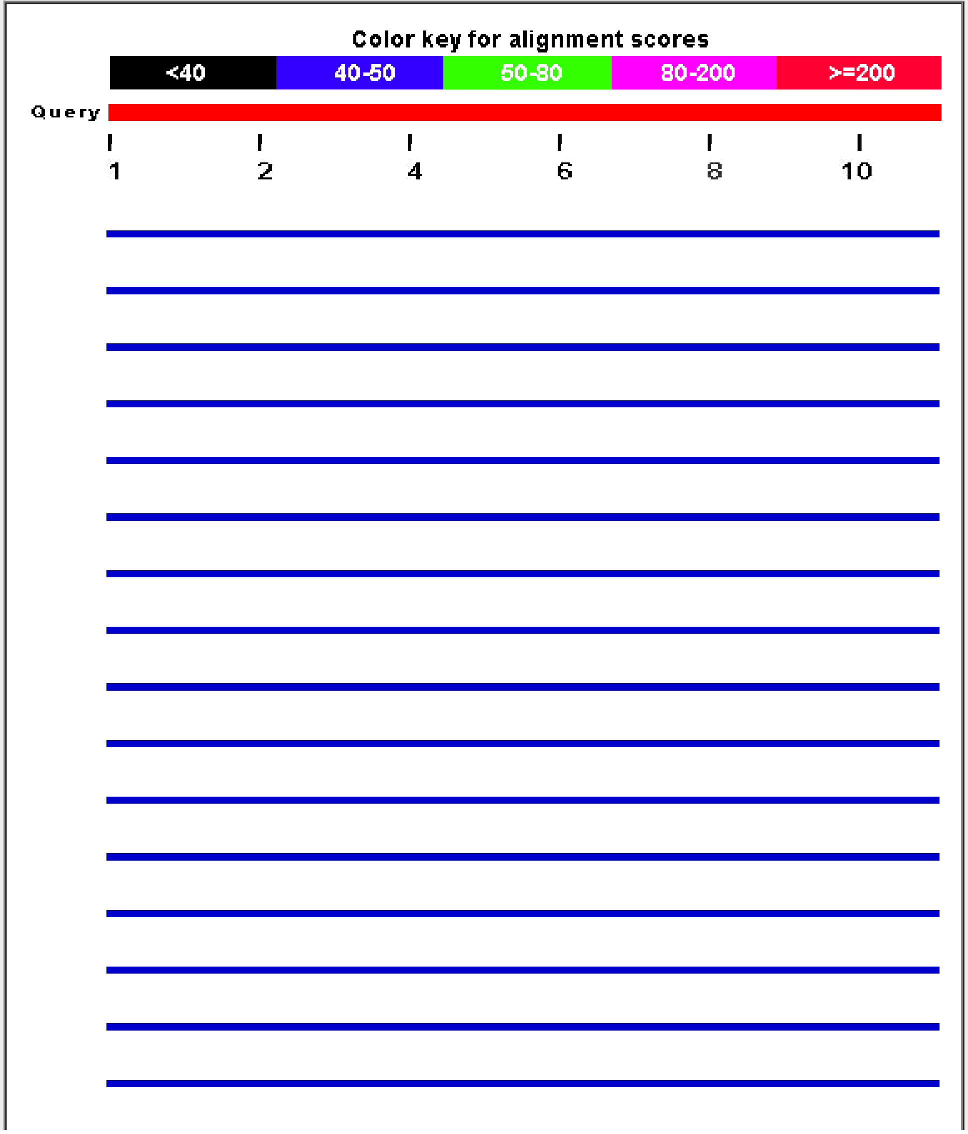
⊟Graphic Summary

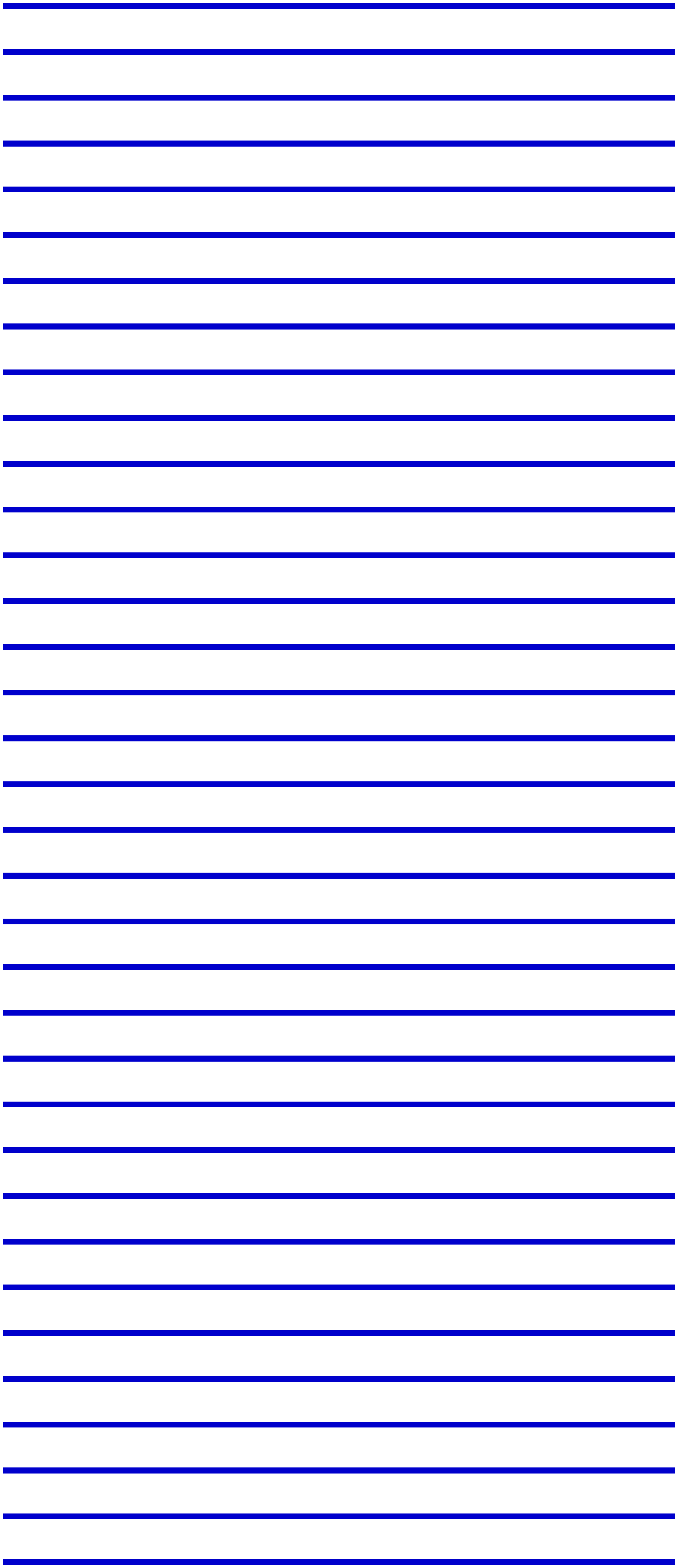
⊟Show Conserved Domains

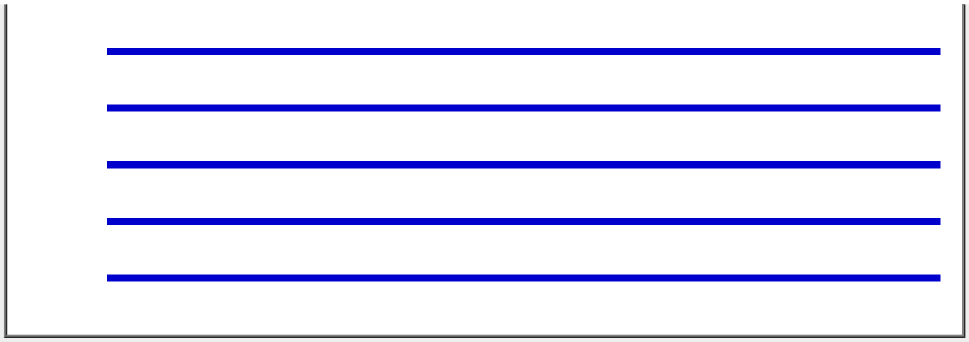
No putative conserved domains have been detected

Distribution of 113 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	attractin [Ovis aries]	41.4	41.4	100%	0.004	100%	gi|78499351|ABB45710.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	41.4	41.4	100%	0.004	100%	gi|585182065|XP_006742666.1
☐	KIAA0548 protein [Homo sapiens]	41.4	41.4	100%	0.004	100%	gi|3043620|BAA25474.1
☐	attractin [Bos taurus]	41.4	41.4	100%	0.004	100%	gi|190683717|ACE82176.1
☐	Attractin [Tupaia chinensis]	41.4	41.4	100%	0.004	100%	gi|444519420|ELV12829.1
☐	PREDICTED: attractin isoform X2 [Papio anubis]	41.4	41.4	100%	0.004	100%	gi|685567345|XP_009214752.1
☐	attractin [Canis lupus familiaris]	41.4	41.4	100%	0.004	100%	gi|339892849|AEK21787.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	41.4	41.4	100%	0.004	100%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin-like [Physeter catodon]	41.4	41.4	100%	0.004	100%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin [Pongo abelii]	41.4	41.4	100%	0.004	100%	gi|297706621|XP_002830129.1
☐	attractin isoform 1 preproprotein [Camelus ferus]	41.4	41.4	100%	0.004	100%	gi|528759526|EPY79185.1
☐	PREDICTED: attractin-like [Ictidomys tridecemlineatus]	41.4	62.8	100%	0.004	100%	gi|532069682|XP_005320676.1
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	41.4	41.4	100%	0.004	100%	gi|530426021|XP_005260918.1
☐	PREDICTED: attractin isoform X1 [Papio anubis]	41.4	41.4	100%	0.004	100%	gi|685567343|XP_009214751.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	41.4	41.4	100%	0.004	100%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	41.4	41.4	100%	0.004	100%	gi|725600051|XP_010350111.1
☐	PREDICTED: attractin [Nannospalax galili]	41.4	41.4	100%	0.004	100%	gi|674060132|XP_008836714.1
☐	PREDICTED: attractin [Tarsius syrichta]	41.4	41.4	100%	0.004	100%	gi|640796924|XP_008054571.1
☐	unnamed protein product [Homo sapiens]	41.4	41.4	100%	0.004	100%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	41.4	41.4	100%	0.004	100%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	41.4	41.4	100%	0.004	100%	gi|332257827|XP_003278006.1
☐	Attractin [Fukomys damarensis]	41.4	41.4	100%	0.004	100%	gi|676263950|KFO20529.1
☐	Attractin [Myotis davidii]	41.4	63.2	100%	0.004	100%	gi|432111133|ELK34519.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	41.4	41.4	100%	0.004	100%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	41.4	41.4	100%	0.004	100%	gi|694977854|XP_009435012.1
☐	Attractin [Myotis brandtii]	41.4	63.2	100%	0.004	100%	gi|521031210|EPQ12996.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	41.4	41.4	100%	0.004	100%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	41.4	41.4	100%	0.004	100%	gi|4093196|AAD03057.1
☐							

	secreted attractin precursor [Homo sapiens]	41.4	41.4	100%	0.004	100%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	41.4	41.4	100%	0.004	100%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	41.4	41.4	100%	0.004	100%	gi|21450863|NP_647538.1
☐	Mahogany-like protein [Macaca mulatta]	41.4	41.4	100%	0.004	100%	gi|355563316|EHH19878.1
☐	attractin [Rattus norvegicus]	41.4	41.4	100%	0.004	100%	gi|12275312|BAB21018.1
☐	attractin, isoform CRA_a [Rattus norvegicus]	41.4	41.4	100%	0.004	100%	gi|149023319|EDL80213.1
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	41.4	41.4	100%	0.004	100%	gi|594099680|XP_006072965.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Pan paniscus]	41.4	41.4	100%	0.004	100%	gi|675763672|XP_008973079.1
☐	PREDICTED: attractin isoform X2 [Canis lupus familiaris]	41.4	41.4	100%	0.004	100%	gi|545540090|XP_005634905.1
☐	PREDICTED: attractin isoform X2 [Heterocephalus glaber]	41.4	62.8	100%	0.004	100%	gi|512956910|XP_004840783.1
☐	PREDICTED: attractin isoform X2 [Loxodonta africana]	41.4	41.4	100%	0.004	100%	gi|731487307|XP_010589860.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	41.4	41.4	100%	0.004	100%	gi|694977852|XP_009435011.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	41.4	41.4	100%	0.004	100%	gi|530426019|XP_005260917.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	41.4	41.4	100%	0.004	100%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	41.4	41.4	100%	0.004	100%	gi|635021368|XP_008017720.1
☐	Mahogany-like protein [Macaca fascicularis]	41.4	41.4	100%	0.004	100%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin [Myotis davidii]	41.4	63.2	100%	0.004	100%	gi|584075971|XP_006758187.1
☐	PREDICTED: attractin [Panthera tigris altaica]	41.4	41.4	100%	0.004	100%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin [Myotis brandtii]	41.4	63.2	100%	0.004	100%	gi|554560893|XP_005874816.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	41.4	41.4	100%	0.004	100%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	41.4	41.4	100%	0.004	100%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	41.4	41.4	100%	0.004	100%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Capra hircus]	41.4	41.4	100%	0.004	100%	gi|548490191|XP_005688293.1
☐	Attractin [Heterocephalus glaber]	41.4	62.8	100%	0.004	100%	gi|351701383|EHB04302.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	41.4	41.4	100%	0.004	100%	gi|724902357|XP_010377335.1
☐	PREDICTED: attractin [Camelus ferus]	41.4	41.4	100%	0.004	100%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Sorex araneus]	41.4	41.4	100%	0.004	100%	gi|505831534|XP_004611050.1
☐	PREDICTED: attractin [Myotis lucifugus]	41.4	63.2	100%	0.004	100%	gi|558159591|XP_006096513.1
☐	PREDICTED: attractin [Bos mutus]	41.4	41.4	100%	0.004	100%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Ursus maritimus]	41.4	41.4	100%	0.004	100%	gi|671021680|XP_008701660.1
☐	hypothetical protein PANDA_007354 [Ailuropoda melanoleuca]	41.4	41.4	100%	0.004	100%	gi|281339872|EFB15456.1
☐	PREDICTED: attractin-like [Ailuropoda melanoleuca]	41.4	41.4	100%	0.004	100%	gi|301766802|XP_002918837.1
☐	attractin, isoform CRA_b [Homo sapiens]	41.4	41.4	100%	0.004	100%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	41.4	41.4	100%	0.004	100%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin [Fukomys damarensis]	41.4	41.4	100%	0.004	100%	gi|731281216|XP_010609356.1
☐	PREDICTED: attractin [Heterocephalus glaber]	41.4	62.8	100%	0.004	100%	gi|512849696|XP_004886859.1
☐	PREDICTED: attractin [Ovis aries]	41.4	41.4	100%	0.004	100%	gi|426241795|XP_004014773.1
☐	PREDICTED: attractin [Peromyscus maniculatus bairdii]	41.4	41.4	100%	0.004	100%	gi|589943852|XP_006984624.1
☐	PREDICTED: attractin [Felis catus]	41.4	41.4	100%	0.004	100%	gi|586981105|XP_003983758.2
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	41.4	41.4	100%	0.004	100%	gi|694977850|XP_009435010.1
☐	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	41.4	41.4	100%	0.004	100%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin [Otolemur garnettii]	41.4	41.4	100%	0.004	100%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin [Erinaceus europaeus]	41.4	41.4	100%	0.004	100%	gi|617558695|XP_007539650.1
☐	PREDICTED: attractin [Vicugna pacos]	41.4	41.4	100%	0.004	100%	gi|560970220|XP_006207473.1
☐	attractin [Bos taurus]	41.4	41.4	100%	0.004	100%	gi|253560524|ACT32973.1

☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	41.4	41.4	100%	0.004	100%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin [Eptesicus fuscus]	41.4	41.4	100%	0.004	100%	gi|641701319|XP_008139256.1
☐	attractin [Bos taurus]	41.4	41.4	100%	0.004	100%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	41.4	41.4	100%	0.004	100%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin isoform X3 [Canis lupus familiaris]	41.4	41.4	100%	0.004	100%	gi|73991942|XP_534360.2
☐	PREDICTED: attractin [Orcinus orca]	41.4	41.4	100%	0.004	100%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin [Lipotes vexillifer]	41.4	41.4	100%	0.004	100%	gi|602710450|XP_007465469.1
☐	PREDICTED: attractin [Odobenus rosmarus divergens]	41.4	41.4	100%	0.004	100%	gi|472357214|XP_004398236.1
☐	PREDICTED: attractin [Chrysochloris asiatica]	41.4	41.4	100%	0.004	100%	gi|586488825|XP_006874887.1
☐	PREDICTED: attractin [Elephantulus edwardii]	41.4	41.4	100%	0.004	100%	gi|585689645|XP_006894264.1
☐	PREDICTED: attractin isoform X1 [Heterocephalus glaber]	41.4	62.8	100%	0.004	100%	gi|512956908|XP_004840782.1
☐	PREDICTED: attractin [Orycteropus afer afer]	41.4	41.4	100%	0.004	100%	gi|634830430|XP_007958185.1
☐	PREDICTED: attractin isoform X3 [Chinchilla lanigera]	41.4	41.4	100%	0.004	100%	gi|533131617|XP_005380852.1
☐	PREDICTED: attractin isoform X1 [Oryctolagus cuniculus]	41.4	41.4	100%	0.004	100%	gi|291388868|XP_002710968.1
☐	PREDICTED: attractin isoform X1 [Ictidomys tridecemlineatus]	41.4	62.8	100%	0.004	100%	gi|532069484|XP_005320577.1
☐	PREDICTED: attractin [Ochotona princeps]	41.4	41.4	100%	0.004	100%	gi|504146589|XP_004585711.1
☐	PREDICTED: attractin isoform X1 [Loxodonta africana]	41.4	41.4	100%	0.004	100%	gi|344279766|XP_003411658.1
☐	attractin [Mesocricetus auratus]	41.4	41.4	100%	0.004	100%	gi|528078159|NP_001268565.1
☐	PREDICTED: attractin isoform X3 [Ictidomys tridecemlineatus]	41.4	62.8	100%	0.004	100%	gi|532069488|XP_005320579.1
☐	PREDICTED: attractin [Callithrix jacchus]	41.4	41.4	100%	0.004	100%	gi|296200062|XP_002747358.1
☐	attractin precursor [Mus musculus]	41.4	41.4	100%	0.004	100%	gi|87299635|NP_033860.2
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	41.4	41.4	100%	0.004	100%	gi|332857715|XP_003316827.1
☐	membrane attractin precursor [Homo sapiens]	41.4	41.4	100%	0.004	100%	gi|8118082|AAF72881.1
☐	attractin isoform 1 preproprotein [Homo sapiens]	41.4	41.4	100%	0.004	100%	gi|21450861|NP_647537.1
☐	PREDICTED: attractin isoform X2 [Ictidomys tridecemlineatus]	41.4	62.8	100%	0.004	100%	gi|532069486|XP_005320578.1
☐	PREDICTED: attractin [Jaculus jaculus]	41.4	41.4	100%	0.004	100%	gi|507555530|XP_004661535.1
☐	PREDICTED: attractin isoform X2 [Macaca fascicularis]	41.4	41.4	100%	0.004	100%	gi|544464512|XP_005568510.1

⊟ Alignments

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

attractin [Ovis aries]

Sequence ID: gi|78499351|gb|ABB45710.1| **Length:** 242 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 79 to 89 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.4 bits(90)	0.004	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    KCINQSICEKC  11
            KCINQSICEKC
Sbjct  79   KCINQSICEKC  89
```

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PREDICTED: attractin-like [Leptonychotes weddellii]

Sequence ID: gi|585182065|ref|XP_006742666.1| **Length:** 290 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 14 to 24 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.4 bits(90)	0.004	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    KCINQSICEKC  11
```

```
             KCINQSICEKC
Sbjct  14  KCINQSICEKC  24
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

KIAA0548 protein [Homo sapiens]

Sequence ID: gi|3043620|dbj|BAA25474.1| **Length:** 452 **Number of Matches:** 1

Range 1: 93 to 103 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.4 bits(90)	0.004	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    KCINQSICEKC  11
            KCINQSICEKC
Sbjct  93   KCINQSICEKC  103
```

Related Information

Gene - associated gene details

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

attractin [Bos taurus]

Sequence ID: gi|190683717|gb|ACE82176.1| **Length:** 670 **Number of Matches:** 1

Range 1: 311 to 321 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.4 bits(90)	0.004	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    KCINQSICEKC  11
            KCINQSICEKC
Sbjct  311  KCINQSICEKC  321
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Attractin [Tupaia chinensis]

Sequence ID: gi|444519420|gb|ELV12829.1| **Length:** 860 **Number of Matches:** 1

Range 1: 639 to 649 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.4 bits(90)	0.004	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    KCINQSICEKC  11
            KCINQSICEKC
Sbjct  639  KCINQSICEKC  649
```

Related Information

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - BHBVBBRG014

Edit and Resubmit | Save Search Strategies | Formatting options | Download

ATRN_KGPVKMPSQAPTGNFYPQPLLDSSMCLEDSRY_Mod

How to read this page | Blast report description

RID BHBVBBRG014 (Expires on 01-17 13:27 pm)

Query ID lcl|90002
Description None
Molecule type amino acid
Query Length 32

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

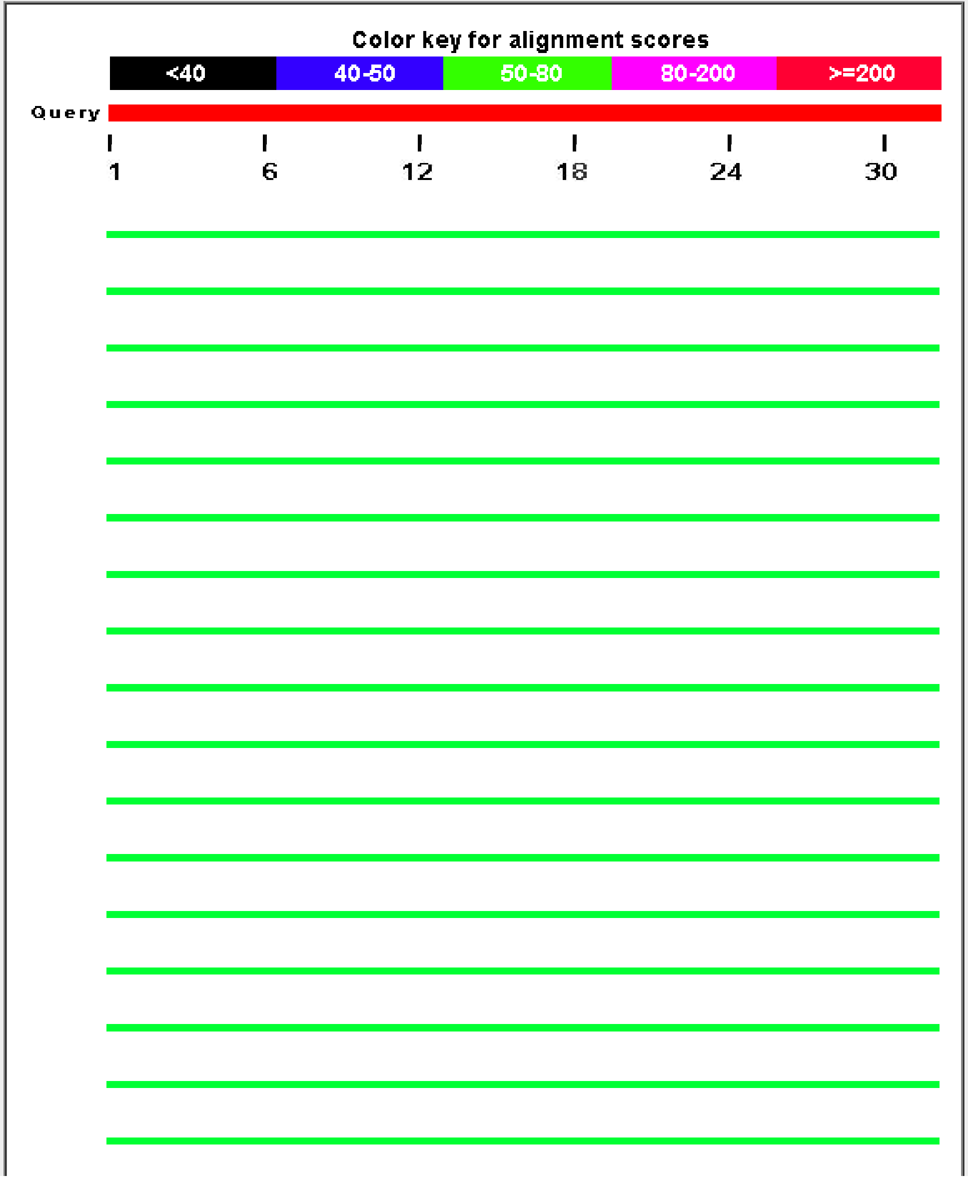
Graphic Summary

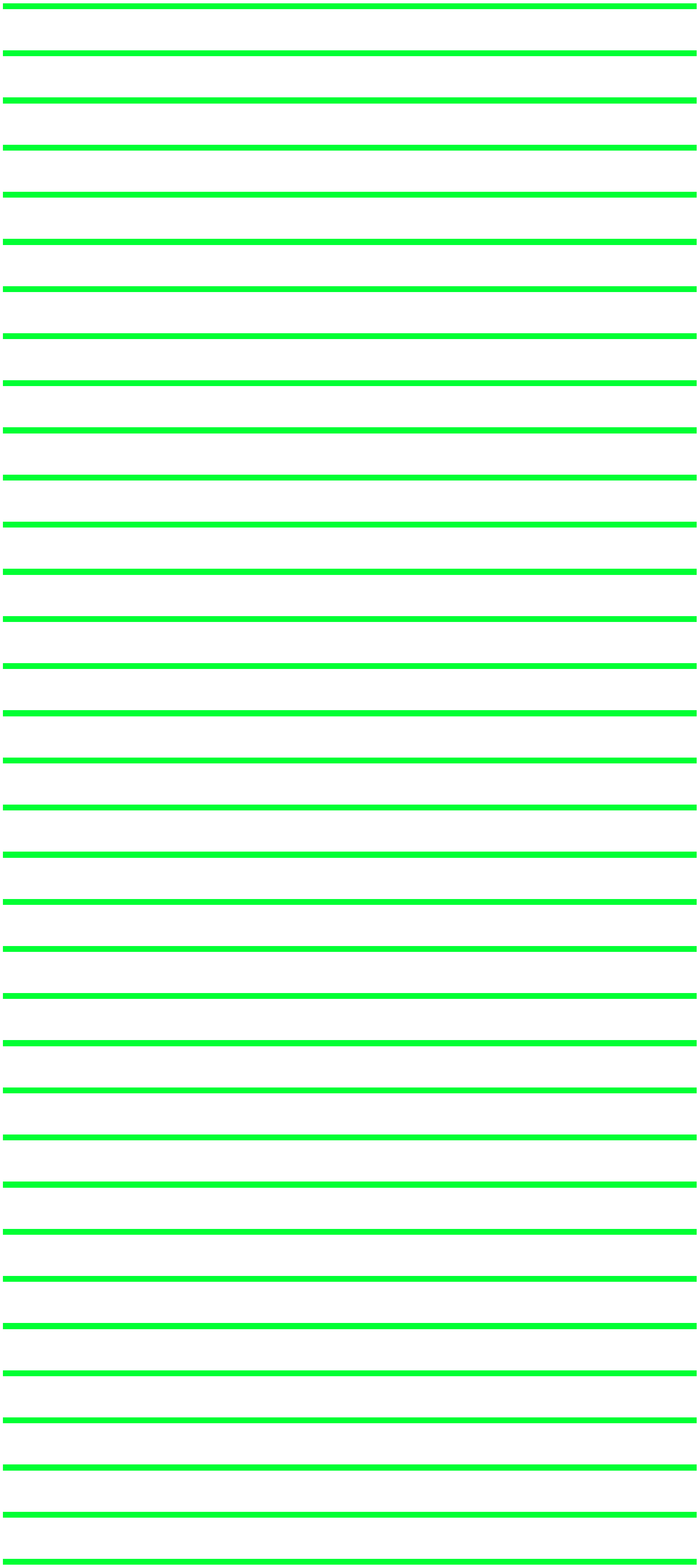
Show Conserved Domains

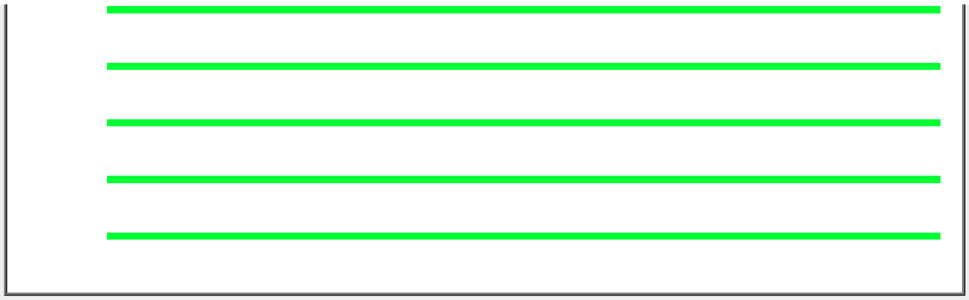
No putative conserved domains have been detected

Distribution of 98 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: attractin-like [Pan paniscus]	70.1	70.1	100%	2e-13	97%	gi|397513332|XP_003826972.1
☐	KIAA0548 protein [Homo sapiens]	70.1	70.1	100%	7e-13	97%	gi|3043620|BAA25474.1
☐	PREDICTED: attractin isoform X2 [Papio anubis]	70.1	70.1	100%	1e-12	97%	gi|685567345|XP_009214752.1
☐	PREDICTED: attractin [Pongo abelii]	70.1	70.1	100%	2e-12	97%	gi|297706621|XP_002830129.1
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	70.1	70.1	100%	2e-12	97%	gi|530426021|XP_005260918.1
☐	PREDICTED: attractin isoform X1 [Papio anubis]	70.1	70.1	100%	2e-12	97%	gi|685567343|XP_009214751.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	67.0	67.0	100%	2e-12	94%	gi|667345974|XP_008563464.1
☐	unnamed protein product [Homo sapiens]	70.1	70.1	100%	2e-12	97%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	70.1	70.1	100%	2e-12	97%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	70.1	70.1	100%	2e-12	97%	gi|332257827|XP_003278006.1
☐	PREDICTED: attractin [Gorilla gorilla gorilla]	70.1	70.1	100%	2e-12	97%	gi|426390844|XP_004061806.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	70.1	70.1	100%	2e-12	97%	gi|694977854|XP_009435012.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	70.1	70.1	100%	2e-12	97%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	70.1	70.1	100%	2e-12	97%	gi|4093196|AAD03057.1
☐	secreted attractin precursor [Homo sapiens]	70.1	70.1	100%	2e-12	97%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	70.1	70.1	100%	2e-12	97%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	70.1	70.1	100%	2e-12	97%	gi|21450863|NP_647538.1
☐	Mahogany-like protein [Macaca mulatta]	70.1	70.1	100%	2e-12	97%	gi|355563316|EHH19878.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	70.1	70.1	100%	2e-12	97%	gi|694977852|XP_009435011.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	70.1	70.1	100%	2e-12	97%	gi|530426019|XP_005260917.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	70.1	70.1	100%	2e-12	97%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	70.1	70.1	100%	2e-12	97%	gi|635021368|XP_008017720.1
☐	Mahogany-like protein [Macaca fascicularis]	70.1	70.1	100%	2e-12	97%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	70.1	70.1	100%	2e-12	97%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	70.1	70.1	100%	2e-12	97%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	70.1	70.1	100%	2e-12	97%	gi|724902357|XP_010377335.1
☐	attractin, isoform CRA_b [Homo sapiens]	70.1	70.1	100%	2e-12	97%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	70.1	70.1	100%	2e-12	97%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	70.1	70.1	100%	2e-12	97%	gi|694977850|XP_009435010.1
☐							

	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	70.1	70.1	100%	2e-12	97%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin [Otolemur garnettii]	70.1	70.1	100%	2e-12	97%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	70.1	70.1	100%	2e-12	97%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin [Ochotona princeps]	70.1	70.1	100%	2e-12	97%	gi|504146589|XP_004585711.1
☐	PREDICTED: attractin [Callithrix jacchus]	70.1	70.1	100%	2e-12	97%	gi|296200062|XP_002747358.1
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	70.1	70.1	100%	2e-12	97%	gi|332857715|XP_003316827.1
☐	membrane attractin precursor [Homo sapiens]	70.1	70.1	100%	2e-12	97%	gi|8118082|AAF72881.1
☐	attractin isoform 1 preproprotein [Homo sapiens]	70.1	70.1	100%	2e-12	97%	gi|21450861|NP_647537.1
☐	PREDICTED: attractin isoform X2 [Macaca fascicularis]	70.1	70.1	100%	2e-12	97%	gi|544464512|XP_005568510.1
☐	PREDICTED: attractin [Macaca mulatta]	70.1	70.1	100%	2e-12	97%	gi|109092720|XP_001115192.1
☐	PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	70.1	70.1	100%	2e-12	97%	gi|635021360|XP_008017700.1
☐	PREDICTED: attractin isoform X1 [Macaca fascicularis]	70.1	70.1	100%	2e-12	97%	gi|544464510|XP_005568509.1
☐	PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	70.1	70.1	100%	2e-12	97%	gi|635021370|XP_008017729.1
☐	PREDICTED: attractin isoform X2 [Pteropus alecto]	70.1	70.1	100%	2e-12	97%	gi|586533634|XP_006921706.1
☐	PREDICTED: attractin [Lipotes vexillifer]	68.9	68.9	100%	4e-12	94%	gi|602710450|XP_007465469.1
☐	attractin [Ovis aries]	65.5	65.5	100%	6e-12	91%	gi|78499351|ABB45710.1
☐	Attractin [Myotis davidii]	68.2	68.2	100%	7e-12	94%	gi|432111133|ELK34519.1
☐	PREDICTED: attractin [Myotis davidii]	68.2	68.2	100%	8e-12	94%	gi|584075971|XP_006758187.1
☐	PREDICTED: attractin [Tarsius syrichta]	67.8	67.8	100%	1e-11	94%	gi|640796924|XP_008054571.1
☐	Attractin [Myotis brandtii]	67.8	67.8	100%	1e-11	94%	gi|521031210|EPQ12996.1
☐	PREDICTED: attractin [Myotis brandtii]	67.8	67.8	100%	1e-11	94%	gi|554560893|XP_005874816.1
☐	PREDICTED: attractin [Myotis lucifugus]	67.8	67.8	100%	1e-11	94%	gi|558159591|XP_006096513.1
☐	PREDICTED: attractin [Eptesicus fuscus]	67.8	67.8	100%	1e-11	94%	gi|641701319|XP_008139256.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	67.0	67.0	100%	2e-11	94%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin-like [Physeter catodon]	67.0	67.0	100%	2e-11	94%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin [Equus przewalskii]	67.0	67.0	100%	2e-11	94%	gi|664773944|XP_008506219.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	67.0	67.0	100%	2e-11	94%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	67.0	67.0	100%	2e-11	94%	gi|725600051|XP_010350111.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	67.0	67.0	100%	2e-11	94%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin [Orcinus orca]	67.0	67.0	100%	2e-11	94%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin [Orycteropus afer afer]	67.0	67.0	100%	2e-11	94%	gi|634830430|XP_007958185.1
☐	attractin [Bos taurus]	65.5	65.5	100%	5e-11	91%	gi|190683717|ACE82176.1
☐	PREDICTED: attractin [Jaculus jaculus]	65.9	65.9	100%	5e-11	91%	gi|507555530|XP_004661535.1
☐	PREDICTED: attractin isoform X1 [Bos taurus]	65.5	65.5	100%	6e-11	91%	gi|741947708|XP_005214542.2
☐	PREDICTED: attractin [Capra hircus]	65.5	65.5	100%	6e-11	91%	gi|548490191|XP_005688293.1
☐	PREDICTED: attractin [Bos mutus]	65.5	65.5	100%	6e-11	91%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Ovis aries]	65.5	65.5	100%	7e-11	91%	gi|426241795|XP_004014773.1
☐	attractin [Bos taurus]	65.5	65.5	100%	7e-11	91%	gi|253560524|ACT32973.1
☐	attractin [Bos taurus]	65.5	65.5	100%	7e-11	91%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin [Bison bison bison]	65.5	65.5	100%	7e-11	91%	gi|742104093|XP_010834932.1
☐	attractin [Canis lupus familiaris]	65.1	65.1	100%	8e-11	91%	gi|339892849|AEK21787.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	65.1	65.1	100%	8e-11	91%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin isoform X2 [Canis lupus familiaris]	65.1	65.1	100%	9e-11	91%	gi|545540090|XP_005634905.1
☐	PREDICTED: attractin [Panthera tigris altaica]	65.1	65.1	100%	9e-11	91%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin [Felis catus]	65.1	65.1	100%	9e-11	91%	gi|586981105|XP_003983758.2

☐	PREDICTED: attractin isoform X3 [Canis lupus familiaris]	65.1	65.1	100%	9e-11	91%	gi|73991942|XP_534360.2
☐	PREDICTED: attractin [Tupaia chinensis]	65.1	65.1	100%	9e-11	91%	gi|562872246|XP_006164056.1
☐	PREDICTED: attractin isoform X1 [Canis lupus familiaris]	65.1	65.1	100%	9e-11	91%	gi|545540087|XP_005634904.1
☐	PREDICTED: attractin isoform X1 [Oryctolagus cuniculus]	64.7	64.7	100%	1e-10	91%	gi|291388868|XP_002710968.1
☐	PREDICTED: attractin isoform X2 [Oryctolagus cuniculus]	64.7	64.7	100%	1e-10	91%	gi|655716500|XP_008254470.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	63.9	63.9	100%	2e-10	88%	gi|585160208|XP_006732353.1
☐	attractin isoform 1 preproprotein [Camelus ferus]	63.9	63.9	100%	2e-10	91%	gi|528759526|EPY79185.1
☐	PREDICTED: attractin isoform X2 [Mustela putorius furo]	63.9	63.9	100%	2e-10	88%	gi|511906947|XP_004772933.1
☐	PREDICTED: attractin [Camelus ferus]	63.9	63.9	100%	2e-10	91%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Camelus dromedarius]	63.9	63.9	100%	2e-10	91%	gi|744589171|XP_010986570.1
☐	PREDICTED: attractin [Camelus bactrianus]	63.9	63.9	100%	2e-10	91%	gi|743752427|XP_010971103.1
☐	PREDICTED: attractin [Mustela putorius furo]	63.9	63.9	100%	2e-10	88%	gi|511947743|XP_004792355.1
☐	PREDICTED: attractin [Vicugna pacos]	63.9	63.9	100%	2e-10	91%	gi|560970220|XP_006207473.1
☐	PREDICTED: attractin [Odobenus rosmarus divergens]	63.9	63.9	100%	2e-10	88%	gi|472357214|XP_004398236.1
☐	PREDICTED: attractin isoform X1 [Mustela putorius furo]	63.9	63.9	100%	2e-10	88%	gi|511906945|XP_004772932.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	63.5	63.5	100%	3e-10	88%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin [Sus scrofa]	63.5	63.5	100%	3e-10	88%	gi|545879723|XP_001927324.5
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	63.5	63.5	100%	3e-10	88%	gi|594099680|XP_006072965.1
☐	attractin [Sus scrofa]	63.5	63.5	100%	3e-10	88%	gi|146741346|BAF62328.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	63.5	63.5	100%	3e-10	88%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin isoform X1 [Bubalus bubalis]	63.5	63.5	100%	3e-10	88%	gi|594099676|XP_006072963.1
☐	PREDICTED: attractin isoform 2 [Ceratotherium simum simum]	63.2	63.2	100%	4e-10	91%	gi|478519276|XP_004433860.1
☐	PREDICTED: attractin isoform 1 [Ceratotherium simum simum]	63.2	63.2	100%	4e-10	91%	gi|478519274|XP_004433859.1
☐	PREDICTED: attractin [Chrysochloris asiatica]	63.2	63.2	100%	4e-10	88%	gi|586488825|XP_006874887.1

⊖ Alignments

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PREDICTED: attractin-like [Pan paniscus]

Sequence ID: gi|397513332|ref|XP_003826972.1| **Length:** 265 **Number of Matches:** 1

Range 1: 210 to 241 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.1 bits(170)	2e-13	31/32(97%)	32/32(100%)	0/32(0%)

```
Query  1    KGPVKMPSQAPTGNFYPQPLLDSSMCLEDSRY  32
            KGPVKMPSQAPTGNFYPQPLL+SSMCLEDSRY
Sbjct  210  KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY  241
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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KIAA0548 protein [Homo sapiens]

Sequence ID: gi|3043620|dbj|BAA25474.1| **Length:** 452 **Number of Matches:** 1

Range 1: 45 to 76 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.1 bits(170)	7e-13	31/32(97%)	32/32(100%)	0/32(0%)

```
Query  1   KGPVKMPSQAPTGNFYPQPLLDSSMCLEDSRY  32
           KGPVKMPSQAPTGNFYPQPLL+SSMCLEDSRY
Sbjct  45  KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY  76
```

Related Information

Gene - associated gene details

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PREDICTED: attractin isoform X2 [Papio anubis]

Sequence ID: gi|685567345|ref|XP_009214752.1| **Length:** 989 **Number of Matches:** 1

Range 1: 712 to 743 GenPept Graphics

Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
70.1 bits(170)	1e-12	31/32(97%)	32/32(100%)	0/32(0%)

```
Query  1    KGPVKMPSQAPTGNFYPQPLLDSSMCLEDSRY  32
            KGPVKMPSQAPTGNFYPQPLL+SSMCLEDSRY
Sbjct  712  KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY  743
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: attractin, partial [Pongo abelii]

Sequence ID: gi|297706621|ref|XP_002830129.1| **Length:** 1058 **Number of Matches:** 1

Range 1: 651 to 682 GenPept Graphics

Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
70.1 bits(170)	2e-12	31/32(97%)	32/32(100%)	0/32(0%)

```
Query  1    KGPVKMPSQAPTGNFYPQPLLDSSMCLEDSRY  32
            KGPVKMPSQAPTGNFYPQPLL+SSMCLEDSRY
Sbjct  651  KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY  682
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: attractin isoform X2 [Homo sapiens]

Sequence ID: gi|530426021|ref|XP_005260918.1| **Length:** 1111 **Number of Matches:** 1

Range 1: 1022 to 1053 GenPept Graphics

Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
70.1 bits(170)	2e-12	31/32(97%)	32/32(100%)	0/32(0%)

```
Query  1     KGPVKMPSQAPTGNFYPQPLLDSSMCLEDSRY  32
             KGPVKMPSQAPTGNFYPQPLL+SSMCLEDSRY
Sbjct  1022  KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY  1053
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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NCBI/ BLAST/ blastp suite/ **Formatting Results - B90YVEXC01R**

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How to read this page Blast report description

ATRN_KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY_NonMod

RID B90YVEXC01R (Expires on 01-14 09:32 am)

Query ID	lcl|78725	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	32		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

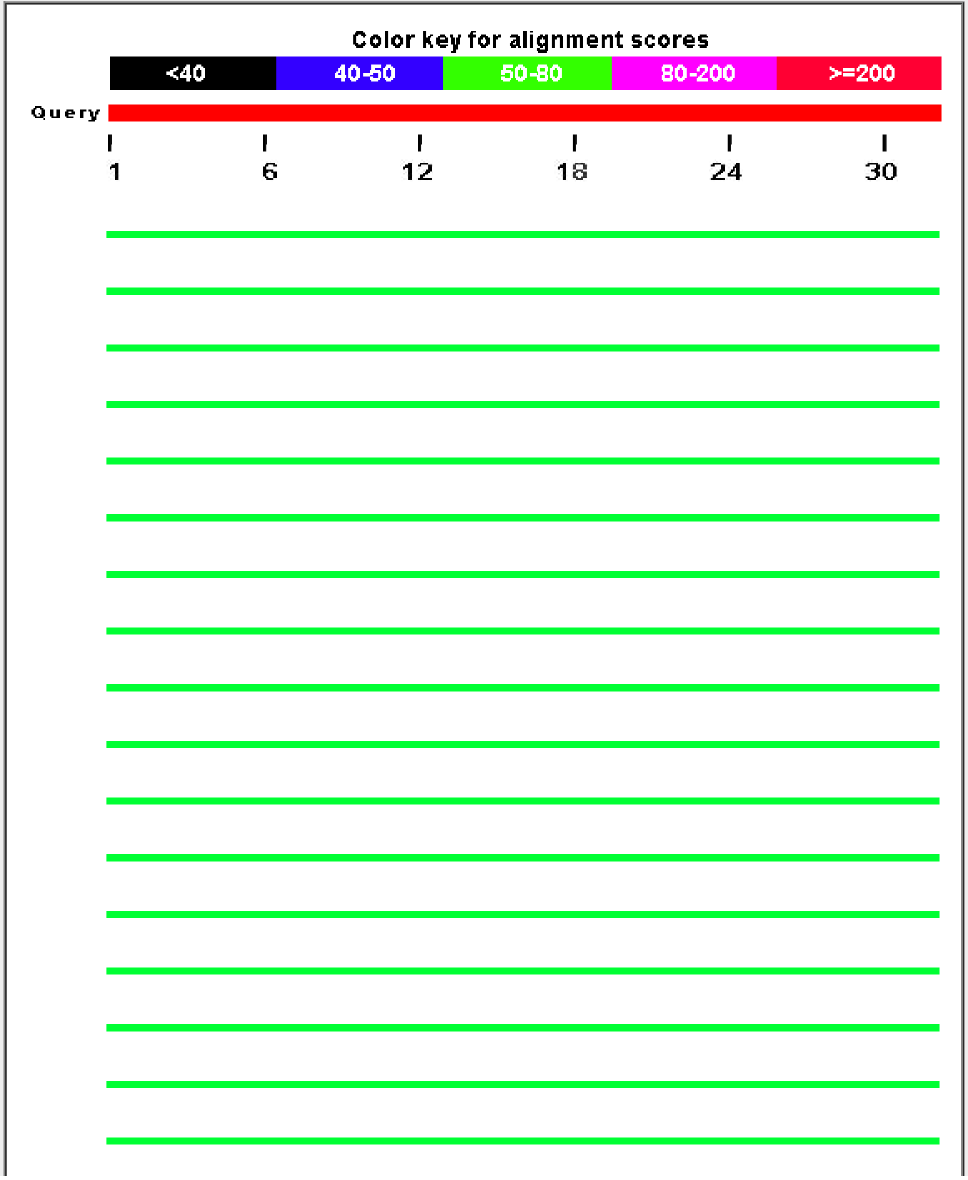
Graphic Summary

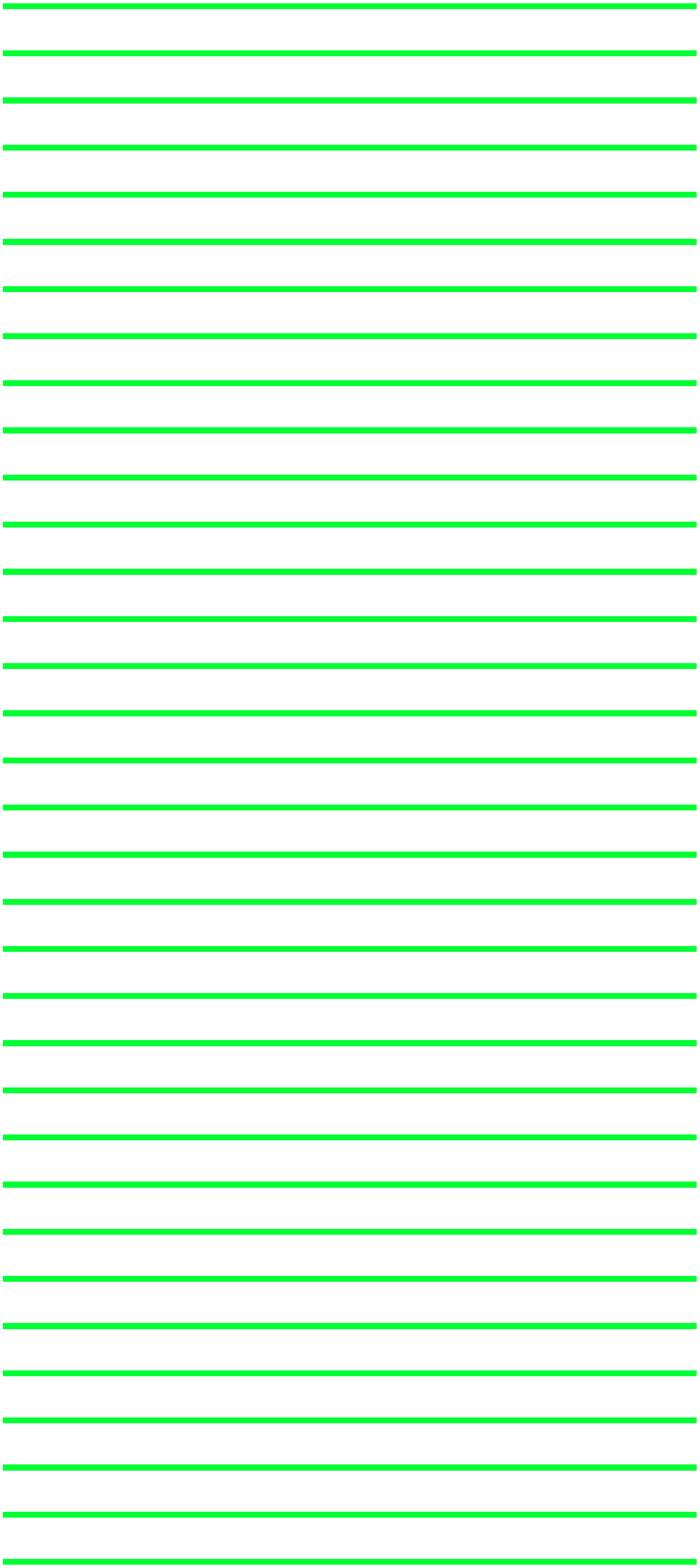
Show Conserved Domains

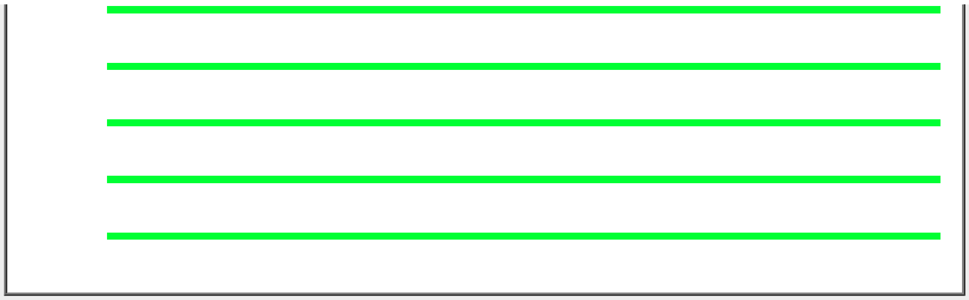
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: attractin-like [Pan paniscus]	72.0	72.0	100%	3e-14	100%	gi|397513332|XP_003826972.1
☐	KIAA0548 protein [Homo sapiens]	72.0	72.0	100%	1e-13	100%	gi|3043620|BAA25474.1
☐	PREDICTED: attractin isoform X2 [Papio anubis]	72.0	72.0	100%	3e-13	100%	gi|685567345|XP_009214752.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	68.9	68.9	100%	3e-13	97%	gi|667345974|XP_008563464.1
☐	PREDICTED: attractin [Pongo abelii]	72.0	72.0	100%	3e-13	100%	gi|297706621|XP_002830129.1
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	72.0	72.0	100%	3e-13	100%	gi|530426021|XP_005260918.1
☐	PREDICTED: attractin isoform X1 [Papio anubis]	72.0	72.0	100%	3e-13	100%	gi|685567343|XP_009214751.1
☐	unnamed protein product [Homo sapiens]	72.0	72.0	100%	3e-13	100%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	72.0	72.0	100%	3e-13	100%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	72.0	72.0	100%	3e-13	100%	gi|332257827|XP_003278006.1
☐	PREDICTED: attractin [Gorilla gorilla gorilla]	72.0	72.0	100%	3e-13	100%	gi|426390844|XP_004061806.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	72.0	72.0	100%	3e-13	100%	gi|694977854|XP_009435012.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	72.0	72.0	100%	3e-13	100%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	72.0	72.0	100%	3e-13	100%	gi|4093196|AAD03057.1
☐	secreted attractin precursor [Homo sapiens]	72.0	72.0	100%	3e-13	100%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	72.0	72.0	100%	3e-13	100%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	72.0	72.0	100%	3e-13	100%	gi|21450863|NP_647538.1
☐	Mahogany-like protein [Macaca mulatta]	72.0	72.0	100%	3e-13	100%	gi|355563316|EHH19878.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	72.0	72.0	100%	3e-13	100%	gi|694977852|XP_009435011.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	72.0	72.0	100%	3e-13	100%	gi|530426019|XP_005260917.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	72.0	72.0	100%	3e-13	100%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	72.0	72.0	100%	3e-13	100%	gi|635021368|XP_008017720.1
☐	Mahogany-like protein [Macaca fascicularis]	72.0	72.0	100%	3e-13	100%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	72.0	72.0	100%	3e-13	100%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	72.0	72.0	100%	3e-13	100%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	72.0	72.0	100%	3e-13	100%	gi|724902357|XP_010377335.1
☐	attractin, isoform CRA_b [Homo sapiens]	72.0	72.0	100%	3e-13	100%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	72.0	72.0	100%	3e-13	100%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	72.0	72.0	100%	3e-13	100%	gi|694977850|XP_009435010.1
☐							

	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	72.0	72.0	100%	3e-13	100%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin [Otolemur garnettii]	72.0	72.0	100%	3e-13	100%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	72.0	72.0	100%	3e-13	100%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin [Ochotona princeps]	72.0	72.0	100%	3e-13	100%	gi|504146589|XP_004585711.1
☐	PREDICTED: attractin [Callithrix jacchus]	72.0	72.0	100%	3e-13	100%	gi|296200062|XP_002747358.1
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	72.0	72.0	100%	3e-13	100%	gi|332857715|XP_003316827.1
☐	membrane attractin precursor [Homo sapiens]	72.0	72.0	100%	3e-13	100%	gi|8118082|AAF72881.1
☐	attractin isoform 1 preproprotein [Homo sapiens]	72.0	72.0	100%	3e-13	100%	gi|21450861|NP_647537.1
☐	PREDICTED: attractin isoform X2 [Macaca fascicularis]	72.0	72.0	100%	3e-13	100%	gi|544464512|XP_005568510.1
☐	PREDICTED: attractin [Macaca mulatta]	72.0	72.0	100%	3e-13	100%	gi|109092720|XP_001115192.1
☐	PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	72.0	72.0	100%	3e-13	100%	gi|635021360|XP_008017700.1
☐	PREDICTED: attractin isoform X1 [Macaca fascicularis]	72.0	72.0	100%	3e-13	100%	gi|544464510|XP_005568509.1
☐	PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	72.0	72.0	100%	3e-13	100%	gi|635021370|XP_008017729.1
☐	PREDICTED: attractin isoform X2 [Pteropus alecto]	72.0	72.0	100%	3e-13	100%	gi|586533634|XP_006921706.1
☐	PREDICTED: attractin [Lipotes vexillifer]	70.9	70.9	100%	8e-13	97%	gi|602710450|XP_007465469.1
☐	attractin [Ovis aries]	67.4	67.4	100%	1e-12	94%	gi|78499351|ABB45710.1
☐	Attractin [Myotis davidii]	70.1	70.1	100%	1e-12	97%	gi|432111133|ELK34519.1
☐	PREDICTED: attractin [Myotis davidii]	70.1	70.1	100%	2e-12	97%	gi|584075971|XP_006758187.1
☐	PREDICTED: attractin [Tarsius syrichta]	69.7	69.7	100%	2e-12	97%	gi|640796924|XP_008054571.1
☐	Attractin [Myotis brandtii]	69.7	69.7	100%	2e-12	97%	gi|521031210|EPQ12996.1
☐	PREDICTED: attractin [Myotis brandtii]	69.7	69.7	100%	2e-12	97%	gi|554560893|XP_005874816.1
☐	PREDICTED: attractin [Myotis lucifugus]	69.7	69.7	100%	2e-12	97%	gi|558159591|XP_006096513.1
☐	PREDICTED: attractin [Eptesicus fuscus]	69.7	69.7	100%	2e-12	97%	gi|641701319|XP_008139256.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	68.9	68.9	100%	4e-12	97%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin-like [Physeter catodon]	68.9	68.9	100%	4e-12	97%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin [Equus przewalskii]	68.9	68.9	100%	4e-12	97%	gi|664773944|XP_008506219.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	68.9	68.9	100%	4e-12	97%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	68.9	68.9	100%	4e-12	97%	gi|725600051|XP_010350111.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	68.9	68.9	100%	4e-12	97%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin [Orcinus orca]	68.9	68.9	100%	4e-12	97%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin [Orycteropus afer afer]	68.9	68.9	100%	4e-12	97%	gi|634830430|XP_007958185.1
☐	attractin [Bos taurus]	67.4	67.4	100%	1e-11	94%	gi|190683717|ACE82176.1
☐	PREDICTED: attractin [Jaculus jaculus]	67.8	67.8	100%	1e-11	94%	gi|507555530|XP_004661535.1
☐	PREDICTED: attractin [Capra hircus]	67.4	67.4	100%	1e-11	94%	gi|548490191|XP_005688293.1
☐	PREDICTED: attractin [Bos mutus]	67.4	67.4	100%	1e-11	94%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Ovis aries]	67.4	67.4	100%	1e-11	94%	gi|426241795|XP_004014773.1
☐	attractin [Bos taurus]	67.4	67.4	100%	1e-11	94%	gi|253560524|ACT32973.1
☐	attractin [Bos taurus]	67.4	67.4	100%	1e-11	94%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X2 [Bos taurus]	67.4	67.4	100%	1e-11	94%	gi|528973313|XP_005214542.1
☐	PREDICTED: attractin isoform X1 [Bos taurus]	67.4	67.4	100%	1e-11	94%	gi|528973311|XP_005214541.1
☐	attractin [Canis lupus familiaris]	67.0	67.0	100%	2e-11	94%	gi|339892849|AEK21787.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	67.0	67.0	100%	2e-11	94%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin isoform X2 [Canis lupus familiaris]	67.0	67.0	100%	2e-11	94%	gi|545540090|XP_005634905.1
☐	PREDICTED: attractin [Panthera tigris altaica]	67.0	67.0	100%	2e-11	94%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin [Felis catus]	67.0	67.0	100%	2e-11	94%	gi|586981105|XP_003983758.2

☐	PREDICTED: attractin isoform X3 [Canis lupus familiaris]	67.0	67.0	100%	2e-11	94%	gi|73991942|XP_534360.2
☐	PREDICTED: attractin [Tupaia chinensis]	67.0	67.0	100%	2e-11	94%	gi|562872246|XP_006164056.1
☐	PREDICTED: attractin isoform X1 [Canis lupus familiaris]	67.0	67.0	100%	2e-11	94%	gi|545540087|XP_005634904.1
☐	PREDICTED: attractin isoform X1 [Oryctolagus cuniculus]	66.6	66.6	100%	2e-11	94%	gi|291388868|XP_002710968.1
☐	PREDICTED: attractin isoform X2 [Oryctolagus cuniculus]	66.6	66.6	100%	3e-11	94%	gi|655716500|XP_008254470.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	65.9	65.9	100%	4e-11	91%	gi|585160208|XP_006732353.1
☐	attractin isoform 1 preproprotein [Camelus ferus]	65.9	65.9	100%	4e-11	94%	gi|528759526|EPY79185.1
☐	PREDICTED: attractin isoform X2 [Mustela putorius furo]	65.9	65.9	100%	4e-11	91%	gi|511906947|XP_004772933.1
☐	PREDICTED: attractin [Camelus ferus]	65.9	65.9	100%	5e-11	94%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Mustela putorius furo]	65.9	65.9	100%	5e-11	91%	gi|511947743|XP_004792355.1
☐	PREDICTED: attractin [Vicugna pacos]	65.9	65.9	100%	5e-11	94%	gi|560970220|XP_006207473.1
☐	PREDICTED: attractin [Odobenus rosmarus divergens]	65.9	65.9	100%	5e-11	91%	gi|472357214|XP_004398236.1
☐	PREDICTED: attractin isoform X1 [Mustela putorius furo]	65.9	65.9	100%	5e-11	91%	gi|511906945|XP_004772932.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	65.5	65.5	100%	6e-11	91%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin [Sus scrofa]	65.5	65.5	100%	6e-11	91%	gi|545879723|XP_001927324.5
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	65.5	65.5	100%	6e-11	91%	gi|594099680|XP_006072965.1
☐	attractin [Sus scrofa]	65.5	65.5	100%	6e-11	91%	gi|146741346|BAF62328.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	65.5	65.5	100%	6e-11	91%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin isoform X1 [Bubalus bubalis]	65.5	65.5	100%	6e-11	91%	gi|594099676|XP_006072963.1
☐	PREDICTED: attractin isoform 2 [Ceratotherium simum simum]	65.1	65.1	100%	8e-11	94%	gi|478519276|XP_004433860.1
☐	PREDICTED: attractin isoform 1 [Ceratotherium simum simum]	65.1	65.1	100%	8e-11	94%	gi|478519274|XP_004433859.1
☐	PREDICTED: attractin [Chrysochloris asiatica]	65.1	65.1	100%	9e-11	91%	gi|586488825|XP_006874887.1
☐	Attractin [Cricetulus griseus]	64.7	64.7	100%	1e-10	88%	gi|344236321|EGV92424.1
☐	PREDICTED: attractin isoform X2 [Cricetulus griseus]	64.7	64.7	100%	1e-10	88%	gi|625260840|XP_007621856.1
☐	PREDICTED: attractin [Nannospalax galili]	64.7	64.7	100%	1e-10	91%	gi|674060132|XP_008836714.1
☐	attractin [Cricetulus griseus]	64.7	64.7	100%	1e-10	88%	gi|537146168|ERE69758.1

⊟ Alignments

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PREDICTED: attractin-like [Pan paniscus]

Sequence ID: gi|397513332|ref|XP_003826972.1| **Length:** 265 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 210 to 241 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.0 bits(175)	3e-14	32/32(100%)	32/32(100%)	0/32(0%)

```
Query  1    KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY  32
            KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY
Sbjct  210  KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY  241
```

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KIAA0548 protein [Homo sapiens]

Sequence ID: gi|3043620|dbj|BAA25474.1| **Length:** 452 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 45 to 76 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.0 bits(175)	1e-13	32/32(100%)	32/32(100%)	0/32(0%)

```
Query  1   KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY  32
           KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY
Sbjct  45  KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY  76
```

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PREDICTED: attractin isoform X2 [Papio anubis]

Sequence ID: gi|685567345|ref|XP_009214752.1| **Length:** 989 **Number of Matches:** 1

Range 1: 712 to 743 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.0 bits(175)	3e-13	32/32(100%)	32/32(100%)	0/32(0%)

```
Query  1    KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY  32
            KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY
Sbjct  712  KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY  743
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: attractin-like, partial [Galeopterus variegatus]

Sequence ID: gi|667345974|ref|XP_008563464.1| **Length:** 213 **Number of Matches:** 1

Range 1: 174 to 205 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(167)	3e-13	31/32(97%)	31/32(96%)	0/32(0%)

```
Query  1    KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY  32
            KGPVKMPSQA TGNFYPQPLLNSSMCLEDSRY
Sbjct  174  KGPVKMPSQASTGNFYPQPLLNSSMCLEDSRY  205
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: attractin, partial [Pongo abelii]

Sequence ID: gi|297706621|ref|XP_002830129.1| **Length:** 1058 **Number of Matches:** 1

Range 1: 651 to 682 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.0 bits(175)	3e-13	32/32(100%)	32/32(100%)	0/32(0%)

```
Query  1    KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY  32
            KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY
Sbjct  651  KGPVKMPSQAPTGNFYPQPLLNSSMCLEDSRY  682
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BHDT94FP014**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download

How to read this page | Blast report description

ATRN_KIDSTGDVTNELRV_Mod

RID BHDT94FP014 (Expires on 01-17 14:00 pm)

Query ID lcl|86384

Description None

Molecule type amino acid

Query Length 14

Database Name nr

Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects

Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

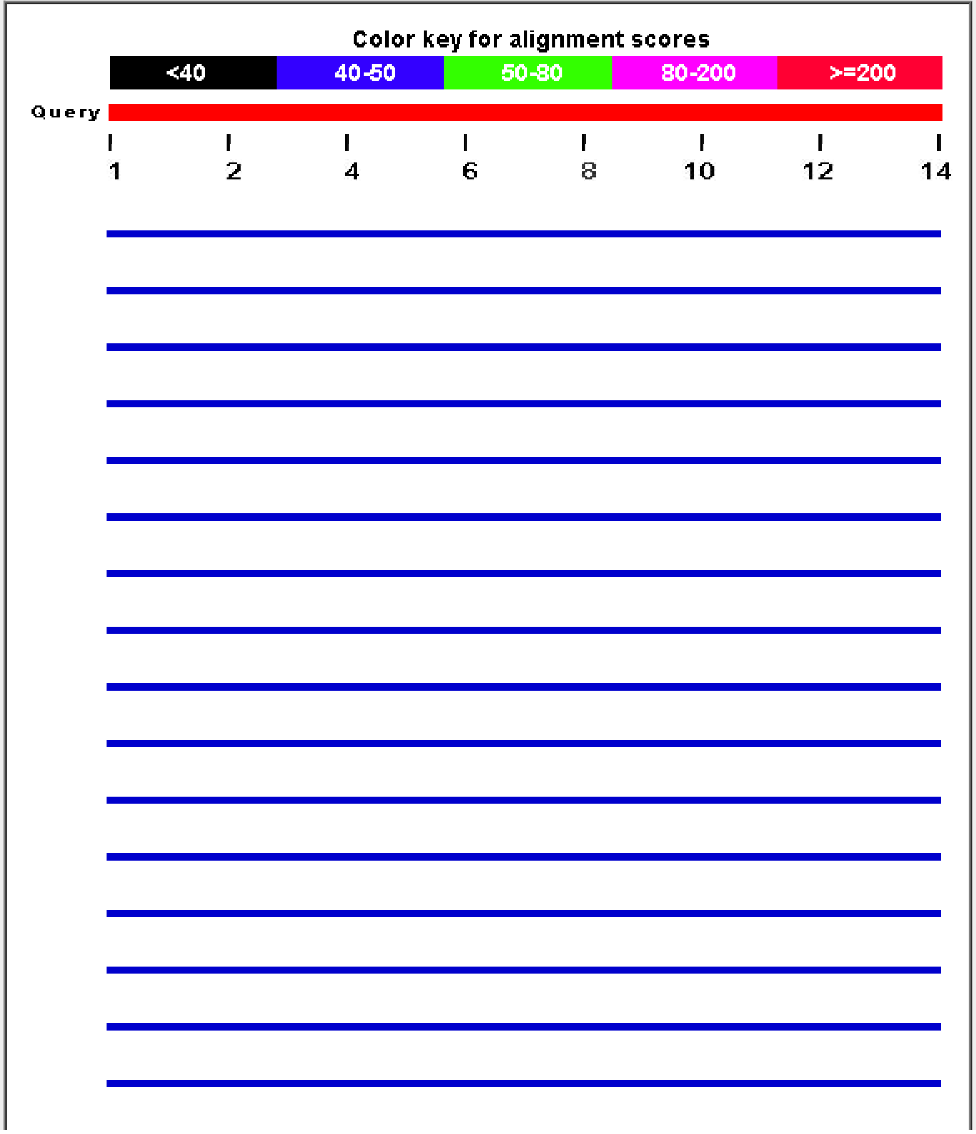
Graphic Summary

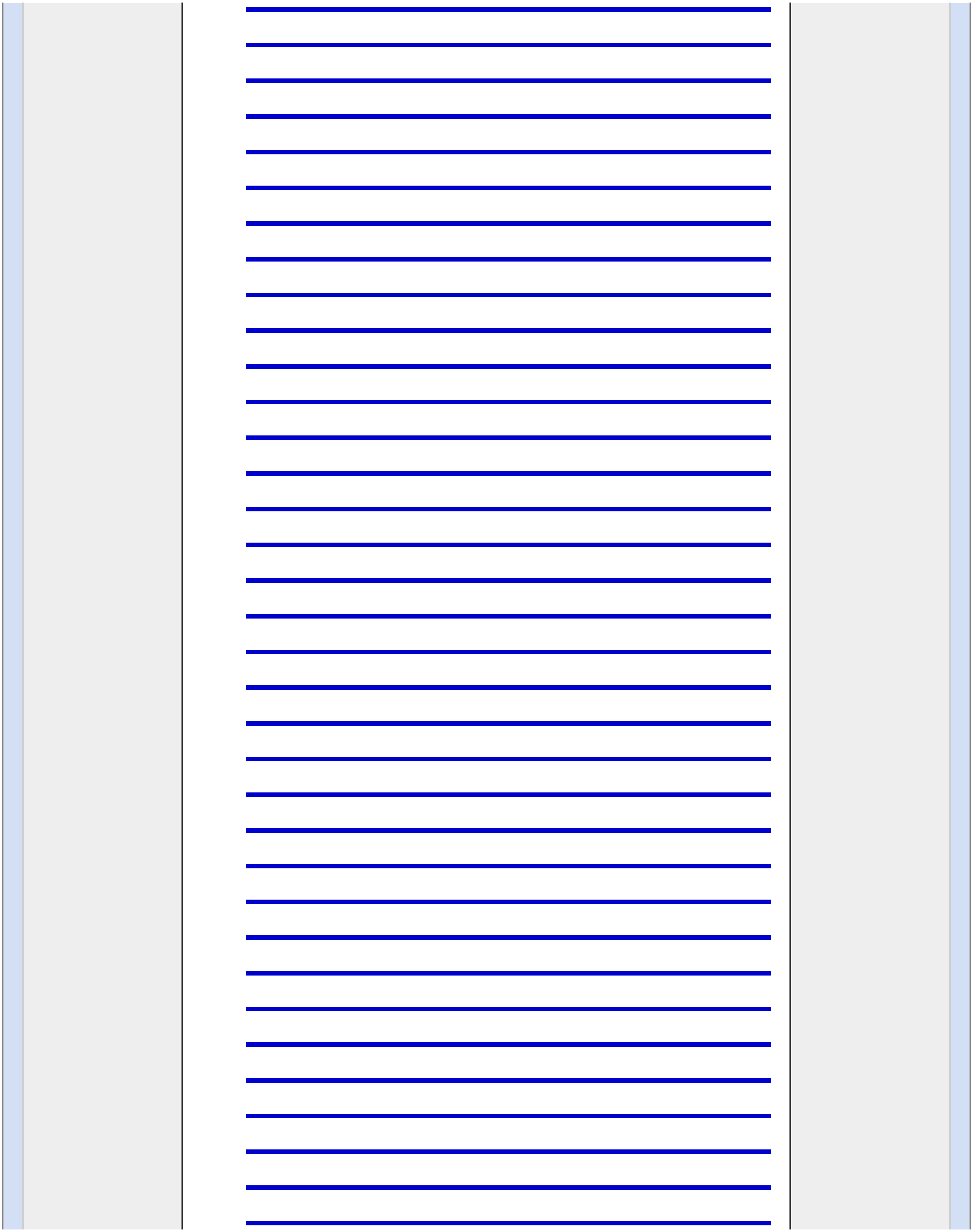
Show Conserved Domains

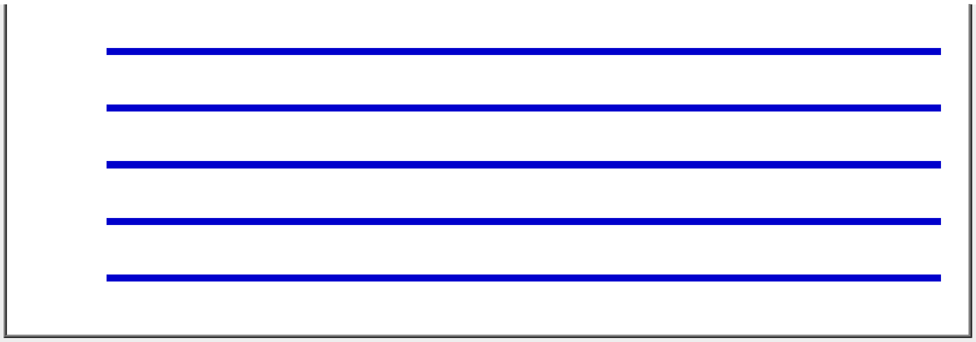
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Attractin [Fukomys damarensis]	43.9	43.9	100%	0.001	93%	gi|676269096|KFO24512.1
☐	Attractin [Tupaia chinensis]	43.9	43.9	100%	0.001	93%	gi|444519420|ELV12829.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	43.9	43.9	100%	0.001	93%	gi|585160208|XP_006732353.1
☐	PREDICTED: attractin isoform X2 [Papio anubis]	43.9	43.9	100%	0.001	93%	gi|685567345|XP_009214752.1
☐	attractin [Canis lupus familiaris]	43.9	43.9	100%	0.001	93%	gi|339892849|AEK21787.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	43.9	43.9	100%	0.001	93%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin-like [Physeter catodon]	43.9	43.9	100%	0.001	93%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin [Pongo abelii]	43.9	43.9	100%	0.001	93%	gi|297706621|XP_002830129.1
☐	mKIAA0548 protein [Mus musculus]	43.9	43.9	100%	0.001	93%	gi|26006173|BAC41429.1
☐	Attractin [Cricetulus griseus]	43.9	43.9	100%	0.001	93%	gi|344236321|EGV92424.1
☐	PREDICTED: attractin [Sarcophilus harrisii]	43.9	43.9	100%	0.001	93%	gi|395543190|XP_003773503.1
☐	attractin isoform 1 preproprotein [Camelus ferus]	43.9	43.9	100%	0.001	93%	gi|528759526|EPY79185.1
☐	PREDICTED: attractin isoform X2 [Cricetulus griseus]	43.9	43.9	100%	0.001	93%	gi|625260840|XP_007621856.1
☐	PREDICTED: attractin-like [Ictidomys tridecemlineatus]	43.9	43.9	100%	0.001	93%	gi|532069682|XP_005320676.1
☐	PREDICTED: attractin [Equus przewalskii]	43.9	43.9	100%	0.001	93%	gi|664773944|XP_008506219.1
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	43.9	43.9	100%	0.001	93%	gi|530426021|XP_005260918.1
☐	PREDICTED: attractin isoform X1 [Papio anubis]	43.9	43.9	100%	0.001	93%	gi|685567343|XP_009214751.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	43.9	43.9	100%	0.001	93%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	43.9	43.9	100%	0.001	93%	gi|725600051|XP_010350111.1
☐	PREDICTED: attractin [Nannospalax galili]	43.9	43.9	100%	0.001	93%	gi|674060132|XP_008836714.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	43.9	43.9	100%	0.001	93%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin [Tarsius syrichta]	43.9	43.9	100%	0.001	93%	gi|640796924|XP_008054571.1
☐	unnamed protein product [Homo sapiens]	43.9	43.9	100%	0.001	93%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	43.9	43.9	100%	0.001	93%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	43.9	43.9	100%	0.001	93%	gi|332257827|XP_003278006.1
☐	PREDICTED: attractin isoform 2 [Dasypus novemcinctus]	43.9	43.9	100%	0.001	93%	gi|488545593|XP_004464327.1
☐	attractin [Cricetulus griseus]	43.9	43.9	100%	0.001	93%	gi|537146168|ERE69758.1
☐	Attractin [Fukomys damarensis]	43.9	43.9	100%	0.001	93%	gi|676263950|KFO20529.1
☐							

	Attractin [Myotis davidii]	43.9	43.9	100%	0.001	93%	gi|432111133|ELK34519.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	43.9	43.9	100%	0.001	93%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin [Sus scrofa]	43.9	43.9	100%	0.001	93%	gi|545879723|XP_001927324.5
☐	PREDICTED: attractin isoform 2 [Ceratotherium simum simum]	43.9	43.9	100%	0.001	93%	gi|478519276|XP_004433860.1
☐	PREDICTED: attractin isoform X2 [Condylura cristata]	43.9	43.9	100%	0.001	93%	gi|507961710|XP_004687418.1
☐	PREDICTED: attractin [Gorilla gorilla gorilla]	43.9	43.9	100%	0.001	93%	gi|426390844|XP_004061806.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	43.9	43.9	100%	0.001	93%	gi|694977854|XP_009435012.1
☐	Attractin [Myotis brandtii]	43.9	43.9	100%	0.001	93%	gi|521031210|EPQ12996.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	43.9	43.9	100%	0.001	93%	gi|332257825|XP_003278005.1
☐	secreted attractin precursor [Homo sapiens]	43.9	43.9	100%	0.001	93%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	43.9	43.9	100%	0.001	93%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	43.9	43.9	100%	0.001	93%	gi|21450863|NP_647538.1
☐	Mahogany-like protein [Macaca mulatta]	43.9	43.9	100%	0.001	93%	gi|355563316|EHH19878.1
☐	attractin [Rattus norvegicus]	43.9	43.9	100%	0.001	93%	gi|12275312|BAB21018.1
☐	attractin, isoform CRA_a [Rattus norvegicus]	43.9	43.9	100%	0.001	93%	gi|149023319|EDL80213.1
☐	PREDICTED: attractin isoform X1 [Bos taurus]	43.9	43.9	100%	0.001	93%	gi|741947708|XP_005214542.2
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	43.9	43.9	100%	0.001	93%	gi|594099680|XP_006072965.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Pan paniscus]	43.9	43.9	100%	0.001	93%	gi|675763672|XP_008973079.1
☐	PREDICTED: attractin isoform X2 [Canis lupus familiaris]	43.9	43.9	100%	0.001	93%	gi|545540090|XP_005634905.1
☐	PREDICTED: attractin isoform X2 [Heterocephalus glaber]	43.9	43.9	100%	0.001	93%	gi|512956910|XP_004840783.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	43.9	43.9	100%	0.001	93%	gi|694977852|XP_009435011.1
☐	attractin [Sus scrofa]	43.9	43.9	100%	0.001	93%	gi|146741346|BAF62328.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	43.9	43.9	100%	0.001	93%	gi|530426019|XP_005260917.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	43.9	43.9	100%	0.001	93%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	43.9	43.9	100%	0.001	93%	gi|635021368|XP_008017720.1
☐	PREDICTED: attractin isoform X2 [Mustela putorius furo]	43.9	43.9	100%	0.001	93%	gi|511906947|XP_004772933.1
☐	Mahogany-like protein [Macaca fascicularis]	43.9	43.9	100%	0.001	93%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin [Myotis davidii]	43.9	43.9	100%	0.001	93%	gi|584075971|XP_006758187.1
☐	PREDICTED: attractin [Panthera tigris altaica]	43.9	43.9	100%	0.001	93%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin [Myotis brandtii]	43.9	43.9	100%	0.001	93%	gi|554560893|XP_005874816.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	43.9	43.9	100%	0.001	93%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	43.9	43.9	100%	0.001	93%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	43.9	43.9	100%	0.001	93%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Capra hircus]	43.9	43.9	100%	0.001	93%	gi|548490191|XP_005688293.1
☐	Attractin [Heterocephalus glaber]	43.9	43.9	100%	0.001	93%	gi|351701383|EHB04302.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	43.9	43.9	100%	0.001	93%	gi|724902357|XP_010377335.1
☐	PREDICTED: attractin isoform 1 [Dasypus novemcinctus]	43.9	43.9	100%	0.001	93%	gi|488545591|XP_004464326.1
☐	PREDICTED: attractin isoform X1 [Cricetulus griseus]	43.9	43.9	100%	0.001	93%	gi|354473756|XP_003499099.1
☐	PREDICTED: attractin [Camelus ferus]	43.9	43.9	100%	0.001	93%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Sorex araneus]	43.9	43.9	100%	0.001	93%	gi|505831534|XP_004611050.1
☐	PREDICTED: attractin [Myotis lucifugus]	43.9	43.9	100%	0.001	93%	gi|558159591|XP_006096513.1
☐	attractin [Cricetulus griseus]	43.9	43.9	100%	0.001	93%	gi|537146167|ERE69757.1
☐	PREDICTED: attractin [Camelus dromedarius]	43.9	43.9	100%	0.001	93%	gi|744589171|XP_010986570.1
☐	PREDICTED: attractin [Bos mutus]	43.9	43.9	100%	0.001	93%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Ursus maritimus]	43.9	43.9	100%	0.001	93%	gi|671021680|XP_008701660.1

☐	hypothetical protein PANDA_007354 [Ailuropoda melanoleuca]	43.9	43.9	100%	0.001	93%	gi|281339872|EFB15456.1
☐	PREDICTED: attractin-like [Ailuropoda melanoleuca]	43.9	43.9	100%	0.001	93%	gi|301766802|XP_002918837.1
☐	PREDICTED: attractin [Camelus bactrianus]	43.9	43.9	100%	0.001	93%	gi|743752427|XP_010971103.1
☐	PREDICTED: attractin [Mustela putorius furo]	43.9	43.9	100%	0.001	93%	gi|511947743|XP_004792355.1
☐	attractin, isoform CRA_b [Homo sapiens]	43.9	43.9	100%	0.001	93%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	43.9	43.9	100%	0.001	93%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin [Fukomys damarensis]	43.9	43.9	100%	0.001	93%	gi|731281216|XP_010609356.1
☐	PREDICTED: attractin [Heterocephalus glaber]	43.9	43.9	100%	0.001	93%	gi|512849696|XP_004886859.1
☐	PREDICTED: attractin [Ovis aries]	43.9	43.9	100%	0.001	93%	gi|426241795|XP_004014773.1
☐	PREDICTED: attractin [Peromyscus maniculatus bairdii]	43.9	43.9	100%	0.001	93%	gi|589943852|XP_006984624.1
☐	PREDICTED: attractin [Felis catus]	43.9	43.9	100%	0.001	93%	gi|586981105|XP_003983758.2
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	43.9	43.9	100%	0.001	93%	gi|694977850|XP_009435010.1
☐	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	43.9	43.9	100%	0.001	93%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin [Otolemur garnettii]	43.9	43.9	100%	0.001	93%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin [Erinaceus europaeus]	43.9	43.9	100%	0.001	93%	gi|617558695|XP_007539650.1
☐	PREDICTED: attractin [Vicugna pacos]	43.9	43.9	100%	0.001	93%	gi|560970220|XP_006207473.1
☐	PREDICTED: attractin [Echinops telfairi]	43.9	43.9	100%	0.001	93%	gi|507626122|XP_004697922.1
☐	attractin [Bos taurus]	43.9	43.9	100%	0.001	93%	gi|253560524|ACT32973.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	43.9	43.9	100%	0.001	93%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin [Eptesicus fuscus]	43.9	43.9	100%	0.001	93%	gi|641701319|XP_008139256.1
☐	attractin [Bos taurus]	43.9	43.9	100%	0.001	93%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	43.9	43.9	100%	0.001	93%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin isoform X3 [Canis lupus familiaris]	43.9	43.9	100%	0.001	93%	gi|73991942|XP_534360.2
☐	PREDICTED: attractin isoform 1 [Ceratotherium simum simum]	43.9	43.9	100%	0.001	93%	gi|478519274|XP_004433859.1
☐	PREDICTED: attractin [Orcinus orca]	43.9	43.9	100%	0.001	93%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin [Lipotes vexillifer]	43.9	43.9	100%	0.001	93%	gi|602710450|XP_007465469.1
☐	PREDICTED: attractin isoform X1 [Condylura cristata]	43.9	43.9	100%	0.001	93%	gi|507961707|XP_004687417.1

Alignments

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Attractin [Fukomys damarensis]

Sequence ID: gi|676269096|gb|KFO24512.1| **Length:** 740 **Number of Matches:** 1

Related Information

Range 1: 322 to 335 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
43.9 bits(96)	0.001	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KIDSTGDVTNELRV  14
            KIDSTG+VTNELRV
Sbjct  322  KIDSTGNVTNELRV  335
```

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Attractin [Tupaia chinensis]

Sequence ID: gi|444519420|gb|ELV12829.1| **Length:** 860 **Number of Matches:** 1

Related Information

Range 1: 57 to 70 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
43.9 bits(96)	0.001	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1   KIDSTGDVTNELRV  14
```

```
               KIDSTG+VTNELRV
Sbjct  57  KIDSTGNVTNELRV  70
```

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PREDICTED: attractin-like [Leptonychotes weddellii]

Sequence ID: gi|585160208|ref|XP_006732353.1| **Length:** 899 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 213 to 226 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
43.9 bits(96)	0.001	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KIDSTGDVTNELRV  14
            KIDSTG+VTNELRV
Sbjct  213  KIDSTGNVTNELRV  226
```

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PREDICTED: attractin isoform X2 [Papio anubis]

Sequence ID: gi|685567345|ref|XP_009214752.1| **Length:** 989 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 100 to 113 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
43.9 bits(96)	0.001	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KIDSTGDVTNELRV  14
            KIDSTG+VTNELRV
Sbjct  100  KIDSTGNVTNELRV  113
```

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attractin [Canis lupus familiaris]

Sequence ID: gi|339892849|gb|AEK21787.1| **Length:** 1001 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 308 to 321 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
43.9 bits(96)	0.001	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KIDSTGDVTNELRV  14
            KIDSTG+VTNELRV
Sbjct  308  KIDSTGNVTNELRV  321
```

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Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download

How to read this page   Blast report description

ATRN_KIDSTGNVTNELRV_NonMod

RID B915AFEV01R (Expires on 01-14 09:36 am)

Query ID lcl|144908
Description None
Molecule type amino acid
Query Length 14

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

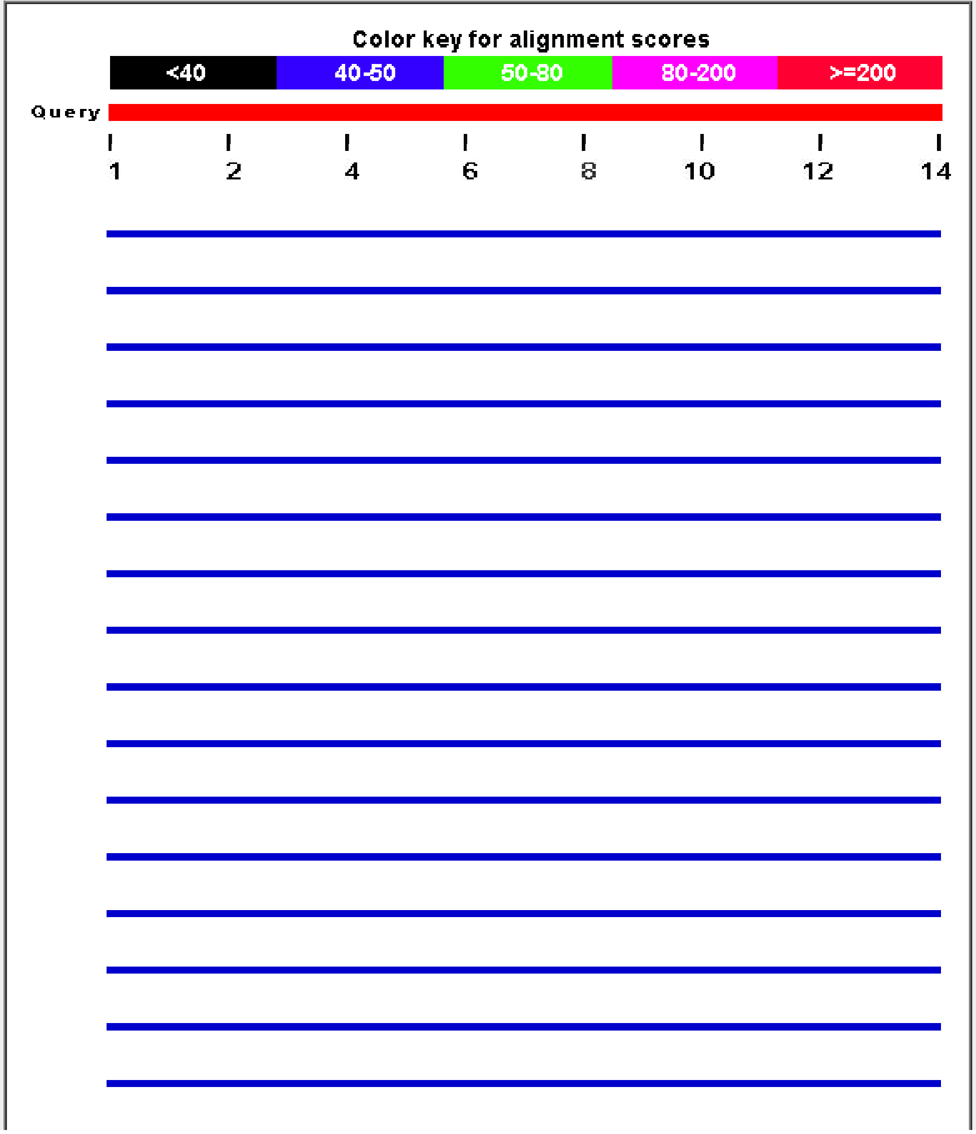
⊟ Graphic Summary

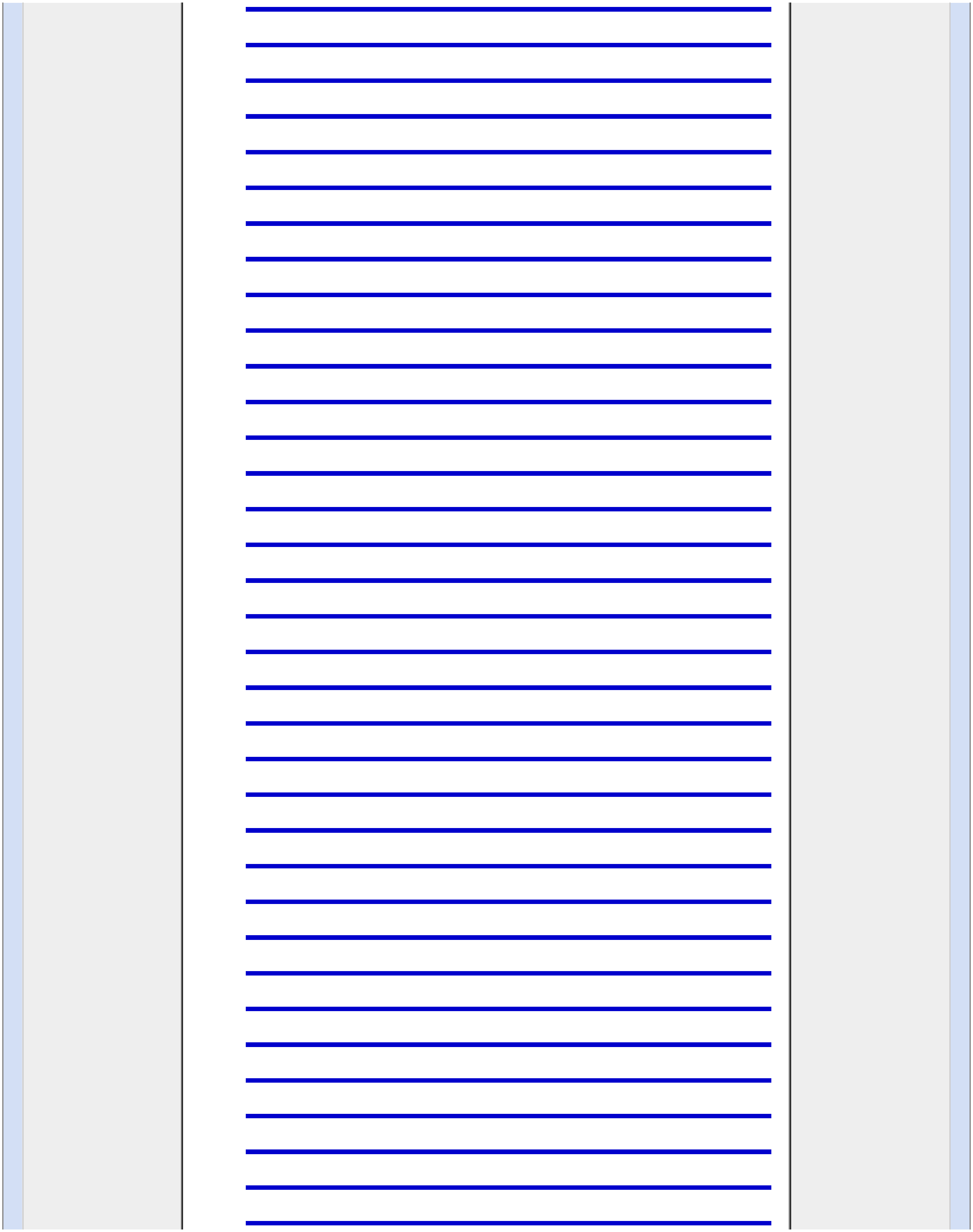
⊟ Show Conserved Domains

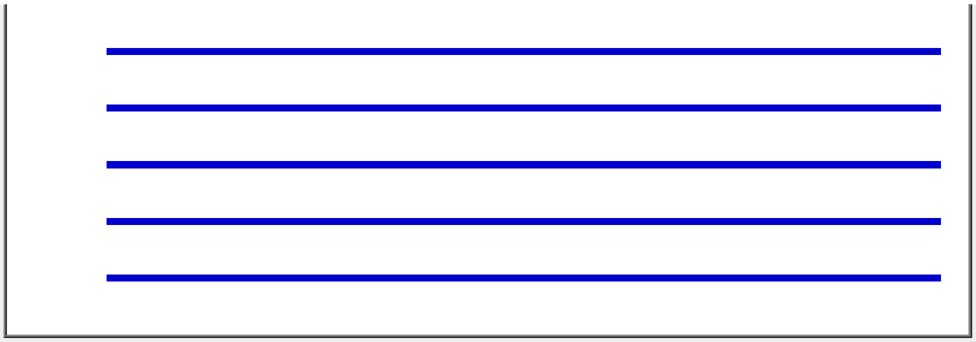
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Attractin [Fukomys damarensis]	46.4	46.4	100%	1e-04	100%	gi|676269096|KFO24512.1
☐	Attractin [Tupaia chinensis]	46.4	46.4	100%	1e-04	100%	gi|444519420|ELV12829.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	46.4	46.4	100%	1e-04	100%	gi|585160208|XP_006732353.1
☐	PREDICTED: attractin isoform X2 [Papio anubis]	46.4	46.4	100%	1e-04	100%	gi|685567345|XP_009214752.1
☐	attractin [Canis lupus familiaris]	46.4	46.4	100%	1e-04	100%	gi|339892849|AEK21787.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	46.4	46.4	100%	1e-04	100%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin-like [Physeter catodon]	46.4	46.4	100%	1e-04	100%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin [Pongo abelii]	46.4	46.4	100%	1e-04	100%	gi|297706621|XP_002830129.1
☐	mKIAA0548 protein [Mus musculus]	46.4	46.4	100%	1e-04	100%	gi|26006173|BAC41429.1
☐	Attractin [Cricetulus griseus]	46.4	46.4	100%	1e-04	100%	gi|344236321|EGV92424.1
☐	PREDICTED: attractin [Sarcophilus harrisii]	46.4	46.4	100%	1e-04	100%	gi|395543190|XP_003773503.1
☐	attractin isoform 1 preproprotein [Camelus ferus]	46.4	46.4	100%	1e-04	100%	gi|528759526|EPY79185.1
☐	PREDICTED: attractin isoform X2 [Cricetulus griseus]	46.4	46.4	100%	1e-04	100%	gi|625260840|XP_007621856.1
☐	PREDICTED: attractin-like [Ictidomys tridecemlineatus]	46.4	46.4	100%	1e-04	100%	gi|532069682|XP_005320676.1
☐	PREDICTED: attractin [Equus przewalskii]	46.4	46.4	100%	1e-04	100%	gi|664773944|XP_008506219.1
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	46.4	46.4	100%	1e-04	100%	gi|530426021|XP_005260918.1
☐	PREDICTED: attractin isoform X1 [Papio anubis]	46.4	46.4	100%	1e-04	100%	gi|685567343|XP_009214751.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	46.4	46.4	100%	1e-04	100%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	46.4	46.4	100%	1e-04	100%	gi|725600051|XP_010350111.1
☐	PREDICTED: attractin [Nannospalax galili]	46.4	46.4	100%	1e-04	100%	gi|674060132|XP_008836714.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	46.4	46.4	100%	1e-04	100%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin [Tarsius syrichta]	46.4	46.4	100%	1e-04	100%	gi|640796924|XP_008054571.1
☐	unnamed protein product [Homo sapiens]	46.4	46.4	100%	1e-04	100%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	46.4	46.4	100%	1e-04	100%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	46.4	46.4	100%	1e-04	100%	gi|332257827|XP_003278006.1
☐	PREDICTED: attractin isoform 2 [Dasypus novemcinctus]	46.4	46.4	100%	1e-04	100%	gi|488545593|XP_004464327.1
☐	attractin [Cricetulus griseus]	46.4	46.4	100%	1e-04	100%	gi|537146168|ERE69758.1
☐	Attractin [Fukomys damarensis]	46.4	46.4	100%	1e-04	100%	gi|676263950|KFO20529.1
☐							

	Attractin [Myotis davidii]	46.4	46.4	100%	1e-04	100%	gi|432111133|ELK34519.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	46.4	46.4	100%	1e-04	100%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin [Sus scrofa]	46.4	46.4	100%	1e-04	100%	gi|545879723|XP_001927324.5
☐	PREDICTED: attractin isoform 2 [Ceratotherium simum simum]	46.4	46.4	100%	1e-04	100%	gi|478519276|XP_004433860.1
☐	PREDICTED: attractin isoform X2 [Condylura cristata]	46.4	46.4	100%	1e-04	100%	gi|507961710|XP_004687418.1
☐	PREDICTED: attractin [Gorilla gorilla gorilla]	46.4	46.4	100%	1e-04	100%	gi|426390844|XP_004061806.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	46.4	46.4	100%	1e-04	100%	gi|694977854|XP_009435012.1
☐	Attractin [Myotis brandtii]	46.4	46.4	100%	1e-04	100%	gi|521031210|EPQ12996.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	46.4	46.4	100%	1e-04	100%	gi|332257825|XP_003278005.1
☐	secreted attractin precursor [Homo sapiens]	46.4	46.4	100%	1e-04	100%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	46.4	46.4	100%	1e-04	100%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	46.4	46.4	100%	1e-04	100%	gi|21450863|NP_647538.1
☐	Mahogany-like protein [Macaca mulatta]	46.4	46.4	100%	1e-04	100%	gi|355563316|EHH19878.1
☐	attractin [Rattus norvegicus]	46.4	46.4	100%	1e-04	100%	gi|12275312|BAB21018.1
☐	attractin, isoform CRA_a [Rattus norvegicus]	46.4	46.4	100%	1e-04	100%	gi|149023319|EDL80213.1
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	46.4	46.4	100%	1e-04	100%	gi|594099680|XP_006072965.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Pan paniscus]	46.4	46.4	100%	1e-04	100%	gi|675763672|XP_008973079.1
☐	PREDICTED: attractin isoform X2 [Canis lupus familiaris]	46.4	46.4	100%	1e-04	100%	gi|545540090|XP_005634905.1
☐	PREDICTED: attractin isoform X2 [Heterocephalus glaber]	46.4	46.4	100%	1e-04	100%	gi|512956910|XP_004840783.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	46.4	46.4	100%	1e-04	100%	gi|694977852|XP_009435011.1
☐	attractin [Sus scrofa]	46.4	46.4	100%	1e-04	100%	gi|146741346|BAF62328.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	46.4	46.4	100%	1e-04	100%	gi|530426019|XP_005260917.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	46.4	46.4	100%	1e-04	100%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	46.4	46.4	100%	1e-04	100%	gi|635021368|XP_008017720.1
☐	PREDICTED: attractin isoform X2 [Mustela putorius furo]	46.4	46.4	100%	1e-04	100%	gi|511906947|XP_004772933.1
☐	Mahogany-like protein [Macaca fascicularis]	46.4	46.4	100%	1e-04	100%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin [Myotis davidii]	46.4	46.4	100%	1e-04	100%	gi|584075971|XP_006758187.1
☐	PREDICTED: attractin [Panthera tigris altaica]	46.4	46.4	100%	1e-04	100%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin [Myotis brandtii]	46.4	46.4	100%	1e-04	100%	gi|554560893|XP_005874816.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	46.4	46.4	100%	1e-04	100%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	46.4	46.4	100%	1e-04	100%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	46.4	46.4	100%	1e-04	100%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Capra hircus]	46.4	46.4	100%	1e-04	100%	gi|548490191|XP_005688293.1
☐	Attractin [Heterocephalus glaber]	46.4	46.4	100%	1e-04	100%	gi|351701383|EHB04302.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	46.4	46.4	100%	1e-04	100%	gi|724902357|XP_010377335.1
☐	PREDICTED: attractin isoform 1 [Dasypus novemcinctus]	46.4	46.4	100%	1e-04	100%	gi|488545591|XP_004464326.1
☐	PREDICTED: attractin isoform X1 [Cricetulus griseus]	46.4	46.4	100%	1e-04	100%	gi|354473756|XP_003499099.1
☐	PREDICTED: attractin [Camelus ferus]	46.4	46.4	100%	1e-04	100%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Sorex araneus]	46.4	46.4	100%	1e-04	100%	gi|505831534|XP_004611050.1
☐	PREDICTED: attractin [Myotis lucifugus]	46.4	46.4	100%	1e-04	100%	gi|558159591|XP_006096513.1
☐	attractin [Cricetulus griseus]	46.4	46.4	100%	1e-04	100%	gi|537146167|ERE69757.1
☐	PREDICTED: attractin [Bos mutus]	46.4	46.4	100%	1e-04	100%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Ursus maritimus]	46.4	46.4	100%	1e-04	100%	gi|671021680|XP_008701660.1
☐	hypothetical protein PANDA_007354 [Ailuropoda melanoleuca]	46.4	46.4	100%	1e-04	100%	gi|281339872|EFB15456.1
☐	PREDICTED: attractin-like [Ailuropoda melanoleuca]	46.4	46.4	100%	1e-04	100%	gi|301766802|XP_002918837.1

☐	PREDICTED: attractin [Mustela putorius furo]	46.4	46.4	100%	1e-04	100%	gi|511947743|XP_004792355.1
☐	attractin, isoform CRA_b [Homo sapiens]	46.4	46.4	100%	1e-04	100%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	46.4	46.4	100%	1e-04	100%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin [Fukomys damarensis]	46.4	46.4	100%	1e-04	100%	gi|731281216|XP_010609356.1
☐	PREDICTED: attractin [Heterocephalus glaber]	46.4	46.4	100%	1e-04	100%	gi|512849696|XP_004886859.1
☐	PREDICTED: attractin [Ovis aries]	46.4	46.4	100%	1e-04	100%	gi|426241795|XP_004014773.1
☐	PREDICTED: attractin [Peromyscus maniculatus bairdii]	46.4	46.4	100%	1e-04	100%	gi|589943852|XP_006984624.1
☐	PREDICTED: attractin [Felis catus]	46.4	46.4	100%	1e-04	100%	gi|586981105|XP_003983758.2
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	46.4	46.4	100%	1e-04	100%	gi|694977850|XP_009435010.1
☐	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	46.4	46.4	100%	1e-04	100%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin [Otolemur garnettii]	46.4	46.4	100%	1e-04	100%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin [Erinaceus europaeus]	46.4	46.4	100%	1e-04	100%	gi|617558695|XP_007539650.1
☐	PREDICTED: attractin [Vicugna pacos]	46.4	46.4	100%	1e-04	100%	gi|560970220|XP_006207473.1
☐	PREDICTED: attractin [Echinops telfairi]	46.4	46.4	100%	1e-04	100%	gi|507626122|XP_004697922.1
☐	attractin [Bos taurus]	46.4	46.4	100%	1e-04	100%	gi|253560524|ACT32973.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	46.4	46.4	100%	1e-04	100%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin [Eptesicus fuscus]	46.4	46.4	100%	1e-04	100%	gi|641701319|XP_008139256.1
☐	attractin [Bos taurus]	46.4	46.4	100%	1e-04	100%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	46.4	46.4	100%	1e-04	100%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin isoform X3 [Canis lupus familiaris]	46.4	46.4	100%	1e-04	100%	gi|73991942|XP_534360.2
☐	PREDICTED: attractin isoform 1 [Ceratotherium simum simum]	46.4	46.4	100%	1e-04	100%	gi|478519274|XP_004433859.1
☐	PREDICTED: attractin [Orcinus orca]	46.4	46.4	100%	1e-04	100%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin [Lipotes vexillifer]	46.4	46.4	100%	1e-04	100%	gi|602710450|XP_007465469.1
☐	PREDICTED: attractin isoform X1 [Condylura cristata]	46.4	46.4	100%	1e-04	100%	gi|507961707|XP_004687417.1
☐	PREDICTED: attractin [Odobenus rosmarus divergens]	46.4	46.4	100%	1e-04	100%	gi|472357214|XP_004398236.1
☐	PREDICTED: attractin isoform X1 [Mustela putorius furo]	46.4	46.4	100%	1e-04	100%	gi|511906945|XP_004772932.1
☐	PREDICTED: attractin [Chrysochloris asiatica]	46.4	46.4	100%	1e-04	100%	gi|586488825|XP_006874887.1

⊟ Alignments

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Attractin [Fukomys damarensis]

Sequence ID: gi|676269096|gb|KFO24512.1| **Length:** 740 **Number of Matches:** 1

Related Information

Range 1: 322 to 335 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.4 bits(102)	1e-04	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KIDSTGNVTNELRV  14
            KIDSTGNVTNELRV
Sbjct  322  KIDSTGNVTNELRV  335
```

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Attractin [Tupaia chinensis]

Sequence ID: gi|444519420|gb|ELV12829.1| **Length:** 860 **Number of Matches:** 1

Related Information

Range 1: 57 to 70 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.4 bits(102)	1e-04	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1   KIDSTGNVTNELRV  14
```

```
            KIDSTGNVTNELRV
Sbjct  57   KIDSTGNVTNELRV  70
```

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PREDICTED: attractin-like [Leptonychotes weddellii]

Sequence ID: gi|585160208|ref|XP_006732353.1| **Length:** 899 **Number of Matches:** 1

Range 1: 213 to 226 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.4 bits(102)	1e-04	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KIDSTGNVTNELRV  14
            KIDSTGNVTNELRV
Sbjct  213  KIDSTGNVTNELRV  226
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: attractin isoform X2 [Papio anubis]

Sequence ID: gi|685567345|ref|XP_009214752.1| **Length:** 989 **Number of Matches:** 1

Range 1: 100 to 113 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.4 bits(102)	1e-04	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KIDSTGNVTNELRV  14
            KIDSTGNVTNELRV
Sbjct  100  KIDSTGNVTNELRV  113
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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attractin [Canis lupus familiaris]

Sequence ID: gi|339892849|gb|AEK21787.1| **Length:** 1001 **Number of Matches:** 1

Range 1: 308 to 321 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.4 bits(102)	1e-04	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KIDSTGNVTNELRV  14
            KIDSTGNVTNELRV
Sbjct  308  KIDSTGNVTNELRV  321
```

Related Information

Gene - associated gene details

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BHF0KAZN015**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download

How to read this page | Blast report description

ATRN_KISDSSDTVECECSENWKG_Mod

RID BHF0KAZN015 (Expires on 01-17 14:21 pm)

Query ID	lcl|95636	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	19		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

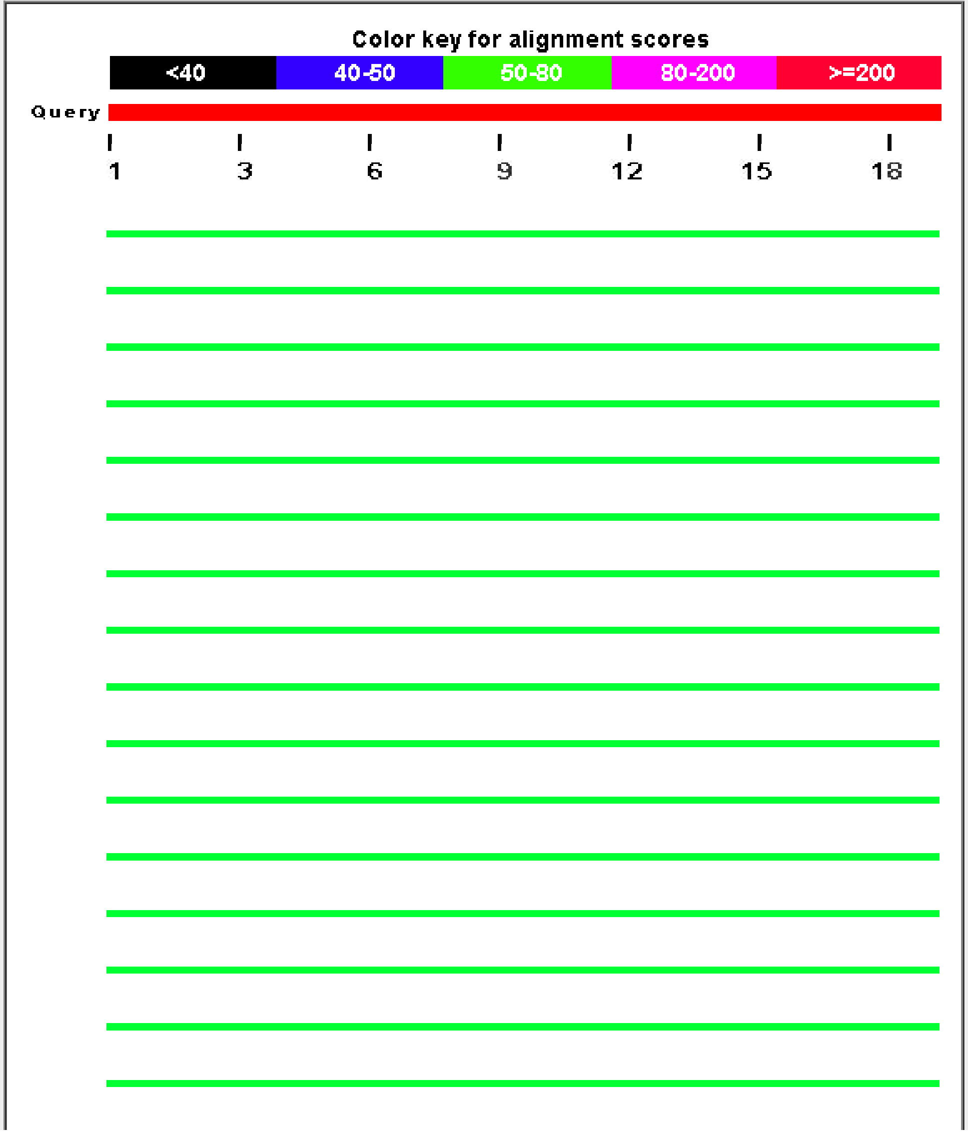
Graphic Summary

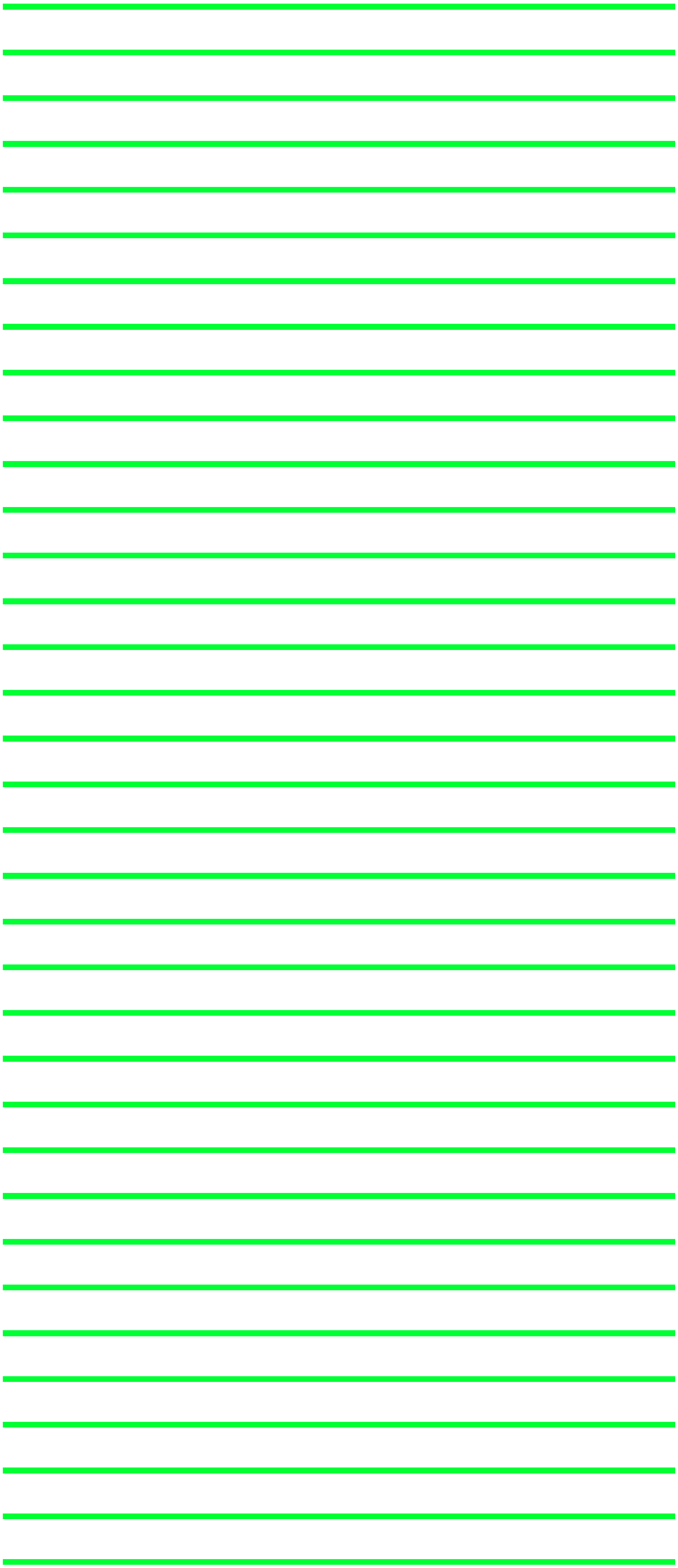
Show Conserved Domains

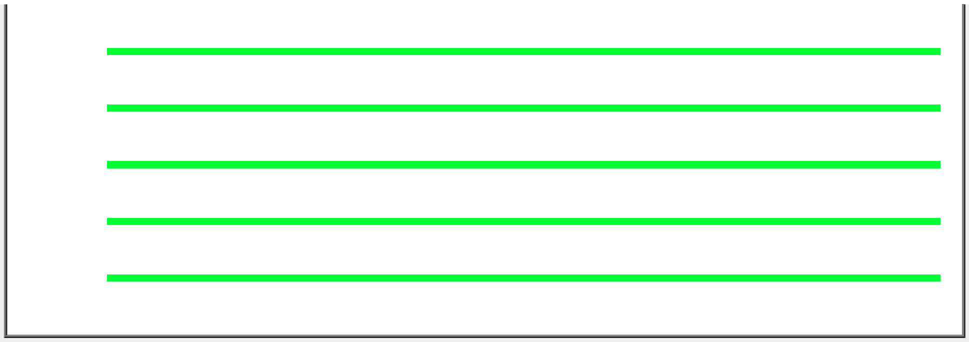
No putative conserved domains have been detected

Distribution of 104 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|530426021|XP_005260918.1
☐	unnamed protein product [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin [Gorilla gorilla gorilla]	63.0	63.0	100%	7e-10	95%	gi|426390844|XP_004061806.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	63.0	63.0	100%	7e-10	95%	gi|694977854|XP_009435012.1
☐	secreted attractin precursor [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|21450863|NP_647538.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Pan paniscus]	63.0	63.0	100%	7e-10	95%	gi|675763672|XP_008973079.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	63.0	63.0	100%	7e-10	95%	gi|694977852|XP_009435011.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|530426019|XP_005260917.1
☐	attractin, isoform CRA_b [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	63.0	63.0	100%	7e-10	95%	gi|694977850|XP_009435010.1
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	63.0	63.0	100%	7e-10	95%	gi|332857715|XP_003316827.1
☐	membrane attractin precursor [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|8118082|AAF72881.1
☐	attractin isoform 1 preproprotein [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|21450861|NP_647537.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	60.4	60.4	100%	5e-09	89%	gi|332257827|XP_003278006.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	60.4	60.4	100%	5e-09	89%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	60.4	60.4	100%	5e-09	89%	gi|4093196|AAD03057.1
☐	PREDICTED: attractin isoform X3 [Chinchilla lanigera]	60.4	60.4	100%	5e-09	89%	gi|533131617|XP_005380852.1
☐	PREDICTED: attractin-like [Octodon degus]	60.4	60.4	100%	5e-09	89%	gi|507657234|XP_004634315.1
☐	PREDICTED: attractin isoform X2 [Chinchilla lanigera]	60.4	60.4	100%	5e-09	89%	gi|533131615|XP_005380851.1
☐	PREDICTED: attractin isoform X1 [Chinchilla lanigera]	60.4	60.4	100%	5e-09	89%	gi|533131613|XP_005380850.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	57.9	57.9	100%	4e-08	84%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	57.9	57.9	100%	4e-08	84%	gi|725600051|XP_010350111.1
☐	Mahogany-like protein [Macaca mulatta]	57.9	57.9	100%	4e-08	84%	gi|355563316|EHH19878.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	57.9	57.9	100%	4e-08	84%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	57.9	57.9	100%	4e-08	84%	gi|635021368|XP_008017720.1
☐							

	Mahogany-like protein [Macaca fascicularis]	57.9	57.9	100%	4e-08	84%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	57.9	57.9	100%	4e-08	84%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	57.9	57.9	100%	4e-08	84%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	57.9	57.9	100%	4e-08	84%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	57.9	57.9	100%	4e-08	84%	gi|724902357|XP_010377335.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	57.9	57.9	100%	4e-08	84%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	57.9	57.9	100%	4e-08	84%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin isoform X2 [Macaca fascicularis]	57.9	57.9	100%	4e-08	84%	gi|544464512|XP_005568510.1
☐	PREDICTED: attractin [Macaca mulatta]	57.9	57.9	100%	4e-08	84%	gi|109092720|XP_001115192.1
☐	PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	57.9	57.9	100%	4e-08	84%	gi|635021360|XP_008017700.1
☐	PREDICTED: attractin isoform X1 [Macaca fascicularis]	57.9	57.9	100%	4e-08	84%	gi|544464510|XP_005568509.1
☐	PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	57.9	57.9	100%	4e-08	84%	gi|635021370|XP_008017729.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	57.5	57.5	100%	5e-08	84%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin-like [Physeter catodon]	57.5	57.5	100%	5e-08	84%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	57.5	57.5	100%	5e-08	84%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin [Sus scrofa]	57.5	57.5	100%	5e-08	84%	gi|545879723|XP_001927324.5
☐	PREDICTED: attractin isoform 2 [Ceratotherium simum simum]	57.5	57.5	100%	5e-08	84%	gi|478519276|XP_004433860.1
☐	PREDICTED: attractin isoform X1 [Bos taurus]	57.5	57.5	100%	5e-08	84%	gi|741947708|XP_005214542.2
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	57.5	57.5	100%	5e-08	84%	gi|594099680|XP_006072965.1
☐	attractin [Sus scrofa]	57.5	57.5	100%	5e-08	84%	gi|146741346|BAF62328.1
☐	PREDICTED: attractin [Panthera tigris altaica]	57.5	57.5	100%	5e-08	84%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin [Capra hircus]	57.5	57.5	100%	5e-08	84%	gi|548490191|XP_005688293.1
☐	PREDICTED: attractin [Bos mutus]	57.5	57.5	100%	5e-08	84%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Ovis aries]	57.5	57.5	100%	5e-08	84%	gi|426241795|XP_004014773.1
☐	PREDICTED: attractin [Felis catus]	57.5	57.5	100%	5e-08	84%	gi|586981105|XP_003983758.2
☐	PREDICTED: attractin [Echinops telfairi]	57.5	57.5	100%	5e-08	84%	gi|507626122|XP_004697922.1
☐	attractin [Bos taurus]	57.5	57.5	100%	5e-08	84%	gi|253560524|ACT32973.1
☐	attractin [Bos taurus]	57.5	57.5	100%	5e-08	84%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	57.5	57.5	100%	5e-08	84%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin isoform 1 [Ceratotherium simum simum]	57.5	57.5	100%	5e-08	84%	gi|478519274|XP_004433859.1
☐	PREDICTED: attractin [Bison bison bison]	57.5	57.5	100%	5e-08	84%	gi|742104093|XP_010834932.1
☐	PREDICTED: attractin isoform X1 [Bubalus bubalis]	57.5	57.5	100%	5e-08	84%	gi|594099676|XP_006072963.1
☐	PREDICTED: attractin [Tupaia chinensis]	57.1	57.1	100%	7e-08	84%	gi|562872246|XP_006164056.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Cavia porcellus]	56.2	56.2	100%	1e-07	84%	gi|514473642|XP_005008408.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	54.9	54.9	100%	4e-07	79%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin isoform X2 [Heterocephalus glaber]	54.9	54.9	100%	4e-07	84%	gi|512956910|XP_004840783.1
☐	PREDICTED: attractin [Trichechus manatus latirostris]	54.9	54.9	100%	4e-07	79%	gi|471400634|XP_004383126.1
☐	Attractin [Heterocephalus glaber]	54.9	54.9	100%	4e-07	84%	gi|351701383|EHB04302.1
☐	PREDICTED: attractin [Camelus ferus]	54.9	54.9	100%	4e-07	79%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Camelus dromedarius]	54.9	54.9	100%	4e-07	79%	gi|744589171|XP_010986570.1
☐	PREDICTED: attractin [Camelus bactrianus]	54.9	54.9	100%	4e-07	79%	gi|743752427|XP_010971103.1
☐	PREDICTED: attractin [Heterocephalus glaber]	54.9	54.9	100%	4e-07	84%	gi|512849696|XP_004886859.1
☐	PREDICTED: attractin isoform X1 [Heterocephalus glaber]	54.9	54.9	100%	4e-07	84%	gi|512956908|XP_004840782.1
☐	PREDICTED: attractin [Callithrix jacchus]	54.9	54.9	100%	4e-07	79%	gi|296200062|XP_002747358.1
☐	PREDICTED: attractin [Tarsius syrichta]	54.5	54.5	100%	5e-07	84%	gi|640796924|XP_008054571.1

☐	PREDICTED: attractin isoform X3 [Cricetulus griseus]	54.1	74.7	94%	5e-07	88%	gi|625288767|XP_007636126.1
☐	attractin [Cricetulus griseus]	54.1	74.7	94%	7e-07	88%	gi|537146168|ERE69758.1
☐	PREDICTED: attractin isoform X1 [Cricetulus griseus]	54.1	74.7	94%	7e-07	88%	gi|354473756|XP_003499099.1
☐	attractin [Cricetulus griseus]	54.1	74.7	94%	7e-07	88%	gi|537146167|ERE69757.1
☐	attractin [Mesocricetus auratus]	54.1	54.1	89%	7e-07	88%	gi|528078159|NP_001268565.1
☐	PREDICTED: attractin [Equus przewalskii]	53.7	53.7	100%	1e-06	79%	gi|664773944|XP_008506219.1
☐	Attractin [Myotis brandtii]	53.7	53.7	100%	1e-06	79%	gi|521031210|EPQ12996.1
☐	PREDICTED: attractin [Myotis brandtii]	53.7	53.7	100%	1e-06	79%	gi|554560893|XP_005874816.1
☐	PREDICTED: attractin [Myotis lucifugus]	53.7	53.7	100%	1e-06	79%	gi|558159591|XP_006096513.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	53.7	53.7	100%	1e-06	79%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin [Orcinus orca]	53.7	53.7	100%	1e-06	79%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin isoform X2 [Pteropus alecto]	53.7	53.7	100%	1e-06	79%	gi|586533634|XP_006921706.1
☐	PREDICTED: attractin isoform X2 [Condylura cristata]	53.2	53.2	100%	1e-06	79%	gi|507961710|XP_004687418.1
☐	PREDICTED: attractin [Otolemur garnettii]	53.2	53.2	100%	1e-06	79%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin isoform X1 [Condylura cristata]	53.2	53.2	100%	1e-06	79%	gi|507961707|XP_004687417.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Nannospalax ga	52.8	52.8	100%	2e-06	79%	gi|674089498|XP_008852735.1
☐	PREDICTED: attractin [Orycteropus afer afer]	52.8	52.8	100%	2e-06	79%	gi|634830430|XP_007958185.1
☐	PREDICTED: attractin [Vicugna pacos]	52.4	52.4	100%	3e-06	74%	gi|560970220|XP_006207473.1
☐	PREDICTED: attractin [Lipotes vexillifer]	52.0	52.0	100%	4e-06	79%	gi|602710450|XP_007465469.1
☐	Attractin [Fukomys damarensis]	51.5	51.5	94%	5e-06	78%	gi|676269096|KFO24512.1
☐	attractin [Rattus norvegicus]	51.5	51.5	89%	5e-06	88%	gi|12275312|BAB21018.1
☐	attractin, isoform CRA_a [Rattus norvegicus]	51.5	51.5	89%	5e-06	88%	gi|149023319|EDL80213.1
☐	PREDICTED: attractin [Microtus ochrogaster]	51.5	51.5	89%	5e-06	88%	gi|532045699|XP_005365652.1
☐	PREDICTED: attractin [Jaculus jaculus]	51.5	51.5	100%	5e-06	74%	gi|507555530|XP_004661535.1
☐	attractin precursor [Rattus norvegicus]	51.5	51.5	89%	5e-06	88%	gi|13786196|NP_112641.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	51.1	51.1	89%	7e-06	82%	gi|585160208|XP_006732353.1
☐	PREDICTED: attractin isoform X2 [Mustela putorius furo]	51.1	51.1	89%	7e-06	82%	gi|511906947|XP_004772933.1

⊟ Alignments

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PREDICTED: attractin isoform X2 [Homo sapiens]

Sequence ID: gi|530426021|ref|XP_005260918.1| **Length:** 1111 **Number of Matches:** 1

Range 1: 261 to 279 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	7e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KISDSSDTVECECSENWKG  19
            KIS+SSDTVECECSENWKG
Sbjct  261  KISNSSDTVECECSENWKG  279
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194380362|dbj|BAG63948.1| **Length:** 1156 **Number of Matches:** 1

Range 1: 145 to 163 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	7e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KISDSSDTVECECSENWKG  19
```

Related Information

Gene - associated gene details

```
                KIS+SSDTVECECSENWKG
Sbjct  145  KISNSSDTVECECSENWKG  163
```

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attractin isoform 4 [Homo sapiens]

Sequence ID: gi|333440461|ref|NP_001193976.1| **Length:** 1156 **Number of Matches:** 1

Range 1: 145 to 163 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	7e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KISDSSDTVECECSENWKG  19
            KIS+SSDTVECECSENWKG
Sbjct  145  KISNSSDTVECECSENWKG  163
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

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PREDICTED: attractin [Gorilla gorilla gorilla]

Sequence ID: gi|426390844|ref|XP_004061806.1| **Length:** 1265 **Number of Matches:** 1

Range 1: 143 to 161 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	7e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KISDSSDTVECECSENWKG  19
            KIS+SSDTVECECSENWKG
Sbjct  143  KISNSSDTVECECSENWKG  161
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: attractin isoform X4 [Pan troglodytes]

Sequence ID: gi|694977854|ref|XP_009435012.1| **Length:** 1269 **Number of Matches:** 1

Range 1: 260 to 278 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	7e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KISDSSDTVECECSENWKG  19
            KIS+SSDTVECECSENWKG
Sbjct  260  KISNSSDTVECECSENWKG  278
```

Related Information

Gene - associated gene details

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How to read this page Blast report description

ATRN_KISNSSDTVECECSENWKG_NonMod

RID B915TPMR01R (Expires on 01-14 09:36 am)

Query ID	lcl|148046	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	19		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

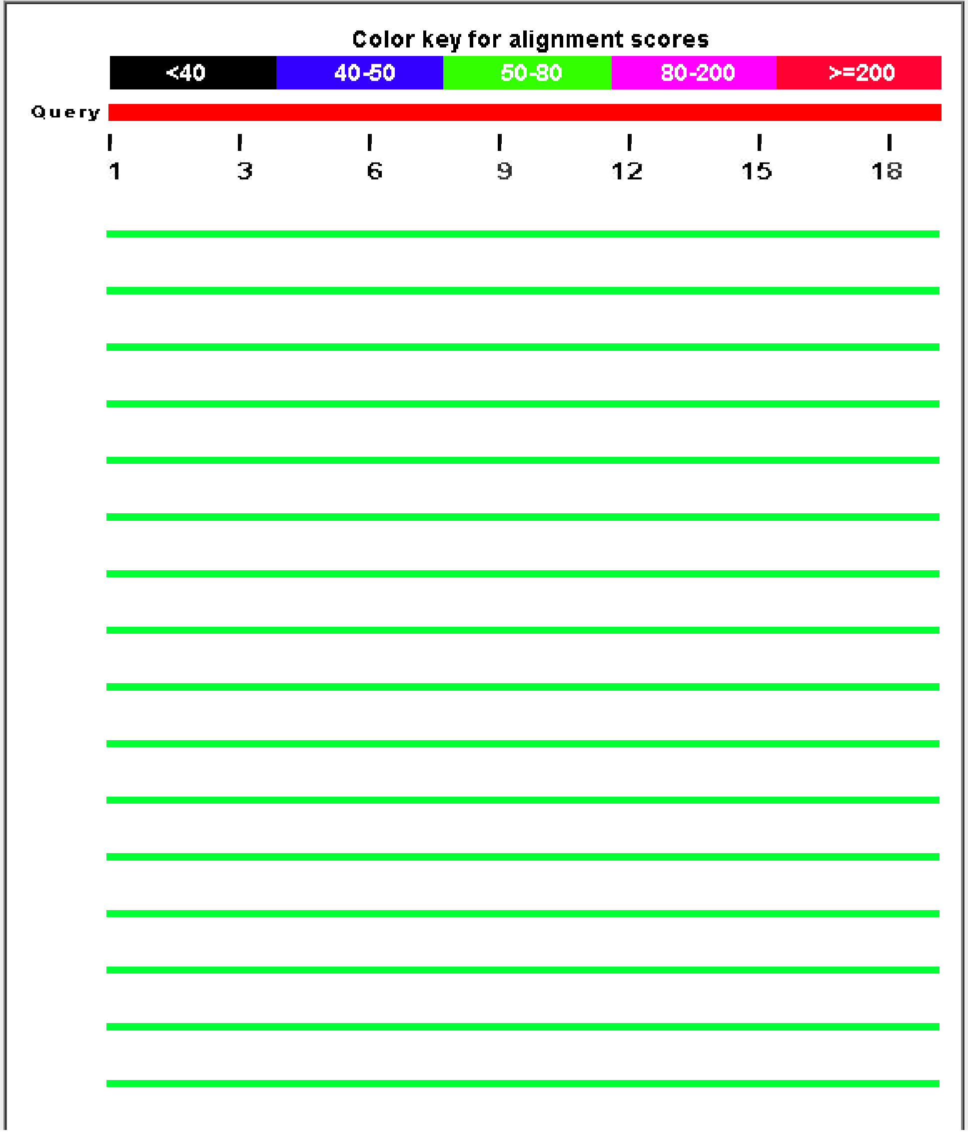
Graphic Summary

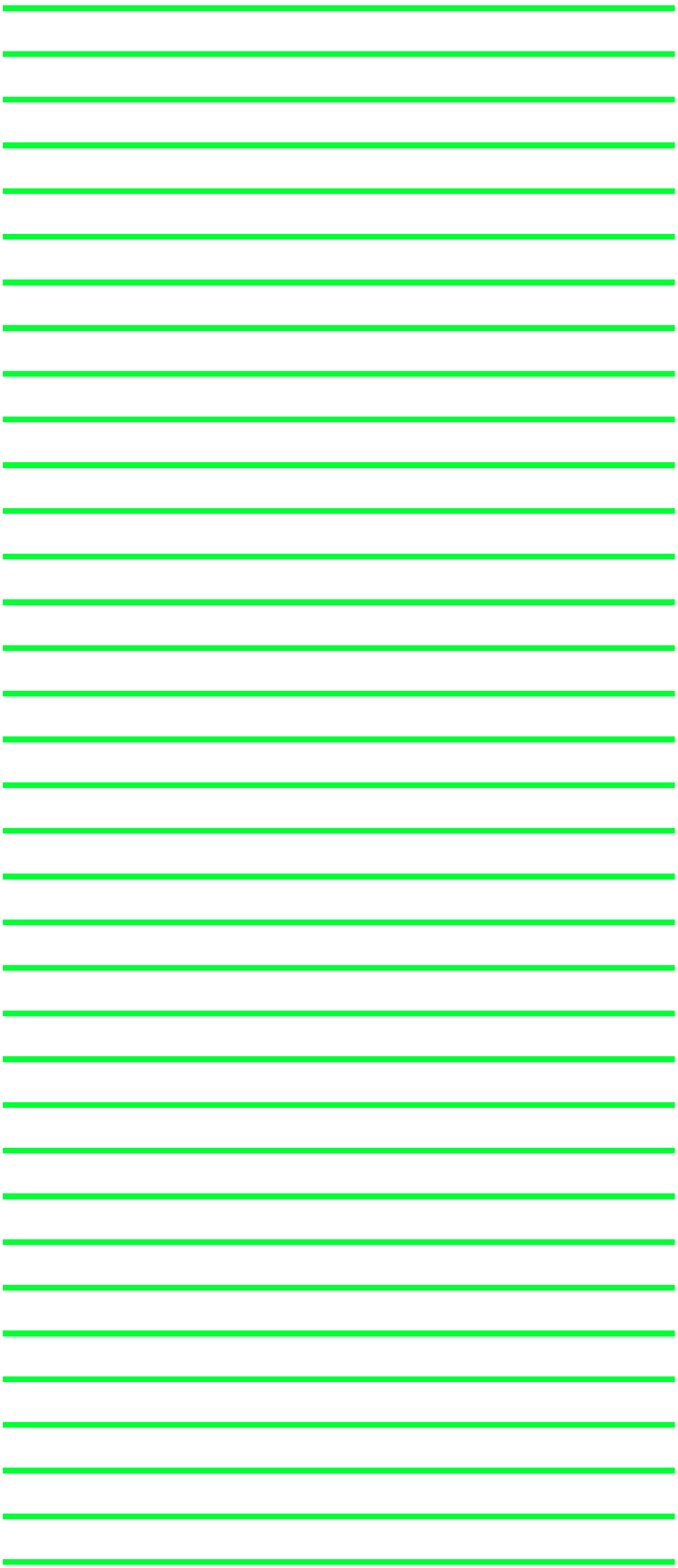
Show Conserved Domains

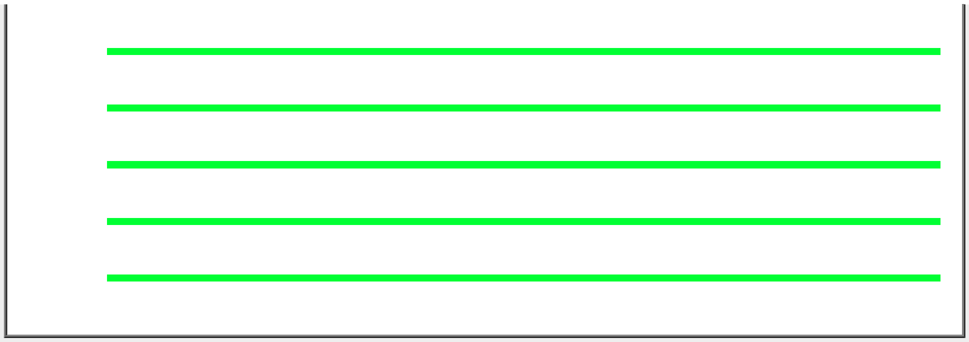
No putative conserved domains have been detected

Distribution of 110 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|530426021|XP_005260918.1
☐	unnamed protein product [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin [Gorilla gorilla gorilla]	65.5	65.5	100%	9e-11	100%	gi|426390844|XP_004061806.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	65.5	65.5	100%	9e-11	100%	gi|694977854|XP_009435012.1
☐	secreted attractin precursor [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|21450863|NP_647538.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Pan paniscus]	65.5	65.5	100%	9e-11	100%	gi|675763672|XP_008973079.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	65.5	65.5	100%	9e-11	100%	gi|694977852|XP_009435011.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|530426019|XP_005260917.1
☐	attractin, isoform CRA_b [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	65.5	65.5	100%	9e-11	100%	gi|694977850|XP_009435010.1
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	65.5	65.5	100%	9e-11	100%	gi|332857715|XP_003316827.1
☐	membrane attractin precursor [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|8118082|AAF72881.1
☐	attractin isoform 1 preproprotein [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|21450861|NP_647537.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	63.0	63.0	100%	6e-10	95%	gi|332257827|XP_003278006.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	63.0	63.0	100%	6e-10	95%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	63.0	63.0	100%	6e-10	95%	gi|4093196|AAD03057.1
☐	PREDICTED: attractin isoform X3 [Chinchilla lanigera]	63.0	85.3	100%	6e-10	95%	gi|533131617|XP_005380852.1
☐	PREDICTED: attractin-like [Octodon degus]	63.0	63.0	100%	6e-10	95%	gi|507657234|XP_004634315.1
☐	PREDICTED: attractin isoform X2 [Chinchilla lanigera]	63.0	85.3	100%	6e-10	95%	gi|533131615|XP_005380851.1
☐	PREDICTED: attractin isoform X1 [Chinchilla lanigera]	63.0	85.3	100%	6e-10	95%	gi|533131613|XP_005380850.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	60.4	60.4	100%	5e-09	89%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	60.4	60.4	100%	5e-09	89%	gi|725600051|XP_010350111.1
☐	Mahogany-like protein [Macaca mulatta]	60.4	60.4	100%	5e-09	89%	gi|355563316|EHH19878.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	60.4	60.4	100%	5e-09	89%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	60.4	60.4	100%	5e-09	89%	gi|635021368|XP_008017720.1
☐							

	Mahogany-like protein [Macaca fascicularis]	60.4	60.4	100%	5e-09	89%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	60.4	60.4	100%	5e-09	89%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	60.4	60.4	100%	5e-09	89%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	60.4	60.4	100%	5e-09	89%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	60.4	60.4	100%	5e-09	89%	gi|724902357|XP_010377335.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	60.4	60.4	100%	5e-09	89%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	60.4	60.4	100%	5e-09	89%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin isoform X2 [Macaca fascicularis]	60.4	60.4	100%	5e-09	89%	gi|544464512|XP_005568510.1
☐	PREDICTED: attractin [Macaca mulatta]	60.4	60.4	100%	5e-09	89%	gi|109092720|XP_001115192.1
☐	PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	60.4	60.4	100%	5e-09	89%	gi|635021360|XP_008017700.1
☐	PREDICTED: attractin isoform X1 [Macaca fascicularis]	60.4	60.4	100%	5e-09	89%	gi|544464510|XP_005568509.1
☐	PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	60.4	60.4	100%	5e-09	89%	gi|635021370|XP_008017729.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	60.0	60.0	100%	6e-09	89%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin-like [Physeter catodon]	60.0	60.0	100%	6e-09	89%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	60.0	60.0	100%	7e-09	89%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin [Sus scrofa]	60.0	60.0	100%	7e-09	89%	gi|545879723|XP_001927324.5
☐	PREDICTED: attractin isoform 2 [Ceratotherium simum simum]	60.0	60.0	100%	7e-09	89%	gi|478519276|XP_004433860.1
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	60.0	60.0	100%	7e-09	89%	gi|594099680|XP_006072965.1
☐	attractin [Sus scrofa]	60.0	60.0	100%	7e-09	89%	gi|146741346|BAF62328.1
☐	PREDICTED: attractin [Panthera tigris altaica]	60.0	60.0	100%	7e-09	89%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin [Capra hircus]	60.0	60.0	100%	7e-09	89%	gi|548490191|XP_005688293.1
☐	PREDICTED: attractin [Bos mutus]	60.0	60.0	100%	7e-09	89%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Ovis aries]	60.0	60.0	100%	7e-09	89%	gi|426241795|XP_004014773.1
☐	PREDICTED: attractin [Felis catus]	60.0	60.0	100%	7e-09	89%	gi|586981105|XP_003983758.2
☐	PREDICTED: attractin [Echinops telfairi]	60.0	60.0	100%	7e-09	89%	gi|507626122|XP_004697922.1
☐	attractin [Bos taurus]	60.0	60.0	100%	7e-09	89%	gi|253560524|ACT32973.1
☐	attractin [Bos taurus]	60.0	60.0	100%	7e-09	89%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	60.0	60.0	100%	7e-09	89%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin isoform 1 [Ceratotherium simum simum]	60.0	60.0	100%	7e-09	89%	gi|478519274|XP_004433859.1
☐	PREDICTED: attractin isoform X2 [Bos taurus]	60.0	60.0	100%	7e-09	89%	gi|528973313|XP_005214542.1
☐	PREDICTED: attractin isoform X1 [Bubalus bubalis]	60.0	60.0	100%	7e-09	89%	gi|594099676|XP_006072963.1
☐	PREDICTED: attractin isoform X1 [Bos taurus]	60.0	60.0	100%	7e-09	89%	gi|528973311|XP_005214541.1
☐	PREDICTED: attractin [Tupaia chinensis]	59.6	59.6	100%	9e-09	89%	gi|562872246|XP_006164056.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Cavia porcellus]	58.7	58.7	100%	2e-08	89%	gi|514473642|XP_005008408.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	57.5	57.5	100%	5e-08	84%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin isoform X2 [Heterocephalus glaber]	57.5	57.5	100%	5e-08	89%	gi|512956910|XP_004840783.1
☐	PREDICTED: attractin [Trichechus manatus latirostris]	57.5	57.5	100%	5e-08	84%	gi|471400634|XP_004383126.1
☐	Attractin [Heterocephalus glaber]	57.5	57.5	100%	5e-08	89%	gi|351701383|EHB04302.1
☐	PREDICTED: attractin [Camelus ferus]	57.5	57.5	100%	5e-08	84%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Heterocephalus glaber]	57.5	57.5	100%	5e-08	89%	gi|512849696|XP_004886859.1
☐	PREDICTED: attractin isoform X1 [Heterocephalus glaber]	57.5	57.5	100%	5e-08	89%	gi|512956908|XP_004840782.1
☐	PREDICTED: attractin [Callithrix jacchus]	57.5	57.5	100%	5e-08	84%	gi|296200062|XP_002747358.1
☐	PREDICTED: attractin [Tarsius syrichta]	57.1	57.1	100%	7e-08	89%	gi|640796924|XP_008054571.1
☐	PREDICTED: attractin isoform X3 [Cricetulus griseus]	56.6	79.7	94%	7e-08	94%	gi|625288767|XP_007636126.1
☐	attractin [Cricetulus griseus]	56.6	79.7	94%	9e-08	94%	gi|537146168|ERE69758.1

☐	PREDICTED: attractin isoform X1 [Cricetulus griseus]	56.6	79.7	94%	9e-08	94%	gi|354473756|XP_003499099.1
☐	attractin [Cricetulus griseus]	56.6	79.7	94%	9e-08	94%	gi|537146167|ERE69757.1
☐	attractin [Mesocricetus auratus]	56.6	56.6	89%	9e-08	94%	gi|528078159|NP_001268565.1
☐	PREDICTED: attractin [Equus przewalskii]	56.2	56.2	100%	1e-07	84%	gi|664773944|XP_008506219.1
☐	Attractin [Myotis brandtii]	56.2	56.2	100%	1e-07	84%	gi|521031210|EPQ12996.1
☐	PREDICTED: attractin [Myotis brandtii]	56.2	56.2	100%	1e-07	84%	gi|554560893|XP_005874816.1
☐	PREDICTED: attractin [Myotis lucifugus]	56.2	56.2	100%	1e-07	84%	gi|558159591|XP_006096513.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	56.2	56.2	100%	1e-07	84%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin [Orcinus orca]	56.2	56.2	100%	1e-07	84%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin isoform X2 [Pteropus alecto]	56.2	56.2	100%	1e-07	84%	gi|586533634|XP_006921706.1
☐	PREDICTED: attractin isoform X2 [Condylura cristata]	55.8	55.8	100%	2e-07	84%	gi|507961710|XP_004687418.1
☐	PREDICTED: attractin [Otolemur garnettii]	55.8	55.8	100%	2e-07	84%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin isoform X1 [Condylura cristata]	55.8	55.8	100%	2e-07	84%	gi|507961707|XP_004687417.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Nannospalax ga	55.4	55.4	100%	2e-07	84%	gi|674089498|XP_008852735.1
☐	PREDICTED: attractin [Orycteropus afer afer]	55.4	55.4	100%	2e-07	84%	gi|634830430|XP_007958185.1
☐	PREDICTED: attractin [Vicugna pacos]	54.9	54.9	100%	3e-07	79%	gi|560970220|XP_006207473.1
☐	PREDICTED: attractin [Lipotes vexillifer]	54.5	54.5	100%	5e-07	84%	gi|602710450|XP_007465469.1
☐	Attractin [Fukomys damarensis]	54.1	54.1	94%	6e-07	83%	gi|676269096|KFO24512.1
☐	attractin [Rattus norvegicus]	54.1	75.5	94%	7e-07	94%	gi|12275312|BAB21018.1
☐	attractin, isoform CRA_a [Rattus norvegicus]	54.1	75.5	94%	7e-07	94%	gi|149023319|EDL80213.1
☐	PREDICTED: attractin [Jaculus jaculus]	54.1	54.1	100%	7e-07	79%	gi|507555530|XP_004661535.1
☐	attractin precursor [Rattus norvegicus]	54.1	75.5	94%	7e-07	94%	gi|13786196|NP_112641.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	53.7	53.7	89%	9e-07	88%	gi|585160208|XP_006732353.1
☐	PREDICTED: attractin isoform X2 [Mustela putorius furo]	53.7	53.7	89%	9e-07	88%	gi|511906947|XP_004772933.1
☐	PREDICTED: attractin [Mustela putorius furo]	53.7	53.7	89%	9e-07	88%	gi|511947743|XP_004792355.1
☐	PREDICTED: attractin [Peromyscus maniculatus bairdii]	53.7	53.7	89%	9e-07	88%	gi|589943852|XP_006984624.1
☐	PREDICTED: attractin isoform X1 [Mustela putorius furo]	53.7	53.7	89%	9e-07	88%	gi|511906945|XP_004772932.1

Alignments

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PREDICTED: attractin isoform X2 [Homo sapiens]

Sequence ID: gi|530426021|ref|XP_005260918.1| **Length:** 1111 **Number of Matches:** 1

Range 1: 261 to 279 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	9e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KISNSSDTVECECSENWKG  19
            KISNSSDTVECECSENWKG
Sbjct  261  KISNSSDTVECECSENWKG  279
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194380362|dbj|BAG63948.1| **Length:** 1156 **Number of Matches:** 1

Range 1: 145 to 163 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	9e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KISNSSDTVECECSENWKG  19
```

Related Information

Gene - associated gene details

```
            KISNSSDTVECECSENWKG
Sbjct  145  KISNSSDTVECECSENWKG  163
```

attractin isoform 4 [Homo sapiens]

Sequence ID: gi|333440461|ref|NP_001193976.1| **Length:** 1156 **Number of Matches:** 1

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Range 1: 145 to 163 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	9e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KISNSSDTVECECSENWKG  19
            KISNSSDTVECECSENWKG
Sbjct  145  KISNSSDTVECECSENWKG  163
```

PREDICTED: attractin [Gorilla gorilla gorilla]

Sequence ID: gi|426390844|ref|XP_004061806.1| **Length:** 1265 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 143 to 161 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	9e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KISNSSDTVECECSENWKG  19
            KISNSSDTVECECSENWKG
Sbjct  143  KISNSSDTVECECSENWKG  161
```

PREDICTED: attractin isoform X4 [Pan troglodytes]

Sequence ID: gi|694977854|ref|XP_009435012.1| **Length:** 1269 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 260 to 278 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	9e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KISNSSDTVECECSENWKG  19
            KISNSSDTVECECSENWKG
Sbjct  260  KISNSSDTVECECSENWKG  278
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

ATRN_KMPSQAPTGNFYPQPLLDSSMCLEDSRY_Mod

RID BHF3AHKM014 (Expires on 01-17 14:23 pm)

Query ID lcl|91517
Description None
Molecule type amino acid
Query Length 28

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

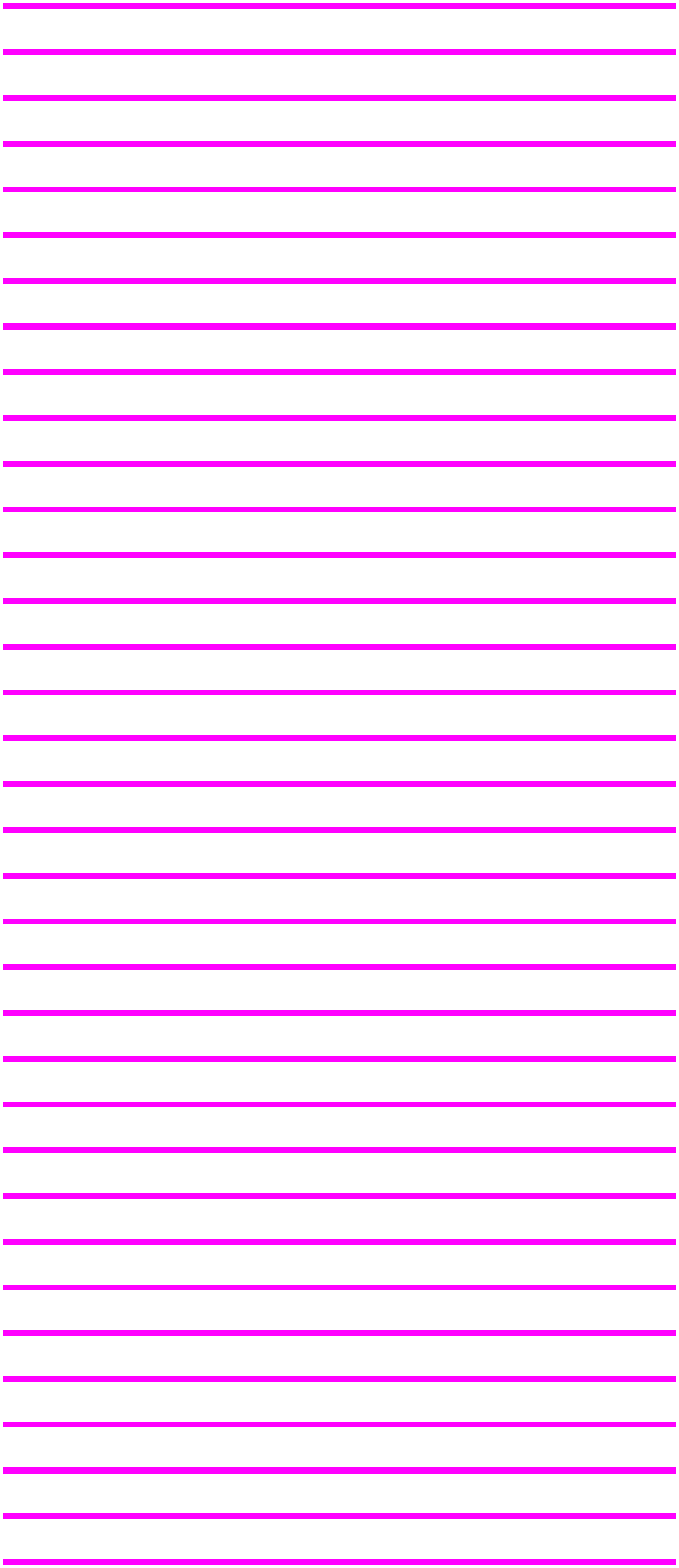
Graphic Summary

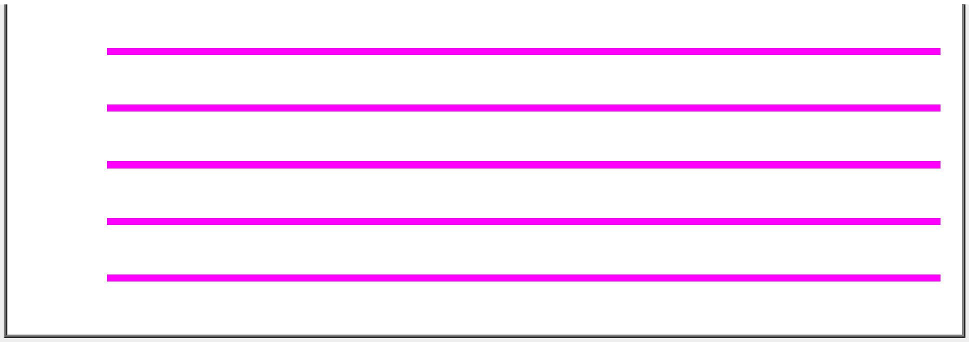
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 98 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: attractin-like [Pan paniscus]	94.0	94.0	100%	4e-20	96%	gi|397513332|XP_003826972.1
☐	KIAA0548 protein [Homo sapiens]	94.0	94.0	100%	5e-20	96%	gi|3043620|BAA25474.1
☐	PREDICTED: attractin isoform X2 [Papio anubis]	94.0	94.0	100%	6e-20	96%	gi|685567345|XP_009214752.1
☐	PREDICTED: attractin [Pongo abelii]	94.0	94.0	100%	6e-20	96%	gi|297706621|XP_002830129.1
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	94.0	94.0	100%	6e-20	96%	gi|530426021|XP_005260918.1
☐	PREDICTED: attractin isoform X1 [Papio anubis]	94.0	94.0	100%	6e-20	96%	gi|685567343|XP_009214751.1
☐	unnamed protein product [Homo sapiens]	94.0	94.0	100%	6e-20	96%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	94.0	94.0	100%	6e-20	96%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	94.0	94.0	100%	6e-20	96%	gi|332257827|XP_003278006.1
☐	PREDICTED: attractin [Gorilla gorilla gorilla]	94.0	94.0	100%	6e-20	96%	gi|426390844|XP_004061806.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	94.0	94.0	100%	6e-20	96%	gi|694977854|XP_009435012.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	94.0	94.0	100%	6e-20	96%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	94.0	94.0	100%	6e-20	96%	gi|4093196|AAD03057.1
☐	secreted attractin precursor [Homo sapiens]	94.0	94.0	100%	6e-20	96%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	94.0	94.0	100%	6e-20	96%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	94.0	94.0	100%	6e-20	96%	gi|21450863|NP_647538.1
☐	Mahogany-like protein [Macaca mulatta]	94.0	94.0	100%	6e-20	96%	gi|355563316|EHH19878.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	94.0	94.0	100%	6e-20	96%	gi|694977852|XP_009435011.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	94.0	94.0	100%	6e-20	96%	gi|530426019|XP_005260917.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	94.0	94.0	100%	6e-20	96%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	94.0	94.0	100%	6e-20	96%	gi|635021368|XP_008017720.1
☐	Mahogany-like protein [Macaca fascicularis]	94.0	94.0	100%	6e-20	96%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	94.0	94.0	100%	6e-20	96%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	94.0	94.0	100%	6e-20	96%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	94.0	94.0	100%	6e-20	96%	gi|724902357|XP_010377335.1
☐	attractin, isoform CRA_b [Homo sapiens]	94.0	94.0	100%	6e-20	96%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	94.0	94.0	100%	6e-20	96%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	94.0	94.0	100%	6e-20	96%	gi|694977850|XP_009435010.1
☐							

	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	94.0	94.0	100%	6e-20	96%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin [Otolemur garnettii]	94.0	94.0	100%	6e-20	96%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	94.0	94.0	100%	6e-20	96%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin [Ochotona princeps]	94.0	94.0	100%	6e-20	96%	gi|504146589|XP_004585711.1
☐	PREDICTED: attractin [Callithrix jacchus]	94.0	94.0	100%	6e-20	96%	gi|296200062|XP_002747358.1
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	94.0	94.0	100%	6e-20	96%	gi|332857715|XP_003316827.1
☐	membrane attractin precursor [Homo sapiens]	94.0	94.0	100%	6e-20	96%	gi|8118082|AAF72881.1
☐	attractin isoform 1 preproprotein [Homo sapiens]	94.0	94.0	100%	6e-20	96%	gi|21450861|NP_647537.1
☐	PREDICTED: attractin isoform X2 [Macaca fascicularis]	94.0	94.0	100%	6e-20	96%	gi|544464512|XP_005568510.1
☐	PREDICTED: attractin [Macaca mulatta]	94.0	94.0	100%	6e-20	96%	gi|109092720|XP_001115192.1
☐	PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	94.0	94.0	100%	6e-20	96%	gi|635021360|XP_008017700.1
☐	PREDICTED: attractin isoform X1 [Macaca fascicularis]	94.0	94.0	100%	6e-20	96%	gi|544464510|XP_005568509.1
☐	PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	94.0	94.0	100%	6e-20	96%	gi|635021370|XP_008017729.1
☐	PREDICTED: attractin isoform X2 [Pteropus alecto]	94.0	94.0	100%	6e-20	96%	gi|586533634|XP_006921706.1
☐	PREDICTED: attractin [Lipotes vexillifer]	91.0	91.0	100%	6e-19	93%	gi|602710450|XP_007465469.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	89.7	89.7	100%	1e-18	93%	gi|667345974|XP_008563464.1
☐	Attractin [Myotis brandtii]	90.1	90.1	100%	1e-18	93%	gi|521031210|EPQ12996.1
☐	PREDICTED: attractin [Myotis brandtii]	90.1	90.1	100%	1e-18	93%	gi|554560893|XP_005874816.1
☐	PREDICTED: attractin [Myotis lucifugus]	90.1	90.1	100%	1e-18	93%	gi|558159591|XP_006096513.1
☐	PREDICTED: attractin [Eptesicus fuscus]	90.1	90.1	100%	1e-18	93%	gi|641701319|XP_008139256.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	89.7	89.7	100%	2e-18	93%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	89.7	89.7	100%	2e-18	93%	gi|725600051|XP_010350111.1
☐	Attractin [Myotis davidii]	89.7	89.7	100%	2e-18	93%	gi|432111133|ELK34519.1
☐	PREDICTED: attractin [Myotis davidii]	89.7	89.7	100%	2e-18	93%	gi|584075971|XP_006758187.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	89.7	89.7	100%	2e-18	93%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin [Tarsius syrichta]	89.3	89.3	100%	2e-18	93%	gi|640796924|XP_008054571.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	87.6	87.6	100%	9e-18	93%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin-like [Physeter catodon]	87.6	87.6	100%	9e-18	93%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin [Equus przewalskii]	87.6	87.6	100%	9e-18	93%	gi|664773944|XP_008506219.1
☐	PREDICTED: attractin [Orcinus orca]	87.6	87.6	100%	9e-18	93%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin [Orycteropus afer afer]	87.6	87.6	100%	9e-18	93%	gi|634830430|XP_007958185.1
☐	attractin isoform 1 preproprotein [Camelus ferus]	86.7	86.7	100%	2e-17	90%	gi|528759526|EPY79185.1
☐	PREDICTED: attractin [Camelus ferus]	86.7	86.7	100%	2e-17	90%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Camelus dromedarius]	86.7	86.7	100%	2e-17	90%	gi|744589171|XP_010986570.1
☐	PREDICTED: attractin [Camelus bactrianus]	86.7	86.7	100%	2e-17	90%	gi|743752427|XP_010971103.1
☐	PREDICTED: attractin [Vicugna pacos]	86.7	86.7	100%	2e-17	90%	gi|560970220|XP_006207473.1
☐	attractin [Ovis aries]	84.2	84.2	100%	9e-17	89%	gi|78499351|ABB45710.1
☐	attractin [Bos taurus]	84.2	84.2	100%	1e-16	89%	gi|190683717|ACE82176.1
☐	attractin [Canis lupus familiaris]	84.2	84.2	100%	1e-16	89%	gi|339892849|AEK21787.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	84.2	84.2	100%	1e-16	89%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin isoform X1 [Bos taurus]	84.2	84.2	100%	1e-16	89%	gi|741947708|XP_005214542.2
☐	PREDICTED: attractin isoform X2 [Canis lupus familiaris]	84.2	84.2	100%	1e-16	89%	gi|545540090|XP_005634905.1
☐	PREDICTED: attractin [Capra hircus]	84.2	84.2	100%	1e-16	89%	gi|548490191|XP_005688293.1
☐	PREDICTED: attractin [Bos mutus]	84.2	84.2	100%	1e-16	89%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Ovis aries]	84.2	84.2	100%	1e-16	89%	gi|426241795|XP_004014773.1

☐	attractin [Bos taurus]	84.2	84.2	100%	1e-16	89%	gi|253560524|ACT32973.1
☐	attractin [Bos taurus]	84.2	84.2	100%	1e-16	89%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X3 [Canis lupus familiaris]	84.2	84.2	100%	1e-16	89%	gi|73991942|XP_534360.2
☐	PREDICTED: attractin [Bison bison bison]	84.2	84.2	100%	1e-16	89%	gi|742104093|XP_010834932.1
☐	PREDICTED: attractin [Tupaia chinensis]	84.2	84.2	100%	1e-16	89%	gi|562872246|XP_006164056.1
☐	PREDICTED: attractin isoform X1 [Canis lupus familiaris]	84.2	84.2	100%	1e-16	89%	gi|545540087|XP_005634904.1
☐	PREDICTED: attractin [Panthera tigris altaica]	83.3	83.3	100%	3e-16	89%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin [Felis catus]	83.3	83.3	100%	3e-16	89%	gi|586981105|XP_003983758.2
☐	PREDICTED: attractin isoform X1 [Oryctolagus cuniculus]	82.9	82.9	100%	4e-16	89%	gi|291388868|XP_002710968.1
☐	PREDICTED: attractin isoform X2 [Oryctolagus cuniculus]	82.9	82.9	100%	4e-16	89%	gi|655716500|XP_008254470.1
☐	PREDICTED: attractin [Jaculus jaculus]	82.5	82.5	100%	5e-16	89%	gi|507555530|XP_004661535.1
☐	PREDICTED: attractin isoform X2 [Mustela putorius furo]	81.7	81.7	100%	1e-15	86%	gi|511906947|XP_004772933.1
☐	PREDICTED: attractin [Mustela putorius furo]	81.7	81.7	100%	1e-15	86%	gi|511947743|XP_004792355.1
☐	PREDICTED: attractin isoform X1 [Mustela putorius furo]	81.7	81.7	100%	1e-15	86%	gi|511906945|XP_004772932.1
☐	PREDICTED: attractin [Sus scrofa]	81.2	81.2	100%	1e-15	86%	gi|545879723|XP_001927324.5
☐	PREDICTED: attractin isoform 2 [Ceratotherium simum simum]	81.2	81.2	100%	1e-15	89%	gi|478519276|XP_004433860.1
☐	attractin [Sus scrofa]	81.2	81.2	100%	1e-15	86%	gi|146741346|BAF62328.1
☐	PREDICTED: attractin isoform 1 [Ceratotherium simum simum]	81.2	81.2	100%	1e-15	89%	gi|478519274|XP_004433859.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	80.8	80.8	100%	2e-15	86%	gi|585160208|XP_006732353.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	80.8	80.8	100%	2e-15	86%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	80.8	80.8	100%	2e-15	86%	gi|594099680|XP_006072965.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	80.8	80.8	100%	2e-15	86%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin [Odobenus rosmarus divergens]	80.8	80.8	100%	2e-15	86%	gi|472357214|XP_004398236.1
☐	PREDICTED: attractin isoform X1 [Bubalus bubalis]	80.8	80.8	100%	2e-15	86%	gi|594099676|XP_006072963.1
☐	PREDICTED: attractin [Chrysochloris asiatica]	80.4	80.4	100%	3e-15	86%	gi|586488825|XP_006874887.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: attractin-like [Pan paniscus]

Sequence ID: gi|397513332|ref|XP_003826972.1| **Length:** 265 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 214 to 241 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.0 bits(214)	4e-20	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    KMPSQAPTGNFYPQPLLDSSMCLEDSRY  28
            KMPSQAPTGNFYPQPLL+SSMCLEDSRY
Sbjct  214  KMPSQAPTGNFYPQPLLNSSMCLEDSRY  241
```

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KIAA0548 protein [Homo sapiens]

Sequence ID: gi|3043620|dbj|BAA25474.1| **Length:** 452 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 49 to 76 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.0 bits(214)	5e-20	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1   KMPSQAPTGNFYPQPLLDSSMCLEDSRY  28
           KMPSQAPTGNFYPQPLL+SSMCLEDSRY
Sbjct  49  KMPSQAPTGNFYPQPLLNSSMCLEDSRY  76
```

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PREDICTED: attractin isoform X2 [Papio anubis]

Sequence ID: gi|685567345|ref|XP_009214752.1| **Length:** 989 **Number of Matches:** 1

Range 1: 716 to 743 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.0 bits(214)	6e-20	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    KMPSQAPTGNFYPQPLLDSSMCLEDSRY  28
            KMPSQAPTGNFYPQPLL+SSMCLEDSRY
Sbjct  716  KMPSQAPTGNFYPQPLLNSSMCLEDSRY  743
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: attractin, partial [Pongo abelii]

Sequence ID: gi|297706621|ref|XP_002830129.1| **Length:** 1058 **Number of Matches:** 1

Range 1: 655 to 682 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.0 bits(214)	6e-20	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    KMPSQAPTGNFYPQPLLDSSMCLEDSRY  28
            KMPSQAPTGNFYPQPLL+SSMCLEDSRY
Sbjct  655  KMPSQAPTGNFYPQPLLNSSMCLEDSRY  682
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: attractin isoform X2 [Homo sapiens]

Sequence ID: gi|530426021|ref|XP_005260918.1| **Length:** 1111 **Number of Matches:** 1

Range 1: 1026 to 1053 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
94.0 bits(214)	6e-20	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1     KMPSQAPTGNFYPQPLLDSSMCLEDSRY  28
             KMPSQAPTGNFYPQPLL+SSMCLEDSRY
Sbjct  1026  KMPSQAPTGNFYPQPLLNSSMCLEDSRY  1053
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - B91Z5M9701R

Your search parameters were adjusted to search for a short input sequence.

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How to read this page | Blast report description

ATRN_KMPSQAPTGNFYPQPLLNSSMCLEDSRY_NonMod

RID B91Z5M9701R (Expires on 01-14 09:50 am)

Query ID	lcl|75302	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	28		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

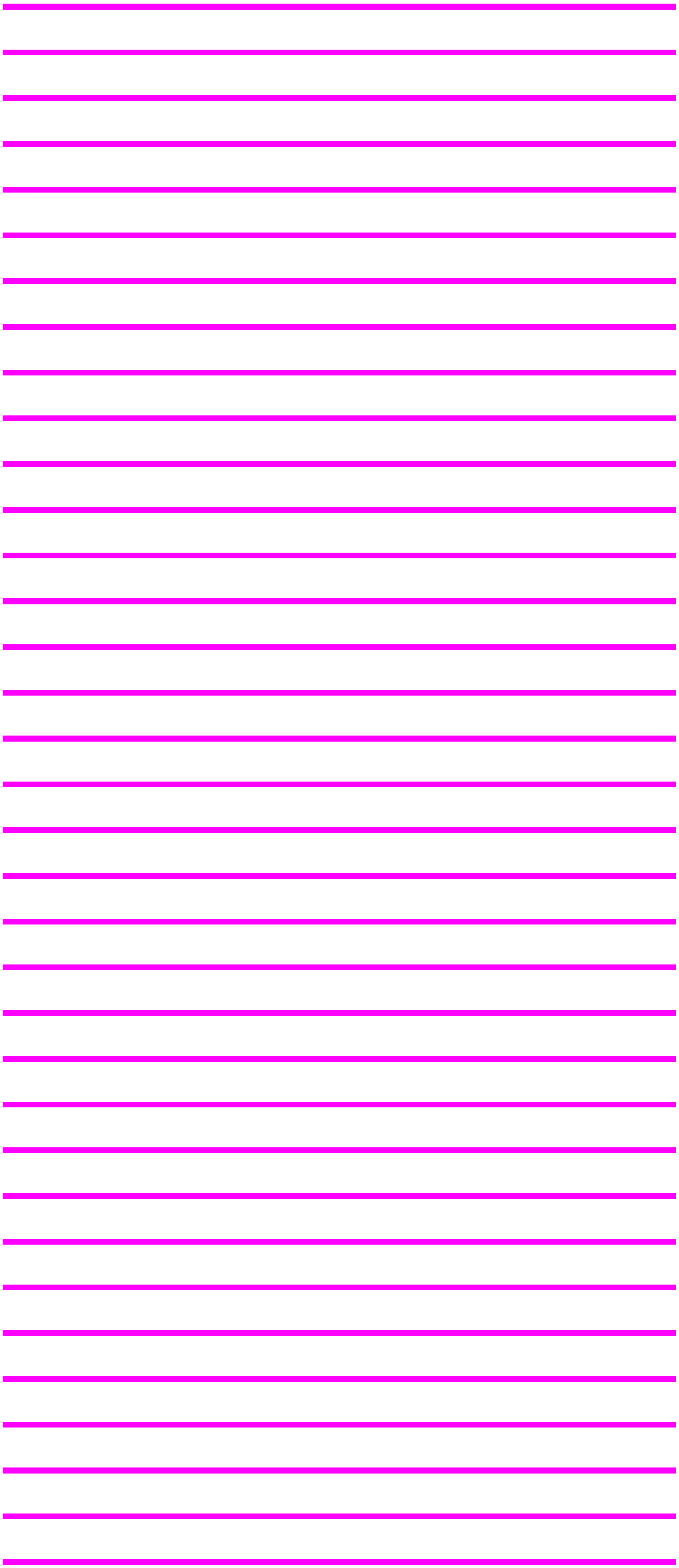
Graphic Summary

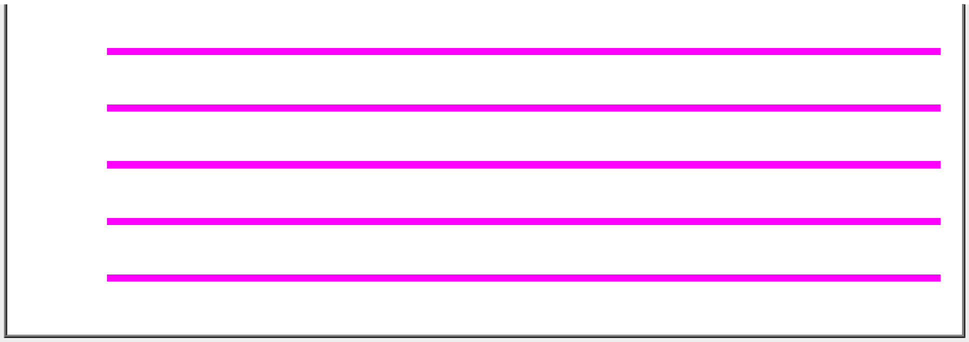
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: attractin-like [Pan paniscus]	96.5	96.5	100%	5e-21	100%	gi|397513332|XP_003826972.1
☐	KIAA0548 protein [Homo sapiens]	96.5	96.5	100%	7e-21	100%	gi|3043620|BAA25474.1
☐	PREDICTED: attractin isoform X2 [Papio anubis]	96.5	96.5	100%	8e-21	100%	gi|685567345|XP_009214752.1
☐	PREDICTED: attractin [Pongo abelii]	96.5	96.5	100%	8e-21	100%	gi|297706621|XP_002830129.1
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	96.5	96.5	100%	8e-21	100%	gi|530426021|XP_005260918.1
☐	PREDICTED: attractin isoform X1 [Papio anubis]	96.5	96.5	100%	8e-21	100%	gi|685567343|XP_009214751.1
☐	unnamed protein product [Homo sapiens]	96.5	96.5	100%	8e-21	100%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	96.5	96.5	100%	8e-21	100%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	96.5	96.5	100%	8e-21	100%	gi|332257827|XP_003278006.1
☐	PREDICTED: attractin [Gorilla gorilla gorilla]	96.5	96.5	100%	8e-21	100%	gi|426390844|XP_004061806.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	96.5	96.5	100%	8e-21	100%	gi|694977854|XP_009435012.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	96.5	96.5	100%	8e-21	100%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	96.5	96.5	100%	8e-21	100%	gi|4093196|AAD03057.1
☐	secreted attractin precursor [Homo sapiens]	96.5	96.5	100%	8e-21	100%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	96.5	96.5	100%	8e-21	100%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	96.5	96.5	100%	8e-21	100%	gi|21450863|NP_647538.1
☐	Mahogany-like protein [Macaca mulatta]	96.5	96.5	100%	8e-21	100%	gi|355563316|EHH19878.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	96.5	96.5	100%	8e-21	100%	gi|694977852|XP_009435011.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	96.5	96.5	100%	8e-21	100%	gi|530426019|XP_005260917.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	96.5	96.5	100%	8e-21	100%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	96.5	96.5	100%	8e-21	100%	gi|635021368|XP_008017720.1
☐	Mahogany-like protein [Macaca fascicularis]	96.5	96.5	100%	8e-21	100%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	96.5	96.5	100%	8e-21	100%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	96.5	96.5	100%	8e-21	100%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	96.5	96.5	100%	8e-21	100%	gi|724902357|XP_010377335.1
☐	attractin, isoform CRA_b [Homo sapiens]	96.5	96.5	100%	8e-21	100%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	96.5	96.5	100%	8e-21	100%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	96.5	96.5	100%	8e-21	100%	gi|694977850|XP_009435010.1
☐							

	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	96.5	96.5	100%	8e-21	100%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin [Otolemur garnettii]	96.5	96.5	100%	8e-21	100%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	96.5	96.5	100%	8e-21	100%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin [Ochotona princeps]	96.5	96.5	100%	8e-21	100%	gi|504146589|XP_004585711.1
☐	PREDICTED: attractin [Callithrix jacchus]	96.5	96.5	100%	8e-21	100%	gi|296200062|XP_002747358.1
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	96.5	96.5	100%	8e-21	100%	gi|332857715|XP_003316827.1
☐	membrane attractin precursor [Homo sapiens]	96.5	96.5	100%	8e-21	100%	gi|8118082|AAF72881.1
☐	attractin isoform 1 preproprotein [Homo sapiens]	96.5	96.5	100%	8e-21	100%	gi|21450861|NP_647537.1
☐	PREDICTED: attractin isoform X2 [Macaca fascicularis]	96.5	96.5	100%	8e-21	100%	gi|544464512|XP_005568510.1
☐	PREDICTED: attractin [Macaca mulatta]	96.5	96.5	100%	8e-21	100%	gi|109092720|XP_001115192.1
☐	PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	96.5	96.5	100%	8e-21	100%	gi|635021360|XP_008017700.1
☐	PREDICTED: attractin isoform X1 [Macaca fascicularis]	96.5	96.5	100%	8e-21	100%	gi|544464510|XP_005568509.1
☐	PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	96.5	96.5	100%	8e-21	100%	gi|635021370|XP_008017729.1
☐	PREDICTED: attractin isoform X2 [Pteropus alecto]	96.5	96.5	100%	8e-21	100%	gi|586533634|XP_006921706.1
☐	PREDICTED: attractin [Lipotes vexillifer]	93.5	93.5	100%	8e-20	96%	gi|602710450|XP_007465469.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	92.3	92.3	100%	1e-19	96%	gi|667345974|XP_008563464.1
☐	Attractin [Myotis brandtii]	92.7	92.7	100%	2e-19	96%	gi|521031210|EPQ12996.1
☐	PREDICTED: attractin [Myotis brandtii]	92.7	92.7	100%	2e-19	96%	gi|554560893|XP_005874816.1
☐	PREDICTED: attractin [Myotis lucifugus]	92.7	92.7	100%	2e-19	96%	gi|558159591|XP_006096513.1
☐	PREDICTED: attractin [Eptesicus fuscus]	92.7	92.7	100%	2e-19	96%	gi|641701319|XP_008139256.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	92.3	92.3	100%	2e-19	96%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	92.3	92.3	100%	2e-19	96%	gi|725600051|XP_010350111.1
☐	Attractin [Myotis davidii]	92.3	92.3	100%	2e-19	96%	gi|432111133|ELK34519.1
☐	PREDICTED: attractin [Myotis davidii]	92.3	92.3	100%	2e-19	96%	gi|584075971|XP_006758187.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	92.3	92.3	100%	2e-19	96%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin [Tarsius syrichta]	91.8	91.8	100%	3e-19	96%	gi|640796924|XP_008054571.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	90.1	90.1	100%	1e-18	96%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin-like [Physeter catodon]	90.1	90.1	100%	1e-18	96%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin [Equus przewalskii]	90.1	90.1	100%	1e-18	96%	gi|664773944|XP_008506219.1
☐	PREDICTED: attractin [Orcinus orca]	90.1	90.1	100%	1e-18	96%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin [Orycteropus afer afer]	90.1	90.1	100%	1e-18	96%	gi|634830430|XP_007958185.1
☐	attractin isoform 1 preproprotein [Camelus ferus]	89.3	89.3	100%	2e-18	93%	gi|528759526|EPY79185.1
☐	PREDICTED: attractin [Camelus ferus]	89.3	89.3	100%	2e-18	93%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Vicugna pacos]	89.3	89.3	100%	2e-18	93%	gi|560970220|XP_006207473.1
☐	attractin [Ovis aries]	86.7	86.7	100%	1e-17	93%	gi|78499351|ABB45710.1
☐	attractin [Bos taurus]	86.7	86.7	100%	2e-17	93%	gi|190683717|ACE82176.1
☐	attractin [Canis lupus familiaris]	86.7	86.7	100%	2e-17	93%	gi|339892849|AEK21787.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	86.7	86.7	100%	2e-17	93%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin isoform X2 [Canis lupus familiaris]	86.7	86.7	100%	2e-17	93%	gi|545540090|XP_005634905.1
☐	PREDICTED: attractin [Capra hircus]	86.7	86.7	100%	2e-17	93%	gi|548490191|XP_005688293.1
☐	PREDICTED: attractin [Bos mutus]	86.7	86.7	100%	2e-17	93%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Ovis aries]	86.7	86.7	100%	2e-17	93%	gi|426241795|XP_004014773.1
☐	attractin [Bos taurus]	86.7	86.7	100%	2e-17	93%	gi|253560524|ACT32973.1
☐	attractin [Bos taurus]	86.7	86.7	100%	2e-17	93%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X3 [Canis lupus familiaris]	86.7	86.7	100%	2e-17	93%	gi|73991942|XP_534360.2

☐	PREDICTED: attractin isoform X2 [Bos taurus]	86.7	86.7	100%	2e-17	93%	gi|528973313|XP_005214542.1
☐	PREDICTED: attractin [Tupaia chinensis]	86.7	86.7	100%	2e-17	93%	gi|562872246|XP_006164056.1
☐	PREDICTED: attractin isoform X1 [Canis lupus familiaris]	86.7	86.7	100%	2e-17	93%	gi|545540087|XP_005634904.1
☐	PREDICTED: attractin isoform X1 [Bos taurus]	86.7	86.7	100%	2e-17	93%	gi|528973311|XP_005214541.1
☐	PREDICTED: attractin [Panthera tigris altaica]	85.9	85.9	100%	3e-17	93%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin [Felis catus]	85.9	85.9	100%	3e-17	93%	gi|586981105|XP_003983758.2
☐	PREDICTED: attractin isoform X1 [Oryctolagus cuniculus]	85.5	85.5	100%	5e-17	93%	gi|291388868|XP_002710968.1
☐	PREDICTED: attractin isoform X2 [Oryctolagus cuniculus]	85.5	85.5	100%	5e-17	93%	gi|655716500|XP_008254470.1
☐	PREDICTED: attractin [Jaculus jaculus]	85.0	85.0	100%	7e-17	93%	gi|507555530|XP_004661535.1
☐	PREDICTED: attractin isoform X2 [Mustela putorius furo]	84.2	84.2	100%	1e-16	89%	gi|511906947|XP_004772933.1
☐	PREDICTED: attractin [Mustela putorius furo]	84.2	84.2	100%	1e-16	89%	gi|511947743|XP_004792355.1
☐	PREDICTED: attractin isoform X1 [Mustela putorius furo]	84.2	84.2	100%	1e-16	89%	gi|511906945|XP_004772932.1
☐	PREDICTED: attractin [Sus scrofa]	83.8	83.8	100%	2e-16	89%	gi|545879723|XP_001927324.5
☐	PREDICTED: attractin isoform 2 [Ceratotherium simum simum]	83.8	83.8	100%	2e-16	93%	gi|478519276|XP_004433860.1
☐	attractin [Sus scrofa]	83.8	83.8	100%	2e-16	89%	gi|146741346|BAF62328.1
☐	PREDICTED: attractin isoform 1 [Ceratotherium simum simum]	83.8	83.8	100%	2e-16	93%	gi|478519274|XP_004433859.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	83.3	83.3	100%	2e-16	89%	gi|585160208|XP_006732353.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	83.3	83.3	100%	2e-16	89%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	83.3	83.3	100%	2e-16	89%	gi|594099680|XP_006072965.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	83.3	83.3	100%	3e-16	89%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin [Odobenus rosmarus divergens]	83.3	83.3	100%	3e-16	89%	gi|472357214|XP_004398236.1
☐	PREDICTED: attractin isoform X1 [Bubalus bubalis]	83.3	83.3	100%	3e-16	89%	gi|594099676|XP_006072963.1
☐	PREDICTED: attractin [Chrysochloris asiatica]	82.9	82.9	100%	3e-16	89%	gi|586488825|XP_006874887.1
☐	PREDICTED: attractin [Nannospalax galili]	82.5	82.5	100%	5e-16	89%	gi|674060132|XP_008836714.1
☐	Attractin [Cricetulus griseus]	82.1	82.1	96%	7e-16	93%	gi|344236321|EGV92424.1
☐	PREDICTED: attractin isoform X2 [Cricetulus griseus]	82.1	82.1	96%	7e-16	93%	gi|625260840|XP_007621856.1
☐	attractin [Cricetulus griseus]	82.1	82.1	96%	7e-16	93%	gi|537146168|ERE69758.1

⊟ Alignments

Download ⌄ GenPept Graphics ▼ Next ▲ Previous ▲ Descriptions

PREDICTED: attractin-like [Pan paniscus]

Sequence ID: gi|397513332|ref|XP_003826972.1| **Length:** 265 **Number of Matches:** 1

Range 1: 214 to 241 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
96.5 bits(220)	5e-21	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    KMPSQAPTGNFYPQPLLNSSMCLEDSRY  28
            KMPSQAPTGNFYPQPLLNSSMCLEDSRY
Sbjct  214  KMPSQAPTGNFYPQPLLNSSMCLEDSRY  241
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Download ⌄ GenPept Graphics ▼ Next ▲ Previous ▲ Descriptions

KIAA0548 protein [Homo sapiens]

Sequence ID: gi|3043620|dbj|BAA25474.1| **Length:** 452 **Number of Matches:** 1

Range 1: 49 to 76 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
96.5 bits(220)	7e-21	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1   KMPSQAPTGNFYPQPLLNSSMCLEDSRY  28
```

Related Information

Gene - associated gene details

```
                KMPSQAPTGNFYPQPLLNSSMCLEDSRY
Sbjct  49   KMPSQAPTGNFYPQPLLNSSMCLEDSRY  76
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: attractin isoform X2 [Papio anubis]

Sequence ID: gi|685567345|ref|XP_009214752.1| **Length:** 989 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 716 to 743 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
96.5 bits(220)	8e-21	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1     KMPSQAPTGNFYPQPLLNSSMCLEDSRY  28
             KMPSQAPTGNFYPQPLLNSSMCLEDSRY
Sbjct  716   KMPSQAPTGNFYPQPLLNSSMCLEDSRY  743
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: attractin, partial [Pongo abelii]

Sequence ID: gi|297706621|ref|XP_002830129.1| **Length:** 1058 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 655 to 682 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
96.5 bits(220)	8e-21	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1     KMPSQAPTGNFYPQPLLNSSMCLEDSRY  28
             KMPSQAPTGNFYPQPLLNSSMCLEDSRY
Sbjct  655   KMPSQAPTGNFYPQPLLNSSMCLEDSRY  682
```

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PREDICTED: attractin isoform X2 [Homo sapiens]

Sequence ID: gi|530426021|ref|XP_005260918.1| **Length:** 1111 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 1026 to 1053 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
96.5 bits(220)	8e-21	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1      KMPSQAPTGNFYPQPLLNSSMCLEDSRY  28
              KMPSQAPTGNFYPQPLLNSSMCLEDSRY
Sbjct  1026   KMPSQAPTGNFYPQPLLNSSMCLEDSRY  1053
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BHF5J1Y0014**

Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

ATRN_RGCSCFSDWQGPGCSVPVPADQSFWTRE_Mod

RID	BHF5J1Y0014 (Expires on 01-17 14:24 pm)
Query ID	lcl|69569
Description	None
Molecule type	amino acid
Query Length	28

Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

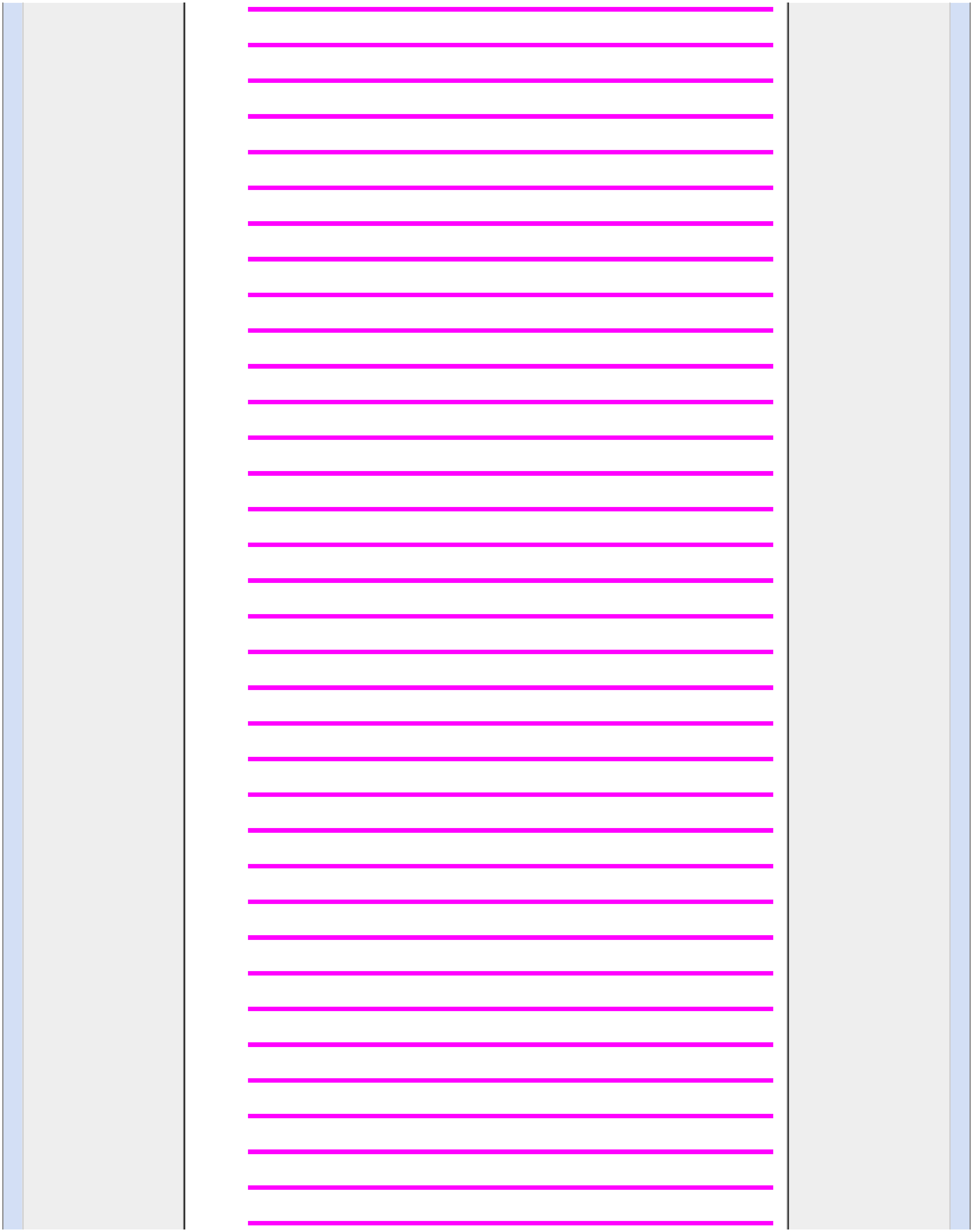
Graphic Summary

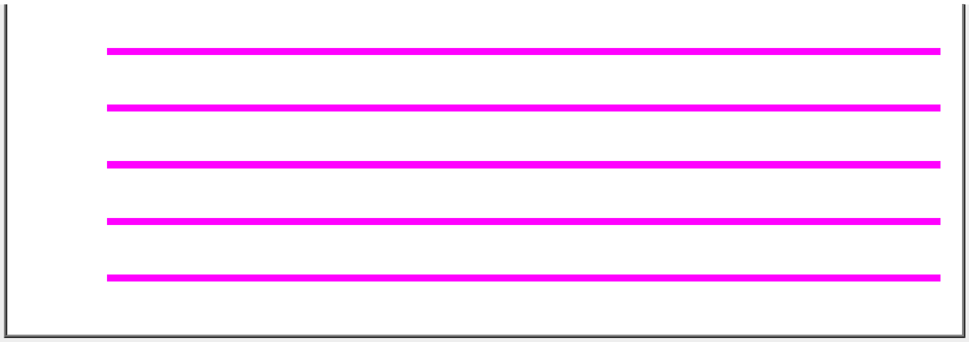
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 98 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	95.2	95.2	100%	2e-20	96%	gi|530426021|XP_005260918.1
☐	unnamed protein product [Homo sapiens]	95.2	95.2	100%	2e-20	96%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	95.2	95.2	100%	2e-20	96%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	95.2	95.2	100%	2e-20	96%	gi|332257827|XP_003278006.1
☐	PREDICTED: attractin [Gorilla gorilla gorilla]	95.2	95.2	100%	2e-20	96%	gi|426390844|XP_004061806.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	95.2	95.2	100%	2e-20	96%	gi|694977854|XP_009435012.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	95.2	95.2	100%	2e-20	96%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	95.2	95.2	100%	2e-20	96%	gi|4093196|AAD03057.1
☐	secreted attractin precursor [Homo sapiens]	95.2	95.2	100%	2e-20	96%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	95.2	95.2	100%	2e-20	96%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	95.2	95.2	100%	2e-20	96%	gi|21450863|NP_647538.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Pan paniscus]	95.2	95.2	100%	2e-20	96%	gi|675763672|XP_008973079.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	95.2	95.2	100%	2e-20	96%	gi|694977852|XP_009435011.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	95.2	95.2	100%	2e-20	96%	gi|530426019|XP_005260917.1
☐	attractin, isoform CRA_b [Homo sapiens]	95.2	95.2	100%	2e-20	96%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	95.2	95.2	100%	2e-20	96%	gi|694977850|XP_009435010.1
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	95.2	95.2	100%	2e-20	96%	gi|332857715|XP_003316827.1
☐	membrane attractin precursor [Homo sapiens]	95.2	95.2	100%	2e-20	96%	gi|8118082|AAF72881.1
☐	attractin isoform 1 preproprotein [Homo sapiens]	95.2	95.2	100%	2e-20	96%	gi|21450861|NP_647537.1
☐	PREDICTED: attractin-like [Octodon degus]	93.1	93.1	100%	1e-19	93%	gi|507657234|XP_004634315.1
☐	PREDICTED: attractin-like [Physeter catodon]	92.7	92.7	100%	2e-19	93%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	92.7	92.7	100%	2e-19	93%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin [Sus scrofa]	92.7	92.7	100%	2e-19	93%	gi|545879723|XP_001927324.5
☐	PREDICTED: attractin isoform X1 [Bos taurus]	92.7	92.7	100%	2e-19	93%	gi|741947708|XP_005214542.2
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	92.7	92.7	100%	2e-19	93%	gi|594099680|XP_006072965.1
☐	attractin [Sus scrofa]	92.7	92.7	100%	2e-19	93%	gi|146741346|BAF62328.1
☐	PREDICTED: attractin [Capra hircus]	92.7	92.7	100%	2e-19	93%	gi|548490191|XP_005688293.1
☐	PREDICTED: attractin [Bos mutus]	92.7	92.7	100%	2e-19	93%	gi|555963925|XP_005894036.1
☐							

	PREDICTED: attractin [Ovis aries]	92.7	92.7	100%	2e-19	93%	gi|426241795|XP_004014773.1
☐	attractin [Bos taurus]	92.7	92.7	100%	2e-19	93%	gi|253560524|ACT32973.1
☐	attractin [Bos taurus]	92.7	92.7	100%	2e-19	93%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	92.7	92.7	100%	2e-19	93%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin isoform X3 [Chinchilla lanigera]	92.7	92.7	100%	2e-19	93%	gi|533131617|XP_005380852.1
☐	PREDICTED: attractin isoform X1 [Ictidomys tridecemlineatus]	92.7	92.7	100%	2e-19	93%	gi|532069484|XP_005320577.1
☐	PREDICTED: attractin isoform X3 [Ictidomys tridecemlineatus]	92.7	92.7	100%	2e-19	93%	gi|532069488|XP_005320579.1
☐	PREDICTED: attractin isoform X2 [Ictidomys tridecemlineatus]	92.7	92.7	100%	2e-19	93%	gi|532069486|XP_005320578.1
☐	PREDICTED: attractin isoform X2 [Chinchilla lanigera]	92.7	92.7	100%	2e-19	93%	gi|533131615|XP_005380851.1
☐	PREDICTED: attractin [Bison bison bison]	92.7	92.7	100%	2e-19	93%	gi|742104093|XP_010834932.1
☐	PREDICTED: attractin isoform X1 [Chinchilla lanigera]	92.7	92.7	100%	2e-19	93%	gi|533131613|XP_005380850.1
☐	PREDICTED: attractin isoform X1 [Bubalus bubalis]	92.7	92.7	100%	2e-19	93%	gi|594099676|XP_006072963.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	91.8	91.8	100%	3e-19	93%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin isoform X2 [Pteropus alecto]	91.8	91.8	100%	3e-19	93%	gi|586533634|XP_006921706.1
☐	PREDICTED: attractin [Equus przewalskii]	90.6	90.6	100%	9e-19	89%	gi|664773944|XP_008506219.1
☐	Mahogany-like protein [Macaca mulatta]	90.6	90.6	100%	9e-19	93%	gi|355563316|EHH19878.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	90.6	90.6	100%	9e-19	93%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	90.6	90.6	100%	9e-19	93%	gi|635021368|XP_008017720.1
☐	Mahogany-like protein [Macaca fascicularis]	90.6	90.6	100%	9e-19	93%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	90.6	90.6	100%	9e-19	93%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	90.6	90.6	100%	9e-19	89%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	90.6	90.6	100%	9e-19	93%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	90.6	90.6	100%	9e-19	93%	gi|724902357|XP_010377335.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	90.6	90.6	100%	9e-19	93%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	90.6	90.6	100%	9e-19	93%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin [Otolemur garnettii]	90.6	90.6	100%	9e-19	89%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin [Orycteropus afer afer]	90.6	90.6	100%	9e-19	89%	gi|634830430|XP_007958185.1
☐	PREDICTED: attractin isoform X2 [Macaca fascicularis]	90.6	90.6	100%	9e-19	93%	gi|544464512|XP_005568510.1
☐	PREDICTED: attractin [Macaca mulatta]	90.6	90.6	100%	9e-19	93%	gi|109092720|XP_001115192.1
☐	PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	90.6	90.6	100%	9e-19	93%	gi|635021360|XP_008017700.1
☐	PREDICTED: attractin isoform X1 [Macaca fascicularis]	90.6	90.6	100%	9e-19	93%	gi|544464510|XP_005568509.1
☐	PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	90.6	90.6	100%	9e-19	93%	gi|635021370|XP_008017729.1
☐	PREDICTED: attractin [Tupaia chinensis]	90.6	90.6	100%	9e-19	89%	gi|562872246|XP_006164056.1
☐	PREDICTED: attractin [Felis catus]	89.7	89.7	100%	2e-18	89%	gi|586981105|XP_003983758.2
☐	PREDICTED: attractin isoform 2 [Ceratotherium simum simum]	89.3	89.3	100%	2e-18	89%	gi|478519276|XP_004433860.1
☐	PREDICTED: attractin isoform 1 [Ceratotherium simum simum]	89.3	89.3	100%	2e-18	89%	gi|478519274|XP_004433859.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	88.9	88.9	100%	3e-18	93%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	88.9	88.9	100%	3e-18	93%	gi|725600051|XP_010350111.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	88.4	88.4	100%	5e-18	89%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin [Camelus dromedarius]	88.4	88.4	100%	5e-18	89%	gi|744589171|XP_010986570.1
☐	PREDICTED: attractin [Vicugna pacos]	88.4	88.4	100%	5e-18	89%	gi|560970220|XP_006207473.1
☐	PREDICTED: attractin [Orcinus orca]	88.4	88.4	100%	5e-18	89%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin [Lipotes vexillifer]	88.4	88.4	100%	5e-18	89%	gi|602710450|XP_007465469.1
☐	PREDICTED: attractin isoform X2 [Heterocephalus glaber]	88.0	88.0	100%	7e-18	89%	gi|512956910|XP_004840783.1
☐	Attractin [Heterocephalus glaber]	88.0	88.0	100%	7e-18	89%	gi|351701383|EHB04302.1

☐	PREDICTED: attractin [Heterocephalus glaber]	88.0	88.0	100%	7e-18	89%	gi|512849696|XP_004886859.1
☐	PREDICTED: attractin [Echinops telfairi]	88.0	88.0	100%	7e-18	86%	gi|507626122|XP_004697922.1
☐	PREDICTED: attractin [Chrysochloris asiatica]	88.0	88.0	100%	7e-18	86%	gi|586488825|XP_006874887.1
☐	PREDICTED: attractin isoform X1 [Heterocephalus glaber]	88.0	88.0	100%	7e-18	89%	gi|512956908|XP_004840782.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Cavia porcellus]	87.6	87.6	100%	9e-18	89%	gi|514473642|XP_005008408.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	87.2	87.2	100%	1e-17	86%	gi|585160208|XP_006732353.1
☐	attractin [Canis lupus familiaris]	87.2	87.2	100%	1e-17	86%	gi|339892849|AEK21787.1
☐	PREDICTED: attractin isoform X2 [Canis lupus familiaris]	87.2	87.2	100%	1e-17	86%	gi|545540090|XP_005634905.1
☐	PREDICTED: attractin isoform X2 [Mustela putorius furo]	87.2	87.2	100%	1e-17	86%	gi|511906947|XP_004772933.1
☐	PREDICTED: attractin [Ursus maritimus]	87.2	87.2	100%	1e-17	86%	gi|671021680|XP_008701660.1
☐	hypothetical protein PANDA_007354 [Ailuropoda melanoleuca]	87.2	87.2	100%	1e-17	86%	gi|281339872|EFB15456.1
☐	PREDICTED: attractin-like [Ailuropoda melanoleuca]	87.2	87.2	100%	1e-17	86%	gi|301766802|XP_002918837.1
☐	PREDICTED: attractin [Mustela putorius furo]	87.2	87.2	100%	1e-17	86%	gi|511947743|XP_004792355.1
☐	PREDICTED: attractin isoform X3 [Canis lupus familiaris]	87.2	87.2	100%	1e-17	86%	gi|73991942|XP_534360.2
☐	PREDICTED: attractin [Odobenus rosmarus divergens]	87.2	87.2	100%	1e-17	86%	gi|472357214|XP_004398236.1
☐	PREDICTED: attractin isoform X1 [Mustela putorius furo]	87.2	87.2	100%	1e-17	86%	gi|511906945|XP_004772932.1
☐	PREDICTED: attractin [Callithrix jacchus]	87.2	87.2	100%	1e-17	89%	gi|296200062|XP_002747358.1
☐	PREDICTED: attractin isoform X1 [Canis lupus familiaris]	87.2	87.2	100%	1e-17	86%	gi|545540087|XP_005634904.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	86.7	86.7	100%	2e-17	89%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin isoform 2 [Dasypus novemcinctus]	86.3	86.3	100%	3e-17	86%	gi|488545593|XP_004464327.1
☐	PREDICTED: attractin [Alligator mississippiensis]	86.3	86.3	100%	3e-17	86%	gi|564227650|XP_006258288.1
☐	PREDICTED: attractin isoform 1 [Dasypus novemcinctus]	86.3	86.3	100%	3e-17	86%	gi|488545591|XP_004464326.1
☐	PREDICTED: attractin [Tarsius syrichta]	85.5	85.5	100%	5e-17	86%	gi|640796924|XP_008054571.1
☐	PREDICTED: attractin [Panthera tigris altaica]	85.5	85.5	100%	5e-17	86%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin [Elephantulus edwardii]	85.5	85.5	100%	5e-17	86%	gi|585689645|XP_006894264.1

Alignments

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PREDICTED: attractin isoform X2 [Homo sapiens]

Sequence ID: gi|530426021|ref|XP_005260918.1| **Length:** 1111 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 305 to 332 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
95.2 bits(217)	2e-20	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    RGCSCFSDWQGPGCSVPVPADQSFWTRE  28
            RGCSCFSDWQGPGCSVPVPA+QSFWTRE
Sbjct  305  RGCSCFSDWQGPGCSVPVPANQSFWTRE  332
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194380362|dbj|BAG63948.1| **Length:** 1156 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 189 to 216 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
95.2 bits(217)	2e-20	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    RGCSCFSDWQGPGCSVPVPADQSFWTRE  28
            RGCSCFSDWQGPGCSVPVPA+QSFWTRE
Sbjct  189  RGCSCFSDWQGPGCSVPVPANQSFWTRE  216
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

attractin isoform 4 [Homo sapiens]

Sequence ID: gi|333440461|ref|NP_001193976.1| **Length:** 1156 **Number of Matches:** 1

Range 1: 189 to 216 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
95.2 bits(217)	2e-20	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    RGCSCFSDWQGPGCSVPVPADQSFWTRE  28
            RGCSCFSDWQGPGCSVPVPA+QSFWTRE
Sbjct  189  RGCSCFSDWQGPGCSVPVPANQSFWTRE  216
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: attractin isoform 2 [Nomascus leucogenys]

Sequence ID: gi|332257827|ref|XP_003278006.1| **Length:** 1156 **Number of Matches:** 1

Range 1: 189 to 216 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
95.2 bits(217)	2e-20	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    RGCSCFSDWQGPGCSVPVPADQSFWTRE  28
            RGCSCFSDWQGPGCSVPVPA+QSFWTRE
Sbjct  189  RGCSCFSDWQGPGCSVPVPANQSFWTRE  216
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: attractin [Gorilla gorilla gorilla]

Sequence ID: gi|426390844|ref|XP_004061806.1| **Length:** 1265 **Number of Matches:** 1

Range 1: 187 to 214 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
95.2 bits(217)	2e-20	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    RGCSCFSDWQGPGCSVPVPADQSFWTRE  28
            RGCSCFSDWQGPGCSVPVPA+QSFWTRE
Sbjct  187  RGCSCFSDWQGPGCSVPVPANQSFWTRE  214
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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NCBI/ BLAST/ blastp suite/ Formatting Results - B916RTUM01R

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How to read this page   Blast report description

ATRN_RGCSCFSDWQGPGCSVPVPANQSFWTRE_NonMod

RID	B916RTUM01R (Expires on 01-14 09:37 am)
Query ID	lcl|222662
Description	None
Molecule type	amino acid
Query Length	28

Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

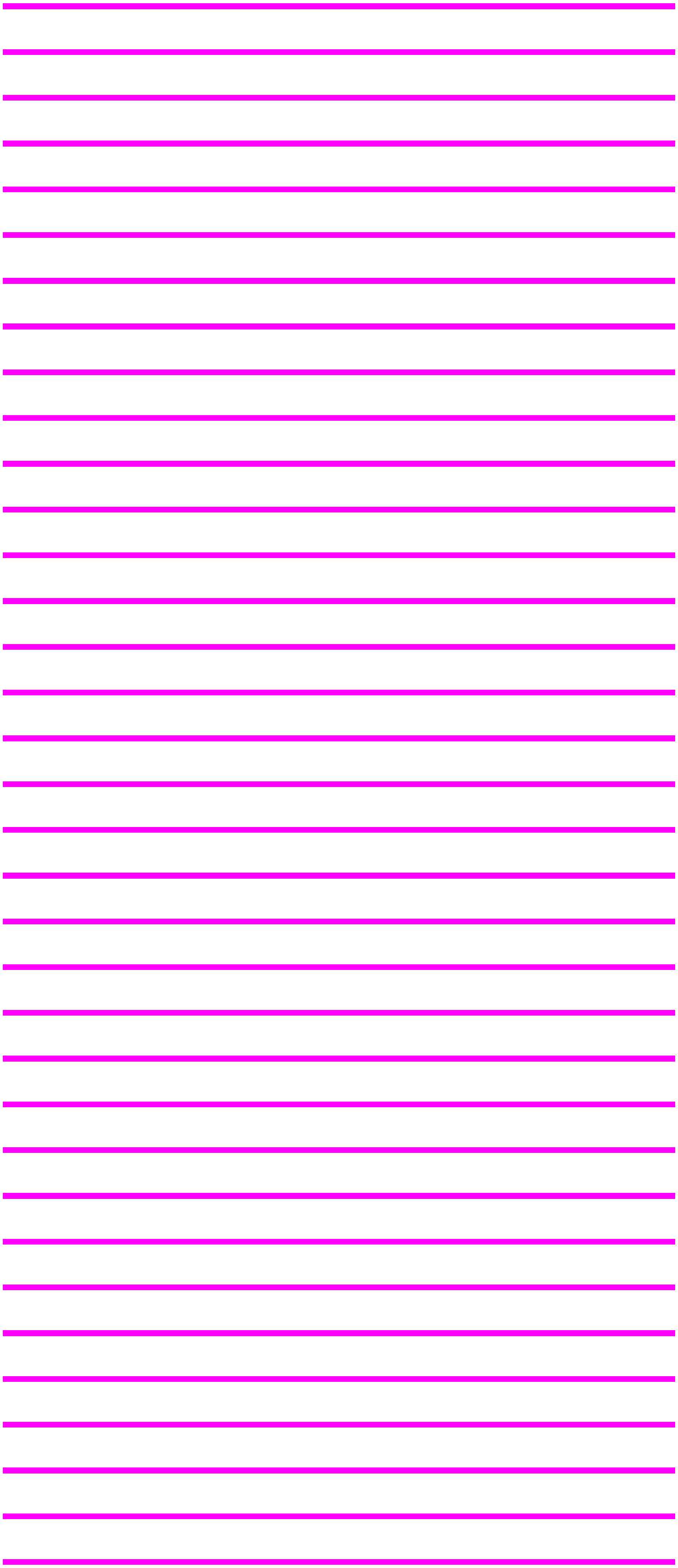
Graphic Summary

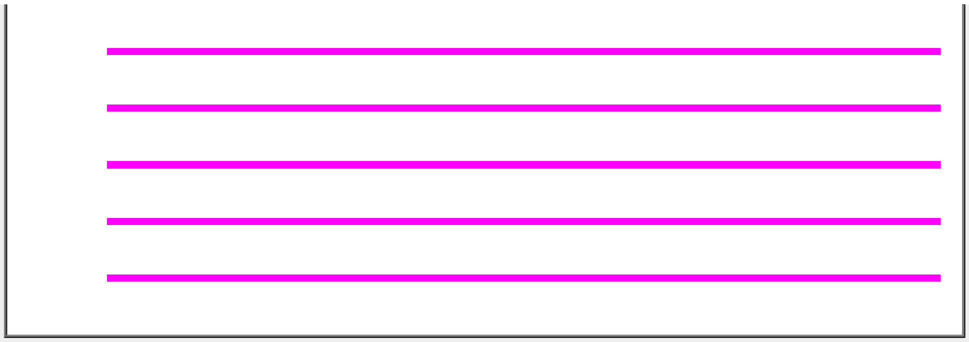
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	97.8	97.8	100%	3e-21	100%	gi|530426021|XP_005260918.1
☐	unnamed protein product [Homo sapiens]	97.8	97.8	100%	3e-21	100%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	97.8	97.8	100%	3e-21	100%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	97.8	97.8	100%	3e-21	100%	gi|332257827|XP_003278006.1
☐	PREDICTED: attractin [Gorilla gorilla gorilla]	97.8	97.8	100%	3e-21	100%	gi|426390844|XP_004061806.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	97.8	97.8	100%	3e-21	100%	gi|694977854|XP_009435012.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	97.8	97.8	100%	3e-21	100%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	97.8	97.8	100%	3e-21	100%	gi|4093196|AAD03057.1
☐	secreted attractin precursor [Homo sapiens]	97.8	97.8	100%	3e-21	100%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	97.8	97.8	100%	3e-21	100%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	97.8	97.8	100%	3e-21	100%	gi|21450863|NP_647538.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Pan paniscus]	97.8	97.8	100%	3e-21	100%	gi|675763672|XP_008973079.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	97.8	97.8	100%	3e-21	100%	gi|694977852|XP_009435011.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	97.8	97.8	100%	3e-21	100%	gi|530426019|XP_005260917.1
☐	attractin, isoform CRA_b [Homo sapiens]	97.8	97.8	100%	3e-21	100%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	97.8	97.8	100%	3e-21	100%	gi|694977850|XP_009435010.1
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	97.8	97.8	100%	3e-21	100%	gi|332857715|XP_003316827.1
☐	membrane attractin precursor [Homo sapiens]	97.8	97.8	100%	3e-21	100%	gi|8118082|AAF72881.1
☐	attractin isoform 1 preproprotein [Homo sapiens]	97.8	97.8	100%	3e-21	100%	gi|21450861|NP_647537.1
☐	PREDICTED: attractin-like [Octodon degus]	95.6	95.6	100%	2e-20	96%	gi|507657234|XP_004634315.1
☐	PREDICTED: attractin-like [Physeter catodon]	95.2	95.2	100%	2e-20	96%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	95.2	95.2	100%	2e-20	96%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin [Sus scrofa]	95.2	95.2	100%	2e-20	96%	gi|545879723|XP_001927324.5
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	95.2	95.2	100%	2e-20	96%	gi|594099680|XP_006072965.1
☐	attractin [Sus scrofa]	95.2	95.2	100%	2e-20	96%	gi|146741346|BAF62328.1
☐	PREDICTED: attractin [Capra hircus]	95.2	95.2	100%	2e-20	96%	gi|548490191|XP_005688293.1
☐	PREDICTED: attractin [Bos mutus]	95.2	95.2	100%	2e-20	96%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Ovis aries]	95.2	95.2	100%	2e-20	96%	gi|426241795|XP_004014773.1
☐							

	attractin [Bos taurus]	95.2	95.2	100%	2e-20	96%	gi|253560524|ACT32973.1
☐	attractin [Bos taurus]	95.2	95.2	100%	2e-20	96%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	95.2	95.2	100%	2e-20	96%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin isoform X3 [Chinchilla lanigera]	95.2	95.2	100%	2e-20	96%	gi|533131617|XP_005380852.1
☐	PREDICTED: attractin isoform X1 [Ictidomys tridecemlineatus]	95.2	95.2	100%	2e-20	96%	gi|532069484|XP_005320577.1
☐	PREDICTED: attractin isoform X3 [Ictidomys tridecemlineatus]	95.2	95.2	100%	2e-20	96%	gi|532069488|XP_005320579.1
☐	PREDICTED: attractin isoform X2 [Ictidomys tridecemlineatus]	95.2	95.2	100%	2e-20	96%	gi|532069486|XP_005320578.1
☐	PREDICTED: attractin isoform X2 [Bos taurus]	95.2	95.2	100%	2e-20	96%	gi|528973313|XP_005214542.1
☐	PREDICTED: attractin isoform X2 [Chinchilla lanigera]	95.2	95.2	100%	2e-20	96%	gi|533131615|XP_005380851.1
☐	PREDICTED: attractin isoform X1 [Chinchilla lanigera]	95.2	95.2	100%	2e-20	96%	gi|533131613|XP_005380850.1
☐	PREDICTED: attractin isoform X1 [Bubalus bubalis]	95.2	95.2	100%	2e-20	96%	gi|594099676|XP_006072963.1
☐	PREDICTED: attractin isoform X1 [Bos taurus]	95.2	95.2	100%	2e-20	96%	gi|528973311|XP_005214541.1
☐	PREDICTED: attractin [Equus przewalskii]	93.1	93.1	100%	1e-19	93%	gi|664773944|XP_008506219.1
☐	Mahogany-like protein [Macaca mulatta]	93.1	93.1	100%	1e-19	96%	gi|355563316|EHH19878.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	93.1	93.1	100%	1e-19	96%	gi|544464516|XP_005568512.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	93.1	93.1	100%	1e-19	96%	gi|635021368|XP_008017720.1
☐	Mahogany-like protein [Macaca fascicularis]	93.1	93.1	100%	1e-19	96%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	93.1	93.1	100%	1e-19	96%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	93.1	93.1	100%	1e-19	93%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	93.1	93.1	100%	1e-19	96%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	93.1	93.1	100%	1e-19	96%	gi|724902357|XP_010377335.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	93.1	93.1	100%	1e-19	96%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	93.1	93.1	100%	1e-19	96%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin [Otolemur garnettii]	93.1	93.1	100%	1e-19	93%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin [Orycteropus afer afer]	93.1	93.1	100%	1e-19	93%	gi|634830430|XP_007958185.1
☐	PREDICTED: attractin isoform X2 [Macaca fascicularis]	93.1	93.1	100%	1e-19	96%	gi|544464512|XP_005568510.1
☐	PREDICTED: attractin [Macaca mulatta]	93.1	93.1	100%	1e-19	96%	gi|109092720|XP_001115192.1
☐	PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	93.1	93.1	100%	1e-19	96%	gi|635021360|XP_008017700.1
☐	PREDICTED: attractin isoform X1 [Macaca fascicularis]	93.1	93.1	100%	1e-19	96%	gi|544464510|XP_005568509.1
☐	PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	93.1	93.1	100%	1e-19	96%	gi|635021370|XP_008017729.1
☐	PREDICTED: attractin [Tupaia chinensis]	93.1	93.1	100%	1e-19	93%	gi|562872246|XP_006164056.1
☐	PREDICTED: attractin [Felis catus]	92.3	92.3	100%	2e-19	93%	gi|586981105|XP_003983758.2
☐	PREDICTED: attractin isoform 2 [Ceratotherium simum simum]	91.8	91.8	100%	3e-19	93%	gi|478519276|XP_004433860.1
☐	PREDICTED: attractin isoform 1 [Ceratotherium simum simum]	91.8	91.8	100%	3e-19	93%	gi|478519274|XP_004433859.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	91.4	91.4	100%	4e-19	96%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	91.4	91.4	100%	4e-19	96%	gi|725600051|XP_010350111.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	91.0	91.0	100%	6e-19	93%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin [Vicugna pacos]	91.0	91.0	100%	6e-19	93%	gi|560970220|XP_006207473.1
☐	PREDICTED: attractin [Orcinus orca]	91.0	91.0	100%	6e-19	93%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin [Lipotes vexillifer]	91.0	91.0	100%	6e-19	93%	gi|602710450|XP_007465469.1
☐	PREDICTED: attractin isoform X2 [Heterocephalus glaber]	90.6	90.6	100%	9e-19	93%	gi|512956910|XP_004840783.1
☐	Attractin [Heterocephalus glaber]	90.6	90.6	100%	9e-19	93%	gi|351701383|EHB04302.1
☐	PREDICTED: attractin [Heterocephalus glaber]	90.6	90.6	100%	9e-19	93%	gi|512849696|XP_004886859.1
☐	PREDICTED: attractin [Echinops telfairi]	90.6	90.6	100%	9e-19	89%	gi|507626122|XP_004697922.1
☐	PREDICTED: attractin [Chrysochloris asiatica]	90.6	90.6	100%	9e-19	89%	gi|586488825|XP_006874887.1

☐	PREDICTED: attractin isoform X1 [Heterocephalus glaber]	90.6	90.6	100%	9e-19	93%	gi|512956908|XP_004840782.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Cavia porcellus]	90.1	90.1	100%	1e-18	93%	gi|514473642|XP_005008408.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	89.7	89.7	100%	2e-18	89%	gi|585160208|XP_006732353.1
☐	attractin [Canis lupus familiaris]	89.7	89.7	100%	2e-18	89%	gi|339892849|AEK21787.1
☐	PREDICTED: attractin isoform X2 [Canis lupus familiaris]	89.7	89.7	100%	2e-18	89%	gi|545540090|XP_005634905.1
☐	PREDICTED: attractin isoform X2 [Mustela putorius furo]	89.7	89.7	100%	2e-18	89%	gi|511906947|XP_004772933.1
☐	PREDICTED: attractin [Ursus maritimus]	89.7	89.7	100%	2e-18	89%	gi|671021680|XP_008701660.1
☐	hypothetical protein PANDA_007354 [Ailuropoda melanoleuca]	89.7	89.7	100%	2e-18	89%	gi|281339872|EFB15456.1
☐	PREDICTED: attractin-like [Ailuropoda melanoleuca]	89.7	89.7	100%	2e-18	89%	gi|301766802|XP_002918837.1
☐	PREDICTED: attractin [Mustela putorius furo]	89.7	89.7	100%	2e-18	89%	gi|511947743|XP_004792355.1
☐	PREDICTED: attractin isoform X3 [Canis lupus familiaris]	89.7	89.7	100%	2e-18	89%	gi|73991942|XP_534360.2
☐	PREDICTED: attractin [Odobenus rosmarus divergens]	89.7	89.7	100%	2e-18	89%	gi|472357214|XP_004398236.1
☐	PREDICTED: attractin isoform X1 [Mustela putorius furo]	89.7	89.7	100%	2e-18	89%	gi|511906945|XP_004772932.1
☐	PREDICTED: attractin [Callithrix jacchus]	89.7	89.7	100%	2e-18	93%	gi|296200062|XP_002747358.1
☐	PREDICTED: attractin isoform X1 [Canis lupus familiaris]	89.7	89.7	100%	2e-18	89%	gi|545540087|XP_005634904.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	89.3	89.3	100%	2e-18	93%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	89.3	89.3	100%	2e-18	89%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin isoform X2 [Pteropus alecto]	89.3	89.3	100%	2e-18	89%	gi|586533634|XP_006921706.1
☐	PREDICTED: attractin isoform 2 [Dasypus novemcinctus]	88.9	88.9	100%	3e-18	89%	gi|488545593|XP_004464327.1
☐	PREDICTED: attractin [Alligator mississippiensis]	88.9	88.9	100%	3e-18	89%	gi|564227650|XP_006258288.1
☐	PREDICTED: attractin isoform 1 [Dasypus novemcinctus]	88.9	88.9	100%	3e-18	89%	gi|488545591|XP_004464326.1
☐	PREDICTED: attractin [Tarsius syrichta]	88.0	88.0	100%	6e-18	89%	gi|640796924|XP_008054571.1
☐	PREDICTED: attractin [Panthera tigris altaica]	88.0	88.0	100%	6e-18	89%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin [Elephantulus edwardii]	88.0	88.0	100%	6e-18	89%	gi|585689645|XP_006894264.1
☐	PREDICTED: attractin [Alligator sinensis]	87.6	87.6	100%	9e-18	89%	gi|557275553|XP_006020974.1
☐	attractin [Rattus norvegicus]	87.2	87.2	100%	1e-17	89%	gi|12275312|BAB21018.1
☐	attractin, isoform CRA_a [Rattus norvegicus]	87.2	87.2	100%	1e-17	89%	gi|149023319|EDL80213.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: attractin isoform X2 [Homo sapiens]

Sequence ID: gi|530426021|ref|XP_005260918.1| **Length:** 1111 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 305 to 332 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
97.8 bits(223)	3e-21	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    RGCSCFSDWQGPGCSVPVPANQSFWTRE  28
            RGCSCFSDWQGPGCSVPVPANQSFWTRE
Sbjct  305  RGCSCFSDWQGPGCSVPVPANQSFWTRE  332
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194380362|dbj|BAG63948.1| **Length:** 1156 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 189 to 216 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
97.8 bits(223)	3e-21	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    RGCSCFSDWQGPGCSVPVPANQSFWTRE  28
```

```
           RGCSCFSDWQGPGCSVPVPANQSFWTRE
Sbjct  189  RGCSCFSDWQGPGCSVPVPANQSFWTRE  216
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

attractin isoform 4 [Homo sapiens]

Sequence ID: gi|333440461|ref|NP_001193976.1| **Length:** 1156 **Number of Matches:** 1

Range 1: 189 to 216 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
97.8 bits(223)	3e-21	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    RGCSCFSDWQGPGCSVPVPANQSFWTRE  28
           RGCSCFSDWQGPGCSVPVPANQSFWTRE
Sbjct  189  RGCSCFSDWQGPGCSVPVPANQSFWTRE  216
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: attractin isoform 2 [Nomascus leucogenys]

Sequence ID: gi|332257827|ref|XP_003278006.1| **Length:** 1156 **Number of Matches:** 1

Range 1: 189 to 216 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
97.8 bits(223)	3e-21	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    RGCSCFSDWQGPGCSVPVPANQSFWTRE  28
           RGCSCFSDWQGPGCSVPVPANQSFWTRE
Sbjct  189  RGCSCFSDWQGPGCSVPVPANQSFWTRE  216
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: attractin [Gorilla gorilla gorilla]

Sequence ID: gi|426390844|ref|XP_004061806.1| **Length:** 1265 **Number of Matches:** 1

Range 1: 187 to 214 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
97.8 bits(223)	3e-21	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    RGCSCFSDWQGPGCSVPVPANQSFWTRE  28
           RGCSCFSDWQGPGCSVPVPANQSFWTRE
Sbjct  187  RGCSCFSDWQGPGCSVPVPANQSFWTRE  214
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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NCBI/ BLAST/ blastp suite/ Formatting Results - BHFKSX4K014

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download

How to read this page Blast report description

ATRN_RGICDSSDVRG_Mod

RID BHFKSX4K014 (Expires on 01-17 14:32 pm)

Query ID lcl|55418
Description None
Molecule type amino acid
Query Length 11

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

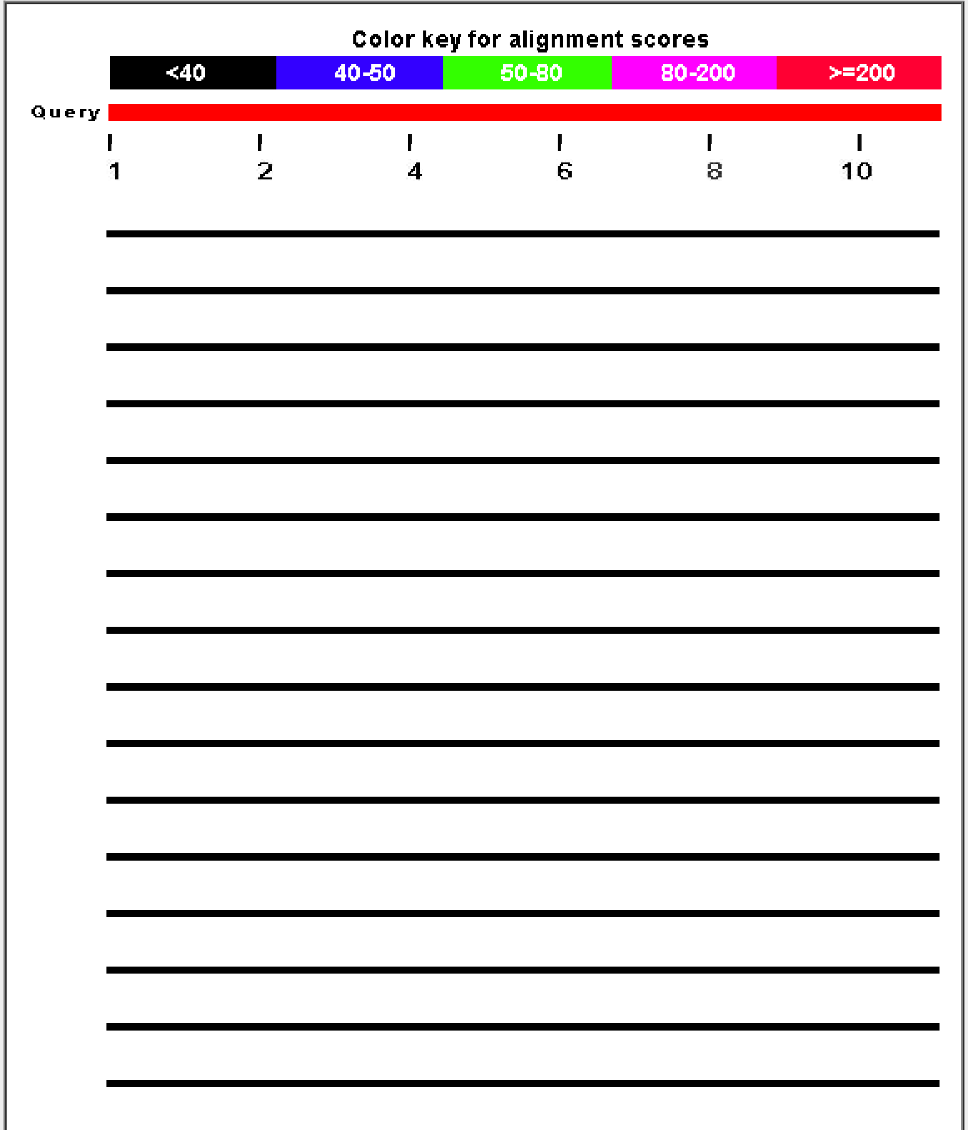
⊟ Graphic Summary

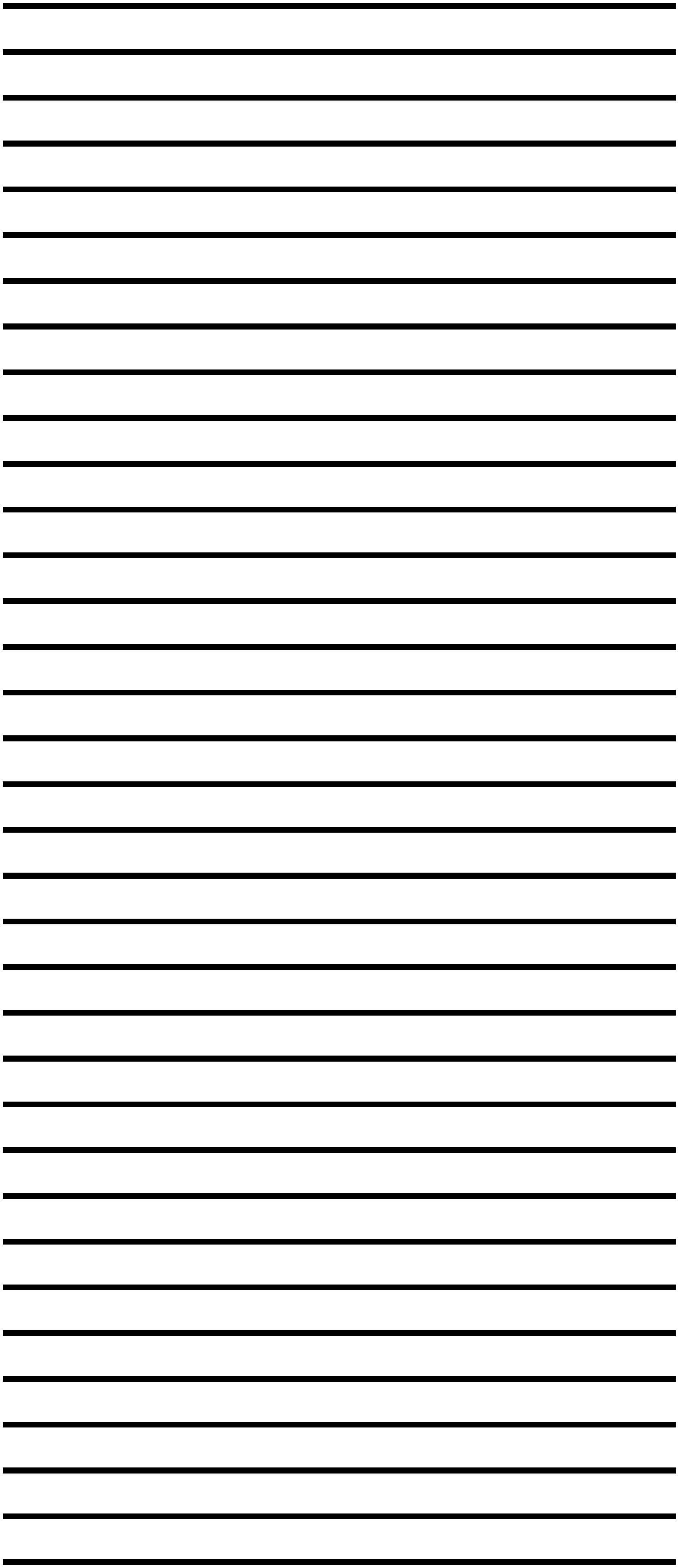
⊟ Show Conserved Domains

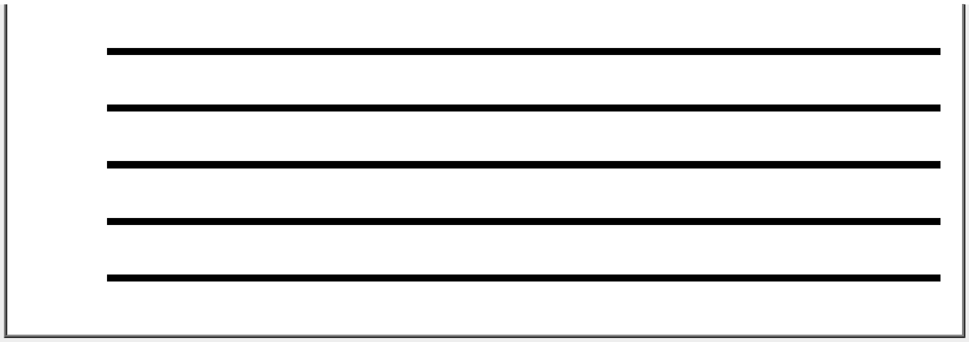
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: attractin [Fukomys damarensis]	37.5	37.5	100%	0.088	100%	gi|731281216|XP_010609356.1
☐	Attractin [Fukomys damarensis]	35.0	35.0	100%	0.60	91%	gi|676269096|KFO24512.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	35.0	35.0	100%	0.60	91%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin-like [Physeter catodon]	35.0	35.0	100%	0.60	91%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	35.0	35.0	100%	0.60	91%	gi|530426021|XP_005260918.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	35.0	35.0	100%	0.60	91%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	35.0	35.0	100%	0.61	91%	gi|725600051|XP_010350111.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	35.0	35.0	100%	0.61	91%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin [Tarsius syrichta]	35.0	35.0	100%	0.61	91%	gi|640796924|XP_008054571.1
☐	unnamed protein product [Homo sapiens]	35.0	35.0	100%	0.61	91%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	35.0	35.0	100%	0.61	91%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	35.0	35.0	100%	0.61	91%	gi|332257827|XP_003278006.1
☐	PREDICTED: attractin isoform 2 [Dasypus novemcinctus]	35.0	35.0	100%	0.61	91%	gi|488545593|XP_004464327.1
☐	Attractin [Myotis davidii]	35.0	35.0	100%	0.61	91%	gi|432111133|ELK34519.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	35.0	35.0	100%	0.61	91%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin [Sus scrofa]	35.0	35.0	100%	0.61	91%	gi|545879723|XP_001927324.5
☐	PREDICTED: attractin [Gorilla gorilla gorilla]	35.0	35.0	100%	0.61	91%	gi|426390844|XP_004061806.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	35.0	35.0	100%	0.61	91%	gi|694977854|XP_009435012.1
☐	Attractin [Myotis brandtii]	35.0	35.0	100%	0.61	91%	gi|521031210|EPQ12996.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	35.0	35.0	100%	0.61	91%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	35.0	35.0	100%	0.61	91%	gi|4093196|AAD03057.1
☐	secreted attractin precursor [Homo sapiens]	35.0	35.0	100%	0.61	91%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	35.0	35.0	100%	0.61	91%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	35.0	35.0	100%	0.61	91%	gi|21450863|NP_647538.1
☐	Mahogany-like protein [Macaca mulatta]	35.0	35.0	100%	0.61	91%	gi|355563316|EHH19878.1
☐	PREDICTED: attractin isoform X1 [Bos taurus]	35.0	35.0	100%	0.61	91%	gi|741947708|XP_005214542.2
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	35.0	35.0	100%	0.61	91%	gi|594099680|XP_006072965.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Pan paniscus]	35.0	35.0	100%	0.61	91%	gi|675763672|XP_008973079.1
☐							

	PREDICTED: attractin isoform X2 [Heterocephalus glaber]	35.0	35.0	100%	0.61	91%	gi|512956910|XP_004840783.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	35.0	35.0	100%	0.61	91%	gi|694977852|XP_009435011.1
☐	attractin [Sus scrofa]	35.0	35.0	100%	0.61	91%	gi|146741346|BAF62328.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	35.0	35.0	100%	0.61	91%	gi|530426019|XP_005260917.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	35.0	35.0	100%	0.61	91%	gi|544464516|XP_005568512.1
☐	Mahogany-like protein [Macaca fascicularis]	35.0	35.0	100%	0.61	91%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin [Myotis davidii]	35.0	35.0	100%	0.61	91%	gi|584075971|XP_006758187.1
☐	PREDICTED: attractin [Panthera tigris altaica]	35.0	35.0	100%	0.61	91%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin [Myotis brandtii]	35.0	35.0	100%	0.61	91%	gi|554560893|XP_005874816.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	35.0	35.0	100%	0.61	91%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	35.0	35.0	100%	0.61	91%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin [Capra hircus]	35.0	35.0	100%	0.61	91%	gi|548490191|XP_005688293.1
☐	PREDICTED: attractin [Trichechus manatus latirostris]	35.0	35.0	100%	0.61	91%	gi|471400634|XP_004383126.1
☐	Attractin [Heterocephalus glaber]	35.0	35.0	100%	0.61	91%	gi|351701383|EHB04302.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	35.0	35.0	100%	0.61	91%	gi|724902357|XP_010377335.1
☐	PREDICTED: attractin isoform 1 [Dasypus novemcinctus]	35.0	35.0	100%	0.61	91%	gi|488545591|XP_004464326.1
☐	PREDICTED: attractin [Camelus ferus]	35.0	35.0	100%	0.61	91%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Myotis lucifugus]	35.0	35.0	100%	0.61	91%	gi|558159591|XP_006096513.1
☐	PREDICTED: attractin [Camelus dromedarius]	35.0	35.0	100%	0.61	91%	gi|744589171|XP_010986570.1
☐	PREDICTED: attractin [Bos mutus]	35.0	35.0	100%	0.61	91%	gi|555963925|XP_005894036.1
☐	PREDICTED: attractin [Camelus bactrianus]	35.0	35.0	100%	0.61	91%	gi|743752427|XP_010971103.1
☐	attractin, isoform CRA_b [Homo sapiens]	35.0	35.0	100%	0.61	91%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin [Heterocephalus glaber]	35.0	35.0	100%	0.61	91%	gi|512849696|XP_004886859.1
☐	PREDICTED: attractin [Ovis aries]	35.0	35.0	100%	0.61	91%	gi|426241795|XP_004014773.1
☐	PREDICTED: attractin [Felis catus]	35.0	35.0	100%	0.61	91%	gi|586981105|XP_003983758.2
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	35.0	35.0	100%	0.61	91%	gi|694977850|XP_009435010.1
☐	PREDICTED: attractin [Otolemur garnettii]	35.0	35.0	100%	0.61	91%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin [Vicugna pacos]	35.0	35.0	100%	0.61	91%	gi|560970220|XP_006207473.1
☐	attractin [Bos taurus]	35.0	35.0	100%	0.61	91%	gi|253560524|ACT32973.1
☐	PREDICTED: attractin [Eptesicus fuscus]	35.0	35.0	100%	0.61	91%	gi|641701319|XP_008139256.1
☐	attractin [Bos taurus]	35.0	35.0	100%	0.61	91%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	35.0	35.0	100%	0.61	91%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin [Orcinus orca]	35.0	35.0	100%	0.61	91%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin [Odobenus rosmarus divergens]	35.0	35.0	100%	0.61	91%	gi|472357214|XP_004398236.1
☐	PREDICTED: attractin [Chrysochloris asiatica]	35.0	35.0	100%	0.61	91%	gi|586488825|XP_006874887.1
☐	PREDICTED: attractin isoform X1 [Heterocephalus glaber]	35.0	35.0	100%	0.61	91%	gi|512956908|XP_004840782.1
☐	PREDICTED: attractin-like [Octodon degus]	35.0	35.0	100%	0.61	91%	gi|507657234|XP_004634315.1
☐	PREDICTED: attractin isoform X1 [Ictidomys tridecemlineatus]	35.0	35.0	100%	0.61	91%	gi|532069484|XP_005320577.1
☐	PREDICTED: attractin isoform X3 [Ictidomys tridecemlineatus]	35.0	35.0	100%	0.61	91%	gi|532069488|XP_005320579.1
☐	PREDICTED: attractin [Callithrix jacchus]	35.0	35.0	100%	0.61	91%	gi|296200062|XP_002747358.1
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	35.0	35.0	100%	0.61	91%	gi|332857715|XP_003316827.1
☐	membrane attractin precursor [Homo sapiens]	35.0	35.0	100%	0.61	91%	gi|8118082|AAF72881.1
☐	attractin isoform 1 preproprotein [Homo sapiens]	35.0	35.0	100%	0.61	91%	gi|21450861|NP_647537.1
☐	PREDICTED: attractin isoform X2 [Ictidomys tridecemlineatus]	35.0	35.0	100%	0.61	91%	gi|532069486|XP_005320578.1
☐	PREDICTED: attractin [Jaculus jaculus]	35.0	35.0	100%	0.61	91%	gi|507555530|XP_004661535.1

☐	PREDICTED: attractin isoform X2 [Macaca fascicularis]	35.0	35.0	100%	0.61	91%	gi|544464512|XP_005568510.1
☐	PREDICTED: attractin [Macaca mulatta]	35.0	35.0	100%	0.61	91%	gi|109092720|XP_001115192.1
☐	PREDICTED: attractin isoform X1 [Macaca fascicularis]	35.0	35.0	100%	0.61	91%	gi|544464510|XP_005568509.1
☐	PREDICTED: attractin [Bison bison bison]	35.0	35.0	100%	0.61	91%	gi|742104093|XP_010834932.1
☐	PREDICTED: attractin [Tupaia chinensis]	35.0	35.0	100%	0.61	91%	gi|562872246|XP_006164056.1
☐	PREDICTED: attractin isoform X1 [Bubalus bubalis]	35.0	35.0	100%	0.61	91%	gi|594099676|XP_006072963.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	32.9	32.9	100%	3.0	82%	gi|635021368|XP_008017720.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	32.9	32.9	100%	3.0	82%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	32.9	32.9	100%	3.0	82%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	32.9	32.9	100%	3.0	82%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	32.9	32.9	100%	3.0	82%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin isoform X3 [Chinchilla lanigera]	32.9	32.9	100%	3.0	82%	gi|533131617|XP_005380852.1
☐	PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	32.9	32.9	100%	3.0	82%	gi|635021360|XP_008017700.1
☐	PREDICTED: attractin isoform X2 [Chinchilla lanigera]	32.9	32.9	100%	3.0	82%	gi|533131615|XP_005380851.1
☐	PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	32.9	32.9	100%	3.0	82%	gi|635021370|XP_008017729.1
☐	PREDICTED: attractin isoform X1 [Chinchilla lanigera]	32.9	32.9	100%	3.0	82%	gi|533131613|XP_005380850.1
☐	PREDICTED: attractin isoform X2 [Pteropus alecto]	32.9	32.9	100%	3.0	82%	gi|586533634|XP_006921706.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	32.5	32.5	100%	4.1	82%	gi|585160208|XP_006732353.1
☐	PREDICTED: attractin isoform X2 [Mustela putorius furo]	32.5	32.5	100%	4.1	82%	gi|511906947|XP_004772933.1
☐	PREDICTED: attractin [Ursus maritimus]	32.5	32.5	100%	4.1	82%	gi|671021680|XP_008701660.1
☐	hypothetical protein PANDA_007354 [Ailuropoda melanoleuca]	32.5	32.5	100%	4.1	82%	gi|281339872|EFB15456.1
☐	PREDICTED: attractin-like [Ailuropoda melanoleuca]	32.5	32.5	100%	4.1	82%	gi|301766802|XP_002918837.1
☐	PREDICTED: attractin [Mustela putorius furo]	32.5	32.5	100%	4.1	82%	gi|511947743|XP_004792355.1
☐	PREDICTED: attractin [Peromyscus maniculatus bairdii]	32.5	32.5	100%	4.1	82%	gi|589943852|XP_006984624.1
☐	PREDICTED: attractin isoform X1 [Mustela putorius furo]	32.5	32.5	100%	4.1	82%	gi|511906945|XP_004772932.1
☐	PREDICTED: attractin [Elephantulus edwardii]	32.5	32.5	100%	4.1	82%	gi|585689645|XP_006894264.1
☐	attractin [Mesocricetus auratus]	32.5	32.5	100%	4.1	82%	gi|528078159|NP_001268565.1

Alignments

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PREDICTED: attractin [Fukomys damarensis]

Sequence ID: gi|731281216|ref|XP_010609356.1| **Length:** 1377 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 244 to 254 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
37.5 bits(81)	0.088	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RGICDSSDVRG  11
            RGICDSSDVRG
Sbjct  244  RGICDSSDVRG  254
```

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Attractin [Fukomys damarensis]

Sequence ID: gi|676269096|gb|KFO24512.1| **Length:** 740 **Number of Matches:** 1

Related Information

Range 1: 208 to 218 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
35.0 bits(75)	0.60	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    RGICDSSDVRG  11
```

```
                RGIC+SSDVRG
Sbjct  208  RGICNSSDVRG  218
```

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PREDICTED: attractin-like [Tursiops truncatus]

Sequence ID: gi|470629747|ref|XP_004321558.1| **Length:** 1003 **Number of Matches:** 1

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

Range 1: 127 to 137 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
35.0 bits(75)	0.60	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    RGICDSSDVRG  11
            RGIC+SSDVRG
Sbjct  127  RGICNSSDVRG  137
```

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PREDICTED: attractin-like, partial [Physeter catodon]

Sequence ID: gi|593773084|ref|XP_007124834.1| **Length:** 1035 **Number of Matches:** 1

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

Range 1: 159 to 169 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
35.0 bits(75)	0.60	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    RGICDSSDVRG  11
            RGIC+SSDVRG
Sbjct  159  RGICNSSDVRG  169
```

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PREDICTED: attractin isoform X2 [Homo sapiens]

Sequence ID: gi|530426021|ref|XP_005260918.1| **Length:** 1111 **Number of Matches:** 1

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

Range 1: 296 to 306 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
35.0 bits(75)	0.60	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    RGICDSSDVRG  11
            RGIC+SSDVRG
Sbjct  296  RGICNSSDVRG  306
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - B91768AM01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download

How to read this page | Blast report description

ATRN_RGICNSSDVRG_NonMod

RID B91768AM01R (Expires on 01-14 09:37 am)

Query ID	lcl|225884	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	11		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

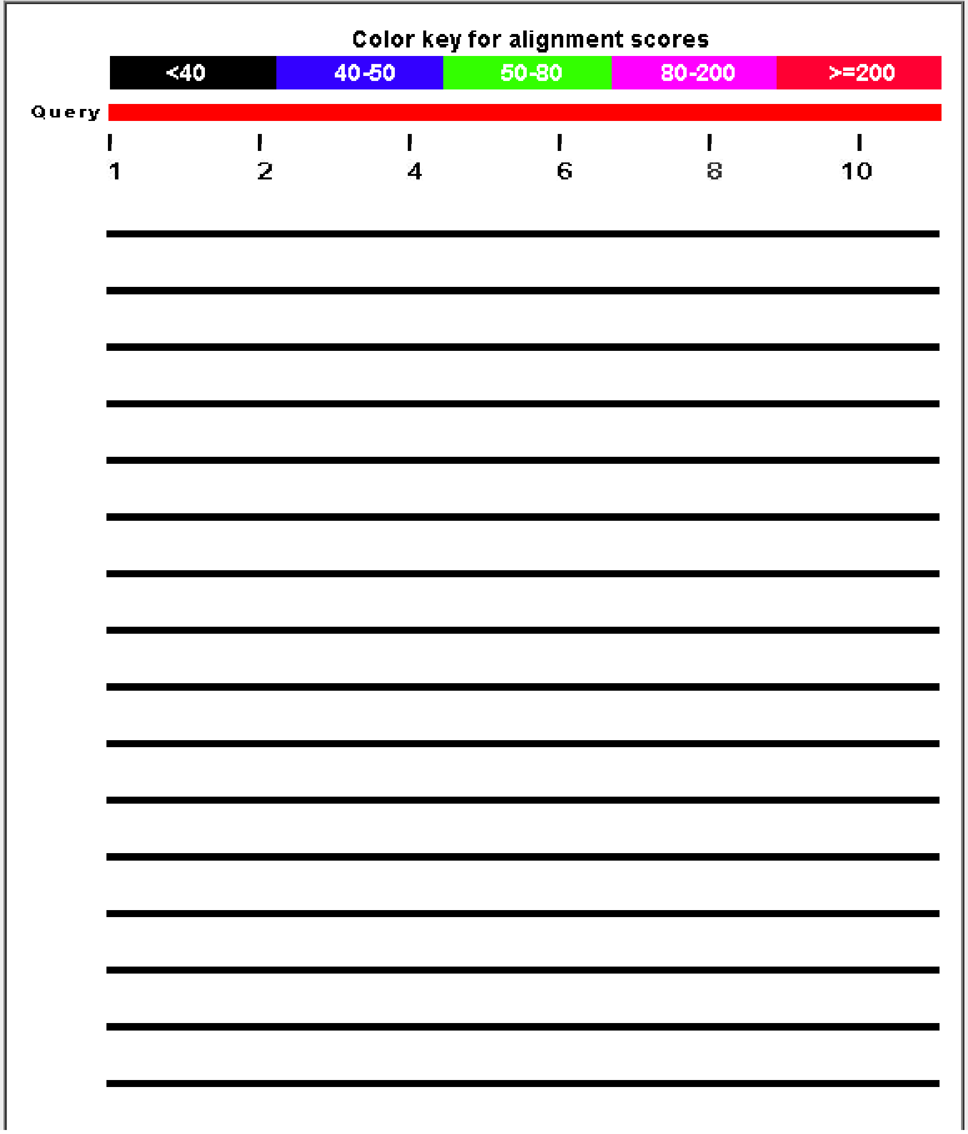
Graphic Summary

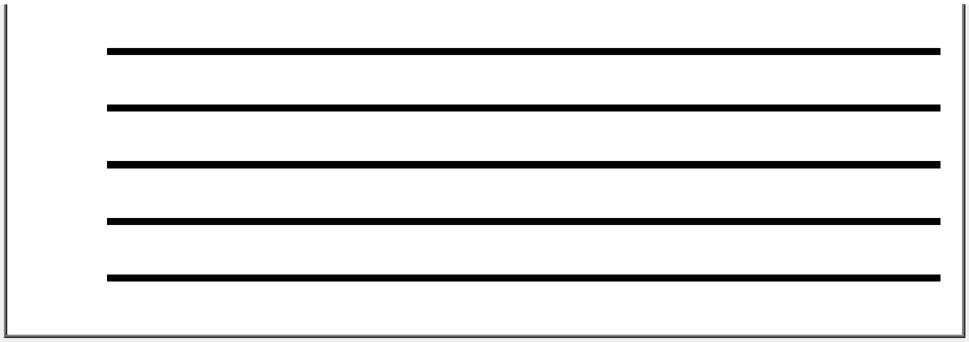
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 116 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





⊖ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Attractin [Fukomys damarensis]	37.5	37.5	100%	0.082	100%	gi|676269096|KFO24512.1
☐	PREDICTED: attractin-like [Tursiops truncatus]	37.5	37.5	100%	0.083	100%	gi|470629747|XP_004321558.1
☐	PREDICTED: attractin-like [Physeter catodon]	37.5	37.5	100%	0.083	100%	gi|593773084|XP_007124834.1
☐	PREDICTED: attractin isoform X2 [Homo sapiens]	37.5	55.6	100%	0.083	100%	gi|530426021|XP_005260918.1
☐	PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]	37.5	37.5	100%	0.083	100%	gi|725600053|XP_010350112.1
☐	PREDICTED: attractin isoform X1 [Saimiri boliviensis boliviensis]	37.5	37.5	100%	0.083	100%	gi|725600051|XP_010350111.1
☐	PREDICTED: attractin [Balaenoptera acutorostrata scammoni]	37.5	37.5	100%	0.083	100%	gi|594697511|XP_007195912.1
☐	PREDICTED: attractin [Tarsius syrichta]	37.5	37.5	100%	0.083	100%	gi|640796924|XP_008054571.1
☐	unnamed protein product [Homo sapiens]	37.5	55.6	100%	0.083	100%	gi|194380362|BAG63948.1
☐	attractin isoform 4 [Homo sapiens]	37.5	55.6	100%	0.083	100%	gi|333440461|NP_001193976.1
☐	PREDICTED: attractin isoform 2 [Nomascus leucogenys]	37.5	37.5	100%	0.083	100%	gi|332257827|XP_003278006.1
☐	PREDICTED: attractin isoform 2 [Dasypus novemcinctus]	37.5	37.5	100%	0.083	100%	gi|488545593|XP_004464327.1
☐	Attractin [Myotis davidii]	37.5	37.5	100%	0.083	100%	gi|432111133|ELK34519.1
☐	PREDICTED: attractin [Pantholops hodgsonii]	37.5	37.5	100%	0.083	100%	gi|556758951|XP_005974805.1
☐	PREDICTED: attractin [Sus scrofa]	37.5	37.5	100%	0.083	100%	gi|545879723|XP_001927324.5
☐	PREDICTED: attractin [Gorilla gorilla gorilla]	37.5	55.6	100%	0.083	100%	gi|426390844|XP_004061806.1
☐	PREDICTED: attractin isoform X4 [Pan troglodytes]	37.5	55.6	100%	0.083	100%	gi|694977854|XP_009435012.1
☐	Attractin [Myotis brandtii]	37.5	37.5	100%	0.083	100%	gi|521031210|EPQ12996.1
☐	PREDICTED: attractin isoform 1 [Nomascus leucogenys]	37.5	37.5	100%	0.083	100%	gi|332257825|XP_003278005.1
☐	attractin-2 [Homo sapiens]	37.5	37.5	100%	0.083	100%	gi|4093196|AAD03057.1
☐	secreted attractin precursor [Homo sapiens]	37.5	55.6	100%	0.083	100%	gi|8118083|AAF72882.1
☐	unnamed protein product [Homo sapiens]	37.5	55.6	100%	0.083	100%	gi|158259481|BAF85699.1
☐	attractin isoform 2 preproprotein [Homo sapiens]	37.5	55.6	100%	0.083	100%	gi|21450863|NP_647538.1
☐	Mahogany-like protein [Macaca mulatta]	37.5	37.5	100%	0.083	100%	gi|355563316|EHH19878.1
☐	PREDICTED: attractin isoform X3 [Bubalus bubalis]	37.5	37.5	100%	0.083	100%	gi|594099680|XP_006072965.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Pan paniscus]	37.5	55.6	100%	0.083	100%	gi|675763672|XP_008973079.1
☐	PREDICTED: attractin isoform X2 [Heterocephalus glaber]	37.5	37.5	100%	0.083	100%	gi|512956910|XP_004840783.1
☐	PREDICTED: attractin isoform X3 [Pan troglodytes]	37.5	55.6	100%	0.083	100%	gi|694977852|XP_009435011.1
☐							

	attractin [Sus scrofa]	37.5	37.5	100%	0.083	100%	gi|146741346|BAF62328.1
☐	PREDICTED: attractin isoform X1 [Homo sapiens]	37.5	55.6	100%	0.083	100%	gi|530426019|XP_005260917.1
☐	PREDICTED: attractin isoform X4 [Macaca fascicularis]	37.5	37.5	100%	0.083	100%	gi|544464516|XP_005568512.1
☐	Mahogany-like protein [Macaca fascicularis]	37.5	37.5	100%	0.083	100%	gi|355784657|EHH65508.1
☐	PREDICTED: attractin [Myotis davidii]	37.5	37.5	100%	0.083	100%	gi|584075971|XP_006758187.1
☐	PREDICTED: attractin [Panthera tigris altaica]	37.5	37.5	100%	0.083	100%	gi|591291970|XP_007073329.1
☐	PREDICTED: attractin [Myotis brandtii]	37.5	37.5	100%	0.083	100%	gi|554560893|XP_005874816.1
☐	PREDICTED: attractin isoform X3 [Macaca fascicularis]	37.5	37.5	100%	0.083	100%	gi|544464514|XP_005568511.1
☐	PREDICTED: attractin-like [Galeopterus variegatus]	37.5	37.5	100%	0.083	100%	gi|667324076|XP_008589101.1
☐	PREDICTED: attractin [Capra hircus]	37.5	37.5	100%	0.083	100%	gi|548490191|XP_005688293.1
☐	PREDICTED: attractin [Trichechus manatus latirostris]	37.5	37.5	100%	0.083	100%	gi|471400634|XP_004383126.1
☐	Attractin [Heterocephalus glaber]	37.5	37.5	100%	0.083	100%	gi|351701383|EHB04302.1
☐	PREDICTED: attractin [Rhinopithecus roxellana]	37.5	37.5	100%	0.083	100%	gi|724902357|XP_010377335.1
☐	PREDICTED: attractin isoform 1 [Dasypus novemcinctus]	37.5	37.5	100%	0.083	100%	gi|488545591|XP_004464326.1
☐	PREDICTED: attractin [Camelus ferus]	37.5	37.5	100%	0.083	100%	gi|560921992|XP_006187198.1
☐	PREDICTED: attractin [Myotis lucifugus]	37.5	37.5	100%	0.083	100%	gi|558159591|XP_006096513.1
☐	PREDICTED: attractin [Bos mutus]	37.5	37.5	100%	0.083	100%	gi|555963925|XP_005894036.1
☐	attractin, isoform CRA_b [Homo sapiens]	37.5	55.6	100%	0.083	100%	gi|119630936|EAX10531.1
☐	PREDICTED: attractin [Heterocephalus glaber]	37.5	37.5	100%	0.083	100%	gi|512849696|XP_004886859.1
☐	PREDICTED: attractin [Ovis aries]	37.5	37.5	100%	0.083	100%	gi|426241795|XP_004014773.1
☐	PREDICTED: attractin [Felis catus]	37.5	37.5	100%	0.083	100%	gi|586981105|XP_003983758.2
☐	PREDICTED: attractin isoform X2 [Pan troglodytes]	37.5	55.6	100%	0.083	100%	gi|694977850|XP_009435010.1
☐	PREDICTED: attractin [Otolemur garnettii]	37.5	37.5	100%	0.083	100%	gi|395830288|XP_003788264.1
☐	PREDICTED: attractin [Vicugna pacos]	37.5	37.5	100%	0.083	100%	gi|560970220|XP_006207473.1
☐	attractin [Bos taurus]	37.5	37.5	100%	0.083	100%	gi|253560524|ACT32973.1
☐	PREDICTED: attractin [Eptesicus fuscus]	37.5	37.5	100%	0.083	100%	gi|641701319|XP_008139256.1
☐	attractin [Bos taurus]	37.5	37.5	100%	0.083	100%	gi|27806737|NP_776420.1
☐	PREDICTED: attractin isoform X2 [Bubalus bubalis]	37.5	37.5	100%	0.083	100%	gi|594099678|XP_006072964.1
☐	PREDICTED: attractin [Orcinus orca]	37.5	37.5	100%	0.083	100%	gi|466084723|XP_004285351.1
☐	PREDICTED: attractin [Odobenus rosmarus divergens]	37.5	37.5	100%	0.083	100%	gi|472357214|XP_004398236.1
☐	PREDICTED: attractin [Chrysochloris asiatica]	37.5	37.5	100%	0.083	100%	gi|586488825|XP_006874887.1
☐	PREDICTED: attractin isoform X1 [Heterocephalus glaber]	37.5	37.5	100%	0.083	100%	gi|512956908|XP_004840782.1
☐	PREDICTED: attractin-like [Octodon degus]	37.5	37.5	100%	0.083	100%	gi|507657234|XP_004634315.1
☐	PREDICTED: attractin isoform X1 [Ictidomys tridecemlineatus]	37.5	37.5	100%	0.083	100%	gi|532069484|XP_005320577.1
☐	PREDICTED: attractin isoform X3 [Ictidomys tridecemlineatus]	37.5	37.5	100%	0.083	100%	gi|532069488|XP_005320579.1
☐	PREDICTED: attractin [Callithrix jacchus]	37.5	37.5	100%	0.083	100%	gi|296200062|XP_002747358.1
☐	PREDICTED: attractin isoform X1 [Pan troglodytes]	37.5	55.6	100%	0.083	100%	gi|332857715|XP_003316827.1
☐	membrane attractin precursor [Homo sapiens]	37.5	55.6	100%	0.083	100%	gi|8118082|AAF72881.1
☐	attractin isoform 1 preproprotein [Homo sapiens]	37.5	55.6	100%	0.083	100%	gi|21450861|NP_647537.1
☐	PREDICTED: attractin isoform X2 [Ictidomys tridecemlineatus]	37.5	37.5	100%	0.083	100%	gi|532069486|XP_005320578.1
☐	PREDICTED: attractin [Jaculus jaculus]	37.5	37.5	100%	0.083	100%	gi|507555530|XP_004661535.1
☐	PREDICTED: attractin isoform X2 [Macaca fascicularis]	37.5	37.5	100%	0.083	100%	gi|544464512|XP_005568510.1
☐	PREDICTED: attractin [Macaca mulatta]	37.5	37.5	100%	0.083	100%	gi|109092720|XP_001115192.1
☐	PREDICTED: attractin isoform X2 [Bos taurus]	37.5	37.5	100%	0.083	100%	gi|528973313|XP_005214542.1
☐	PREDICTED: attractin isoform X1 [Macaca fascicularis]	37.5	37.5	100%	0.083	100%	gi|544464510|XP_005568509.1

☐	PREDICTED: attractin [Tupaia chinensis]	37.5	37.5	100%	0.083	100%	gi|562872246|XP_006164056.1
☐	PREDICTED: attractin isoform X1 [Bubalus bubalis]	37.5	37.5	100%	0.083	100%	gi|594099676|XP_006072963.1
☐	PREDICTED: attractin isoform X1 [Bos taurus]	37.5	37.5	100%	0.084	100%	gi|528973311|XP_005214541.1
☐	PREDICTED: attractin isoform X5 [Chlorocebus sabaeus]	35.4	35.4	100%	0.42	91%	gi|635021368|XP_008017720.1
☐	PREDICTED: attractin isoform X4 [Chlorocebus sabaeus]	35.4	35.4	100%	0.42	91%	gi|635021366|XP_008017712.1
☐	PREDICTED: attractin isoform X3 [Chlorocebus sabaeus]	35.4	35.4	100%	0.42	91%	gi|635021364|XP_008017707.1
☐	PREDICTED: attractin isoform X2 [Chlorocebus sabaeus]	35.4	35.4	100%	0.42	91%	gi|635021362|XP_008017704.1
☐	PREDICTED: attractin isoform X1 [Pteropus alecto]	35.4	35.4	100%	0.42	91%	gi|586533632|XP_006921705.1
☐	PREDICTED: attractin isoform X3 [Chinchilla lanigera]	35.4	35.4	100%	0.42	91%	gi|533131617|XP_005380852.1
☐	PREDICTED: attractin isoform X1 [Chlorocebus sabaeus]	35.4	35.4	100%	0.42	91%	gi|635021360|XP_008017700.1
☐	PREDICTED: attractin isoform X2 [Chinchilla lanigera]	35.4	35.4	100%	0.42	91%	gi|533131615|XP_005380851.1
☐	PREDICTED: attractin isoform X6 [Chlorocebus sabaeus]	35.4	35.4	100%	0.42	91%	gi|635021370|XP_008017729.1
☐	PREDICTED: attractin isoform X1 [Chinchilla lanigera]	35.4	35.4	100%	0.42	91%	gi|533131613|XP_005380850.1
☐	PREDICTED: attractin isoform X2 [Pteropus alecto]	35.4	35.4	100%	0.42	91%	gi|586533634|XP_006921706.1
☐	PREDICTED: attractin-like [Leptonychotes weddellii]	35.0	35.0	100%	0.57	91%	gi|585160208|XP_006732353.1
☐	PREDICTED: attractin isoform X2 [Mustela putorius furo]	35.0	35.0	100%	0.58	91%	gi|511906947|XP_004772933.1
☐	PREDICTED: attractin [Ursus maritimus]	35.0	35.0	100%	0.58	91%	gi|671021680|XP_008701660.1
☐	hypothetical protein PANDA_007354 [Ailuropoda melanoleuca]	35.0	35.0	100%	0.58	91%	gi|281339872|EFB15456.1
☐	PREDICTED: attractin-like [Ailuropoda melanoleuca]	35.0	35.0	100%	0.58	91%	gi|301766802|XP_002918837.1
☐	PREDICTED: attractin [Mustela putorius furo]	35.0	35.0	100%	0.58	91%	gi|511947743|XP_004792355.1
☐	PREDICTED: attractin [Fukomys damarensis]	35.0	35.0	100%	0.58	91%	gi|731281216|XP_010609356.1
☐	PREDICTED: attractin [Peromyscus maniculatus bairdii]	35.0	35.0	100%	0.58	91%	gi|589943852|XP_006984624.1
☐	PREDICTED: attractin isoform X1 [Mustela putorius furo]	35.0	35.0	100%	0.58	91%	gi|511906945|XP_004772932.1
☐	PREDICTED: attractin [Elephantulus edwardii]	35.0	35.0	100%	0.58	91%	gi|585689645|XP_006894264.1
☐	attractin [Mesocricetus auratus]	35.0	35.0	100%	0.58	91%	gi|528078159|NP_001268565.1
☐	PREDICTED: LOW QUALITY PROTEIN: attractin [Cavia porcellus]	35.0	35.0	100%	0.58	91%	gi|514473642|XP_005008408.1
☐	PREDICTED: attractin [Lipotes vexillifer]	34.1	34.1	100%	1.1	91%	gi|602710450|XP_007465469.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Attractin [Fukomys damarensis]

Sequence ID: gi|676269096|gb|KFO24512.1| **Length:** 740 **Number of Matches:** 1

Related Information

Range 1: 208 to 218 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
37.5 bits(81)	0.082	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RGICNSSDVRG  11
            RGICNSSDVRG
Sbjct  208  RGICNSSDVRG  218
```

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PREDICTED: attractin-like [Tursiops truncatus]

Sequence ID: gi|470629747|ref|XP_004321558.1| **Length:** 1003 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 127 to 137 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
37.5 bits(81)	0.083	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RGICNSSDVRG  11
```

```
                 RGICNSSDVRG
Sbjct  127  RGICNSSDVRG  137
```

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PREDICTED: attractin-like, partial [Physeter catodon]

Sequence ID: gi|593773084|ref|XP_007124834.1| **Length:** 1035 **Number of Matches:** 1

Range 1: 159 to 169 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
37.5 bits(81)	0.083	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RGICNSSDVRG  11
            RGICNSSDVRG
Sbjct  159  RGICNSSDVRG  169
```

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

Download GenPept Graphics **Sort by:** E value ▼ Next ▲ Previous Descriptions

PREDICTED: attractin isoform X2 [Homo sapiens]

Sequence ID: gi|530426021|ref|XP_005260918.1| **Length:** 1111 **Number of Matches:** 2

Range 1: 296 to 306 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
37.5 bits(81)	0.083	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RGICNSSDVRG  11
            RGICNSSDVRG
Sbjct  296  RGICNSSDVRG  306
```

Range 2: 257 to 267 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
18.0 bits(35)	181692	7/11(64%)	7/11(63%)	3/11(27%)

```
Query  1    RGIC---NSSD  8
            RG C   NSSD
Sbjct  257  RGECKISNSSD  267
```

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

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PREDICTED: attractin isoform X2 [Saimiri boliviensis boliviensis]

Sequence ID: gi|725600053|ref|XP_010350112.1| **Length:** 1128 **Number of Matches:** 1

Range 1: 127 to 137 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
37.5 bits(81)	0.083	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RGICNSSDVRG  11
            RGICNSSDVRG
Sbjct  127  RGICNSSDVRG  137
```

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

BCHE_KYGDPNETQNDSTSWPVFKS_Mod

RID	BHJ2V2AH014 (Expires on 01-17 15:14 pm)		
Query ID	lcl|2924	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	20		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

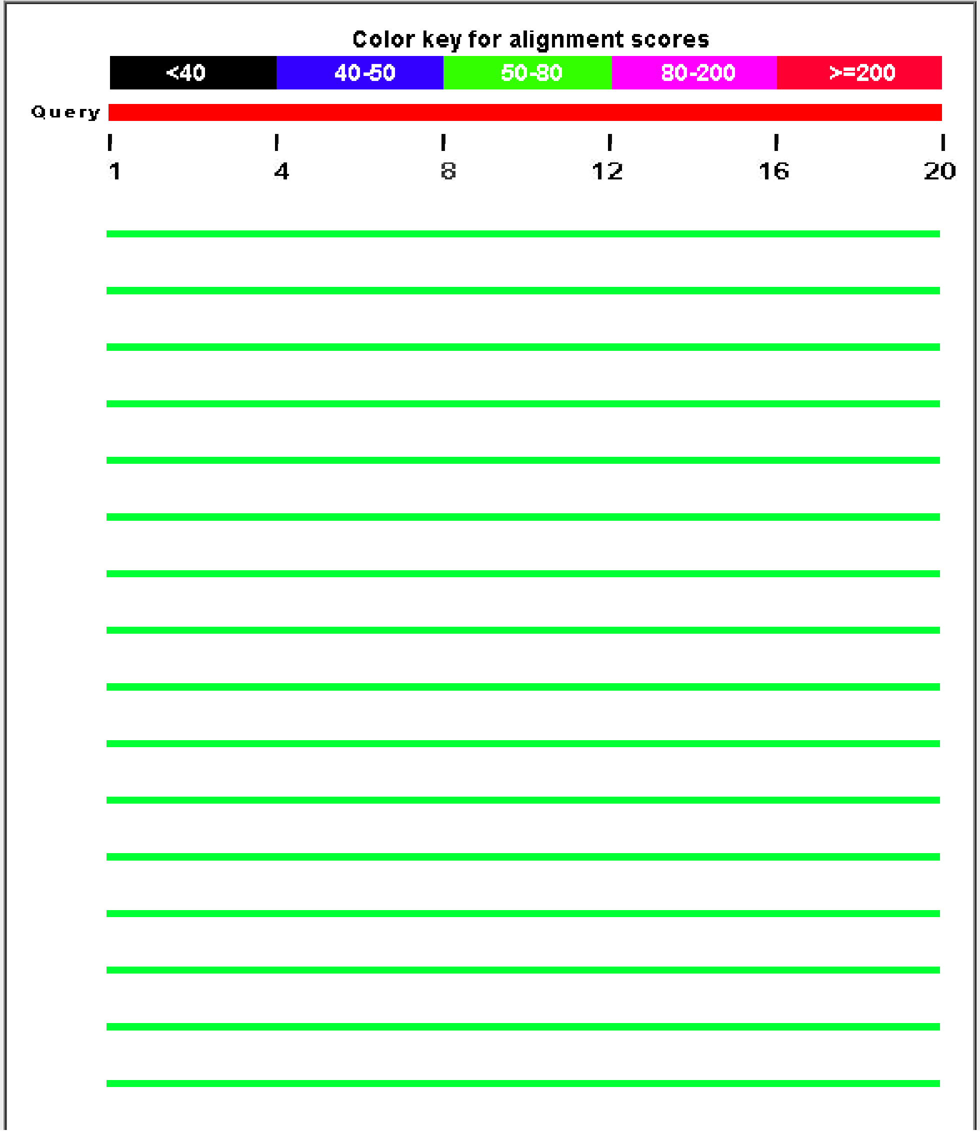
Graphic Summary

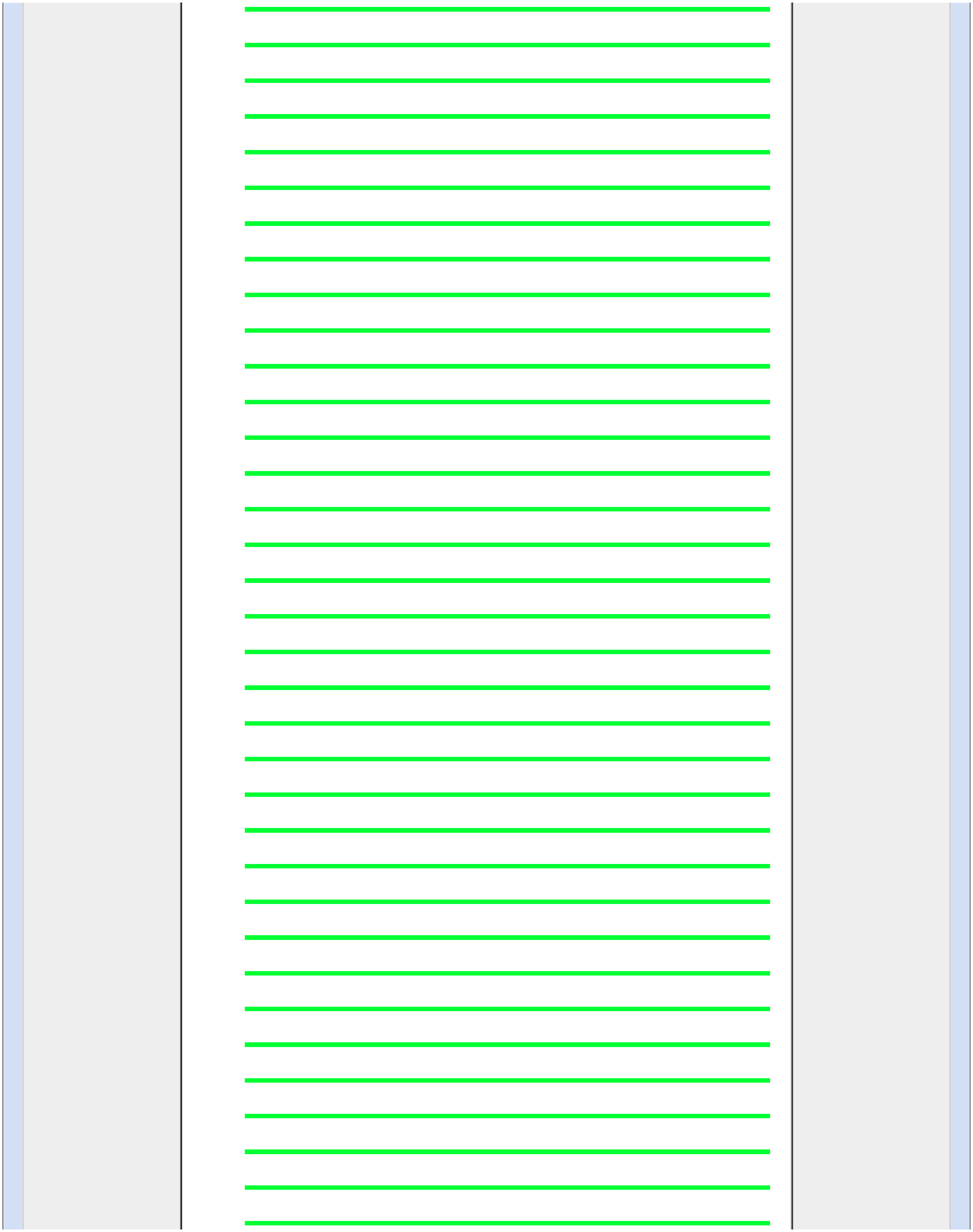
Show Conserved Domains

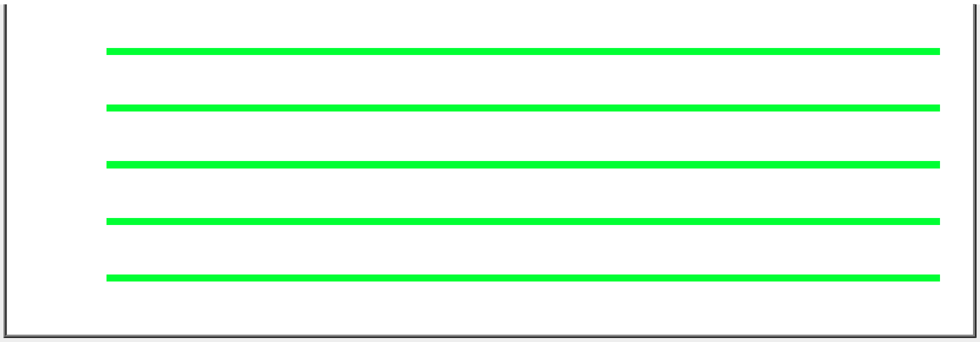
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylchol	63.8	63.8	100%	4e-10	90%	gi|393715367|4AQD_A
☐	monomeric butyrylcholinesterase [synthetic construct]	63.8	63.8	100%	4e-10	90%	gi|388261124|AFK25766.1
☐	Chain A, Co-Crystallization Studies Of Full Length Recombinant Bc	63.8	63.8	100%	4e-10	90%	gi|328877250|3O9M_A
☐	butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|632795270|AHZ34327.1
☐	cholinesterase precursor [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|4557351|NP_000046.1
☐	unnamed protein product [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|158257558|BAF84752.1
☐	butyrylcholinesterase [synthetic construct]	63.8	63.8	100%	4e-10	90%	gi|260766471|ACX50257.1
☐	PREDICTED: cholinesterase isoform X1 [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|530375091|XP_005247742.1
☐	cholinesterase precursor [Pan troglodytes]	60.0	60.0	100%	7e-09	85%	gi|343960913|BAK62046.1
☐	PREDICTED: cholinesterase [Gorilla gorilla gorilla]	60.0	60.0	100%	7e-09	85%	gi|426342776|XP_004038010.1
☐	PREDICTED: cholinesterase [Pan paniscus]	60.0	60.0	100%	7e-09	85%	gi|397493718|XP_003817746.1
☐	PREDICTED: cholinesterase [Pan troglodytes]	60.0	60.0	100%	7e-09	85%	gi|114590210|XP_516857.2
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholinest	59.2	59.2	100%	1e-08	85%	gi|402550232|4AXB_A
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholinest	59.2	59.2	100%	1e-08	85%	gi|402550237|4B0O_A
☐	Chain A, Structure Of Human Butyrylcholinesterase Inhibited By Cb	59.2	59.2	100%	1e-08	85%	gi|340707403|2Y1K_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	59.2	59.2	100%	1e-08	85%	gi|237823652|2WIL_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	59.2	59.2	100%	1e-08	85%	gi|237823648|2WIF_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	59.2	59.2	100%	1e-08	85%	gi|237823647|2WID_A
☐	Chain A, X-Ray Structure Of Human Butyrylcholinesterase Inhibitec	57.5	57.5	100%	5e-08	85%	gi|326634060|2XQF_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	57.5	57.5	100%	5e-08	85%	gi|258588213|2WSL_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	57.5	57.5	100%	5e-08	85%	gi|215794636|3DJY_A
☐	Chain A, Crystal Structure Of Human Butyryl Cholinesterase [Homo	57.5	57.5	100%	5e-08	85%	gi|34810859|1P0I_A
☐	Chain A, G117h Mutant Of Human Butyrylcholinesterase In Comple	57.5	57.5	100%	5e-08	85%	gi|313103512|2XMB_A
☐	Chain A, Crystal Structure Of Recombinant Full Length Human Buty	57.5	57.5	100%	5e-08	85%	gi|158429456|2PM8_A
☐	Chain A, Structure Of Human Butyrylcholinesterase In Complex Wit	57.1	57.1	100%	7e-08	85%	gi|145579736|2J4C_A
☐	PREDICTED: cholinesterase [Eptesicus fuscus]	56.2	56.2	100%	1e-07	85%	gi|641703485|XP_008140478.1
☐	PREDICTED: cholinesterase [Myotis lucifugus]	56.2	56.2	100%	1e-07	85%	gi|558125651|XP_006088951.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhydı	54.9	54.9	100%	4e-07	80%	gi|21362409|P81908.1
☐							

	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhyd	54.9	54.9	100%	4e-07	80%	gi|116354|P21927.1
☐	PREDICTED: cholinesterase [Oryctolagus cuniculus]	54.9	54.9	100%	4e-07	80%	gi|291400118|XP_002716414.1
☐	PREDICTED: cholinesterase [Orcinus orca]	54.9	54.9	100%	4e-07	80%	gi|466076197|XP_004283487.1
☐	cholinesterase precursor [Pongo abelii]	54.9	54.9	100%	4e-07	80%	gi|197097436|NP_001127509.1
☐	PREDICTED: cholinesterase isoform X1 [Sus scrofa]	54.9	54.9	100%	4e-07	80%	gi|335299867|XP_003358712.1
☐	cholinesterase precursor [Bos taurus]	54.9	54.9	100%	4e-07	80%	gi|116004027|NP_001070374.1
☐	PREDICTED: cholinesterase [Bison bison bison]	54.9	54.9	100%	4e-07	80%	gi|742123891|XP_010839228.1
☐	PREDICTED: cholinesterase [Balaenoptera acutorostrata scammo	54.9	54.9	100%	4e-07	80%	gi|594625950|XP_007197616.1
☐	PREDICTED: cholinesterase isoform X1 [Pongo abelii]	54.9	54.9	100%	4e-07	80%	gi|686714306|XP_009237773.1
☐	PREDICTED: cholinesterase [Lipotes vexillifer]	54.9	54.9	100%	4e-07	80%	gi|602681974|XP_007446483.1
☐	PREDICTED: cholinesterase [Pantholops hodgsonii]	54.9	54.9	100%	4e-07	80%	gi|556779632|XP_005984864.1
☐	PREDICTED: cholinesterase [Bos mutus]	54.9	54.9	100%	4e-07	80%	gi|555966690|XP_005895396.1
☐	PREDICTED: cholinesterase [Capra hircus]	54.9	54.9	100%	4e-07	80%	gi|548451269|XP_005675420.1
☐	PREDICTED: cholinesterase [Ovis aries]	54.9	54.9	100%	4e-07	80%	gi|426218006|XP_004003241.1
☐	PREDICTED: cholinesterase-like isoform X1 [Myotis brandtii]	53.7	53.7	100%	1e-06	85%	gi|554526033|XP_005857864.1
☐	Cholinesterase [Myotis brandtii]	53.7	53.7	100%	1e-06	85%	gi|521020653|EPQ02441.1
☐	PREDICTED: cholinesterase isoform X2 [Saimiri boliviensis bolivie	52.8	52.8	100%	2e-06	75%	gi|725560928|XP_010334003.1
☐	PREDICTED: cholinesterase isoform X1 [Saimiri boliviensis bolivie	52.8	52.8	100%	2e-06	75%	gi|403265619|XP_003925023.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase [Callithrix j	52.8	52.8	100%	2e-06	75%	gi|675737963|XP_002807699.3
☐	PREDICTED: cholinesterase [Ictidomys tridecemlineatus]	52.4	52.4	100%	3e-06	80%	gi|532105511|XP_005338342.1
☐	PREDICTED: cholinesterase [Nomascus leucogenys]	52.4	52.4	100%	3e-06	75%	gi|332214651|XP_003256448.1
☐	hypothetical protein EGK_11933 [Macaca mulatta]	51.5	51.5	100%	5e-06	75%	gi|355559896|EHH16624.1
☐	butyrylcholinesterase precursor [Macaca fascicularis]	51.5	51.5	100%	5e-06	75%	gi|290795732|ADD64703.1
☐	cholinesterase precursor [Equus caballus]	51.5	51.5	100%	5e-06	75%	gi|126352540|NP_001075319.1
☐	PREDICTED: cholinesterase-like [Elephantulus edwardii]	51.5	51.5	100%	5e-06	75%	gi|585675683|XP_006890440.1
☐	PREDICTED: cholinesterase [Macaca fascicularis]	51.5	51.5	100%	5e-06	75%	gi|544412493|XP_005546353.1
☐	PREDICTED: cholinesterase isoform X1 [Papio anubis]	51.5	51.5	100%	5e-06	75%	gi|402861047|XP_003894921.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase-like [Maca	51.5	51.5	100%	5e-06	75%	gi|297286482|XP_002808379.1
☐	PREDICTED: cholinesterase isoform X2 [Equus przewalskii]	51.5	51.5	100%	5e-06	75%	gi|664725795|XP_008520036.1
☐	PREDICTED: cholinesterase isoform X1 [Equus przewalskii]	51.5	51.5	100%	5e-06	75%	gi|664725793|XP_008520035.1
☐	PREDICTED: cholinesterase isoform X1 [Chlorocebus sabaeus]	51.5	51.5	100%	5e-06	75%	gi|635084154|XP_007970394.1
☐	PREDICTED: cholinesterase [Ceratotherium simum simum]	51.5	51.5	100%	5e-06	75%	gi|478501043|XP_004424836.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus dromedarius]	51.1	51.1	100%	7e-06	75%	gi|744553709|XP_010974642.1
☐	PREDICTED: cholinesterase isoform X1 [Camelus dromedarius]	51.1	51.1	100%	7e-06	75%	gi|744553706|XP_010974641.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus bactrianus]	51.1	51.1	100%	7e-06	75%	gi|743713601|XP_010950371.1
☐	PREDICTED: cholinesterase [Vicugna pacos]	51.1	51.1	100%	7e-06	75%	gi|560956860|XP_006200907.1
☐	PREDICTED: cholinesterase [Camelus ferus]	51.1	51.1	100%	7e-06	75%	gi|560915255|XP_006183885.1
☐	PREDICTED: cholinesterase [Myotis davidii]	50.7	50.7	90%	1e-05	83%	gi|584083219|XP_006761409.1
☐	PREDICTED: cholinesterase [Orycteropus afer afer]	49.8	49.8	100%	2e-05	75%	gi|634870148|XP_007946910.1
☐	PREDICTED: cholinesterase [Otolemur garnettii]	49.0	49.0	100%	4e-05	75%	gi|395843862|XP_003794691.1
☐	PREDICTED: cholinesterase isoform X1 [Peromyscus maniculatus	49.0	49.0	100%	4e-05	75%	gi|589919054|XP_006972718.1
☐	PREDICTED: cholinesterase [Tarsius syrichta]	48.6	48.6	100%	5e-05	70%	gi|640826885|XP_008070612.1
☐	PREDICTED: cholinesterase-like isoform 1 [Dasypus novemcinctus	48.1	48.1	100%	7e-05	70%	gi|488587231|XP_004478943.1
☐	PREDICTED: cholinesterase-like [Trichechus manatus latirostris]	48.1	48.1	100%	7e-05	70%	gi|471406477|XP_004384938.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhyd	48.1	48.1	100%	7e-05	70%	gi|38502853|O62761.1

☐	cholinesterase precursor [Felis catus]	48.1	48.1	100%	7e-05	70%	gi|57163907|NP_001009364.1
☐	PREDICTED: cholinesterase isoform X1 [Loxodonta africana]	48.1	48.1	100%	7e-05	70%	gi|731499959|XP_003416305.2
☐	PREDICTED: cholinesterase-like [Panthera tigris altaica]	48.1	48.1	100%	7e-05	70%	gi|591300304|XP_007077117.1
☐	PREDICTED: cholinesterase [Galeopterus variegatus]	47.7	47.7	100%	1e-04	70%	gi|667294272|XP_008578862.1
☐	PREDICTED: cholinesterase-like [Chrysochloris asiatica]	47.7	47.7	100%	1e-04	70%	gi|586462448|XP_006861862.1
☐	PREDICTED: cholinesterase-like [Echinops telfairi]	47.7	47.7	100%	1e-04	70%	gi|507651638|XP_004704160.1
☐	PREDICTED: cholinesterase [Ursus maritimus]	47.3	47.3	95%	1e-04	68%	gi|670999264|XP_008690527.1
☐	PREDICTED: cholinesterase isoform X2 [Heterocephalus glaber]	46.9	46.9	100%	2e-04	75%	gi|512824494|XP_004880401.1
☐	PREDICTED: cholinesterase isoform X1 [Chinchilla lanigera]	46.9	46.9	100%	2e-04	75%	gi|533158554|XP_005393194.1
☐	PREDICTED: cholinesterase isoform X1 [Heterocephalus glaber]	46.9	46.9	100%	2e-04	75%	gi|512824490|XP_004880400.1
☐	PREDICTED: cholinesterase isoform X2 [Cavia porcellus]	46.4	46.4	100%	3e-04	70%	gi|514460083|XP_005003514.1
☐	PREDICTED: cholinesterase isoform X1 [Cavia porcellus]	46.4	46.4	100%	3e-04	70%	gi|348567235|XP_003469406.1
☐	PREDICTED: cholinesterase [Rhinopithecus roxellana]	46.4	46.4	100%	3e-04	70%	gi|724956944|XP_010353594.1
☐	Cholinesterase [Pteropus alecto]	46.0	46.0	100%	4e-04	75%	gi|431915168|ELK15855.1
☐	PREDICTED: cholinesterase [Microtus ochrogaster]	46.0	46.0	100%	4e-04	75%	gi|531999261|XP_005344165.1
☐	PREDICTED: cholinesterase [Pteropus alecto]	46.0	46.0	100%	4e-04	75%	gi|586546267|XP_006908236.1
☐	PREDICTED: cholinesterase-like isoform X1 [Mustela putorius furo]	46.0	46.0	95%	4e-04	68%	gi|511910148|XP_004774475.1
☐	hypothetical protein PANDA_007095 [Ailuropoda melanoleuca]	45.6	45.6	95%	5e-04	68%	gi|281337784|EFB13368.1
☐	PREDICTED: cholinesterase-like [Ailuropoda melanoleuca]	45.6	45.6	95%	5e-04	68%	gi|301766374|XP_002918607.1
☐	PREDICTED: cholinesterase [Fukomys damarensis]	44.3	44.3	100%	0.001	70%	gi|731199055|XP_010610068.1
☐	Cholinesterase [Fukomys damarensis]	44.3	44.3	100%	0.001	70%	gi|676283600|KFO36750.1
☐	PREDICTED: cholinesterase [Sarcophilus harrisii]	43.9	43.9	90%	0.002	67%	gi|395528220|XP_003766229.1
☐	PREDICTED: cholinesterase [Tupaia chinensis]	43.5	43.5	100%	0.002	65%	gi|562842605|XP_006150360.1
☐	PREDICTED: cholinesterase-like [Sorex araneus]	43.1	43.1	95%	0.003	68%	gi|505845607|XP_004616283.1
☐	PREDICTED: cholinesterase [Cricetulus griseus]	43.1	43.1	100%	0.003	70%	gi|354496810|XP_003510518.1
☐	PREDICTED: cholinesterase-like [Odobenus rosmarus divergens]	43.1	43.1	90%	0.003	67%	gi|472347065|XP_004393257.1
☐	cholinesterase precursor [Mus musculus]	42.6	42.6	100%	0.004	70%	gi|124487350|NP_033868.3

⊟ Alignments

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Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylcholinesterase

Sequence ID: gi|393715367|pdb|4AQD|A **Length:** 531 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 478 to 497 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGDPNETQNDSTSWPVFKS  20
            KYG+PNETQN+STSWPVFKS
Sbjct  478  KYGNPNETQNNSTSWPVFKS  497
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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monomeric butyrylcholinesterase [synthetic construct]

Sequence ID: gi|388261124|gb|AFK25766.1| **Length:** 557 **Number of Matches:** 1

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

Related Information

```
Query  1    KYGDPNETQNDSTSWPVFKS  20
            KYG+PNETQN+STSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

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Chain A, Co-Crystallization Studies Of Full Length Recombinant Bche With Cocaine Offers Insights Into Cocaine Detoxification

Sequence ID: gi|328877250|pdb|3O9M|A **Length:** 574 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 476 to 495 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGDPNETQNDSTSWPVFKS  20
            KYG+PNETQN+STSWPVFKS
Sbjct  476  KYGNPNETQNNSTSWPVFKS  495
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]

Sequence ID: gi|632795270|gb|AHZ34327.1| **Length:** 602 **Number of Matches:** 1

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGDPNETQNDSTSWPVFKS  20
            KYG+PNETQN+STSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Related Information

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

cholinesterase precursor [Homo sapiens]

Sequence ID: gi|4557351|ref|NP_000046.1| **Length:** 602 **Number of Matches:** 1

▷ See 10 more title(s)

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGDPNETQNDSTSWPVFKS  20
            KYG+PNETQN+STSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Structure - 3D structure displays

PubChem BioAssay - bioactivity screening

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - BHJCM84E014

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download

How to read this page   Blast report description

BCHE_KYGNPDETQDDSTSWPVFKS_Mod

RID	BHJCM84E014 (Expires on 01-17 15:19 pm)
Query ID	lcl|37331
Description	None
Molecule type	amino acid
Query Length	20

Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

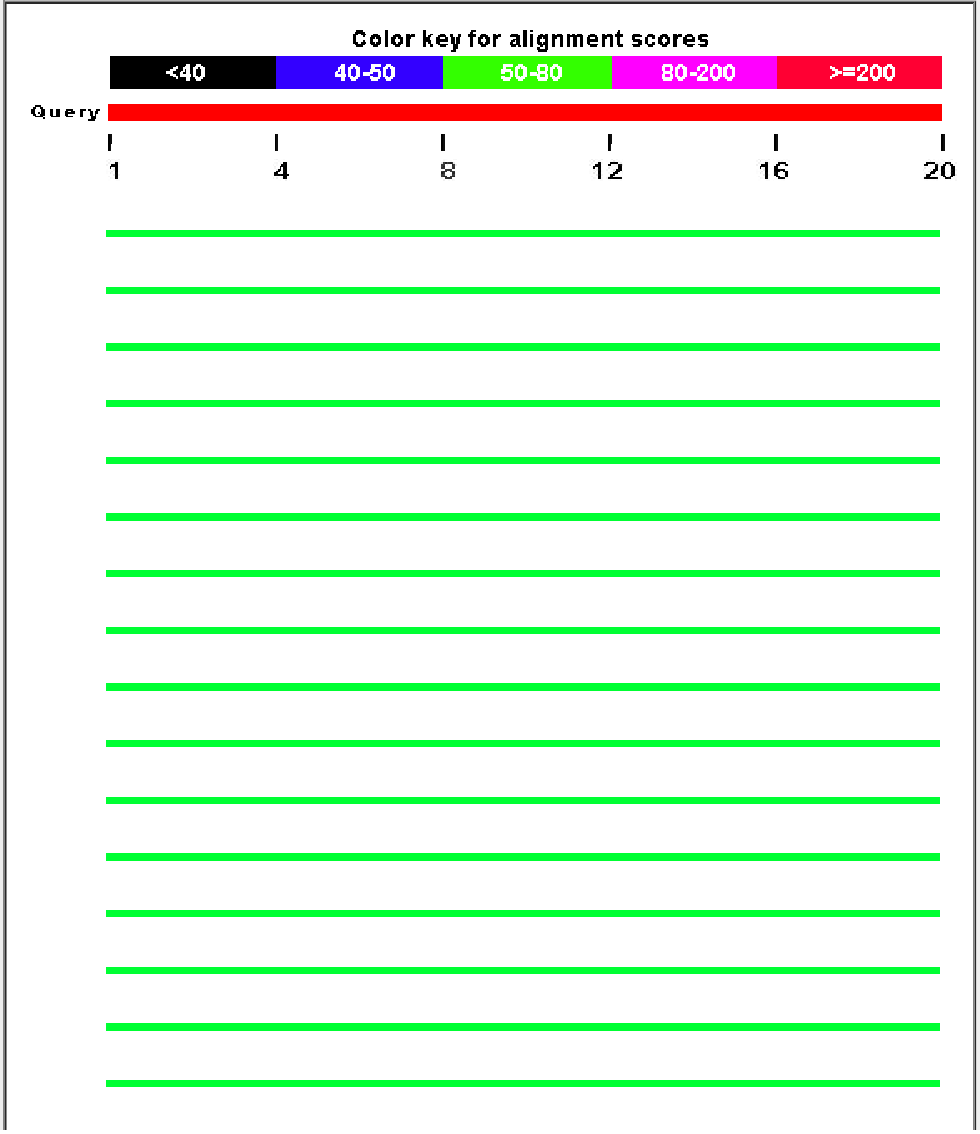
Graphic Summary

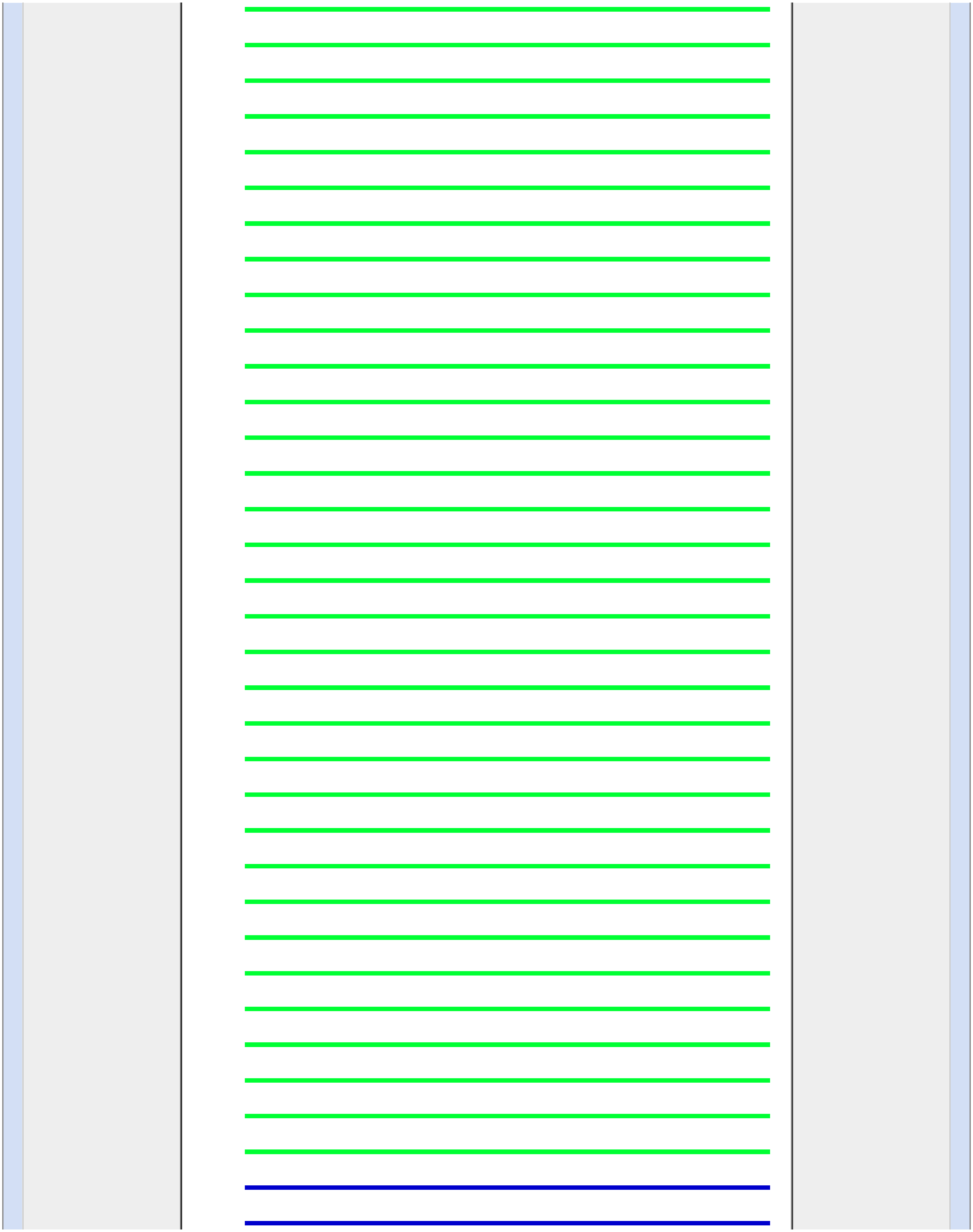
Show Conserved Domains

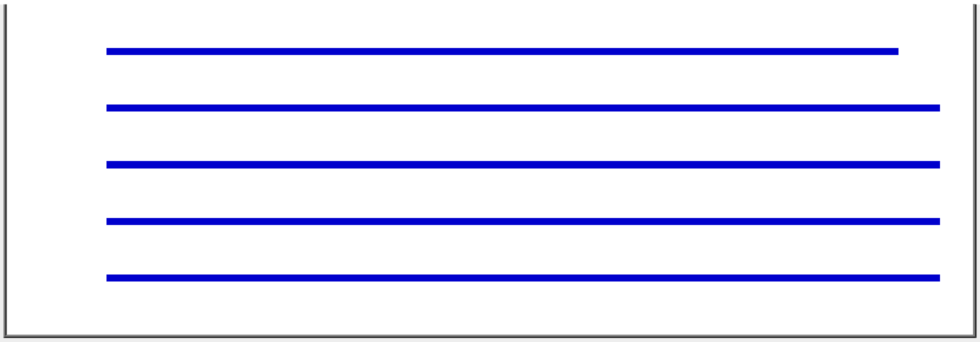
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylchol	61.3	61.3	100%	3e-09	85%	gi|393715367|4AQD_A
☐	monomeric butyrylcholinesterase [synthetic construct]	61.3	61.3	100%	3e-09	85%	gi|388261124|AFK25766.1
☐	Chain A, Co-Crystallization Studies Of Full Length Recombinant Bc	61.3	61.3	100%	3e-09	85%	gi|328877250|3O9M_A
☐	butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]	61.3	61.3	100%	3e-09	85%	gi|632795270|AHZ34327.1
☐	cholinesterase precursor [Homo sapiens]	61.3	61.3	100%	3e-09	85%	gi|4557351|NP_000046.1
☐	unnamed protein product [Homo sapiens]	61.3	61.3	100%	3e-09	85%	gi|158257558|BAF84752.1
☐	butyrylcholinesterase [synthetic construct]	61.3	61.3	100%	3e-09	85%	gi|260766471|ACX50257.1
☐	PREDICTED: cholinesterase isoform X1 [Homo sapiens]	61.3	61.3	100%	3e-09	85%	gi|530375091|XP_005247742.1
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholineste	59.6	59.6	100%	1e-08	85%	gi|402550232|4AXB_A
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholineste	59.6	59.6	100%	1e-08	85%	gi|402550237|4B0O_A
☐	Chain A, Structure Of Human Butyrylcholinesterase Inhibited By Cb	59.6	59.6	100%	1e-08	85%	gi|340707403|2Y1K_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	59.6	59.6	100%	1e-08	85%	gi|237823652|2WIL_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	59.6	59.6	100%	1e-08	85%	gi|237823648|2WIF_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	59.6	59.6	100%	1e-08	85%	gi|237823647|2WID_A
☐	Chain A, X-Ray Structure Of Human Butyrylcholinesterase Inhibitec	57.9	57.9	100%	4e-08	85%	gi|326634060|2XQF_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	57.9	57.9	100%	4e-08	85%	gi|258588213|2WSL_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	57.9	57.9	100%	4e-08	85%	gi|215794636|3DJY_A
☐	Chain A, Crystal Structure Of Human Butyryl Cholinesterase [Homo	57.9	57.9	100%	4e-08	85%	gi|34810859|1P0I_A
☐	Chain A, G117h Mutant Of Human Butyrylcholinesterase In Comple	57.9	57.9	100%	4e-08	85%	gi|313103512|2XMB_A
☐	Chain A, Crystal Structure Of Recombinant Full Length Human Buty	57.9	57.9	100%	4e-08	85%	gi|158429456|2PM8_A
☐	cholinesterase precursor [Pan troglodytes]	57.5	57.5	100%	5e-08	80%	gi|343960913|BAK62046.1
☐	Chain A, Structure Of Human Butyrylcholinesterase In Complex Wit	57.5	57.5	100%	5e-08	85%	gi|145579736|2J4C_A
☐	PREDICTED: cholinesterase [Gorilla gorilla gorilla]	57.5	57.5	100%	5e-08	80%	gi|426342776|XP_004038010.1
☐	PREDICTED: cholinesterase [Pan paniscus]	57.5	57.5	100%	5e-08	80%	gi|397493718|XP_003817746.1
☐	PREDICTED: cholinesterase [Pan troglodytes]	57.5	57.5	100%	5e-08	80%	gi|114590210|XP_516857.2
☐	PREDICTED: cholinesterase [Nomascus leucogenys]	54.9	54.9	100%	4e-07	80%	gi|332214651|XP_003256448.1
☐	PREDICTED: cholinesterase [Eptesicus fuscus]	53.7	53.7	100%	1e-06	80%	gi|641703485|XP_008140478.1
☐	PREDICTED: cholinesterase [Myotis lucifugus]	53.7	53.7	100%	1e-06	80%	gi|558125651|XP_006088951.1
☐							

	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhyd	52.4	52.4	100%	3e-06	75%	gi|21362409|P81908.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhyd	52.4	52.4	100%	3e-06	75%	gi|116354|P21927.1
☐	PREDICTED: cholinesterase [Oryctolagus cuniculus]	52.4	52.4	100%	3e-06	75%	gi|291400118|XP_002716414.1
☐	PREDICTED: cholinesterase [Orcinus orca]	52.4	52.4	100%	3e-06	75%	gi|466076197|XP_004283487.1
☐	cholinesterase precursor [Pongo abelii]	52.4	52.4	100%	3e-06	75%	gi|197097436|NP_001127509.1
☐	PREDICTED: cholinesterase isoform X1 [Sus scrofa]	52.4	52.4	100%	3e-06	75%	gi|335299867|XP_003358712.1
☐	cholinesterase precursor [Bos taurus]	52.4	52.4	100%	3e-06	75%	gi|116004027|NP_001070374.1
☐	PREDICTED: cholinesterase [Bison bison bison]	52.4	52.4	100%	3e-06	75%	gi|742123891|XP_010839228.1
☐	PREDICTED: cholinesterase [Balaenoptera acutorostrata scammo	52.4	52.4	100%	3e-06	75%	gi|594625950|XP_007197616.1
☐	PREDICTED: cholinesterase isoform X1 [Pongo abelii]	52.4	52.4	100%	3e-06	75%	gi|686714306|XP_009237773.1
☐	PREDICTED: cholinesterase [Lipotes vexillifer]	52.4	52.4	100%	3e-06	75%	gi|602681974|XP_007446483.1
☐	PREDICTED: cholinesterase [Pantholops hodgsonii]	52.4	52.4	100%	3e-06	75%	gi|556779632|XP_005984864.1
☐	PREDICTED: cholinesterase [Bos mutus]	52.4	52.4	100%	3e-06	75%	gi|555966690|XP_005895396.1
☐	PREDICTED: cholinesterase [Capra hircus]	52.4	52.4	100%	3e-06	75%	gi|548451269|XP_005675420.1
☐	PREDICTED: cholinesterase [Ovis aries]	52.4	52.4	100%	3e-06	75%	gi|426218006|XP_004003241.1
☐	PREDICTED: cholinesterase-like isoform X1 [Myotis brandtii]	50.3	50.3	100%	1e-05	75%	gi|554526033|XP_005857864.1
☐	PREDICTED: cholinesterase [Orycteropus afer afer]	50.3	50.3	100%	1e-05	75%	gi|634870148|XP_007946910.1
☐	PREDICTED: cholinesterase isoform X2 [Saimiri boliviensis bolivie	50.3	50.3	100%	1e-05	70%	gi|725560928|XP_010334003.1
☐	PREDICTED: cholinesterase isoform X1 [Saimiri boliviensis bolivie	50.3	50.3	100%	1e-05	70%	gi|403265619|XP_003925023.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase [Callithrix j	50.3	50.3	100%	1e-05	70%	gi|675737963|XP_002807699.3
☐	Cholinesterase [Myotis brandtii]	50.3	50.3	100%	1e-05	75%	gi|521020653|EPQ02441.1
☐	cholinesterase precursor [Equus caballus]	49.8	49.8	100%	2e-05	75%	gi|126352540|NP_001075319.1
☐	PREDICTED: cholinesterase-like [Elephantulus edwardii]	49.8	49.8	100%	2e-05	75%	gi|585675683|XP_006890440.1
☐	PREDICTED: cholinesterase [Ursus maritimus]	49.8	49.8	95%	2e-05	74%	gi|670999264|XP_008690527.1
☐	PREDICTED: cholinesterase isoform X2 [Equus przewalskii]	49.8	49.8	100%	2e-05	75%	gi|664725795|XP_008520036.1
☐	PREDICTED: cholinesterase isoform X1 [Equus przewalskii]	49.8	49.8	100%	2e-05	75%	gi|664725793|XP_008520035.1
☐	PREDICTED: cholinesterase [Ceratotherium simum simum]	49.8	49.8	100%	2e-05	75%	gi|478501043|XP_004424836.1
☐	hypothetical protein EGK_11933 [Macaca mulatta]	49.0	49.0	100%	4e-05	70%	gi|355559896|EHH16624.1
☐	butyrylcholinesterase precursor [Macaca fascicularis]	49.0	49.0	100%	4e-05	70%	gi|290795732|ADD64703.1
☐	PREDICTED: cholinesterase [Macaca fascicularis]	49.0	49.0	100%	4e-05	70%	gi|544412493|XP_005546353.1
☐	PREDICTED: cholinesterase isoform X1 [Papio anubis]	49.0	49.0	100%	4e-05	70%	gi|402861047|XP_003894921.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase-like [Maca	49.0	49.0	100%	4e-05	70%	gi|297286482|XP_002808379.1
☐	PREDICTED: cholinesterase [Ictidomys tridecemlineatus]	49.0	49.0	100%	4e-05	70%	gi|532105511|XP_005338342.1
☐	PREDICTED: cholinesterase isoform X1 [Chlorocebus sabaeus]	49.0	49.0	100%	4e-05	70%	gi|635084154|XP_007970394.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus dromedarius]	48.6	48.6	100%	5e-05	70%	gi|744553709|XP_010974642.1
☐	PREDICTED: cholinesterase isoform X1 [Camelus dromedarius]	48.6	48.6	100%	5e-05	70%	gi|744553706|XP_010974641.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus bactrianus]	48.6	48.6	100%	5e-05	70%	gi|743713601|XP_010950371.1
☐	PREDICTED: cholinesterase [Vicugna pacos]	48.6	48.6	100%	5e-05	70%	gi|560956860|XP_006200907.1
☐	PREDICTED: cholinesterase [Camelus ferus]	48.6	48.6	100%	5e-05	70%	gi|560915255|XP_006183885.1
☐	PREDICTED: cholinesterase-like isoform X1 [Mustela putorius furo]	48.6	48.6	95%	5e-05	74%	gi|511910148|XP_004774475.1
☐	hypothetical protein PANDA_007095 [Ailuropoda melanoleuca]	48.1	48.1	95%	7e-05	74%	gi|281337784|EFB13368.1
☐	PREDICTED: cholinesterase [Myotis davidii]	48.1	48.1	90%	7e-05	78%	gi|584083219|XP_006761409.1
☐	PREDICTED: cholinesterase-like [Ailuropoda melanoleuca]	48.1	48.1	95%	7e-05	74%	gi|301766374|XP_002918607.1
☐	PREDICTED: cholinesterase [Fukomys damarensis]	46.9	46.9	100%	2e-04	75%	gi|731199055|XP_010610068.1
☐	Cholinesterase [Fukomys damarensis]	46.9	46.9	100%	2e-04	75%	gi|676283600|KFO36750.1

☐	PREDICTED: cholinesterase [Tarsius syrichta]	46.9	46.9	100%	2e-04	70%	gi|640826885|XP_008070612.1
☐	PREDICTED: cholinesterase [Otolemur garnettii]	46.4	46.4	100%	3e-04	70%	gi|395843862|XP_003794691.1
☐	PREDICTED: cholinesterase-like isoform 1 [Dasypus novemcinctus	46.4	46.4	100%	3e-04	70%	gi|488587231|XP_004478943.1
☐	PREDICTED: cholinesterase-like [Trichechus manatus latirostris]	46.4	46.4	100%	3e-04	70%	gi|471406477|XP_004384938.1
☐	PREDICTED: cholinesterase isoform X1 [Loxodonta africana]	46.4	46.4	100%	3e-04	70%	gi|731499959|XP_003416305.2
☐	PREDICTED: cholinesterase [Galeopterus variegatus]	46.0	46.0	100%	4e-04	70%	gi|667294272|XP_008578862.1
☐	PREDICTED: cholinesterase-like [Sorex araneus]	45.6	45.6	95%	5e-04	74%	gi|505845607|XP_004616283.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhydi	45.6	45.6	100%	5e-04	65%	gi|38502853|O62761.1
☐	cholinesterase precursor [Felis catus]	45.6	45.6	100%	5e-04	65%	gi|57163907|NP_001009364.1
☐	PREDICTED: cholinesterase-like [Panthera tigris altaica]	45.6	45.6	100%	5e-04	65%	gi|591300304|XP_007077117.1
☐	PREDICTED: cholinesterase-like [Odobenus rosmarus divergens]	45.6	45.6	90%	5e-04	72%	gi|472347065|XP_004393257.1
☐	PREDICTED: cholinesterase [Rhinopithecus roxellana]	45.6	45.6	100%	5e-04	70%	gi|724956944|XP_010353594.1
☐	PREDICTED: cholinesterase-like [Chrysochloris asiatica]	45.2	45.2	100%	7e-04	65%	gi|586462448|XP_006861862.1
☐	PREDICTED: cholinesterase-like [Echinops telfairi]	45.2	45.2	100%	7e-04	65%	gi|507651638|XP_004704160.1
☐	PREDICTED: cholinesterase isoform X2 [Heterocephalus glaber]	44.3	44.3	100%	0.001	70%	gi|512824494|XP_004880401.1
☐	PREDICTED: cholinesterase isoform X1 [Chinchilla lanigera]	44.3	44.3	100%	0.001	70%	gi|533158554|XP_005393194.1
☐	PREDICTED: cholinesterase isoform X1 [Heterocephalus glaber]	44.3	44.3	100%	0.001	70%	gi|512824490|XP_004880400.1
☐	PREDICTED: cholinesterase isoform X2 [Cavia porcellus]	43.9	43.9	100%	0.002	65%	gi|514460083|XP_005003514.1
☐	PREDICTED: cholinesterase isoform X1 [Cavia porcellus]	43.9	43.9	100%	0.002	65%	gi|348567235|XP_003469406.1
☐	Cholinesterase [Pteropus alecto]	43.5	43.5	100%	0.002	70%	gi|431915168|ELK15855.1
☐	PREDICTED: cholinesterase [Pteropus alecto]	43.5	43.5	100%	0.002	70%	gi|586546267|XP_006908236.1
☐	PREDICTED: cholinesterase [Microtus ochrogaster]	42.6	42.6	100%	0.004	65%	gi|531999261|XP_005344165.1
☐	PREDICTED: cholinesterase [Erinaceus europaeus]	42.2	42.2	100%	0.006	65%	gi|617605262|XP_007523705.1
☐	PREDICTED: cholinesterase [Canis lupus familiaris]	42.2	42.2	90%	0.006	67%	gi|74003707|XP_545267.2
☐	PREDICTED: cholinesterase isoform X1 [Peromyscus maniculatus	42.2	42.2	100%	0.006	65%	gi|589919054|XP_006972718.1
☐	PREDICTED: cholinesterase-like [Leptonychotes weddellii]	41.8	41.8	90%	0.008	67%	gi|585150385|XP_006727664.1
☐	cholinesterase precursor [Mus musculus]	41.8	41.8	100%	0.008	65%	gi|124487350|NP_033868.3

⊟ Alignments

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Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylcholinesterase

Sequence ID: gi|393715367|pdb|4AQD|A **Length:** 531 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 478 to 497 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	3e-09	17/20(85%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQDDSTSWPVFKS  20
            KYGNP+ETQ++STSWPVFKS
Sbjct  478  KYGNPNETQNNSTSWPVFKS  497
```

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monomeric butyrylcholinesterase [synthetic construct]

Sequence ID: gi|388261124|gb|AFK25766.1| **Length:** 557 **Number of Matches:** 1

Related Information

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	3e-09	17/20(85%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQDDSTSWPVFKS  20
            KYGNP+ETQ++STSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Co-Crystallization Studies Of Full Length Recombinant Bche With Cocaine Offers Insights Into Cocaine Detoxification

Sequence ID: gi|328877250|pdb|3O9M|A **Length:** 574 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 476 to 495 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	3e-09	17/20(85%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQDDSTSWPVFKS  20
            KYGNP+ETQ++STSWPVFKS
Sbjct  476  KYGNPNETQNNSTSWPVFKS  495
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]

Sequence ID: gi|632795270|gb|AHZ34327.1| **Length:** 602 **Number of Matches:** 1

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	3e-09	17/20(85%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQDDSTSWPVFKS  20
            KYGNP+ETQ++STSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Related Information

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

cholinesterase precursor [Homo sapiens]

Sequence ID: gi|4557351|ref|NP_000046.1| **Length:** 602 **Number of Matches:** 1

▷ See 10 more title(s)

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	3e-09	17/20(85%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQDDSTSWPVFKS  20
            KYGNP+ETQ++STSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Structure - 3D structure displays

PubChem BioAssay - bioactivity screening

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - BHJK084D015

Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

BCHE_KYGNPDETQDNSTSWPVFKS_Mod

RID BHJK084D015 (Expires on 01-17 15:22 pm)

Query ID	lcl|50558	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	20		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

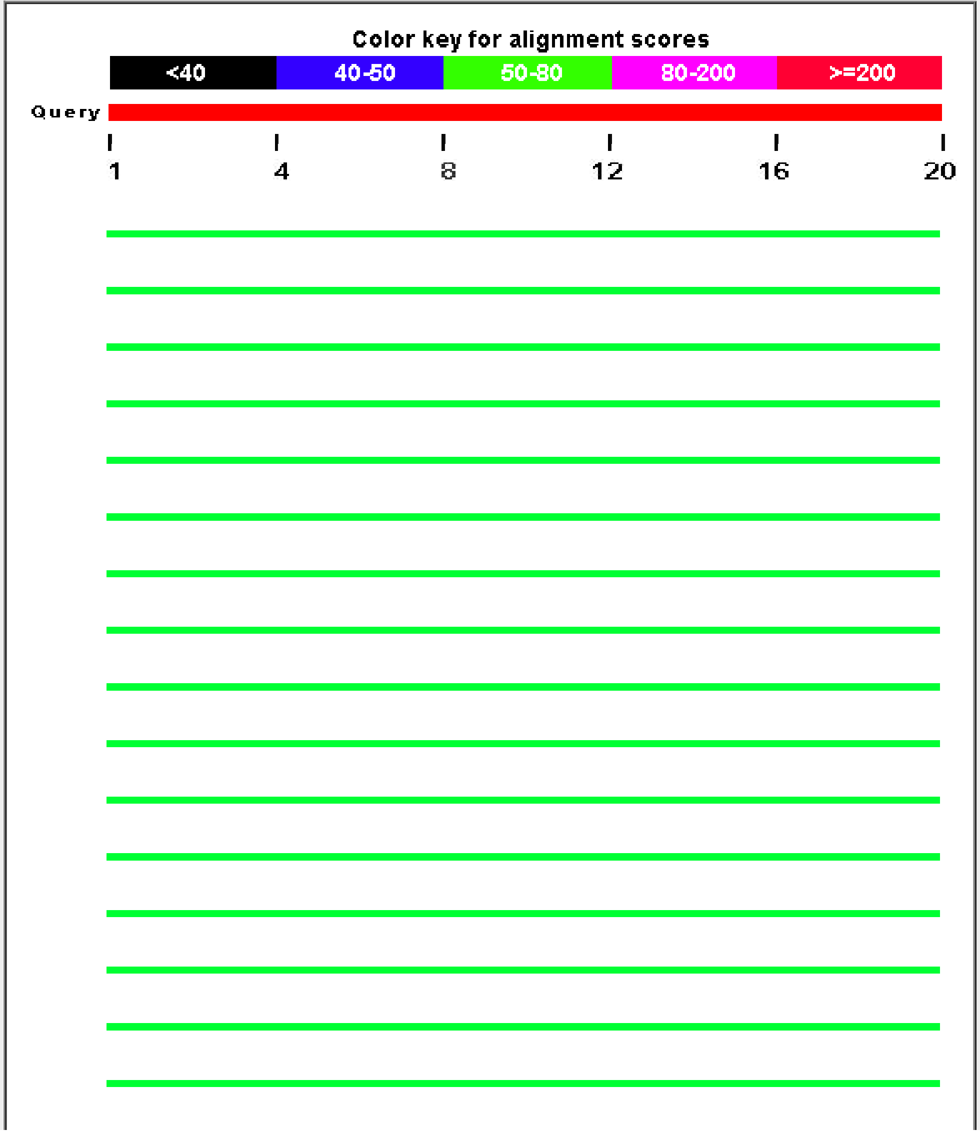
Graphic Summary

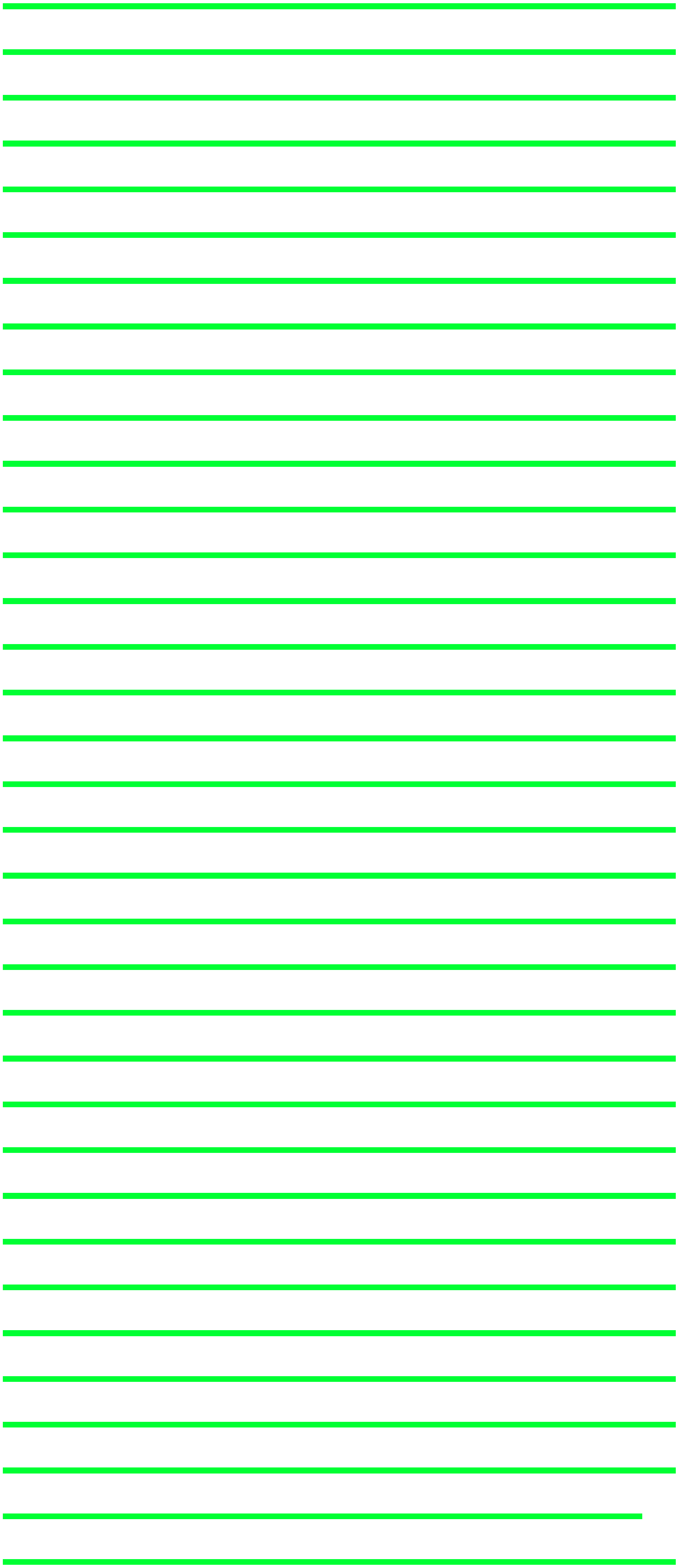
Show Conserved Domains

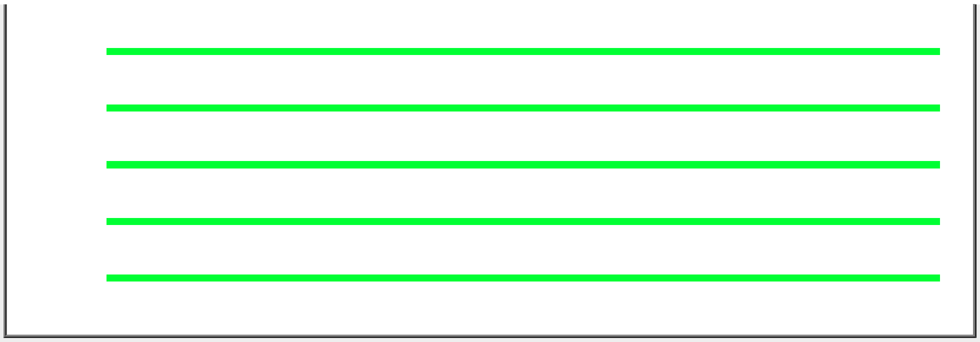
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylchol	63.8	63.8	100%	4e-10	90%	gi|393715367|4AQD_A
☐	monomeric butyrylcholinesterase [synthetic construct]	63.8	63.8	100%	4e-10	90%	gi|388261124|AFK25766.1
☐	Chain A, Co-Crystallization Studies Of Full Length Recombinant Bc	63.8	63.8	100%	4e-10	90%	gi|328877250|3O9M_A
☐	butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|632795270|AHZ34327.1
☐	cholinesterase precursor [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|4557351|NP_000046.1
☐	unnamed protein product [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|158257558|BAF84752.1
☐	butyrylcholinesterase [synthetic construct]	63.8	63.8	100%	4e-10	90%	gi|260766471|ACX50257.1
☐	PREDICTED: cholinesterase isoform X1 [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|530375091|XP_005247742.1
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholineste	62.1	62.1	100%	1e-09	90%	gi|402550232|4AXB_A
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholineste	62.1	62.1	100%	1e-09	90%	gi|402550237|4B0O_A
☐	Chain A, Structure Of Human Butyrylcholinesterase Inhibited By Cb	62.1	62.1	100%	1e-09	90%	gi|340707403|2Y1K_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	62.1	62.1	100%	1e-09	90%	gi|237823652|2WIL_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	62.1	62.1	100%	1e-09	90%	gi|237823648|2WIF_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	62.1	62.1	100%	1e-09	90%	gi|237823647|2WID_A
☐	cholinesterase precursor [Pan troglodytes]	60.0	60.0	100%	7e-09	85%	gi|343960913|BAK62046.1
☐	PREDICTED: cholinesterase [Gorilla gorilla gorilla]	60.0	60.0	100%	7e-09	85%	gi|426342776|XP_004038010.1
☐	PREDICTED: cholinesterase [Pan paniscus]	60.0	60.0	100%	7e-09	85%	gi|397493718|XP_003817746.1
☐	PREDICTED: cholinesterase [Pan troglodytes]	60.0	60.0	100%	7e-09	85%	gi|114590210|XP_516857.2
☐	Chain A, X-Ray Structure Of Human Butyrylcholinesterase Inhibitec	57.5	57.5	100%	5e-08	85%	gi|326634060|2XQF_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	57.5	57.5	100%	5e-08	85%	gi|258588213|2WSL_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	57.5	57.5	100%	5e-08	85%	gi|215794636|3DJY_A
☐	Chain A, Crystal Structure Of Human Butyryl Cholinesterase [Homo	57.5	57.5	100%	5e-08	85%	gi|34810859|1P0I_A
☐	Chain A, G117h Mutant Of Human Butyrylcholinesterase In Comple	57.5	57.5	100%	5e-08	85%	gi|313103512|2XMB_A
☐	Chain A, Crystal Structure Of Recombinant Full Length Human Buty	57.5	57.5	100%	5e-08	85%	gi|158429456|2PM8_A
☐	PREDICTED: cholinesterase [Nomascus leucogenys]	57.5	57.5	100%	5e-08	85%	gi|332214651|XP_003256448.1
☐	Chain A, Structure Of Human Butyrylcholinesterase In Complex Wit	57.1	57.1	100%	7e-08	85%	gi|145579736|2J4C_A
☐	PREDICTED: cholinesterase [Eptesicus fuscus]	55.4	55.4	100%	3e-07	80%	gi|641703485|XP_008140478.1
☐	PREDICTED: cholinesterase [Myotis lucifugus]	55.4	55.4	100%	3e-07	80%	gi|558125651|XP_006088951.1
☐							

	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhyd	54.9	54.9	100%	4e-07	80%	gi|21362409|P81908.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhyd	54.9	54.9	100%	4e-07	80%	gi|116354|P21927.1
☐	PREDICTED: cholinesterase [Oryctolagus cuniculus]	54.9	54.9	100%	4e-07	80%	gi|291400118|XP_002716414.1
☐	PREDICTED: cholinesterase [Orcinus orca]	54.9	54.9	100%	4e-07	80%	gi|466076197|XP_004283487.1
☐	cholinesterase precursor [Pongo abelii]	54.9	54.9	100%	4e-07	80%	gi|197097436|NP_001127509.1
☐	PREDICTED: cholinesterase isoform X1 [Sus scrofa]	54.9	54.9	100%	4e-07	80%	gi|335299867|XP_003358712.1
☐	cholinesterase precursor [Bos taurus]	54.9	54.9	100%	4e-07	80%	gi|116004027|NP_001070374.1
☐	PREDICTED: cholinesterase [Bison bison bison]	54.9	54.9	100%	4e-07	80%	gi|742123891|XP_010839228.1
☐	PREDICTED: cholinesterase [Balaenoptera acutorostrata scammor	54.9	54.9	100%	4e-07	80%	gi|594625950|XP_007197616.1
☐	PREDICTED: cholinesterase isoform X1 [Pongo abelii]	54.9	54.9	100%	4e-07	80%	gi|686714306|XP_009237773.1
☐	PREDICTED: cholinesterase [Lipotes vexillifer]	54.9	54.9	100%	4e-07	80%	gi|602681974|XP_007446483.1
☐	PREDICTED: cholinesterase [Pantholops hodgsonii]	54.9	54.9	100%	4e-07	80%	gi|556779632|XP_005984864.1
☐	PREDICTED: cholinesterase [Bos mutus]	54.9	54.9	100%	4e-07	80%	gi|555966690|XP_005895396.1
☐	PREDICTED: cholinesterase [Capra hircus]	54.9	54.9	100%	4e-07	80%	gi|548451269|XP_005675420.1
☐	PREDICTED: cholinesterase [Ovis aries]	54.9	54.9	100%	4e-07	80%	gi|426218006|XP_004003241.1
☐	PREDICTED: cholinesterase [Orycteropus afer afer]	52.8	52.8	100%	2e-06	80%	gi|634870148|XP_007946910.1
☐	PREDICTED: cholinesterase isoform X2 [Saimiri boliviensis bolivier	52.8	52.8	100%	2e-06	75%	gi|725560928|XP_010334003.1
☐	PREDICTED: cholinesterase isoform X1 [Saimiri boliviensis bolivier	52.8	52.8	100%	2e-06	75%	gi|403265619|XP_003925023.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase [Callithrix j	52.8	52.8	100%	2e-06	75%	gi|675737963|XP_002807699.3
☐	cholinesterase precursor [Equus caballus]	52.4	52.4	100%	3e-06	80%	gi|126352540|NP_001075319.1
☐	PREDICTED: cholinesterase-like [Elephantulus edwardii]	52.4	52.4	100%	3e-06	80%	gi|585675683|XP_006890440.1
☐	PREDICTED: cholinesterase [Ursus maritimus]	52.4	52.4	95%	3e-06	79%	gi|670999264|XP_008690527.1
☐	PREDICTED: cholinesterase isoform X2 [Equus przewalskii]	52.4	52.4	100%	3e-06	80%	gi|664725795|XP_008520036.1
☐	PREDICTED: cholinesterase isoform X1 [Equus przewalskii]	52.4	52.4	100%	3e-06	80%	gi|664725793|XP_008520035.1
☐	PREDICTED: cholinesterase [Ceratotherium simum simum]	52.4	52.4	100%	3e-06	80%	gi|478501043|XP_004424836.1
☐	PREDICTED: cholinesterase-like isoform X1 [Myotis brandtii]	52.0	52.0	100%	4e-06	75%	gi|554526033|XP_005857864.1
☐	Cholinesterase [Myotis brandtii]	52.0	52.0	100%	4e-06	75%	gi|521020653|EPQ02441.1
☐	hypothetical protein EGK_11933 [Macaca mulatta]	51.5	51.5	100%	5e-06	75%	gi|355559896|EHH16624.1
☐	butyrylcholinesterase precursor [Macaca fascicularis]	51.5	51.5	100%	5e-06	75%	gi|290795732|ADD64703.1
☐	PREDICTED: cholinesterase [Macaca fascicularis]	51.5	51.5	100%	5e-06	75%	gi|544412493|XP_005546353.1
☐	PREDICTED: cholinesterase isoform X1 [Papio anubis]	51.5	51.5	100%	5e-06	75%	gi|402861047|XP_003894921.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase-like [Maca	51.5	51.5	100%	5e-06	75%	gi|297286482|XP_002808379.1
☐	PREDICTED: cholinesterase [Ictidomys tridecemlineatus]	51.5	51.5	100%	5e-06	75%	gi|532105511|XP_005338342.1
☐	PREDICTED: cholinesterase isoform X1 [Chlorocebus sabaeus]	51.5	51.5	100%	5e-06	75%	gi|635084154|XP_007970394.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus dromedarius]	51.1	51.1	100%	7e-06	75%	gi|744553709|XP_010974642.1
☐	PREDICTED: cholinesterase isoform X1 [Camelus dromedarius]	51.1	51.1	100%	7e-06	75%	gi|744553706|XP_010974641.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus bactrianus]	51.1	51.1	100%	7e-06	75%	gi|743713601|XP_010950371.1
☐	PREDICTED: cholinesterase [Vicugna pacos]	51.1	51.1	100%	7e-06	75%	gi|560956860|XP_006200907.1
☐	PREDICTED: cholinesterase [Camelus ferus]	51.1	51.1	100%	7e-06	75%	gi|560915255|XP_006183885.1
☐	PREDICTED: cholinesterase-like isoform X1 [Mustela putorius furo]	51.1	51.1	95%	7e-06	79%	gi|511910148|XP_004774475.1
☐	hypothetical protein PANDA_007095 [Ailuropoda melanoleuca]	50.7	50.7	95%	1e-05	79%	gi|281337784|EFB13368.1
☐	PREDICTED: cholinesterase-like [Ailuropoda melanoleuca]	50.7	50.7	95%	1e-05	79%	gi|301766374|XP_002918607.1
☐	PREDICTED: cholinesterase [Myotis davidii]	49.8	49.8	90%	2e-05	78%	gi|584083219|XP_006761409.1
☐	PREDICTED: cholinesterase [Fukomys damarensis]	49.4	49.4	100%	3e-05	80%	gi|731199055|XP_010610068.1
☐	Cholinesterase [Fukomys damarensis]	49.4	49.4	100%	3e-05	80%	gi|676283600|KFO36750.1

☐	PREDICTED: cholinesterase [Tarsius syrichta]	49.4	49.4	100%	3e-05	75%	gi|640826885|XP_008070612.1
☐	PREDICTED: cholinesterase [Otolemur garnettii]	49.0	49.0	100%	4e-05	75%	gi|395843862|XP_003794691.1
☐	PREDICTED: cholinesterase-like isoform 1 [Dasypus novemcinctus	49.0	49.0	100%	4e-05	75%	gi|488587231|XP_004478943.1
☐	PREDICTED: cholinesterase-like [Trichechus manatus latirostris]	49.0	49.0	100%	4e-05	75%	gi|471406477|XP_004384938.1
☐	PREDICTED: cholinesterase isoform X1 [Loxodonta africana]	49.0	49.0	100%	4e-05	75%	gi|731499959|XP_003416305.2
☐	PREDICTED: cholinesterase [Galeopterus variegatus]	48.6	48.6	100%	5e-05	75%	gi|667294272|XP_008578862.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhydı	48.1	48.1	100%	7e-05	70%	gi|38502853|O62761.1
☐	cholinesterase precursor [Felis catus]	48.1	48.1	100%	7e-05	70%	gi|57163907|NP_001009364.1
☐	PREDICTED: cholinesterase-like [Panthera tigris altaica]	48.1	48.1	100%	7e-05	70%	gi|591300304|XP_007077117.1
☐	PREDICTED: cholinesterase-like [Odobenus rosmarus divergens]	48.1	48.1	90%	7e-05	78%	gi|472347065|XP_004393257.1
☐	PREDICTED: cholinesterase [Rhinopithecus roxellana]	48.1	48.1	100%	7e-05	75%	gi|724956944|XP_010353594.1
☐	PREDICTED: cholinesterase-like [Chrysochloris asiatica]	47.7	47.7	100%	1e-04	70%	gi|586462448|XP_006861862.1
☐	PREDICTED: cholinesterase-like [Echinops telfairi]	47.7	47.7	100%	1e-04	70%	gi|507651638|XP_004704160.1
☐	PREDICTED: cholinesterase-like [Sorex araneus]	47.3	47.3	95%	1e-04	74%	gi|505845607|XP_004616283.1
☐	PREDICTED: cholinesterase isoform X2 [Heterocephalus glaber]	46.9	46.9	100%	2e-04	75%	gi|512824494|XP_004880401.1
☐	PREDICTED: cholinesterase isoform X1 [Chinchilla lanigera]	46.9	46.9	100%	2e-04	75%	gi|533158554|XP_005393194.1
☐	PREDICTED: cholinesterase isoform X1 [Heterocephalus glaber]	46.9	46.9	100%	2e-04	75%	gi|512824490|XP_004880400.1
☐	PREDICTED: cholinesterase isoform X2 [Cavia porcellus]	46.4	46.4	100%	3e-04	70%	gi|514460083|XP_005003514.1
☐	PREDICTED: cholinesterase isoform X1 [Cavia porcellus]	46.4	46.4	100%	3e-04	70%	gi|348567235|XP_003469406.1
☐	Cholinesterase [Pteropus alecto]	45.2	45.2	100%	7e-04	70%	gi|431915168|ELK15855.1
☐	PREDICTED: cholinesterase [Pteropus alecto]	45.2	45.2	100%	7e-04	70%	gi|586546267|XP_006908236.1
☐	PREDICTED: cholinesterase [Erinaceus europaeus]	44.8	44.8	100%	0.001	70%	gi|617605262|XP_007523705.1
☐	PREDICTED: cholinesterase [Canis lupus familiaris]	44.8	44.8	90%	0.001	72%	gi|74003707|XP_545267.2
☐	PREDICTED: cholinesterase isoform X1 [Peromyscus maniculatus	44.8	44.8	100%	0.001	70%	gi|589919054|XP_006972718.1
☐	PREDICTED: cholinesterase-like [Leptonychotes weddellii]	44.3	44.3	90%	0.001	72%	gi|585150385|XP_006727664.1
☐	Butyrylcholinesterase [Mus musculus]	44.3	44.3	100%	0.001	70%	gi|71534030|AAH99977.1
☐	cholinesterase precursor [Mus musculus]	44.3	44.3	100%	0.001	70%	gi|124487350|NP_033868.3

⊟ Alignments

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Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylcholinesterase

Sequence ID: gi|393715367|pdb|4AQD|A **Length:** 531 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 478 to 497 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQDNSTSWPVFKS  20
            KYGNP+ETQ+NSTSWPVFKS
Sbjct  478  KYGNPNETQNNSTSWPVFKS  497
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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monomeric butyrylcholinesterase [synthetic construct]

Sequence ID: gi|388261124|gb|AFK25766.1| **Length:** 557 **Number of Matches:** 1

Related Information

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQDNSTSWPVFKS  20
            KYGNP+ETQ+NSTSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Co-Crystallization Studies Of Full Length Recombinant Bche With Cocaine Offers Insights Into Cocaine Detoxification

Sequence ID: gi|328877250|pdb|3O9M|A **Length:** 574 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 476 to 495 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQDNSTSWPVFKS  20
            KYGNP+ETQ+NSTSWPVFKS
Sbjct  476  KYGNPNETQNNSTSWPVFKS  495
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]

Sequence ID: gi|632795270|gb|AHZ34327.1| **Length:** 602 **Number of Matches:** 1

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQDNSTSWPVFKS  20
            KYGNP+ETQ+NSTSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Related Information

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

cholinesterase precursor [Homo sapiens]

Sequence ID: gi|4557351|ref|NP_000046.1| **Length:** 602 **Number of Matches:** 1

▷ See 10 more title(s)

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQDNSTSWPVFKS  20
            KYGNP+ETQ+NSTSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Structure - 3D structure displays

PubChem BioAssay - bioactivity screening

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

BCHE_KYGNPDETQNDSTSWPVFKS_Mod

RID BHJKBYJB014 (Expires on 01-17 15:23 pm)

Query ID	lcl|60926	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	20		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

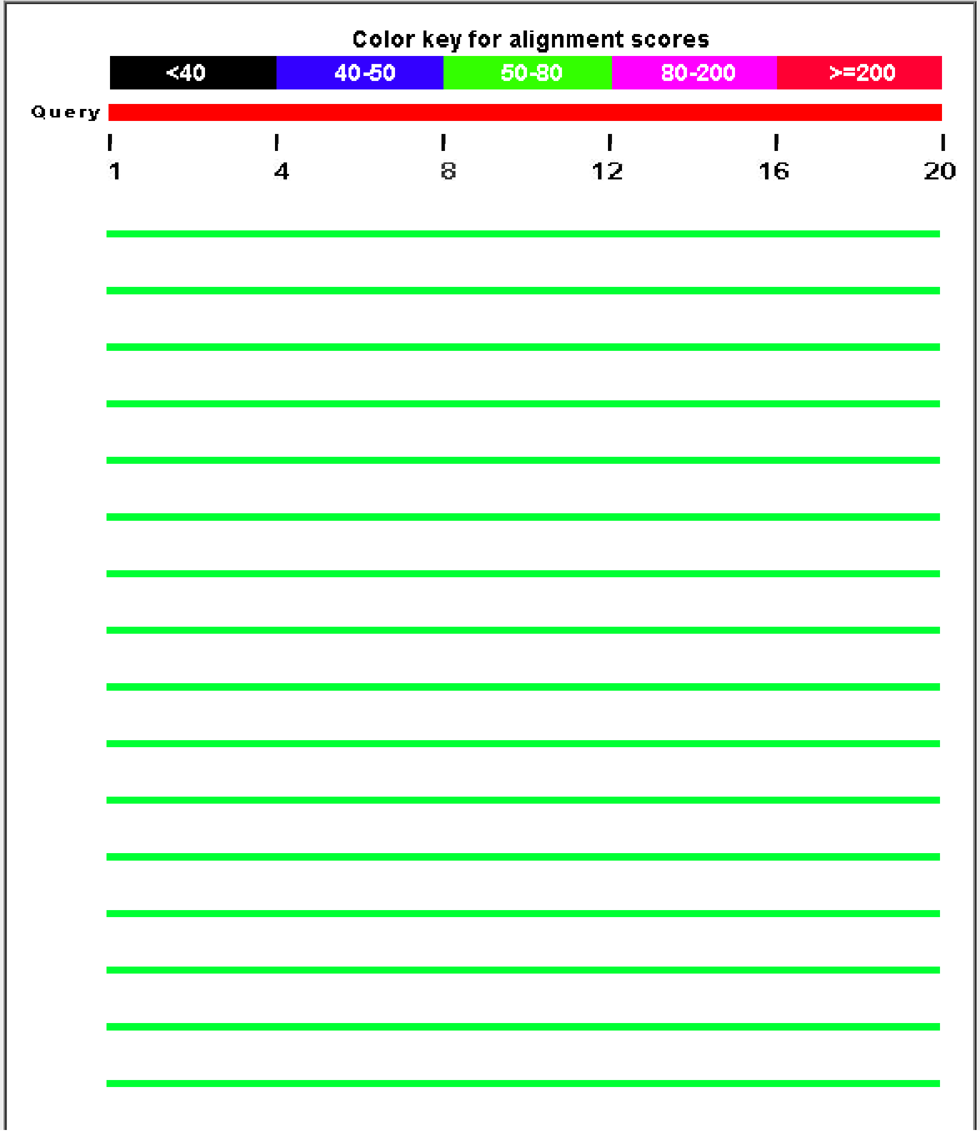
Graphic Summary

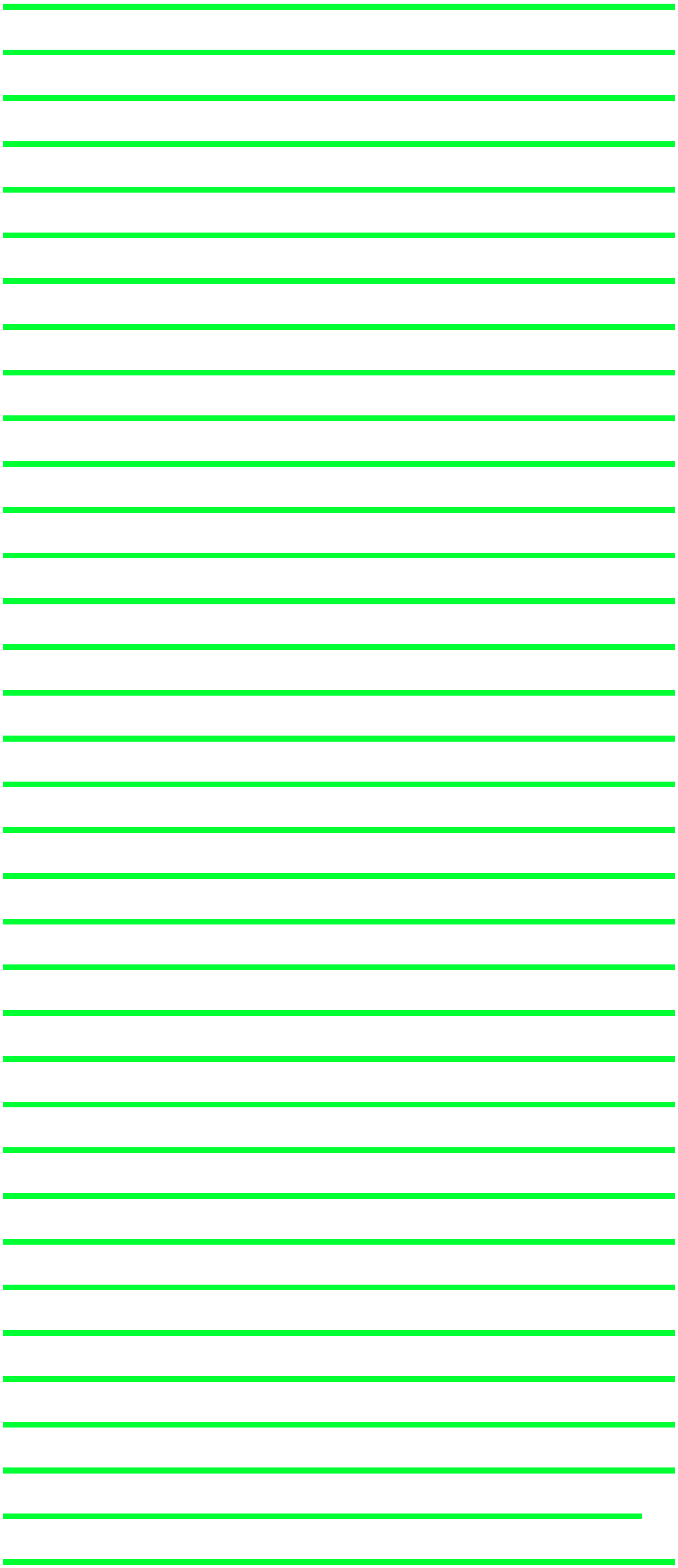
Show Conserved Domains

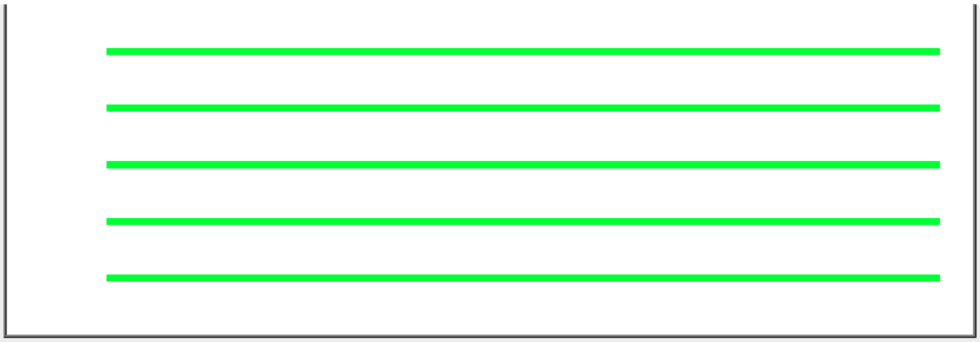
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylchol	63.8	63.8	100%	4e-10	90%	gi|393715367|4AQD_A
☐	monomeric butyrylcholinesterase [synthetic construct]	63.8	63.8	100%	4e-10	90%	gi|388261124|AFK25766.1
☐	Chain A, Co-Crystallization Studies Of Full Length Recombinant Bc	63.8	63.8	100%	4e-10	90%	gi|328877250|3O9M_A
☐	butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|632795270|AHZ34327.1
☐	cholinesterase precursor [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|4557351|NP_000046.1
☐	unnamed protein product [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|158257558|BAF84752.1
☐	butyrylcholinesterase [synthetic construct]	63.8	63.8	100%	4e-10	90%	gi|260766471|ACX50257.1
☐	PREDICTED: cholinesterase isoform X1 [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|530375091|XP_005247742.1
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholineste	62.1	62.1	100%	1e-09	90%	gi|402550232|4AXB_A
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholineste	62.1	62.1	100%	1e-09	90%	gi|402550237|4B0O_A
☐	Chain A, Structure Of Human Butyrylcholinesterase Inhibited By Cb	62.1	62.1	100%	1e-09	90%	gi|340707403|2Y1K_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	62.1	62.1	100%	1e-09	90%	gi|237823652|2WIL_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	62.1	62.1	100%	1e-09	90%	gi|237823648|2WIF_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	62.1	62.1	100%	1e-09	90%	gi|237823647|2WID_A
☐	Chain A, X-Ray Structure Of Human Butyrylcholinesterase Inhibitec	60.4	60.4	100%	5e-09	90%	gi|326634060|2XQF_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	60.4	60.4	100%	5e-09	90%	gi|258588213|2WSL_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	60.4	60.4	100%	5e-09	90%	gi|215794636|3DJY_A
☐	Chain A, Crystal Structure Of Human Butyryl Cholinesterase [Homo	60.4	60.4	100%	5e-09	90%	gi|34810859|1P0I_A
☐	Chain A, G117h Mutant Of Human Butyrylcholinesterase In Comple	60.4	60.4	100%	5e-09	90%	gi|313103512|2XMB_A
☐	Chain A, Crystal Structure Of Recombinant Full Length Human Buty	60.4	60.4	100%	5e-09	90%	gi|158429456|2PM8_A
☐	cholinesterase precursor [Pan troglodytes]	60.0	60.0	100%	7e-09	85%	gi|343960913|BAK62046.1
☐	Chain A, Structure Of Human Butyrylcholinesterase In Complex Wit	60.0	60.0	100%	7e-09	90%	gi|145579736|2J4C_A
☐	PREDICTED: cholinesterase [Gorilla gorilla gorilla]	60.0	60.0	100%	7e-09	85%	gi|426342776|XP_004038010.1
☐	PREDICTED: cholinesterase [Pan paniscus]	60.0	60.0	100%	7e-09	85%	gi|397493718|XP_003817746.1
☐	PREDICTED: cholinesterase [Pan troglodytes]	60.0	60.0	100%	7e-09	85%	gi|114590210|XP_516857.2
☐	PREDICTED: cholinesterase [Nomascus leucogenys]	57.5	57.5	100%	5e-08	85%	gi|332214651|XP_003256448.1
☐	PREDICTED: cholinesterase [Eptesicus fuscus]	56.2	56.2	100%	1e-07	85%	gi|641703485|XP_008140478.1
☐	PREDICTED: cholinesterase [Myotis lucifugus]	56.2	56.2	100%	1e-07	85%	gi|558125651|XP_006088951.1
☐							

	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhyd	54.9	54.9	100%	4e-07	80%	gi|21362409|P81908.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhyd	54.9	54.9	100%	4e-07	80%	gi|116354|P21927.1
☐	PREDICTED: cholinesterase [Oryctolagus cuniculus]	54.9	54.9	100%	4e-07	80%	gi|291400118|XP_002716414.1
☐	PREDICTED: cholinesterase [Orcinus orca]	54.9	54.9	100%	4e-07	80%	gi|466076197|XP_004283487.1
☐	cholinesterase precursor [Pongo abelii]	54.9	54.9	100%	4e-07	80%	gi|197097436|NP_001127509.1
☐	PREDICTED: cholinesterase isoform X1 [Sus scrofa]	54.9	54.9	100%	4e-07	80%	gi|335299867|XP_003358712.1
☐	cholinesterase precursor [Bos taurus]	54.9	54.9	100%	4e-07	80%	gi|116004027|NP_001070374.1
☐	PREDICTED: cholinesterase [Bison bison bison]	54.9	54.9	100%	4e-07	80%	gi|742123891|XP_010839228.1
☐	PREDICTED: cholinesterase [Balaenoptera acutorostrata scammon	54.9	54.9	100%	4e-07	80%	gi|594625950|XP_007197616.1
☐	PREDICTED: cholinesterase isoform X1 [Pongo abelii]	54.9	54.9	100%	4e-07	80%	gi|686714306|XP_009237773.1
☐	PREDICTED: cholinesterase [Lipotes vexillifer]	54.9	54.9	100%	4e-07	80%	gi|602681974|XP_007446483.1
☐	PREDICTED: cholinesterase [Pantholops hodgsonii]	54.9	54.9	100%	4e-07	80%	gi|556779632|XP_005984864.1
☐	PREDICTED: cholinesterase [Bos mutus]	54.9	54.9	100%	4e-07	80%	gi|555966690|XP_005895396.1
☐	PREDICTED: cholinesterase [Capra hircus]	54.9	54.9	100%	4e-07	80%	gi|548451269|XP_005675420.1
☐	PREDICTED: cholinesterase [Ovis aries]	54.9	54.9	100%	4e-07	80%	gi|426218006|XP_004003241.1
☐	PREDICTED: cholinesterase-like isoform X1 [Myotis brandtii]	52.8	52.8	100%	2e-06	80%	gi|554526033|XP_005857864.1
☐	PREDICTED: cholinesterase [Orycteropus afer afer]	52.8	52.8	100%	2e-06	80%	gi|634870148|XP_007946910.1
☐	PREDICTED: cholinesterase isoform X2 [Saimiri boliviensis bolivier	52.8	52.8	100%	2e-06	75%	gi|725560928|XP_010334003.1
☐	PREDICTED: cholinesterase isoform X1 [Saimiri boliviensis bolivier	52.8	52.8	100%	2e-06	75%	gi|403265619|XP_003925023.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase [Callithrix j	52.8	52.8	100%	2e-06	75%	gi|675737963|XP_002807699.3
☐	Cholinesterase [Myotis brandtii]	52.8	52.8	100%	2e-06	80%	gi|521020653|EPQ02441.1
☐	PREDICTED: cholinesterase [Ursus maritimus]	52.4	52.4	95%	3e-06	79%	gi|670999264|XP_008690527.1
☐	hypothetical protein EGK_11933 [Macaca mulatta]	51.5	51.5	100%	5e-06	75%	gi|355559896|EHH16624.1
☐	butyrylcholinesterase precursor [Macaca fascicularis]	51.5	51.5	100%	5e-06	75%	gi|290795732|ADD64703.1
☐	cholinesterase precursor [Equus caballus]	51.5	51.5	100%	5e-06	75%	gi|126352540|NP_001075319.1
☐	PREDICTED: cholinesterase-like [Elephantulus edwardii]	51.5	51.5	100%	5e-06	75%	gi|585675683|XP_006890440.1
☐	PREDICTED: cholinesterase [Macaca fascicularis]	51.5	51.5	100%	5e-06	75%	gi|544412493|XP_005546353.1
☐	PREDICTED: cholinesterase isoform X1 [Papio anubis]	51.5	51.5	100%	5e-06	75%	gi|402861047|XP_003894921.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase-like [Maca	51.5	51.5	100%	5e-06	75%	gi|297286482|XP_002808379.1
☐	PREDICTED: cholinesterase [Ictidomys tridecemlineatus]	51.5	51.5	100%	5e-06	75%	gi|532105511|XP_005338342.1
☐	PREDICTED: cholinesterase isoform X2 [Equus przewalskii]	51.5	51.5	100%	5e-06	75%	gi|664725795|XP_008520036.1
☐	PREDICTED: cholinesterase isoform X1 [Equus przewalskii]	51.5	51.5	100%	5e-06	75%	gi|664725793|XP_008520035.1
☐	PREDICTED: cholinesterase isoform X1 [Chlorocebus sabaeus]	51.5	51.5	100%	5e-06	75%	gi|635084154|XP_007970394.1
☐	PREDICTED: cholinesterase [Ceratotherium simum simum]	51.5	51.5	100%	5e-06	75%	gi|478501043|XP_004424836.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus dromedarius]	51.1	51.1	100%	7e-06	75%	gi|744553709|XP_010974642.1
☐	PREDICTED: cholinesterase isoform X1 [Camelus dromedarius]	51.1	51.1	100%	7e-06	75%	gi|744553706|XP_010974641.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus bactrianus]	51.1	51.1	100%	7e-06	75%	gi|743713601|XP_010950371.1
☐	PREDICTED: cholinesterase [Vicugna pacos]	51.1	51.1	100%	7e-06	75%	gi|560956860|XP_006200907.1
☐	PREDICTED: cholinesterase [Camelus ferus]	51.1	51.1	100%	7e-06	75%	gi|560915255|XP_006183885.1
☐	PREDICTED: cholinesterase-like isoform X1 [Mustela putorius furo]	51.1	51.1	95%	7e-06	79%	gi|511910148|XP_004774475.1
☐	hypothetical protein PANDA_007095 [Ailuropoda melanoleuca]	50.7	50.7	95%	1e-05	79%	gi|281337784|EFB13368.1
☐	PREDICTED: cholinesterase [Myotis davidii]	50.7	50.7	90%	1e-05	83%	gi|584083219|XP_006761409.1
☐	PREDICTED: cholinesterase-like [Ailuropoda melanoleuca]	50.7	50.7	95%	1e-05	79%	gi|301766374|XP_002918607.1
☐	PREDICTED: cholinesterase [Fukomys damarensis]	48.6	48.6	100%	5e-05	75%	gi|731199055|XP_010610068.1
☐	Cholinesterase [Fukomys damarensis]	48.6	48.6	100%	5e-05	75%	gi|676283600|KFO36750.1

☐	PREDICTED: cholinesterase [Tarsius syrichta]	48.6	48.6	100%	5e-05	70%	gi|640826885|XP_008070612.1
☐	PREDICTED: cholinesterase [Otolemur garnettii]	48.1	48.1	100%	7e-05	70%	gi|395843862|XP_003794691.1
☐	PREDICTED: cholinesterase-like [Sorex araneus]	48.1	48.1	95%	7e-05	79%	gi|505845607|XP_004616283.1
☐	PREDICTED: cholinesterase-like isoform 1 [Dasypus novemcinctus	48.1	48.1	100%	7e-05	70%	gi|488587231|XP_004478943.1
☐	PREDICTED: cholinesterase-like [Trichechus manatus latirostris]	48.1	48.1	100%	7e-05	70%	gi|471406477|XP_004384938.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhyd	48.1	48.1	100%	7e-05	70%	gi|38502853|O62761.1
☐	cholinesterase precursor [Felis catus]	48.1	48.1	100%	7e-05	70%	gi|57163907|NP_001009364.1
☐	PREDICTED: cholinesterase isoform X1 [Loxodonta africana]	48.1	48.1	100%	7e-05	70%	gi|731499959|XP_003416305.2
☐	PREDICTED: cholinesterase-like [Panthera tigris altaica]	48.1	48.1	100%	7e-05	70%	gi|591300304|XP_007077117.1
☐	PREDICTED: cholinesterase-like [Odobenus rosmarus divergens]	48.1	48.1	90%	7e-05	78%	gi|472347065|XP_004393257.1
☐	PREDICTED: cholinesterase [Rhinopithecus roxellana]	48.1	48.1	100%	7e-05	75%	gi|724956944|XP_010353594.1
☐	PREDICTED: cholinesterase [Galeopterus variegatus]	47.7	47.7	100%	1e-04	70%	gi|667294272|XP_008578862.1
☐	PREDICTED: cholinesterase-like [Chrysochloris asiatica]	47.7	47.7	100%	1e-04	70%	gi|586462448|XP_006861862.1
☐	PREDICTED: cholinesterase-like [Echinops telfairi]	47.7	47.7	100%	1e-04	70%	gi|507651638|XP_004704160.1
☐	PREDICTED: cholinesterase isoform X2 [Heterocephalus glaber]	46.0	46.0	100%	4e-04	70%	gi|512824494|XP_004880401.1
☐	PREDICTED: cholinesterase isoform X1 [Chinchilla lanigera]	46.0	46.0	100%	4e-04	70%	gi|533158554|XP_005393194.1
☐	Cholinesterase [Pteropus alecto]	46.0	46.0	100%	4e-04	75%	gi|431915168|ELK15855.1
☐	PREDICTED: cholinesterase isoform X1 [Heterocephalus glaber]	46.0	46.0	100%	4e-04	70%	gi|512824490|XP_004880400.1
☐	PREDICTED: cholinesterase [Pteropus alecto]	46.0	46.0	100%	4e-04	75%	gi|586546267|XP_006908236.1
☐	PREDICTED: cholinesterase isoform X2 [Cavia porcellus]	45.6	45.6	100%	5e-04	65%	gi|514460083|XP_005003514.1
☐	PREDICTED: cholinesterase isoform X1 [Cavia porcellus]	45.6	45.6	100%	5e-04	65%	gi|348567235|XP_003469406.1
☐	PREDICTED: cholinesterase [Microtus ochrogaster]	45.2	45.2	100%	7e-04	70%	gi|531999261|XP_005344165.1
☐	PREDICTED: cholinesterase [Erinaceus europaeus]	44.8	44.8	100%	0.001	70%	gi|617605262|XP_007523705.1
☐	PREDICTED: cholinesterase [Canis lupus familiaris]	44.8	44.8	90%	0.001	72%	gi|74003707|XP_545267.2
☐	PREDICTED: cholinesterase-like [Leptonychotes weddellii]	44.3	44.3	90%	0.001	72%	gi|585150385|XP_006727664.1
☐	PREDICTED: cholinesterase [Tupaia chinensis]	44.3	44.3	100%	0.001	70%	gi|562842605|XP_006150360.1
☐	PREDICTED: cholinesterase [Sarcophilus harrisii]	43.9	43.9	90%	0.002	67%	gi|395528220|XP_003766229.1

⊟ Alignments

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Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylcholinesterase

Sequence ID: gi|393715367|pdb|4AQD|A **Length:** 531 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 478 to 497 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQNDSTSWPVFKS  20
            KYGNP+ETQN+STSWPVFKS
Sbjct  478  KYGNPNETQNNSTSWPVFKS  497
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

monomeric butyrylcholinesterase [synthetic construct]

Sequence ID: gi|388261124|gb|AFK25766.1| **Length:** 557 **Number of Matches:** 1

Related Information

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQNDSTSWPVFKS  20
            KYGNP+ETQN+STSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Co-Crystallization Studies Of Full Length Recombinant Bche With Cocaine Offers Insights Into Cocaine Detoxification

Sequence ID: gi|328877250|pdb|3O9M|A **Length:** 574 **Number of Matches:** 1

See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 476 to 495 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQNDSTSWPVFKS  20
            KYGNP+ETQN+STSWPVFKS
Sbjct  476  KYGNPNETQNNSTSWPVFKS  495
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]

Sequence ID: gi|632795270|gb|AHZ34327.1| **Length:** 602 **Number of Matches:** 1

Related Information

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQNDSTSWPVFKS  20
            KYGNP+ETQN+STSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

cholinesterase precursor [Homo sapiens]

Sequence ID: gi|4557351|ref|NP_000046.1| **Length:** 602 **Number of Matches:** 1

See 10 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Structure - 3D structure displays

PubChem BioAssay - bioactivity screening

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQNDSTSWPVFKS  20
            KYGNP+ETQN+STSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BHJAGXXM015**

Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

BCHE_KYGNPDETQNNSTSWPVFKS_Mod

RID BHJAGXXM015 (Expires on 01-17 15:18 pm)

Query ID	lcl|58619	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	20		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

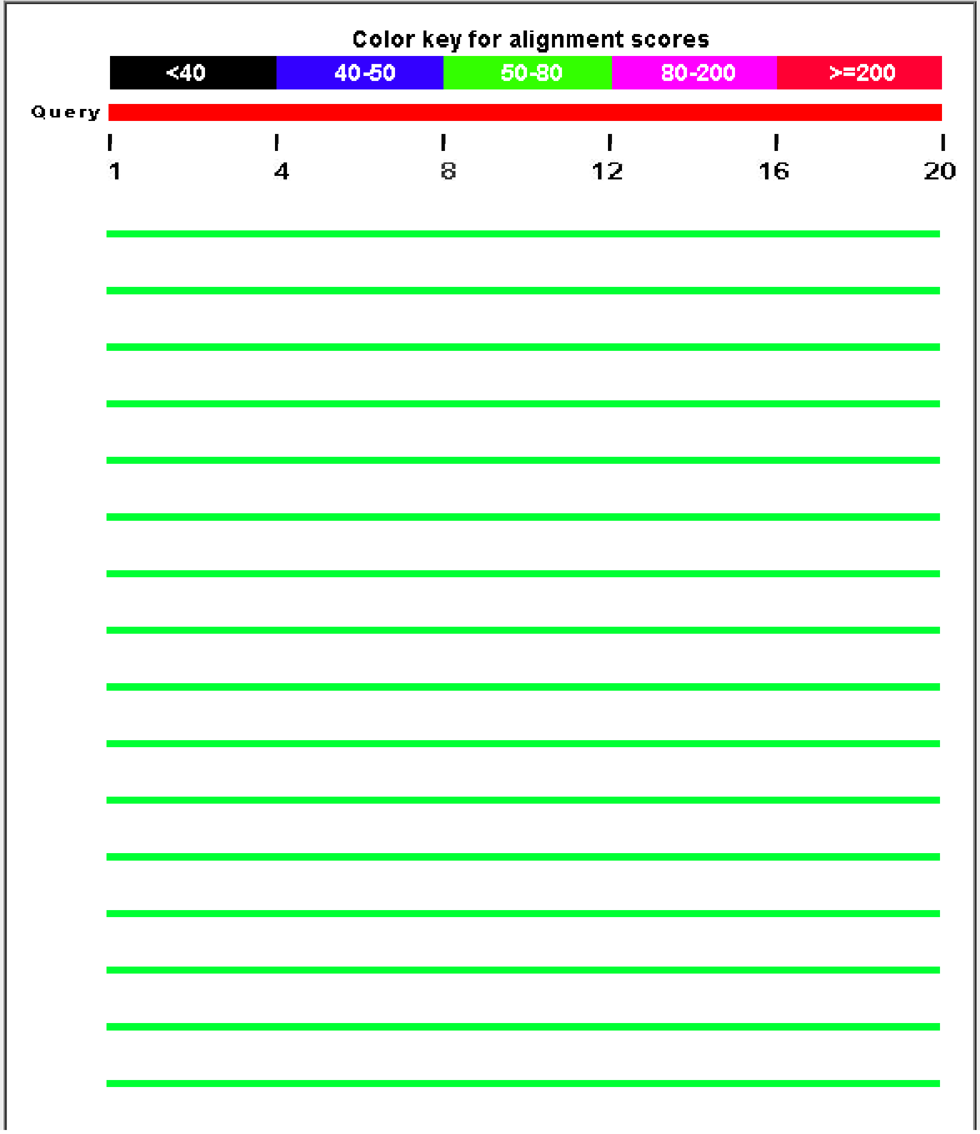
Graphic Summary

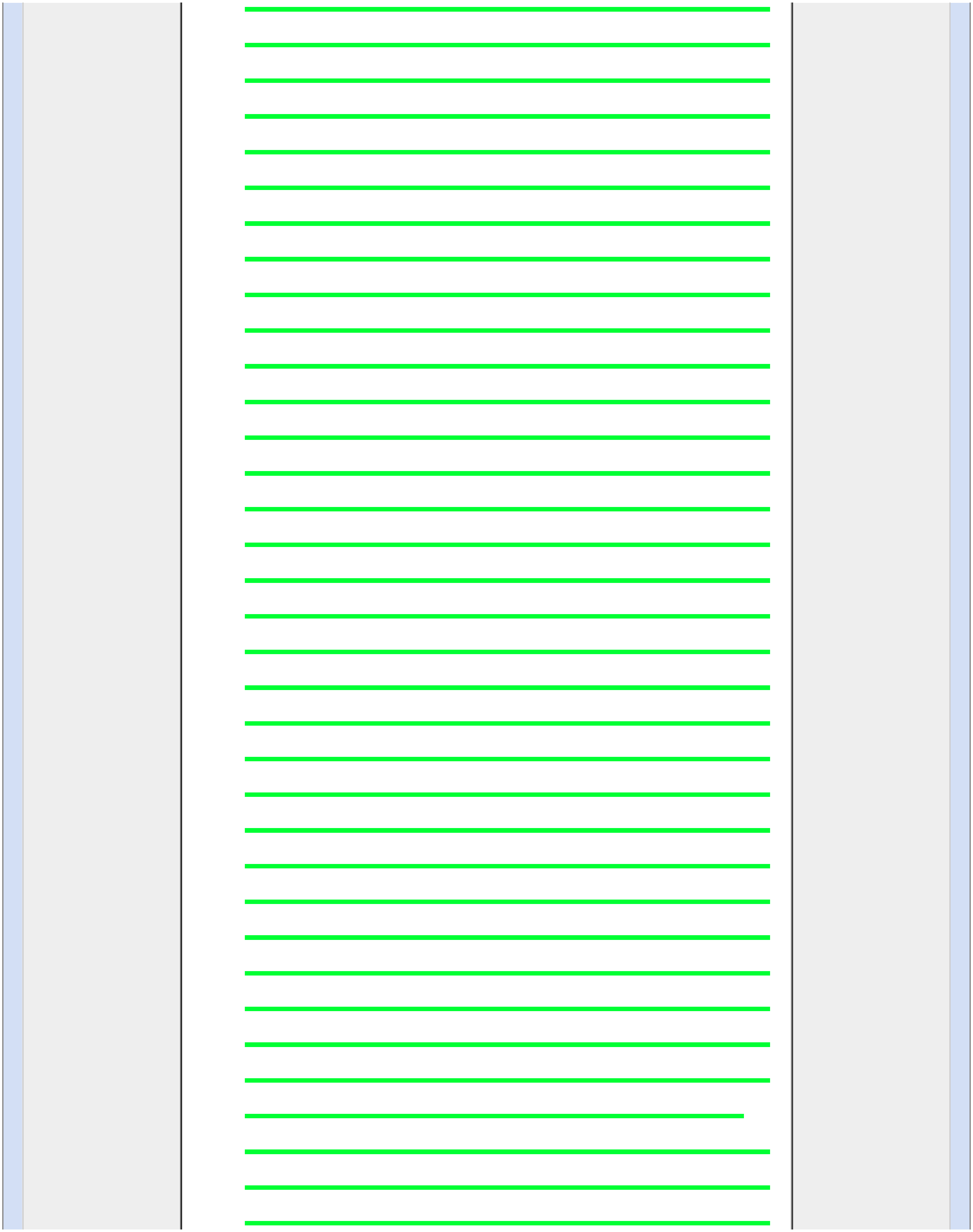
Show Conserved Domains

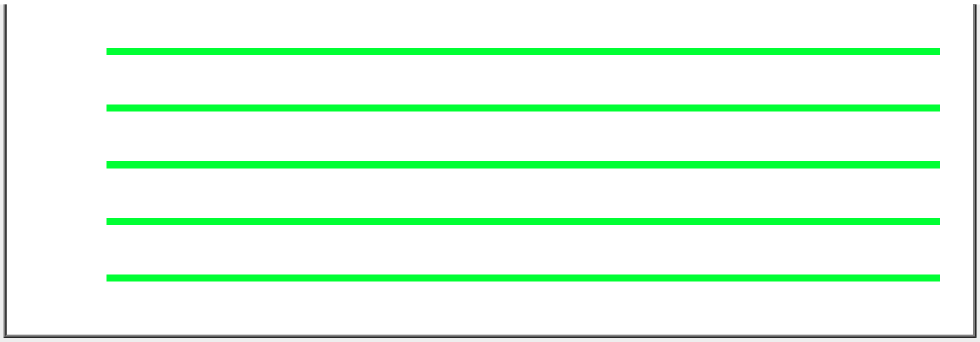
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylchol	66.4	66.4	100%	5e-11	95%	gi|393715367|4AQD_A
☐	monomeric butyrylcholinesterase [synthetic construct]	66.4	66.4	100%	5e-11	95%	gi|388261124|AFK25766.1
☐	Chain A, Co-Crystallization Studies Of Full Length Recombinant Bc	66.4	66.4	100%	5e-11	95%	gi|328877250|3O9M_A
☐	butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]	66.4	66.4	100%	5e-11	95%	gi|632795270|AHZ34327.1
☐	cholinesterase precursor [Homo sapiens]	66.4	66.4	100%	5e-11	95%	gi|4557351|NP_000046.1
☐	unnamed protein product [Homo sapiens]	66.4	66.4	100%	5e-11	95%	gi|158257558|BAF84752.1
☐	butyrylcholinesterase [synthetic construct]	66.4	66.4	100%	5e-11	95%	gi|260766471|ACX50257.1
☐	PREDICTED: cholinesterase isoform X1 [Homo sapiens]	66.4	66.4	100%	5e-11	95%	gi|530375091|XP_005247742.1
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholinest	64.7	64.7	100%	2e-10	95%	gi|402550232|4AXB_A
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholinest	64.7	64.7	100%	2e-10	95%	gi|402550237|4B0O_A
☐	Chain A, Structure Of Human Butyrylcholinesterase Inhibited By Cb	64.7	64.7	100%	2e-10	95%	gi|340707403|2Y1K_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	64.7	64.7	100%	2e-10	95%	gi|237823652|2WIL_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	64.7	64.7	100%	2e-10	95%	gi|237823648|2WIF_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	64.7	64.7	100%	2e-10	95%	gi|237823647|2WID_A
☐	cholinesterase precursor [Pan troglodytes]	62.6	62.6	100%	1e-09	90%	gi|343960913|BAK62046.1
☐	PREDICTED: cholinesterase [Gorilla gorilla gorilla]	62.6	62.6	100%	1e-09	90%	gi|426342776|XP_004038010.1
☐	PREDICTED: cholinesterase [Pan paniscus]	62.6	62.6	100%	1e-09	90%	gi|397493718|XP_003817746.1
☐	PREDICTED: cholinesterase [Pan troglodytes]	62.6	62.6	100%	1e-09	90%	gi|114590210|XP_516857.2
☐	Chain A, X-Ray Structure Of Human Butyrylcholinesterase Inhibitec	60.0	60.0	100%	7e-09	90%	gi|326634060|2XQF_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	60.0	60.0	100%	7e-09	90%	gi|258588213|2WSL_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	60.0	60.0	100%	7e-09	90%	gi|215794636|3DJY_A
☐	Chain A, Crystal Structure Of Human Butyryl Cholinesterase [Homo	60.0	60.0	100%	7e-09	90%	gi|34810859|1P0I_A
☐	Chain A, G117h Mutant Of Human Butyrylcholinesterase In Comple	60.0	60.0	100%	7e-09	90%	gi|313103512|2XMB_A
☐	Chain A, Crystal Structure Of Recombinant Full Length Human Buty	60.0	60.0	100%	7e-09	90%	gi|158429456|2PM8_A
☐	PREDICTED: cholinesterase [Nomascus leucogenys]	60.0	60.0	100%	7e-09	90%	gi|332214651|XP_003256448.1
☐	Chain A, Structure Of Human Butyrylcholinesterase In Complex Wit	59.6	59.6	100%	1e-08	90%	gi|145579736|2J4C_A
☐	PREDICTED: cholinesterase [Eptesicus fuscus]	57.9	57.9	100%	4e-08	85%	gi|641703485|XP_008140478.1
☐	PREDICTED: cholinesterase [Myotis lucifugus]	57.9	57.9	100%	4e-08	85%	gi|558125651|XP_006088951.1
☐							

	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhydr	57.5	57.5	100%	5e-08	85%	gi|21362409|P81908.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhydr	57.5	57.5	100%	5e-08	85%	gi|116354|P21927.1
☐	PREDICTED: cholinesterase [Oryctolagus cuniculus]	57.5	57.5	100%	5e-08	85%	gi|291400118|XP_002716414.1
☐	PREDICTED: cholinesterase [Orcinus orca]	57.5	57.5	100%	5e-08	85%	gi|466076197|XP_004283487.1
☐	cholinesterase precursor [Pongo abelii]	57.5	57.5	100%	5e-08	85%	gi|197097436|NP_001127509.1
☐	PREDICTED: cholinesterase isoform X1 [Sus scrofa]	57.5	57.5	100%	5e-08	85%	gi|335299867|XP_003358712.1
☐	cholinesterase precursor [Bos taurus]	57.5	57.5	100%	5e-08	85%	gi|116004027|NP_001070374.1
☐	PREDICTED: cholinesterase [Bison bison bison]	57.5	57.5	100%	5e-08	85%	gi|742123891|XP_010839228.1
☐	PREDICTED: cholinesterase [Balaenoptera acutorostrata scammor	57.5	57.5	100%	5e-08	85%	gi|594625950|XP_007197616.1
☐	PREDICTED: cholinesterase isoform X1 [Pongo abelii]	57.5	57.5	100%	5e-08	85%	gi|686714306|XP_009237773.1
☐	PREDICTED: cholinesterase [Lipotes vexillifer]	57.5	57.5	100%	5e-08	85%	gi|602681974|XP_007446483.1
☐	PREDICTED: cholinesterase [Pantholops hodgsonii]	57.5	57.5	100%	5e-08	85%	gi|556779632|XP_005984864.1
☐	PREDICTED: cholinesterase [Bos mutus]	57.5	57.5	100%	5e-08	85%	gi|555966690|XP_005895396.1
☐	PREDICTED: cholinesterase [Capra hircus]	57.5	57.5	100%	5e-08	85%	gi|548451269|XP_005675420.1
☐	PREDICTED: cholinesterase [Ovis aries]	57.5	57.5	100%	5e-08	85%	gi|426218006|XP_004003241.1
☐	PREDICTED: cholinesterase [Orycteropus afer afer]	55.4	55.4	100%	3e-07	85%	gi|634870148|XP_007946910.1
☐	PREDICTED: cholinesterase isoform X2 [Saimiri boliviensis bolivier	55.4	55.4	100%	3e-07	80%	gi|725560928|XP_010334003.1
☐	PREDICTED: cholinesterase isoform X1 [Saimiri boliviensis bolivier	55.4	55.4	100%	3e-07	80%	gi|403265619|XP_003925023.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase [Callithrix j	55.4	55.4	100%	3e-07	80%	gi|675737963|XP_002807699.3
☐	PREDICTED: cholinesterase [Ursus maritimus]	54.9	54.9	95%	4e-07	84%	gi|670999264|XP_008690527.1
☐	PREDICTED: cholinesterase-like isoform X1 [Myotis brandtii]	54.5	54.5	100%	5e-07	80%	gi|554526033|XP_005857864.1
☐	Cholinesterase [Myotis brandtii]	54.5	54.5	100%	5e-07	80%	gi|521020653|EPQ02441.1
☐	hypothetical protein EGK_11933 [Macaca mulatta]	54.1	54.1	100%	7e-07	80%	gi|355559896|EHH16624.1
☐	butyrylcholinesterase precursor [Macaca fascicularis]	54.1	54.1	100%	7e-07	80%	gi|290795732|ADD64703.1
☐	cholinesterase precursor [Equus caballus]	54.1	54.1	100%	7e-07	80%	gi|126352540|NP_001075319.1
☐	PREDICTED: cholinesterase-like [Elephantulus edwardii]	54.1	54.1	100%	7e-07	80%	gi|585675683|XP_006890440.1
☐	PREDICTED: cholinesterase [Macaca fascicularis]	54.1	54.1	100%	7e-07	80%	gi|544412493|XP_005546353.1
☐	PREDICTED: cholinesterase isoform X1 [Papio anubis]	54.1	54.1	100%	7e-07	80%	gi|402861047|XP_003894921.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase-like [Maca	54.1	54.1	100%	7e-07	80%	gi|297286482|XP_002808379.1
☐	PREDICTED: cholinesterase [Ictidomys tridecemlineatus]	54.1	54.1	100%	7e-07	80%	gi|532105511|XP_005338342.1
☐	PREDICTED: cholinesterase isoform X2 [Equus przewalskii]	54.1	54.1	100%	7e-07	80%	gi|664725795|XP_008520036.1
☐	PREDICTED: cholinesterase isoform X1 [Equus przewalskii]	54.1	54.1	100%	7e-07	80%	gi|664725793|XP_008520035.1
☐	PREDICTED: cholinesterase isoform X1 [Chlorocebus sabaeus]	54.1	54.1	100%	7e-07	80%	gi|635084154|XP_007970394.1
☐	PREDICTED: cholinesterase [Ceratotherium simum simum]	54.1	54.1	100%	7e-07	80%	gi|478501043|XP_004424836.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus dromedarius]	53.7	53.7	100%	1e-06	80%	gi|744553709|XP_010974642.1
☐	PREDICTED: cholinesterase isoform X1 [Camelus dromedarius]	53.7	53.7	100%	1e-06	80%	gi|744553706|XP_010974641.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus bactrianus]	53.7	53.7	100%	1e-06	80%	gi|743713601|XP_010950371.1
☐	PREDICTED: cholinesterase [Vicugna pacos]	53.7	53.7	100%	1e-06	80%	gi|560956860|XP_006200907.1
☐	PREDICTED: cholinesterase [Camelus ferus]	53.7	53.7	100%	1e-06	80%	gi|560915255|XP_006183885.1
☐	PREDICTED: cholinesterase-like isoform X1 [Mustela putorius furo]	53.7	53.7	95%	1e-06	84%	gi|511910148|XP_004774475.1
☐	hypothetical protein PANDA_007095 [Ailuropoda melanoleuca]	53.2	53.2	95%	1e-06	84%	gi|281337784|EFB13368.1
☐	PREDICTED: cholinesterase-like [Ailuropoda melanoleuca]	53.2	53.2	95%	1e-06	84%	gi|301766374|XP_002918607.1
☐	PREDICTED: cholinesterase [Myotis davidii]	52.4	52.4	90%	3e-06	83%	gi|584083219|XP_006761409.1
☐	PREDICTED: cholinesterase [Fukomys damarensis]	51.1	51.1	100%	7e-06	80%	gi|731199055|XP_010610068.1
☐	Cholinesterase [Fukomys damarensis]	51.1	51.1	100%	7e-06	80%	gi|676283600|KFO36750.1

☐	PREDICTED: cholinesterase [Tarsius syrichta]	51.1	51.1	100%	7e-06	75%	gi|640826885|XP_008070612.1
☐	PREDICTED: cholinesterase [Otolemur garnettii]	50.7	50.7	100%	1e-05	75%	gi|395843862|XP_003794691.1
☐	PREDICTED: cholinesterase-like isoform 1 [Dasypus novemcinctus	50.7	50.7	100%	1e-05	75%	gi|488587231|XP_004478943.1
☐	PREDICTED: cholinesterase-like [Trichechus manatus latirostris]	50.7	50.7	100%	1e-05	75%	gi|471406477|XP_004384938.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhydı	50.7	50.7	100%	1e-05	75%	gi|38502853|O62761.1
☐	cholinesterase precursor [Felis catus]	50.7	50.7	100%	1e-05	75%	gi|57163907|NP_001009364.1
☐	PREDICTED: cholinesterase isoform X1 [Loxodonta africana]	50.7	50.7	100%	1e-05	75%	gi|731499959|XP_003416305.2
☐	PREDICTED: cholinesterase-like [Panthera tigris altaica]	50.7	50.7	100%	1e-05	75%	gi|591300304|XP_007077117.1
☐	PREDICTED: cholinesterase-like [Odobenus rosmarus divergens]	50.7	50.7	90%	1e-05	83%	gi|472347065|XP_004393257.1
☐	PREDICTED: cholinesterase [Rhinopithecus roxellana]	50.7	50.7	100%	1e-05	80%	gi|724956944|XP_010353594.1
☐	PREDICTED: cholinesterase [Galeopterus variegatus]	50.3	50.3	100%	1e-05	75%	gi|667294272|XP_008578862.1
☐	PREDICTED: cholinesterase-like [Chrysochloris asiatica]	50.3	50.3	100%	1e-05	75%	gi|586462448|XP_006861862.1
☐	PREDICTED: cholinesterase-like [Echinops telfairi]	50.3	50.3	100%	1e-05	75%	gi|507651638|XP_004704160.1
☐	PREDICTED: cholinesterase-like [Sorex araneus]	49.8	49.8	95%	2e-05	79%	gi|505845607|XP_004616283.1
☐	PREDICTED: cholinesterase isoform X2 [Heterocephalus glaber]	48.6	48.6	100%	5e-05	75%	gi|512824494|XP_004880401.1
☐	PREDICTED: cholinesterase isoform X1 [Chinchilla lanigera]	48.6	48.6	100%	5e-05	75%	gi|533158554|XP_005393194.1
☐	PREDICTED: cholinesterase isoform X1 [Heterocephalus glaber]	48.6	48.6	100%	5e-05	75%	gi|512824490|XP_004880400.1
☐	PREDICTED: cholinesterase isoform X2 [Cavia porcellus]	48.1	48.1	100%	7e-05	70%	gi|514460083|XP_005003514.1
☐	PREDICTED: cholinesterase isoform X1 [Cavia porcellus]	48.1	48.1	100%	7e-05	70%	gi|348567235|XP_003469406.1
☐	Cholinesterase [Pteropus alecto]	47.7	47.7	100%	1e-04	75%	gi|431915168|ELK15855.1
☐	PREDICTED: cholinesterase [Pteropus alecto]	47.7	47.7	100%	1e-04	75%	gi|586546267|XP_006908236.1
☐	PREDICTED: cholinesterase [Erinaceus europaeus]	47.3	47.3	100%	1e-04	75%	gi|617605262|XP_007523705.1
☐	PREDICTED: cholinesterase [Canis lupus familiaris]	47.3	47.3	90%	1e-04	78%	gi|74003707|XP_545267.2
☐	PREDICTED: cholinesterase-like [Leptonychotes weddellii]	46.9	46.9	90%	2e-04	78%	gi|585150385|XP_006727664.1
☐	PREDICTED: cholinesterase [Sarcophilus harrisii]	46.4	46.4	90%	3e-04	72%	gi|395528220|XP_003766229.1
☐	PREDICTED: cholinesterase isoform X1 [Peromyscus maniculatus	46.4	46.4	100%	3e-04	70%	gi|589919054|XP_006972718.1
☐	PREDICTED: cholinesterase [Jaculus jaculus]	45.2	45.2	100%	7e-04	70%	gi|507536796|XP_004652429.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylcholinesterase

Sequence ID: gi|393715367|pdb|4AQD|A **Length:** 531 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 478 to 497 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
66.4 bits(149)	5e-11	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQNNSTSWPVFKS  20
            KYGNP+ETQNNSTSWPVFKS
Sbjct  478  KYGNPNETQNNSTSWPVFKS  497
```

Related Information

Structure - 3D structure displays
Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

monomeric butyrylcholinesterase [synthetic construct]

Sequence ID: gi|388261124|gb|AFK25766.1| **Length:** 557 **Number of Matches:** 1

Related Information

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
66.4 bits(149)	5e-11	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQNNSTSWPVFKS  20
            KYGNP+ETQNNSTSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Co-Crystallization Studies Of Full Length Recombinant Bche With Cocaine Offers Insights Into Cocaine Detoxification

Sequence ID: gi|328877250|pdb|3O9M|A **Length:** 574 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 476 to 495 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
66.4 bits(149)	5e-11	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQNNSTSWPVFKS  20
            KYGNP+ETQNNSTSWPVFKS
Sbjct  476  KYGNPNETQNNSTSWPVFKS  495
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]

Sequence ID: gi|632795270|gb|AHZ34327.1| **Length:** 602 **Number of Matches:** 1

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
66.4 bits(149)	5e-11	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQNNSTSWPVFKS  20
            KYGNP+ETQNNSTSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Related Information

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

cholinesterase precursor [Homo sapiens]

Sequence ID: gi|4557351|ref|NP_000046.1| **Length:** 602 **Number of Matches:** 1

▷ See 10 more title(s)

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
66.4 bits(149)	5e-11	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPDETQNNSTSWPVFKS  20
            KYGNP+ETQNNSTSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Structure - 3D structure displays

PubChem BioAssay - bioactivity screening

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - BHJGKFFG015

Your search parameters were adjusted to search for a short input sequence.

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How to read this page | Blast report description

BCHE_KYGNPNETQDDSTSWPVFKS_Mod

RID BHJGKFFG015 (Expires on 01-17 15:21 pm)

Query ID lcl|56207
Description None
Molecule type amino acid
Query Length 20

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

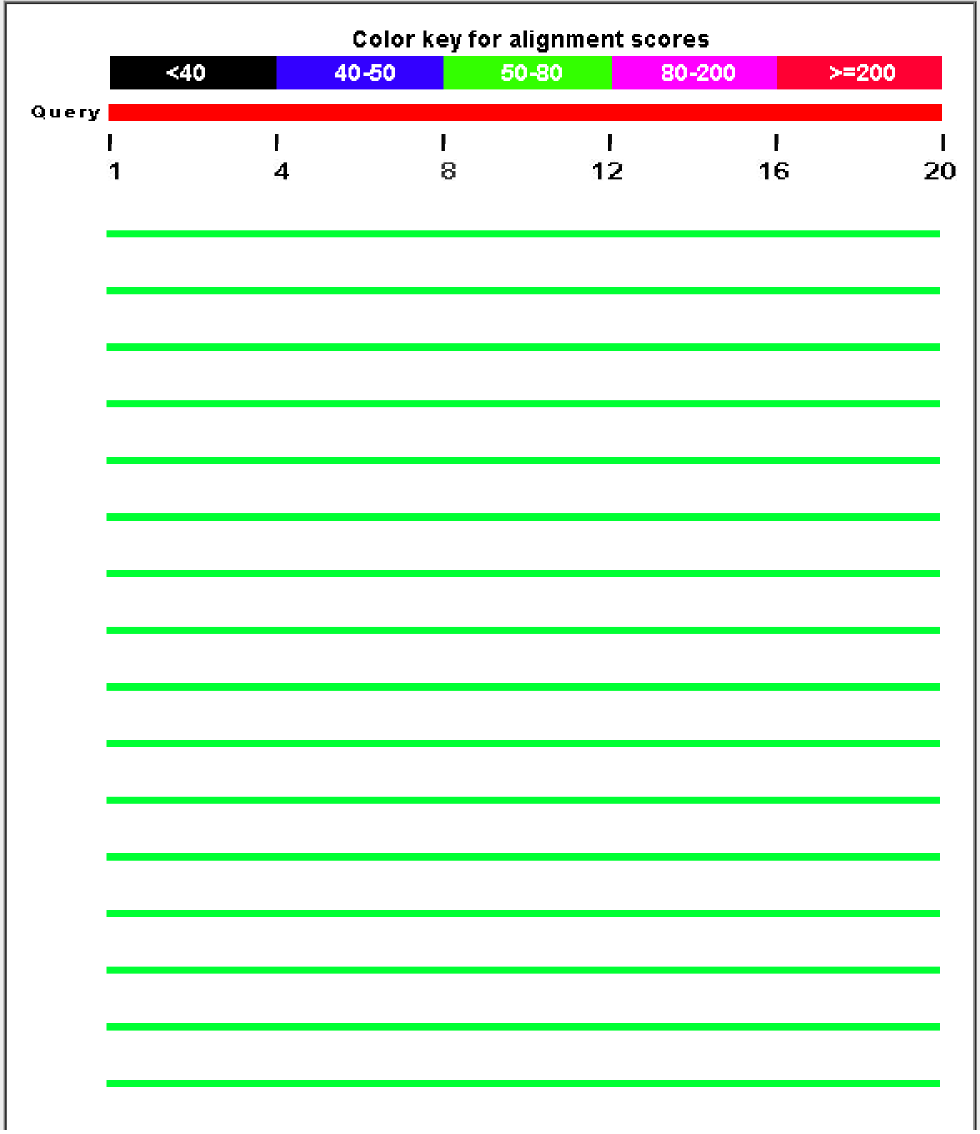
Graphic Summary

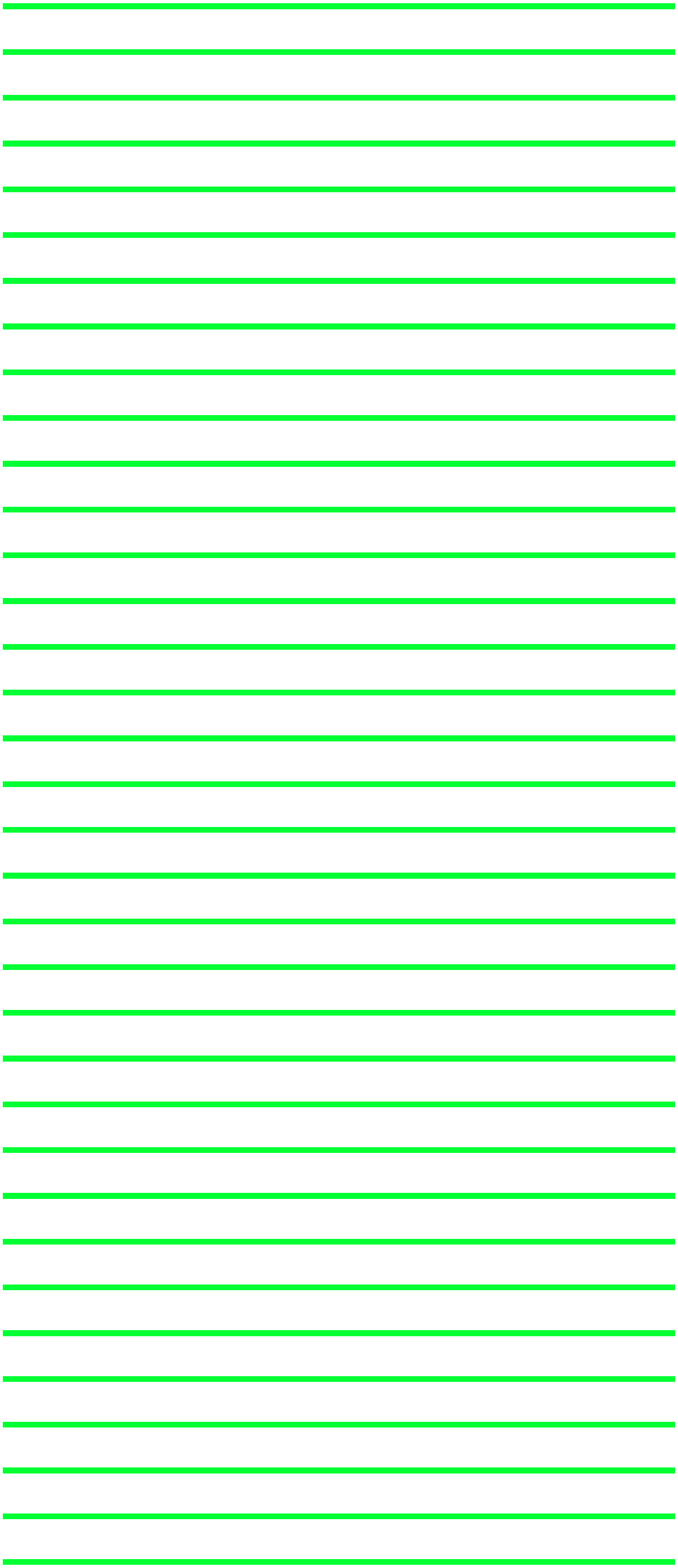
Show Conserved Domains

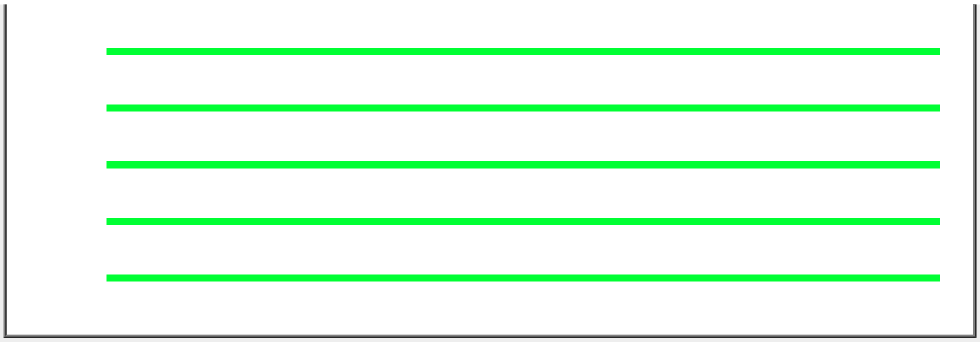
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylchol	63.8	63.8	100%	4e-10	90%	gi|393715367|4AQD_A
☐	monomeric butyrylcholinesterase [synthetic construct]	63.8	63.8	100%	4e-10	90%	gi|388261124|AFK25766.1
☐	Chain A, Co-Crystallization Studies Of Full Length Recombinant Bc	63.8	63.8	100%	4e-10	90%	gi|328877250|3O9M_A
☐	butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|632795270|AHZ34327.1
☐	cholinesterase precursor [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|4557351|NP_000046.1
☐	unnamed protein product [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|158257558|BAF84752.1
☐	butyrylcholinesterase [synthetic construct]	63.8	63.8	100%	4e-10	90%	gi|260766471|ACX50257.1
☐	PREDICTED: cholinesterase isoform X1 [Homo sapiens]	63.8	63.8	100%	4e-10	90%	gi|530375091|XP_005247742.1
☐	cholinesterase precursor [Pan troglodytes]	60.0	60.0	100%	7e-09	85%	gi|343960913|BAK62046.1
☐	PREDICTED: cholinesterase [Gorilla gorilla gorilla]	60.0	60.0	100%	7e-09	85%	gi|426342776|XP_004038010.1
☐	PREDICTED: cholinesterase [Pan paniscus]	60.0	60.0	100%	7e-09	85%	gi|397493718|XP_003817746.1
☐	PREDICTED: cholinesterase [Pan troglodytes]	60.0	60.0	100%	7e-09	85%	gi|114590210|XP_516857.2
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholinest	59.2	59.2	100%	1e-08	85%	gi|402550232|4AXB_A
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholinest	59.2	59.2	100%	1e-08	85%	gi|402550237|4B0O_A
☐	Chain A, Structure Of Human Butyrylcholinesterase Inhibited By Cb	59.2	59.2	100%	1e-08	85%	gi|340707403|2Y1K_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By	59.2	59.2	100%	1e-08	85%	gi|237823652|2WIL_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By	59.2	59.2	100%	1e-08	85%	gi|237823648|2WIF_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited	59.2	59.2	100%	1e-08	85%	gi|237823647|2WID_A
☐	Chain A, X-Ray Structure Of Human Butyrylcholinesterase Inhibite	57.5	57.5	100%	5e-08	85%	gi|326634060|2XQF_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By	57.5	57.5	100%	5e-08	85%	gi|258588213|2WSL_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited	57.5	57.5	100%	5e-08	85%	gi|215794636|3DJY_A
☐	Chain A, Crystal Structure Of Human Butyryl Cholinesterase [Homo	57.5	57.5	100%	5e-08	85%	gi|34810859|1P0I_A
☐	Chain A, G117h Mutant Of Human Butyrylcholinesterase In Comple	57.5	57.5	100%	5e-08	85%	gi|313103512|2XMB_A
☐	Chain A, Crystal Structure Of Recombinant Full Length Human Buty	57.5	57.5	100%	5e-08	85%	gi|158429456|2PM8_A
☐	Chain A, Structure Of Human Butyrylcholinesterase In Complex Wit	57.1	57.1	100%	7e-08	85%	gi|145579736|2J4C_A
☐	PREDICTED: cholinesterase [Eptesicus fuscus]	56.2	56.2	100%	1e-07	85%	gi|641703485|XP_008140478.1
☐	PREDICTED: cholinesterase [Myotis lucifugus]	56.2	56.2	100%	1e-07	85%	gi|558125651|XP_006088951.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhyd	54.9	54.9	100%	4e-07	80%	gi|21362409|P81908.1
☐							

	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhydı	54.9	54.9	100%	4e-07	80%	gi|116354|P21927.1
☐	PREDICTED: cholinesterase [Oryctolagus cuniculus]	54.9	54.9	100%	4e-07	80%	gi|291400118|XP_002716414.1
☐	PREDICTED: cholinesterase [Orcinus orca]	54.9	54.9	100%	4e-07	80%	gi|466076197|XP_004283487.1
☐	cholinesterase precursor [Pongo abelii]	54.9	54.9	100%	4e-07	80%	gi|197097436|NP_001127509.1
☐	PREDICTED: cholinesterase isoform X1 [Sus scrofa]	54.9	54.9	100%	4e-07	80%	gi|335299867|XP_003358712.1
☐	cholinesterase precursor [Bos taurus]	54.9	54.9	100%	4e-07	80%	gi|116004027|NP_001070374.1
☐	PREDICTED: cholinesterase [Bison bison bison]	54.9	54.9	100%	4e-07	80%	gi|742123891|XP_010839228.1
☐	PREDICTED: cholinesterase [Balaenoptera acutorostrata scammor	54.9	54.9	100%	4e-07	80%	gi|594625950|XP_007197616.1
☐	PREDICTED: cholinesterase isoform X1 [Pongo abelii]	54.9	54.9	100%	4e-07	80%	gi|686714306|XP_009237773.1
☐	PREDICTED: cholinesterase [Lipotes vexillifer]	54.9	54.9	100%	4e-07	80%	gi|602681974|XP_007446483.1
☐	PREDICTED: cholinesterase [Pantholops hodgsonii]	54.9	54.9	100%	4e-07	80%	gi|556779632|XP_005984864.1
☐	PREDICTED: cholinesterase [Bos mutus]	54.9	54.9	100%	4e-07	80%	gi|555966690|XP_005895396.1
☐	PREDICTED: cholinesterase [Capra hircus]	54.9	54.9	100%	4e-07	80%	gi|548451269|XP_005675420.1
☐	PREDICTED: cholinesterase [Ovis aries]	54.9	54.9	100%	4e-07	80%	gi|426218006|XP_004003241.1
☐	PREDICTED: cholinesterase-like isoform X1 [Myotis brandtii]	52.8	52.8	100%	2e-06	80%	gi|554526033|XP_005857864.1
☐	PREDICTED: cholinesterase isoform X2 [Saimiri boliviensis bolivier	52.8	52.8	100%	2e-06	75%	gi|725560928|XP_010334003.1
☐	PREDICTED: cholinesterase isoform X1 [Saimiri boliviensis bolivier	52.8	52.8	100%	2e-06	75%	gi|403265619|XP_003925023.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase [Callithrix j	52.8	52.8	100%	2e-06	75%	gi|675737963|XP_002807699.3
☐	Cholinesterase [Myotis brandtii]	52.8	52.8	100%	2e-06	80%	gi|521020653|EPQ02441.1
☐	cholinesterase precursor [Equus caballus]	52.4	52.4	100%	3e-06	80%	gi|126352540|NP_001075319.1
☐	PREDICTED: cholinesterase-like [Elephantulus edwardii]	52.4	52.4	100%	3e-06	80%	gi|585675683|XP_006890440.1
☐	PREDICTED: cholinesterase isoform X2 [Equus przewalskii]	52.4	52.4	100%	3e-06	80%	gi|664725795|XP_008520036.1
☐	PREDICTED: cholinesterase isoform X1 [Equus przewalskii]	52.4	52.4	100%	3e-06	80%	gi|664725793|XP_008520035.1
☐	PREDICTED: cholinesterase [Ceratotherium simum simum]	52.4	52.4	100%	3e-06	80%	gi|478501043|XP_004424836.1
☐	PREDICTED: cholinesterase [Nomascus leucogenys]	52.4	52.4	100%	3e-06	75%	gi|332214651|XP_003256448.1
☐	hypothetical protein EGK_11933 [Macaca mulatta]	51.5	51.5	100%	5e-06	75%	gi|355559896|EHH16624.1
☐	butyrylcholinesterase precursor [Macaca fascicularis]	51.5	51.5	100%	5e-06	75%	gi|290795732|ADD64703.1
☐	PREDICTED: cholinesterase [Macaca fascicularis]	51.5	51.5	100%	5e-06	75%	gi|544412493|XP_005546353.1
☐	PREDICTED: cholinesterase isoform X1 [Papio anubis]	51.5	51.5	100%	5e-06	75%	gi|402861047|XP_003894921.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase-like [Maca	51.5	51.5	100%	5e-06	75%	gi|297286482|XP_002808379.1
☐	PREDICTED: cholinesterase [Ictidomys tridecemlineatus]	51.5	51.5	100%	5e-06	75%	gi|532105511|XP_005338342.1
☐	PREDICTED: cholinesterase isoform X1 [Chlorocebus sabaeus]	51.5	51.5	100%	5e-06	75%	gi|635084154|XP_007970394.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus dromedarius]	51.1	51.1	100%	7e-06	75%	gi|744553709|XP_010974642.1
☐	PREDICTED: cholinesterase isoform X1 [Camelus dromedarius]	51.1	51.1	100%	7e-06	75%	gi|744553706|XP_010974641.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus bactrianus]	51.1	51.1	100%	7e-06	75%	gi|743713601|XP_010950371.1
☐	PREDICTED: cholinesterase [Vicugna pacos]	51.1	51.1	100%	7e-06	75%	gi|560956860|XP_006200907.1
☐	PREDICTED: cholinesterase [Camelus ferus]	51.1	51.1	100%	7e-06	75%	gi|560915255|XP_006183885.1
☐	PREDICTED: cholinesterase [Myotis davidii]	50.7	50.7	90%	1e-05	83%	gi|584083219|XP_006761409.1
☐	PREDICTED: cholinesterase [Orycteropus afer afer]	49.8	49.8	100%	2e-05	75%	gi|634870148|XP_007946910.1
☐	PREDICTED: cholinesterase [Tarsius syrichta]	49.4	49.4	100%	3e-05	75%	gi|640826885|XP_008070612.1
☐	PREDICTED: cholinesterase [Otolemur garnettii]	49.0	49.0	100%	4e-05	75%	gi|395843862|XP_003794691.1
☐	PREDICTED: cholinesterase-like isoform 1 [Dasypus novemcinctus	49.0	49.0	100%	4e-05	75%	gi|488587231|XP_004478943.1
☐	PREDICTED: cholinesterase-like [Trichechus manatus latirostris]	49.0	49.0	100%	4e-05	75%	gi|471406477|XP_004384938.1
☐	PREDICTED: cholinesterase isoform X1 [Loxodonta africana]	49.0	49.0	100%	4e-05	75%	gi|731499959|XP_003416305.2
☐	PREDICTED: cholinesterase [Galeopterus variegatus]	48.6	48.6	100%	5e-05	75%	gi|667294272|XP_008578862.1

☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhyd	48.1	48.1	100%	7e-05	70%	gi|38502853|O62761.1
☐	cholinesterase precursor [Felis catus]	48.1	48.1	100%	7e-05	70%	gi|57163907|NP_001009364.1
☐	PREDICTED: cholinesterase-like [Panthera tigris altaica]	48.1	48.1	100%	7e-05	70%	gi|591300304|XP_007077117.1
☐	PREDICTED: cholinesterase-like [Chrysochloris asiatica]	47.7	47.7	100%	1e-04	70%	gi|586462448|XP_006861862.1
☐	PREDICTED: cholinesterase-like [Echinops telfairi]	47.7	47.7	100%	1e-04	70%	gi|507651638|XP_004704160.1
☐	PREDICTED: cholinesterase [Ursus maritimus]	47.3	47.3	95%	1e-04	68%	gi|670999264|XP_008690527.1
☐	PREDICTED: cholinesterase isoform X2 [Heterocephalus glaber]	46.9	46.9	100%	2e-04	75%	gi|512824494|XP_004880401.1
☐	PREDICTED: cholinesterase isoform X1 [Chinchilla lanigera]	46.9	46.9	100%	2e-04	75%	gi|533158554|XP_005393194.1
☐	PREDICTED: cholinesterase isoform X1 [Heterocephalus glaber]	46.9	46.9	100%	2e-04	75%	gi|512824490|XP_004880400.1
☐	PREDICTED: cholinesterase isoform X2 [Cavia porcellus]	46.4	46.4	100%	3e-04	70%	gi|514460083|XP_005003514.1
☐	PREDICTED: cholinesterase isoform X1 [Cavia porcellus]	46.4	46.4	100%	3e-04	70%	gi|348567235|XP_003469406.1
☐	PREDICTED: cholinesterase [Rhinopithecus roxellana]	46.4	46.4	100%	3e-04	70%	gi|724956944|XP_010353594.1
☐	Cholinesterase [Pteropus alecto]	46.0	46.0	100%	4e-04	75%	gi|431915168|ELK15855.1
☐	PREDICTED: cholinesterase [Pteropus alecto]	46.0	46.0	100%	4e-04	75%	gi|586546267|XP_006908236.1
☐	PREDICTED: cholinesterase-like isoform X1 [Mustela putorius furo]	46.0	46.0	95%	4e-04	68%	gi|511910148|XP_004774475.1
☐	hypothetical protein PANDA_007095 [Ailuropoda melanoleuca]	45.6	45.6	95%	5e-04	68%	gi|281337784|EFB13368.1
☐	PREDICTED: cholinesterase-like [Ailuropoda melanoleuca]	45.6	45.6	95%	5e-04	68%	gi|301766374|XP_002918607.1
☐	PREDICTED: cholinesterase [Microtus ochrogaster]	45.2	45.2	100%	7e-04	70%	gi|531999261|XP_005344165.1
☐	PREDICTED: cholinesterase isoform X1 [Peromyscus maniculatus	44.8	44.8	100%	0.001	70%	gi|589919054|XP_006972718.1
☐	PREDICTED: cholinesterase [Fukomys damarensis]	44.3	44.3	100%	0.001	70%	gi|731199055|XP_010610068.1
☐	Butyrylcholinesterase [Mus musculus]	44.3	44.3	100%	0.001	70%	gi|71534030|AAH99977.1
☐	butyrylcholinesterase [Mus musculus]	44.3	44.3	100%	0.001	70%	gi|191580|AAA37328.1
☐	cholinesterase precursor [Mus musculus]	44.3	44.3	100%	0.001	70%	gi|124487350|NP_033868.3
☐	Cholinesterase [Fukomys damarensis]	44.3	44.3	100%	0.001	70%	gi|676283600|KFO36750.1
☐	cholinesterase precursor [Rattus norvegicus]	43.9	43.9	100%	0.002	70%	gi|12621110|NP_075231.1
☐	PREDICTED: cholinesterase [Sarcophilus harrisii]	43.9	43.9	90%	0.002	67%	gi|395528220|XP_003766229.1
☐	PREDICTED: cholinesterase isoform X1 [Rattus norvegicus]	43.9	43.9	100%	0.002	70%	gi|672042750|XP_008759334.1

⊖ Alignments

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Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylcholinesterase

Sequence ID: gi|393715367|pdb|4AQD|A **Length:** 531 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 478 to 497 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPNETQDDSTSWPVFKS  20
            KYGNPNETQ++STSWPVFKS
Sbjct  478  KYGNPNETQNNSTSWPVFKS  497
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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monomeric butyrylcholinesterase [synthetic construct]

Sequence ID: gi|388261124|gb|AFK25766.1| **Length:** 557 **Number of Matches:** 1

Related Information

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPNETQDDSTSWPVFKS  20
            KYGNPNETQ++STSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Co-Crystallization Studies Of Full Length Recombinant Bche With Cocaine Offers Insights Into Cocaine Detoxification

Sequence ID: gi|328877250|pdb|3O9M|A **Length:** 574 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 476 to 495 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPNETQDDSTSWPVFKS  20
            KYGNPNETQ++STSWPVFKS
Sbjct  476  KYGNPNETQNNSTSWPVFKS  495
```

Related Information

Structure - 3D structure displays
Identical Proteins - Proteins identical to the subject

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butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]

Sequence ID: gi|632795270|gb|AHZ34327.1| **Length:** 602 **Number of Matches:** 1

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPNETQDDSTSWPVFKS  20
            KYGNPNETQ++STSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Related Information

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

cholinesterase precursor [Homo sapiens]

Sequence ID: gi|4557351|ref|NP_000046.1| **Length:** 602 **Number of Matches:** 1

▷ See 10 more title(s)

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	4e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPNETQDDSTSWPVFKS  20
            KYGNPNETQ++STSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Related Information

Gene - associated gene details
UniGene - clustered expressed sequence tags
Structure - 3D structure displays
PubChem BioAssay - bioactivity screening
Map Viewer - aligned genomic context
Identical Proteins - Proteins identical to the subject

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download

How to read this page | Blast report description

BCHE_KYGNPNETQDNSTSWPVFKS_Mod

RID BHJBMR4H015 (Expires on 01-17 15:19 pm)

Query ID lcl|3581
Description None
Molecule type amino acid
Query Length 20

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

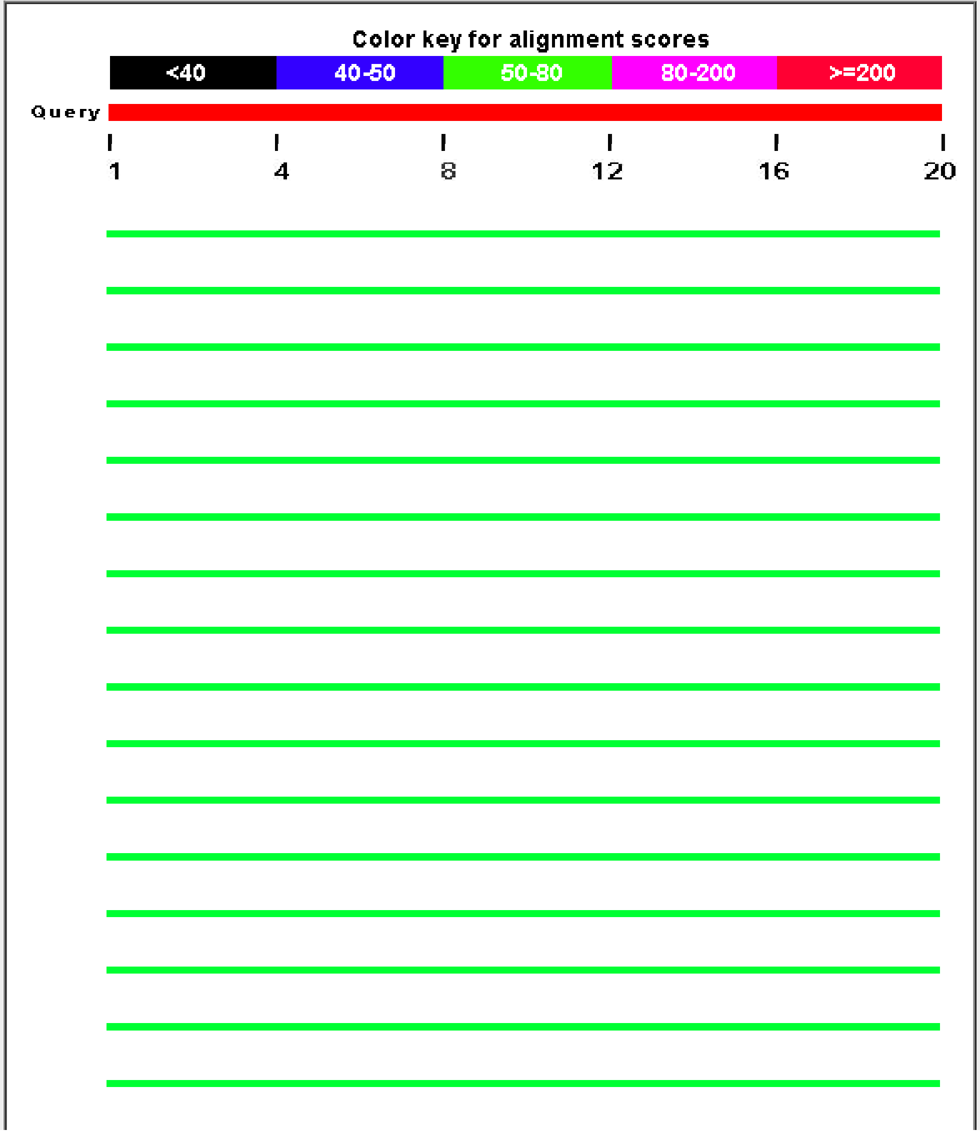
Graphic Summary

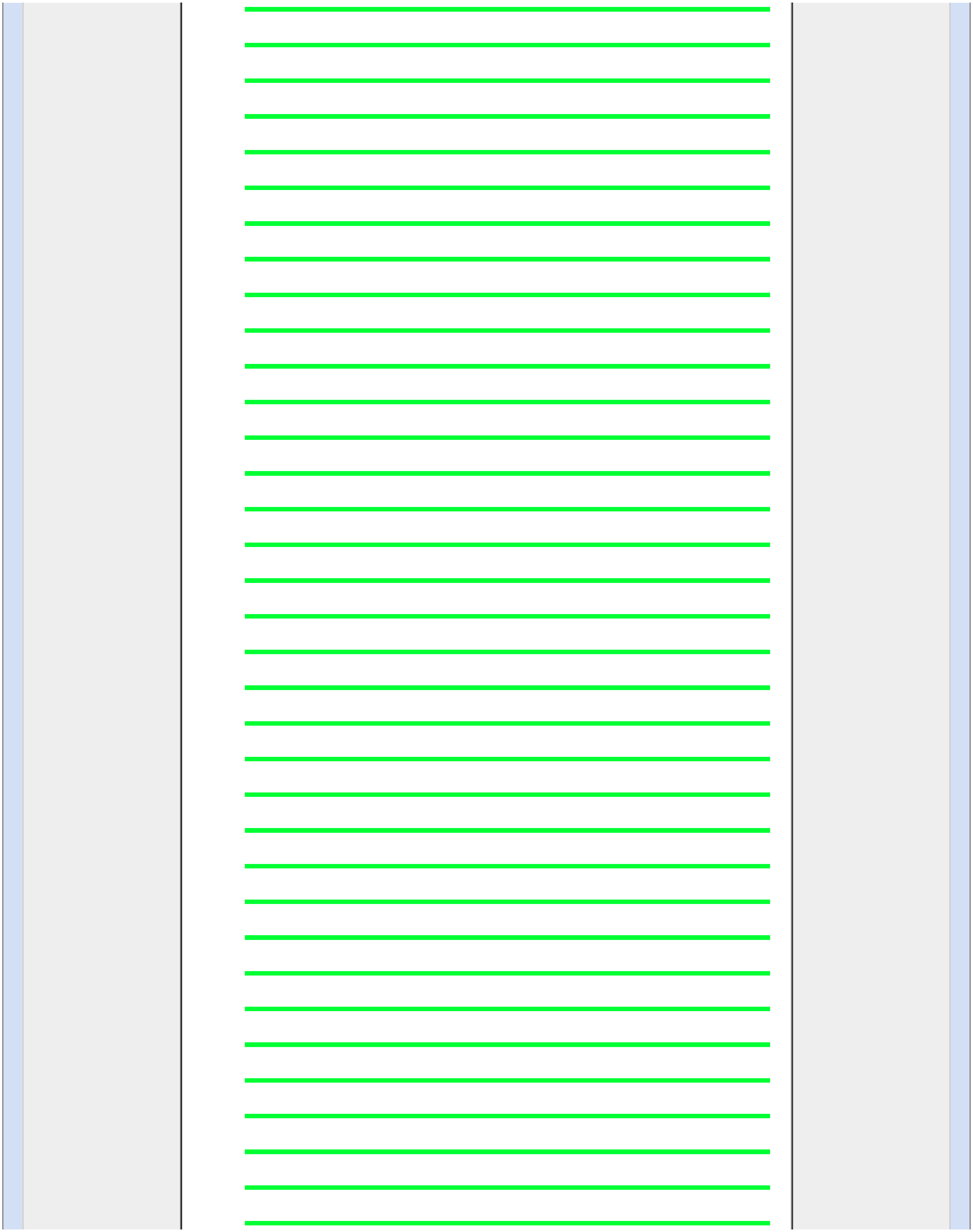
Show Conserved Domains

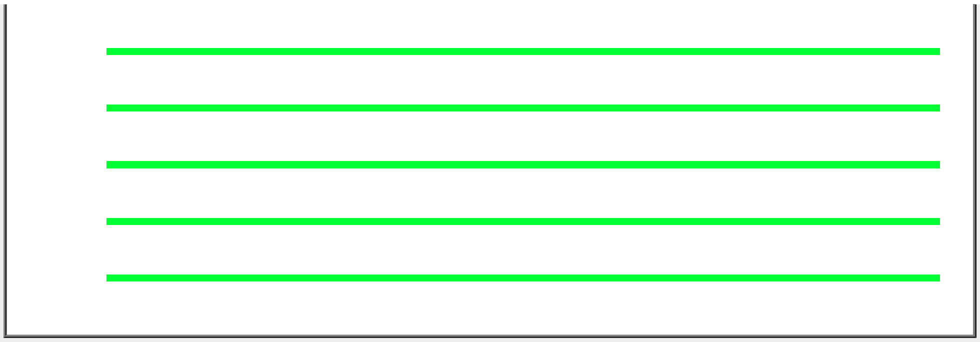
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylchol	66.4	66.4	100%	5e-11	95%	gi|393715367|4AQD_A
☐	monomeric butyrylcholinesterase [synthetic construct]	66.4	66.4	100%	5e-11	95%	gi|388261124|AFK25766.1
☐	Chain A, Co-Crystallization Studies Of Full Length Recombinant Bc	66.4	66.4	100%	5e-11	95%	gi|328877250|3O9M_A
☐	butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]	66.4	66.4	100%	5e-11	95%	gi|632795270|AHZ34327.1
☐	cholinesterase precursor [Homo sapiens]	66.4	66.4	100%	5e-11	95%	gi|4557351|NP_000046.1
☐	unnamed protein product [Homo sapiens]	66.4	66.4	100%	5e-11	95%	gi|158257558|BAF84752.1
☐	butyrylcholinesterase [synthetic construct]	66.4	66.4	100%	5e-11	95%	gi|260766471|ACX50257.1
☐	PREDICTED: cholinesterase isoform X1 [Homo sapiens]	66.4	66.4	100%	5e-11	95%	gi|530375091|XP_005247742.1
☐	cholinesterase precursor [Pan troglodytes]	62.6	62.6	100%	1e-09	90%	gi|343960913|BAK62046.1
☐	PREDICTED: cholinesterase [Gorilla gorilla gorilla]	62.6	62.6	100%	1e-09	90%	gi|426342776|XP_004038010.1
☐	PREDICTED: cholinesterase [Pan paniscus]	62.6	62.6	100%	1e-09	90%	gi|397493718|XP_003817746.1
☐	PREDICTED: cholinesterase [Pan troglodytes]	62.6	62.6	100%	1e-09	90%	gi|114590210|XP_516857.2
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholinest	61.7	61.7	100%	2e-09	90%	gi|402550232|4AXB_A
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholinest	61.7	61.7	100%	2e-09	90%	gi|402550237|4B0O_A
☐	Chain A, Structure Of Human Butyrylcholinesterase Inhibited By Cb	61.7	61.7	100%	2e-09	90%	gi|340707403|2Y1K_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	61.7	61.7	100%	2e-09	90%	gi|237823652|2WIL_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	61.7	61.7	100%	2e-09	90%	gi|237823648|2WIF_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	61.7	61.7	100%	2e-09	90%	gi|237823647|2WID_A
☐	PREDICTED: cholinesterase [Eptesicus fuscus]	57.9	57.9	100%	4e-08	85%	gi|641703485|XP_008140478.1
☐	PREDICTED: cholinesterase [Myotis lucifugus]	57.9	57.9	100%	4e-08	85%	gi|558125651|XP_006088951.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhydı	57.5	57.5	100%	5e-08	85%	gi|21362409|P81908.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhydı	57.5	57.5	100%	5e-08	85%	gi|116354|P21927.1
☐	PREDICTED: cholinesterase [Oryctolagus cuniculus]	57.5	57.5	100%	5e-08	85%	gi|291400118|XP_002716414.1
☐	PREDICTED: cholinesterase [Orcinus orca]	57.5	57.5	100%	5e-08	85%	gi|466076197|XP_004283487.1
☐	cholinesterase precursor [Pongo abelii]	57.5	57.5	100%	5e-08	85%	gi|197097436|NP_001127509.1
☐	PREDICTED: cholinesterase isoform X1 [Sus scrofa]	57.5	57.5	100%	5e-08	85%	gi|335299867|XP_003358712.1
☐	cholinesterase precursor [Bos taurus]	57.5	57.5	100%	5e-08	85%	gi|116004027|NP_001070374.1
☐	PREDICTED: cholinesterase [Bison bison bison]	57.5	57.5	100%	5e-08	85%	gi|742123891|XP_010839228.1
☐							

	PREDICTED: cholinesterase [Balaenoptera acutorostrata scammon	57.5	57.5	100%	5e-08	85%	gi|594625950|XP_007197616.1
☐	PREDICTED: cholinesterase isoform X1 [Pongo abelii]	57.5	57.5	100%	5e-08	85%	gi|686714306|XP_009237773.1
☐	PREDICTED: cholinesterase [Lipotes vexillifer]	57.5	57.5	100%	5e-08	85%	gi|602681974|XP_007446483.1
☐	PREDICTED: cholinesterase [Pantholops hodgsonii]	57.5	57.5	100%	5e-08	85%	gi|556779632|XP_005984864.1
☐	PREDICTED: cholinesterase [Bos mutus]	57.5	57.5	100%	5e-08	85%	gi|555966690|XP_005895396.1
☐	PREDICTED: cholinesterase [Capra hircus]	57.5	57.5	100%	5e-08	85%	gi|548451269|XP_005675420.1
☐	PREDICTED: cholinesterase [Ovis aries]	57.5	57.5	100%	5e-08	85%	gi|426218006|XP_004003241.1
☐	Chain A, X-Ray Structure Of Human Butyrylcholinesterase Inhibitec	57.1	57.1	100%	7e-08	85%	gi|326634060|2XQF_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	57.1	57.1	100%	7e-08	85%	gi|258588213|2WSL_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	57.1	57.1	100%	7e-08	85%	gi|215794636|3DJY_A
☐	Chain A, Crystal Structure Of Human Butyryl Cholinesterase [Homo	57.1	57.1	100%	7e-08	85%	gi|34810859|1P0I_A
☐	Chain A, G117h Mutant Of Human Butyrylcholinesterase In Comple	57.1	57.1	100%	7e-08	85%	gi|313103512|2XMB_A
☐	Chain A, Crystal Structure Of Recombinant Full Length Human Buty	57.1	57.1	100%	7e-08	85%	gi|158429456|2PM8_A
☐	Chain A, Structure Of Human Butyrylcholinesterase In Complex Wit	56.6	56.6	100%	1e-07	85%	gi|145579736|2J4C_A
☐	PREDICTED: cholinesterase isoform X2 [Saimiri boliviensis bolivier	55.4	55.4	100%	3e-07	80%	gi|725560928|XP_010334003.1
☐	PREDICTED: cholinesterase isoform X1 [Saimiri boliviensis bolivier	55.4	55.4	100%	3e-07	80%	gi|403265619|XP_003925023.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase [Callithrix j	55.4	55.4	100%	3e-07	80%	gi|675737963|XP_002807699.3
☐	cholinesterase precursor [Equus caballus]	54.9	54.9	100%	4e-07	85%	gi|126352540|NP_001075319.1
☐	PREDICTED: cholinesterase-like [Elephantulus edwardii]	54.9	54.9	100%	4e-07	85%	gi|585675683|XP_006890440.1
☐	PREDICTED: cholinesterase isoform X2 [Equus przewalskii]	54.9	54.9	100%	4e-07	85%	gi|664725795|XP_008520036.1
☐	PREDICTED: cholinesterase isoform X1 [Equus przewalskii]	54.9	54.9	100%	4e-07	85%	gi|664725793|XP_008520035.1
☐	PREDICTED: cholinesterase [Ceratotherium simum simum]	54.9	54.9	100%	4e-07	85%	gi|478501043|XP_004424836.1
☐	PREDICTED: cholinesterase [Nomascus leucogenys]	54.9	54.9	100%	4e-07	80%	gi|332214651|XP_003256448.1
☐	PREDICTED: cholinesterase-like isoform X1 [Myotis brandtii]	54.5	54.5	100%	5e-07	80%	gi|554526033|XP_005857864.1
☐	Cholinesterase [Myotis brandtii]	54.5	54.5	100%	5e-07	80%	gi|521020653|EPQ02441.1
☐	hypothetical protein EGK_11933 [Macaca mulatta]	54.1	54.1	100%	7e-07	80%	gi|355559896|EHH16624.1
☐	butyrylcholinesterase precursor [Macaca fascicularis]	54.1	54.1	100%	7e-07	80%	gi|290795732|ADD64703.1
☐	PREDICTED: cholinesterase [Macaca fascicularis]	54.1	54.1	100%	7e-07	80%	gi|544412493|XP_005546353.1
☐	PREDICTED: cholinesterase isoform X1 [Papio anubis]	54.1	54.1	100%	7e-07	80%	gi|402861047|XP_003894921.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase-like [Maca	54.1	54.1	100%	7e-07	80%	gi|297286482|XP_002808379.1
☐	PREDICTED: cholinesterase [Ictidomys tridecemlineatus]	54.1	54.1	100%	7e-07	80%	gi|532105511|XP_005338342.1
☐	PREDICTED: cholinesterase isoform X1 [Chlorocebus sabaeus]	54.1	54.1	100%	7e-07	80%	gi|635084154|XP_007970394.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus dromedarius]	53.7	53.7	100%	1e-06	80%	gi|744553709|XP_010974642.1
☐	PREDICTED: cholinesterase isoform X1 [Camelus dromedarius]	53.7	53.7	100%	1e-06	80%	gi|744553706|XP_010974641.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus bactrianus]	53.7	53.7	100%	1e-06	80%	gi|743713601|XP_010950371.1
☐	PREDICTED: cholinesterase [Vicugna pacos]	53.7	53.7	100%	1e-06	80%	gi|560956860|XP_006200907.1
☐	PREDICTED: cholinesterase [Camelus ferus]	53.7	53.7	100%	1e-06	80%	gi|560915255|XP_006183885.1
☐	PREDICTED: cholinesterase [Myotis davidii]	52.4	52.4	90%	3e-06	83%	gi|584083219|XP_006761409.1
☐	PREDICTED: cholinesterase [Orycteropus afer afer]	52.4	52.4	100%	3e-06	80%	gi|634870148|XP_007946910.1
☐	PREDICTED: cholinesterase [Tarsius syrichta]	52.0	52.0	100%	4e-06	80%	gi|640826885|XP_008070612.1
☐	PREDICTED: cholinesterase [Otolemur garnettii]	51.5	51.5	100%	5e-06	80%	gi|395843862|XP_003794691.1
☐	PREDICTED: cholinesterase-like isoform 1 [Dasypus novemcinctus	51.5	51.5	100%	5e-06	80%	gi|488587231|XP_004478943.1
☐	PREDICTED: cholinesterase-like [Trichechus manatus latirostris]	51.5	51.5	100%	5e-06	80%	gi|471406477|XP_004384938.1
☐	PREDICTED: cholinesterase isoform X1 [Loxodonta africana]	51.5	51.5	100%	5e-06	80%	gi|731499959|XP_003416305.2
☐	PREDICTED: cholinesterase [Galeopterus variegatus]	51.1	51.1	100%	7e-06	80%	gi|667294272|XP_008578862.1

☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhydı	50.7	50.7	100%	1e-05	75%	gi|38502853|O62761.1
☐	cholinesterase precursor [Felis catus]	50.7	50.7	100%	1e-05	75%	gi|57163907|NP_001009364.1
☐	PREDICTED: cholinesterase-like [Panthera tigris altaica]	50.7	50.7	100%	1e-05	75%	gi|591300304|XP_007077117.1
☐	PREDICTED: cholinesterase-like [Chrysochloris asiatica]	50.3	50.3	100%	1e-05	75%	gi|586462448|XP_006861862.1
☐	PREDICTED: cholinesterase-like [Echinops telfairi]	50.3	50.3	100%	1e-05	75%	gi|507651638|XP_004704160.1
☐	PREDICTED: cholinesterase [Ursus maritimus]	49.8	49.8	95%	2e-05	74%	gi|670999264|XP_008690527.1
☐	PREDICTED: cholinesterase isoform X2 [Heterocephalus glaber]	49.4	49.4	100%	3e-05	80%	gi|512824494|XP_004880401.1
☐	PREDICTED: cholinesterase isoform X1 [Chinchilla lanigera]	49.4	49.4	100%	3e-05	80%	gi|533158554|XP_005393194.1
☐	PREDICTED: cholinesterase isoform X1 [Heterocephalus glaber]	49.4	49.4	100%	3e-05	80%	gi|512824490|XP_004880400.1
☐	PREDICTED: cholinesterase isoform X2 [Cavia porcellus]	49.0	49.0	100%	4e-05	75%	gi|514460083|XP_005003514.1
☐	PREDICTED: cholinesterase isoform X1 [Cavia porcellus]	49.0	49.0	100%	4e-05	75%	gi|348567235|XP_003469406.1
☐	PREDICTED: cholinesterase [Rhinopithecus roxellana]	49.0	49.0	100%	4e-05	75%	gi|724956944|XP_010353594.1
☐	PREDICTED: cholinesterase-like isoform X1 [Mustela putorius furo]	48.6	48.6	95%	5e-05	74%	gi|511910148|XP_004774475.1
☐	hypothetical protein PANDA_007095 [Ailuropoda melanoleuca]	48.1	48.1	95%	7e-05	74%	gi|281337784|EFB13368.1
☐	PREDICTED: cholinesterase-like [Ailuropoda melanoleuca]	48.1	48.1	95%	7e-05	74%	gi|301766374|XP_002918607.1
☐	Cholinesterase [Pteropus alecto]	47.7	47.7	100%	1e-04	75%	gi|431915168|ELK15855.1
☐	PREDICTED: cholinesterase [Pteropus alecto]	47.7	47.7	100%	1e-04	75%	gi|586546267|XP_006908236.1
☐	PREDICTED: cholinesterase isoform X1 [Peromyscus maniculatus	47.3	47.3	100%	1e-04	75%	gi|589919054|XP_006972718.1
☐	PREDICTED: cholinesterase [Fukomys damarensis]	46.9	46.9	100%	2e-04	75%	gi|731199055|XP_010610068.1
☐	Butyrylcholinesterase [Mus musculus]	46.9	46.9	100%	2e-04	75%	gi|71534030|AAH99977.1
☐	butyrylcholinesterase [Mus musculus]	46.9	46.9	100%	2e-04	75%	gi|191580|AAA37328.1
☐	cholinesterase precursor [Mus musculus]	46.9	46.9	100%	2e-04	75%	gi|124487350|NP_033868.3
☐	Cholinesterase [Fukomys damarensis]	46.9	46.9	100%	2e-04	75%	gi|676283600|KFO36750.1
☐	cholinesterase precursor [Rattus norvegicus]	46.4	46.4	100%	3e-04	75%	gi|12621110|NP_075231.1
☐	PREDICTED: cholinesterase [Sarcophilus harrisii]	46.4	46.4	90%	3e-04	72%	gi|395528220|XP_003766229.1
☐	PREDICTED: cholinesterase isoform X1 [Rattus norvegicus]	46.4	46.4	100%	3e-04	75%	gi|672042750|XP_008759334.1
☐	PREDICTED: cholinesterase [Jaculus jaculus]	46.0	46.0	100%	4e-04	75%	gi|507536796|XP_004652429.1

⊟ Alignments

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Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylcholinesterase

Sequence ID: gi|393715367|pdb|4AQD|A **Length:** 531 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 478 to 497 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
66.4 bits(149)	5e-11	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPNETQDNSTSWPVFKS  20
            KYGNPNETQ+NSTSWPVFKS
Sbjct  478  KYGNPNETQNNSTSWPVFKS  497
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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monomeric butyrylcholinesterase [synthetic construct]

Sequence ID: gi|388261124|gb|AFK25766.1| **Length:** 557 **Number of Matches:** 1

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
66.4 bits(149)	5e-11	19/20(95%)	20/20(100%)	0/20(0%)

Related Information

```
Query  1    KYGNPNETQDNSTSWPVFKS  20
            KYGNPNETQ+NSTSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Co-Crystallization Studies Of Full Length Recombinant Bche With Cocaine Offers Insights Into Cocaine Detoxification

Sequence ID: gi|328877250|pdb|3O9M|A **Length:** 574 **Number of Matches:** 1

See 1 more title(s)

Range 1: 476 to 495 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
66.4 bits(149)	5e-11	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPNETQDNSTSWPVFKS  20
            KYGNPNETQ+NSTSWPVFKS
Sbjct  476  KYGNPNETQNNSTSWPVFKS  495
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]

Sequence ID: gi|632795270|gb|AHZ34327.1| **Length:** 602 **Number of Matches:** 1

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
66.4 bits(149)	5e-11	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPNETQDNSTSWPVFKS  20
            KYGNPNETQ+NSTSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Related Information

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

cholinesterase precursor [Homo sapiens]

Sequence ID: gi|4557351|ref|NP_000046.1| **Length:** 602 **Number of Matches:** 1

See 10 more title(s)

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
66.4 bits(149)	5e-11	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPNETQDNSTSWPVFKS  20
            KYGNPNETQ+NSTSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Structure - 3D structure displays

PubChem BioAssay - bioactivity screening

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - B92844B301R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download

How to read this page | Blast report description

BCHE_KYGNPNETQNNSTSWPVFKS_NonMod

RID B92844B301R (Expires on 01-14 09:55 am)

Query ID lcl|195965
Description None
Molecule type amino acid
Query Length 20

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

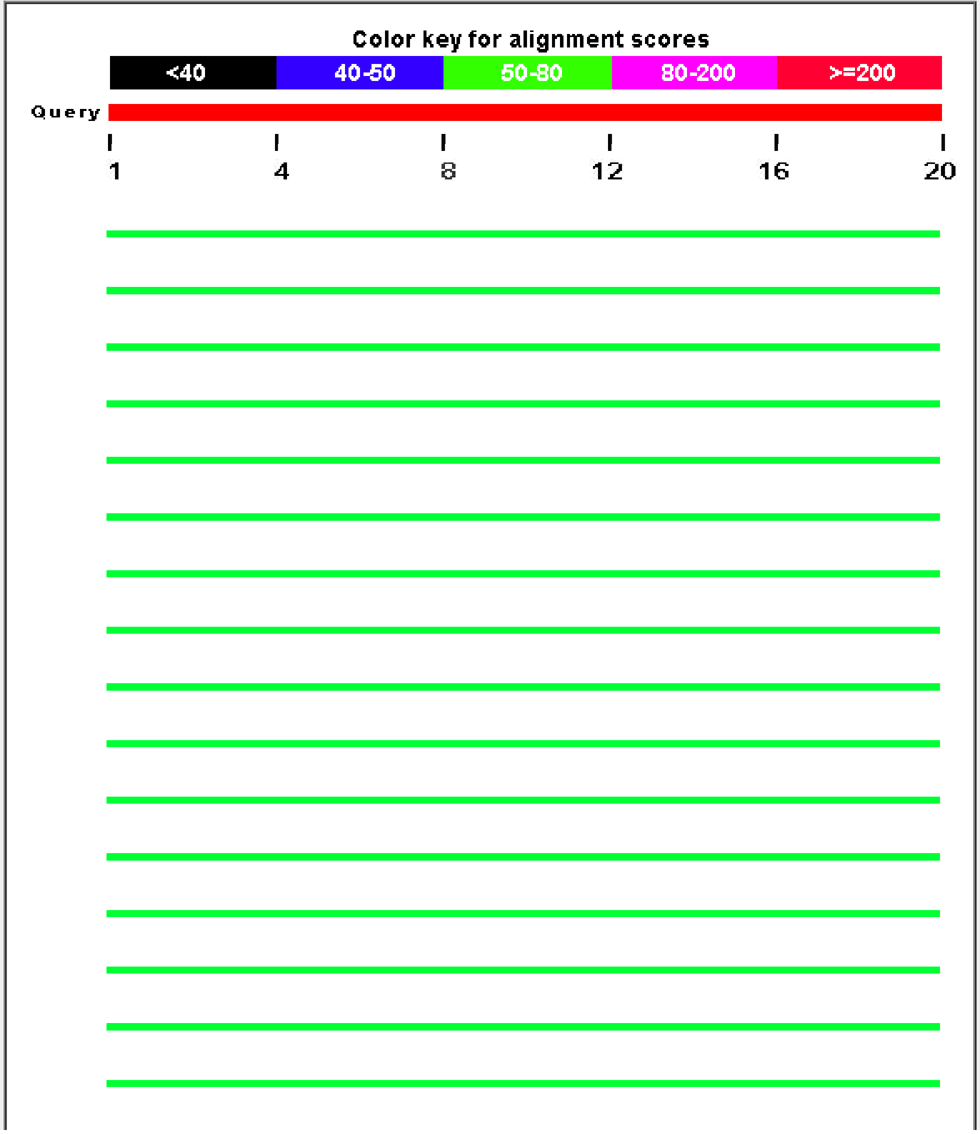
Graphic Summary

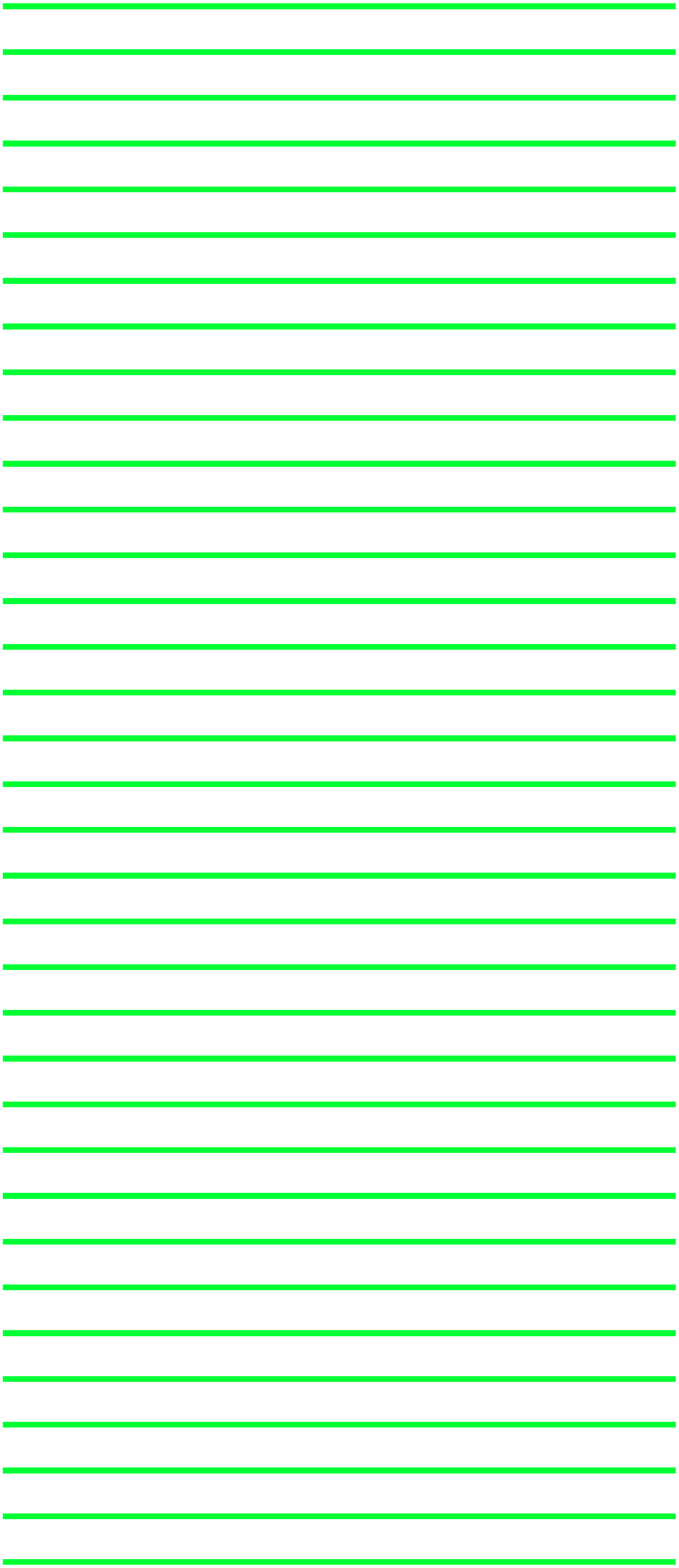
Show Conserved Domains

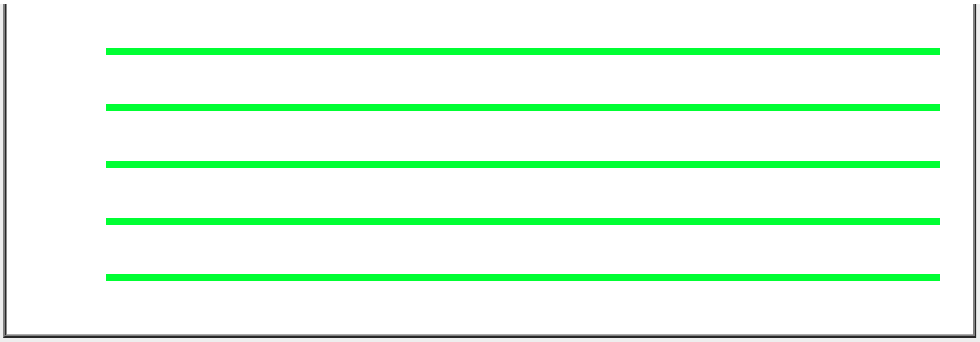
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylchol	68.9	68.9	100%	6e-12	100%	gi|393715367|4AQD_A
☐	monomeric butyrylcholinesterase [synthetic construct]	68.9	68.9	100%	6e-12	100%	gi|388261124|AFK25766.1
☐	Chain A, Co-Crystallization Studies Of Full Length Recombinant Bc	68.9	68.9	100%	6e-12	100%	gi|328877250|3O9M_A
☐	butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]	68.9	68.9	100%	6e-12	100%	gi|632795270|AHZ34327.1
☐	cholinesterase precursor [Homo sapiens]	68.9	68.9	100%	6e-12	100%	gi|4557351|NP_000046.1
☐	unnamed protein product [Homo sapiens]	68.9	68.9	100%	6e-12	100%	gi|158257558|BAF84752.1
☐	butyrylcholinesterase [synthetic construct]	68.9	68.9	100%	7e-12	100%	gi|260766471|ACX50257.1
☐	PREDICTED: cholinesterase isoform X1 [Homo sapiens]	68.9	68.9	100%	7e-12	100%	gi|530375091|XP_005247742.1
☐	cholinesterase precursor [Pan troglodytes]	65.1	65.1	100%	1e-10	95%	gi|343960913|BAK62046.1
☐	PREDICTED: cholinesterase [Gorilla gorilla gorilla]	65.1	65.1	100%	1e-10	95%	gi|426342776|XP_004038010.1
☐	PREDICTED: cholinesterase [Pan paniscus]	65.1	65.1	100%	1e-10	95%	gi|397493718|XP_003817746.1
☐	PREDICTED: cholinesterase [Pan troglodytes]	65.1	65.1	100%	1e-10	95%	gi|114590210|XP_516857.2
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholinest	64.3	64.3	100%	3e-10	95%	gi|402550232|4AXB_A
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholinest	64.3	64.3	100%	3e-10	95%	gi|402550237|4B0O_A
☐	Chain A, Structure Of Human Butyrylcholinesterase Inhibited By Cb	64.3	64.3	100%	3e-10	95%	gi|340707403|2Y1K_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	64.3	64.3	100%	3e-10	95%	gi|237823652|2WIL_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	64.3	64.3	100%	3e-10	95%	gi|237823648|2WIF_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	64.3	64.3	100%	3e-10	95%	gi|237823647|2WID_A
☐	PREDICTED: cholinesterase [Eptesicus fuscus]	60.4	60.4	100%	5e-09	90%	gi|641703485|XP_008140478.1
☐	PREDICTED: cholinesterase [Myotis lucifugus]	60.4	60.4	100%	5e-09	90%	gi|558125651|XP_006088951.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhydı	60.0	60.0	100%	7e-09	90%	gi|21362409|P81908.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhydı	60.0	60.0	100%	7e-09	90%	gi|116354|P21927.1
☐	PREDICTED: cholinesterase [Oryctolagus cuniculus]	60.0	60.0	100%	7e-09	90%	gi|291400118|XP_002716414.1
☐	PREDICTED: cholinesterase [Orcinus orca]	60.0	60.0	100%	7e-09	90%	gi|466076197|XP_004283487.1
☐	cholinesterase precursor [Pongo abelii]	60.0	60.0	100%	7e-09	90%	gi|197097436|NP_001127509.1
☐	PREDICTED: cholinesterase isoform X1 [Sus scrofa]	60.0	60.0	100%	7e-09	90%	gi|335299867|XP_003358712.1
☐	cholinesterase precursor [Bos taurus]	60.0	60.0	100%	7e-09	90%	gi|116004027|NP_001070374.1
☐	PREDICTED: cholinesterase [Balaenoptera acutorostrata scammor	60.0	60.0	100%	7e-09	90%	gi|594625950|XP_007197616.1
☐							

	PREDICTED: cholinesterase isoform X1 [Pongo abelii]	60.0	60.0	100%	7e-09	90%	gi|686714306|XP_009237773.1
☐	PREDICTED: cholinesterase [Lipotes vexillifer]	60.0	60.0	100%	7e-09	90%	gi|602681974|XP_007446483.1
☐	PREDICTED: cholinesterase [Pantholops hodgsonii]	60.0	60.0	100%	7e-09	90%	gi|556779632|XP_005984864.1
☐	PREDICTED: cholinesterase [Bos mutus]	60.0	60.0	100%	7e-09	90%	gi|555966690|XP_005895396.1
☐	PREDICTED: cholinesterase [Capra hircus]	60.0	60.0	100%	7e-09	90%	gi|548451269|XP_005675420.1
☐	PREDICTED: cholinesterase [Ovis aries]	60.0	60.0	100%	7e-09	90%	gi|426218006|XP_004003241.1
☐	Chain A, X-Ray Structure Of Human Butyrylcholinesterase Inhibite	59.6	59.6	100%	1e-08	90%	gi|326634060|2XQF_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By	59.6	59.6	100%	1e-08	90%	gi|258588213|2WSL_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited	59.6	59.6	100%	1e-08	90%	gi|215794636|3DJY_A
☐	Chain A, Crystal Structure Of Human Butyryl Cholinesterase [Homo	59.6	59.6	100%	1e-08	90%	gi|34810859|1P0I_A
☐	Chain A, G117h Mutant Of Human Butyrylcholinesterase In Comple	59.6	59.6	100%	1e-08	90%	gi|313103512|2XMB_A
☐	Chain A, Crystal Structure Of Recombinant Full Length Human Buty	59.6	59.6	100%	1e-08	90%	gi|158429456|2PM8_A
☐	Chain A, Structure Of Human Butyrylcholinesterase In Complex Wit	59.2	59.2	100%	1e-08	90%	gi|145579736|2J4C_A
☐	PREDICTED: cholinesterase isoform X2 [Saimiri boliviensis bolivie	57.9	57.9	100%	4e-08	85%	gi|725560928|XP_010334003.1
☐	PREDICTED: cholinesterase isoform X1 [Saimiri boliviensis bolivie	57.9	57.9	100%	4e-08	85%	gi|403265619|XP_003925023.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase [Callithrix j	57.9	57.9	100%	4e-08	85%	gi|675737963|XP_002807699.3
☐	PREDICTED: cholinesterase [Nomascus leucogenys]	57.5	57.5	100%	5e-08	85%	gi|332214651|XP_003256448.1
☐	PREDICTED: cholinesterase-like isoform X1 [Myotis brandtii]	57.1	57.1	100%	7e-08	85%	gi|554526033|XP_005857864.1
☐	Cholinesterase [Myotis brandtii]	57.1	57.1	100%	7e-08	85%	gi|521020653|EPQ02441.1
☐	hypothetical protein EGK_11933 [Macaca mulatta]	56.6	56.6	100%	1e-07	85%	gi|355559896|EHH16624.1
☐	butyrylcholinesterase precursor [Macaca fascicularis]	56.6	56.6	100%	1e-07	85%	gi|290795732|ADD64703.1
☐	cholinesterase precursor [Equus caballus]	56.6	56.6	100%	1e-07	85%	gi|126352540|NP_001075319.1
☐	PREDICTED: cholinesterase-like [Elephantulus edwardii]	56.6	56.6	100%	1e-07	85%	gi|585675683|XP_006890440.1
☐	PREDICTED: cholinesterase [Macaca fascicularis]	56.6	56.6	100%	1e-07	85%	gi|544412493|XP_005546353.1
☐	PREDICTED: cholinesterase isoform X1 [Papio anubis]	56.6	56.6	100%	1e-07	85%	gi|402861047|XP_003894921.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase-like [Maca	56.6	56.6	100%	1e-07	85%	gi|297286482|XP_002808379.1
☐	PREDICTED: cholinesterase [Ictidomys tridecemlineatus]	56.6	56.6	100%	1e-07	85%	gi|532105511|XP_005338342.1
☐	PREDICTED: cholinesterase isoform X2 [Equus przewalskii]	56.6	56.6	100%	1e-07	85%	gi|664725795|XP_008520036.1
☐	PREDICTED: cholinesterase isoform X1 [Equus przewalskii]	56.6	56.6	100%	1e-07	85%	gi|664725793|XP_008520035.1
☐	PREDICTED: cholinesterase isoform X1 [Chlorocebus sabaeus]	56.6	56.6	100%	1e-07	85%	gi|635084154|XP_007970394.1
☐	PREDICTED: cholinesterase [Ceratotherium simum simum]	56.6	56.6	100%	1e-07	85%	gi|478501043|XP_004424836.1
☐	PREDICTED: cholinesterase [Vicugna pacos]	56.2	56.2	100%	1e-07	85%	gi|560956860|XP_006200907.1
☐	PREDICTED: cholinesterase [Camelus ferus]	56.2	56.2	100%	1e-07	85%	gi|560915255|XP_006183885.1
☐	PREDICTED: cholinesterase [Myotis davidii]	54.9	54.9	90%	4e-07	89%	gi|584083219|XP_006761409.1
☐	PREDICTED: cholinesterase [Orycteropus afer afer]	54.9	54.9	100%	4e-07	85%	gi|634870148|XP_007946910.1
☐	PREDICTED: cholinesterase [Tarsius syrichta]	53.7	53.7	100%	1e-06	80%	gi|640826885|XP_008070612.1
☐	PREDICTED: cholinesterase [Otolemur garnettii]	53.2	53.2	100%	1e-06	80%	gi|395843862|XP_003794691.1
☐	PREDICTED: cholinesterase-like isoform 1 [Dasypus novemcinctus	53.2	53.2	100%	1e-06	80%	gi|488587231|XP_004478943.1
☐	PREDICTED: cholinesterase-like [Trichechus manatus latirostris]	53.2	53.2	100%	1e-06	80%	gi|471406477|XP_004384938.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhyd	53.2	53.2	100%	1e-06	80%	gi|38502853|O62761.1
☐	cholinesterase precursor [Felis catus]	53.2	53.2	100%	1e-06	80%	gi|57163907|NP_001009364.1
☐	PREDICTED: cholinesterase isoform X1 [Loxodonta africana]	53.2	53.2	100%	1e-06	80%	gi|731499959|XP_003416305.2
☐	PREDICTED: cholinesterase-like [Panthera tigris altaica]	53.2	53.2	100%	1e-06	80%	gi|591300304|XP_007077117.1
☐	PREDICTED: cholinesterase [Galeopterus variegatus]	52.8	52.8	100%	2e-06	80%	gi|667294272|XP_008578862.1
☐	PREDICTED: cholinesterase-like [Chrysochloris asiatica]	52.8	52.8	100%	2e-06	80%	gi|586462448|XP_006861862.1

☐	PREDICTED: cholinesterase-like [Echinops telfairi]	52.8	52.8	100%	2e-06	80%	gi|507651638|XP_004704160.1
☐	PREDICTED: cholinesterase [Ursus maritimus]	52.4	52.4	95%	3e-06	79%	gi|670999264|XP_008690527.1
☐	PREDICTED: cholinesterase [Rhinopithecus roxellana]	51.5	51.5	100%	5e-06	80%	gi|724956944|XP_010353594.1
☐	PREDICTED: cholinesterase isoform X2 [Heterocephalus glaber]	51.1	51.1	100%	7e-06	80%	gi|512824494|XP_004880401.1
☐	PREDICTED: cholinesterase isoform X1 [Chinchilla lanigera]	51.1	51.1	100%	7e-06	80%	gi|533158554|XP_005393194.1
☐	PREDICTED: cholinesterase isoform X1 [Heterocephalus glaber]	51.1	51.1	100%	7e-06	80%	gi|512824490|XP_004880400.1
☐	PREDICTED: cholinesterase-like isoform X1 [Mustela putorius furo]	51.1	51.1	95%	7e-06	79%	gi|511910148|XP_004774475.1
☐	PREDICTED: cholinesterase isoform X2 [Cavia porcellus]	50.7	50.7	100%	1e-05	75%	gi|514460083|XP_005003514.1
☐	hypothetical protein PANDA_007095 [Ailuropoda melanoleuca]	50.7	50.7	95%	1e-05	79%	gi|281337784|EFB13368.1
☐	PREDICTED: cholinesterase isoform X1 [Cavia porcellus]	50.7	50.7	100%	1e-05	75%	gi|348567235|XP_003469406.1
☐	PREDICTED: cholinesterase-like [Ailuropoda melanoleuca]	50.7	50.7	95%	1e-05	79%	gi|301766374|XP_002918607.1
☐	Cholinesterase [Pteropus alecto]	50.3	50.3	100%	1e-05	80%	gi|431915168|ELK15855.1
☐	PREDICTED: cholinesterase [Pteropus alecto]	50.3	50.3	100%	1e-05	80%	gi|586546267|XP_006908236.1
☐	PREDICTED: cholinesterase [Sarcophilus harrisii]	49.0	49.0	90%	4e-05	78%	gi|395528220|XP_003766229.1
☐	PREDICTED: cholinesterase isoform X1 [Peromyscus maniculatus	49.0	49.0	100%	4e-05	75%	gi|589919054|XP_006972718.1
☐	PREDICTED: cholinesterase [Fukomys damarensis]	48.6	48.6	100%	5e-05	75%	gi|731199055|XP_010610068.1
☐	Cholinesterase [Fukomys damarensis]	48.6	48.6	100%	5e-05	75%	gi|676283600|KFO36750.1
☐	PREDICTED: cholinesterase-like [Odobenus rosmarus divergens]	48.1	48.1	90%	7e-05	78%	gi|472347065|XP_004393257.1
☐	PREDICTED: cholinesterase [Jaculus jaculus]	47.7	47.7	100%	9e-05	75%	gi|507536796|XP_004652429.1
☐	PREDICTED: cholinesterase-like [Sorex araneus]	47.3	47.3	95%	1e-04	74%	gi|505845607|XP_004616283.1
☐	PREDICTED: cholinesterase [Cricetulus griseus]	47.3	47.3	100%	1e-04	75%	gi|354496810|XP_003510518.1
☐	Butyrylcholinesterase [Mus musculus]	46.9	46.9	100%	2e-04	75%	gi|71534030|AAH99977.1
☐	butyrylcholinesterase [Mus musculus]	46.9	46.9	100%	2e-04	75%	gi|191580|AAA37328.1
☐	cholinesterase precursor [Mus musculus]	46.9	46.9	100%	2e-04	75%	gi|124487350|NP_033868.3
☐	cholinesterase precursor [Rattus norvegicus]	46.4	46.4	100%	2e-04	75%	gi|12621110|NP_075231.1
☐	PREDICTED: cholinesterase isoform X1 [Rattus norvegicus]	46.4	46.4	100%	2e-04	75%	gi|672042750|XP_008759334.1
☐	PREDICTED: cholinesterase-like [Octodon degus]	45.6	45.6	100%	5e-04	70%	gi|507706867|XP_004646055.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylcholinesterase

Sequence ID: gi|393715367|pdb|4AQD|A **Length:** 531 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 478 to 497 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(155)	6e-12	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPNETQNNSTSWPVFKS  20
            KYGNPNETQNNSTSWPVFKS
Sbjct  478  KYGNPNETQNNSTSWPVFKS  497
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

monomeric butyrylcholinesterase [synthetic construct]

Sequence ID: gi|388261124|gb|AFK25766.1| **Length:** 557 **Number of Matches:** 1

Related Information

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(155)	6e-12	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPNETQNNSTSWPVFKS  20
            KYGNPNETQNNSTSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Co-Crystallization Studies Of Full Length Recombinant Bche With Cocaine Offers Insights Into Cocaine Detoxification

Sequence ID: gi|328877250|pdb|3O9M|A **Length:** 574 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 476 to 495 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(155)	6e-12	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPNETQNNSTSWPVFKS  20
            KYGNPNETQNNSTSWPVFKS
Sbjct  476  KYGNPNETQNNSTSWPVFKS  495
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]

Sequence ID: gi|632795270|gb|AHZ34327.1| **Length:** 602 **Number of Matches:** 1

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(155)	6e-12	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPNETQNNSTSWPVFKS  20
            KYGNPNETQNNSTSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Related Information

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

cholinesterase precursor [Homo sapiens]

Sequence ID: gi|4557351|ref|NP_000046.1| **Length:** 602 **Number of Matches:** 1

▷ See 10 more title(s)

Range 1: 504 to 523 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(155)	6e-12	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KYGNPNETQNNSTSWPVFKS  20
            KYGNPNETQNNSTSWPVFKS
Sbjct  504  KYGNPNETQNNSTSWPVFKS  523
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Structure - 3D structure displays

PubChem BioAssay - bioactivity screening

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

BCHE_RDDYTKAEEILSRS_Mod

RID BHK7FBBM014 (Expires on 01-17 15:33 pm)

Query ID	lcl|85898	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	14		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

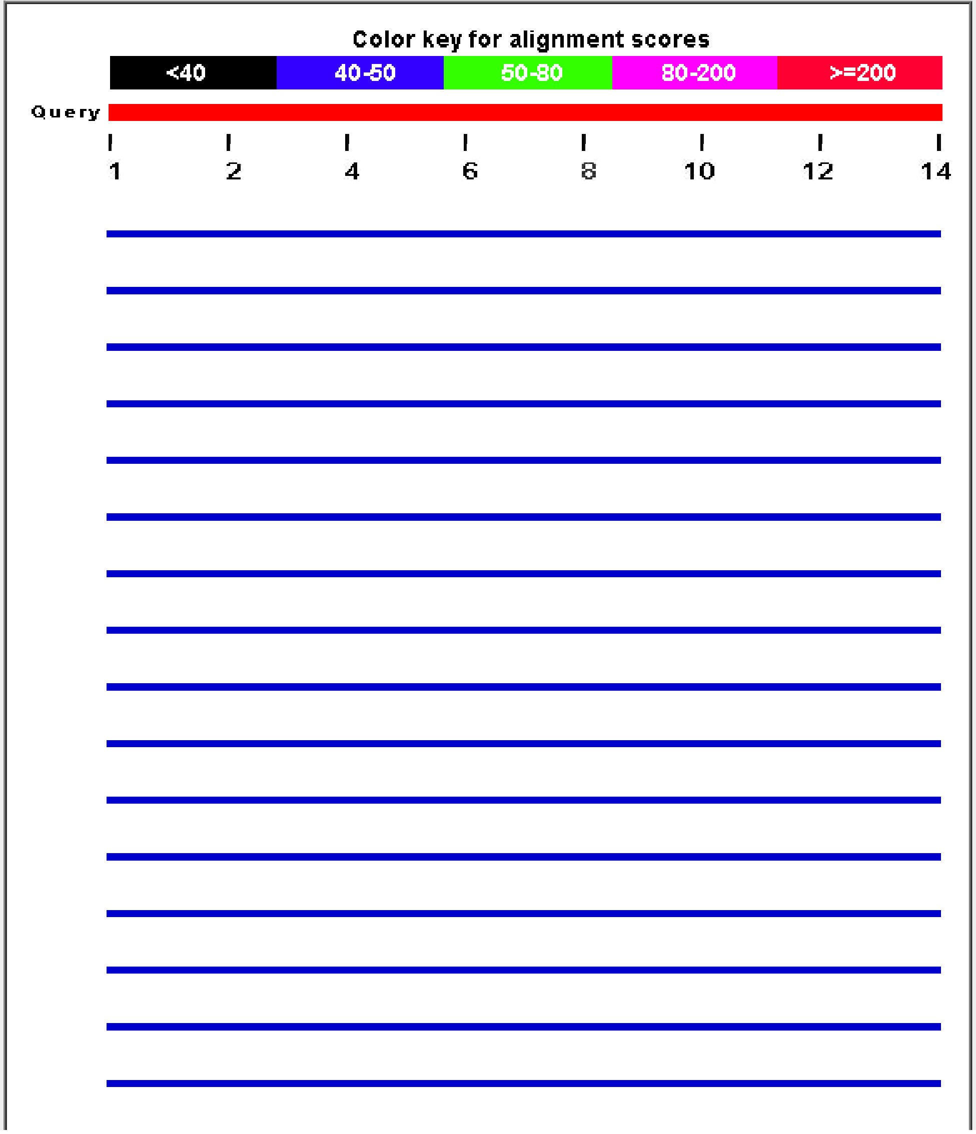
Graphic Summary

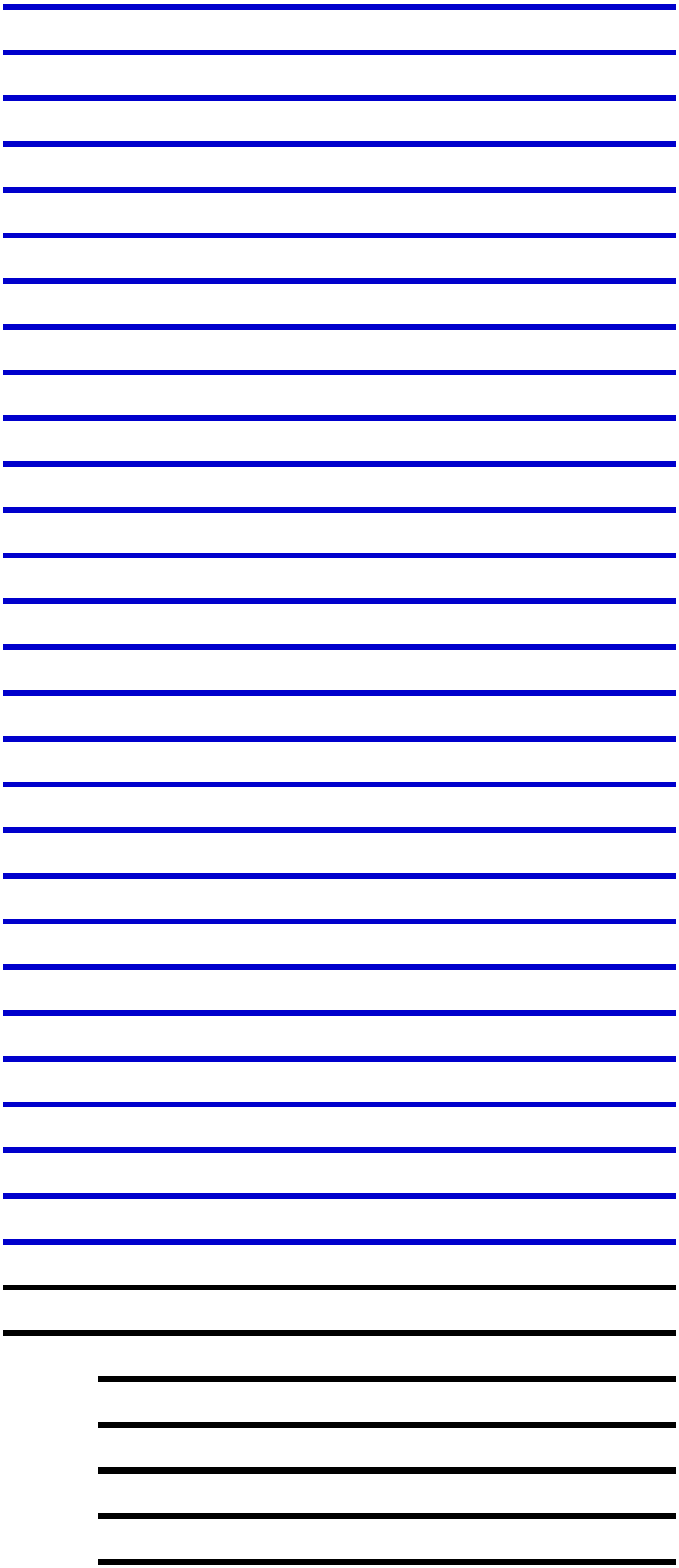
Show Conserved Domains

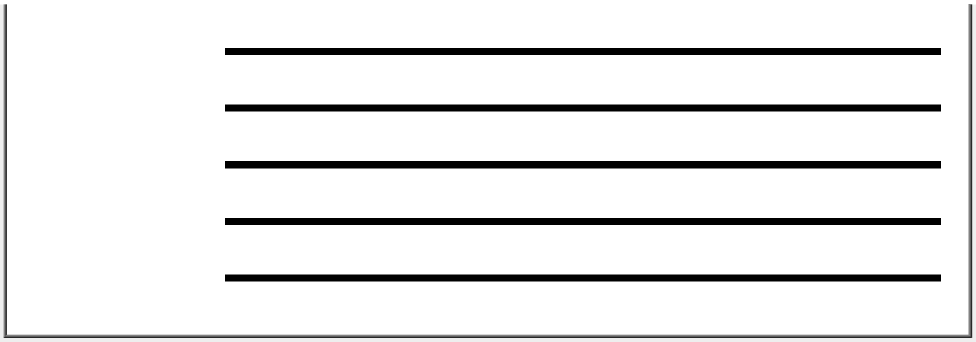
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	cholinesterase precursor [Pan troglodytes]	45.2	45.2	100%	3e-04	93%	gi|343960913|BAK62046.1
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	45.2	45.2	100%	3e-04	93%	gi|237823652|2WIL_A
☐	Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylchol	45.2	45.2	100%	3e-04	93%	gi|393715367|4AQD_A
☐	monomeric butyrylcholinesterase [synthetic construct]	45.2	45.2	100%	3e-04	93%	gi|388261124|AFK25766.1
☐	Chain A, Co-Crystallization Studies Of Full Length Recombinant Bc	45.2	45.2	100%	3e-04	93%	gi|328877250|3O9M_A
☐	butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|632795270|AHZ34327.1
☐	cholinesterase precursor [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|4557351|NP_000046.1
☐	unnamed protein product [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|158257558|BAF84752.1
☐	butyrylcholinesterase [synthetic construct]	45.2	45.2	100%	4e-04	93%	gi|260766471|ACX50257.1
☐	PREDICTED: cholinesterase [Gorilla gorilla gorilla]	45.2	45.2	100%	4e-04	93%	gi|426342776|XP_004038010.1
☐	PREDICTED: cholinesterase [Pan paniscus]	45.2	45.2	100%	4e-04	93%	gi|397493718|XP_003817746.1
☐	PREDICTED: cholinesterase isoform X1 [Homo sapiens]	45.2	45.2	100%	4e-04	93%	gi|530375091|XP_005247742.1
☐	PREDICTED: cholinesterase [Pan troglodytes]	45.2	45.2	100%	4e-04	93%	gi|114590210|XP_516857.2
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholineste	43.5	43.5	100%	0.001	93%	gi|402550232|4AXB_A
☐	Chain A, X-Ray Structure Of Human Butyrylcholinesterase Inhibitec	43.5	43.5	100%	0.001	93%	gi|326634060|2XQF_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	43.5	43.5	100%	0.001	93%	gi|258588213|2WSL_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	43.5	43.5	100%	0.001	93%	gi|215794636|3DJY_A
☐	Chain A, Crystal Structure Of Human Butyryl Cholinesterase [Homo	43.5	43.5	100%	0.001	93%	gi|34810859|1P0I_A
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholineste	43.5	43.5	100%	0.001	93%	gi|402550237|4B0O_A
☐	Chain A, Structure Of Human Butyrylcholinesterase Inhibited By Cb	43.5	43.5	100%	0.001	93%	gi|340707403|2Y1K_A
☐	Chain A, G117h Mutant Of Human Butyrylcholinesterase In Comple	43.5	43.5	100%	0.001	93%	gi|313103512|2XMB_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	43.5	43.5	100%	0.001	93%	gi|237823648|2WIF_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	43.5	43.5	100%	0.001	93%	gi|237823647|2WID_A
☐	Chain A, Structure Of Human Butyrylcholinesterase In Complex Wit	43.5	43.5	100%	0.001	93%	gi|145579736|2J4C_A
☐	Chain A, Crystal Structure Of Recombinant Full Length Human Buty	43.5	43.5	100%	0.001	93%	gi|158429456|2PM8_A
☐	PREDICTED: cholinesterase isoform X3 [Heterocephalus glaber]	42.6	42.6	100%	0.002	86%	gi|512824498|XP_004880402.1
☐	PREDICTED: cholinesterase isoform X2 [Heterocephalus glaber]	42.6	42.6	100%	0.002	86%	gi|512824494|XP_004880401.1
☐	PREDICTED: cholinesterase isoform X1 [Heterocephalus glaber]	42.6	42.6	100%	0.002	86%	gi|512824490|XP_004880400.1
☐							

	cholinesterase precursor [Pongo abelii]	41.4	41.4	100%	0.007	86%	gi|197097436|NP_001127509.1
☐	PREDICTED: cholinesterase isoform X1 [Pongo abelii]	41.4	41.4	100%	0.007	86%	gi|686714306|XP_009237773.1
☐	PREDICTED: cholinesterase isoform X2 [Sus scrofa]	40.5	40.5	100%	0.012	86%	gi|545864567|XP_005670020.1
☐	PREDICTED: cholinesterase-like isoform X2 [Mustela putorius furo]	40.5	40.5	100%	0.013	86%	gi|511910151|XP_004774476.1
☐	PREDICTED: cholinesterase [Nestor notabilis]	40.5	40.5	100%	0.013	86%	gi|701300599|XP_010010752.1
☐	PREDICTED: cholinesterase [Eptesicus fuscus]	40.5	40.5	100%	0.013	86%	gi|641703485|XP_008140478.1
☐	hypothetical protein PANDA_007095 [Ailuropoda melanoleuca]	40.5	40.5	100%	0.013	86%	gi|281337784|EFB13368.1
☐	PREDICTED: cholinesterase [Canis lupus familiaris]	40.5	40.5	100%	0.013	86%	gi|74003707|XP_545267.2
☐	PREDICTED: cholinesterase-like [Leptonychotes weddellii]	40.5	40.5	100%	0.013	86%	gi|585150385|XP_006727664.1
☐	PREDICTED: cholinesterase isoform X1 [Sus scrofa]	40.5	40.5	100%	0.013	86%	gi|335299867|XP_003358712.1
☐	PREDICTED: cholinesterase isoform X2 [Saimiri boliviensis bolivier	40.5	40.5	100%	0.013	86%	gi|725560928|XP_010334003.1
☐	PREDICTED: cholinesterase-like [Odobenus rosmarus divergens]	40.5	40.5	100%	0.013	86%	gi|472347065|XP_004393257.1
☐	PREDICTED: cholinesterase [Ursus maritimus]	40.5	40.5	100%	0.013	86%	gi|670999264|XP_008690527.1
☐	PREDICTED: cholinesterase-like isoform X1 [Mustela putorius furo]	40.5	40.5	100%	0.013	86%	gi|511910148|XP_004774475.1
☐	PREDICTED: cholinesterase isoform X1 [Saimiri boliviensis bolivier	40.5	40.5	100%	0.013	86%	gi|403265619|XP_003925023.1
☐	PREDICTED: cholinesterase-like [Ailuropoda melanoleuca]	40.5	40.5	100%	0.013	86%	gi|301766374|XP_002918607.1
☐	PREDICTED: cholinesterase isoform X2 [Loxodonta africana]	38.8	38.8	100%	0.045	86%	gi|731499961|XP_010594355.1
☐	PREDICTED: cholinesterase isoform X1 [Loxodonta africana]	38.8	38.8	100%	0.046	86%	gi|731499959|XP_003416305.2
☐	PREDICTED: cholinesterase [Balearica pavonina gibbericeps]	38.4	38.4	85%	0.062	92%	gi|723546565|XP_010296638.1
☐	PREDICTED: cholinesterase [Phaethon lepturus]	38.4	38.4	85%	0.062	92%	gi|723122346|XP_010287090.1
☐	PREDICTED: cholinesterase [Tyto alba]	38.4	38.4	85%	0.062	92%	gi|701367577|XP_009962519.1
☐	PREDICTED: cholinesterase [Gavia stellata]	38.4	38.4	85%	0.062	92%	gi|698412479|XP_009811650.1
☐	PREDICTED: cholinesterase [Cariama cristata]	38.4	38.4	85%	0.062	92%	gi|698406540|XP_009708153.1
☐	PREDICTED: cholinesterase [Phalacrocorax carbo]	38.4	38.4	85%	0.062	92%	gi|695141055|XP_009513025.1
☐	PREDICTED: cholinesterase [Merops nubicus]	38.4	38.4	85%	0.062	92%	gi|675619693|XP_008937822.1
☐	cholinesterase precursor [Camelus ferus]	38.4	38.4	85%	0.062	92%	gi|528762213|EPY81872.1
☐	PREDICTED: cholinesterase-like [Tursiops truncatus]	38.4	38.4	85%	0.062	92%	gi|470638951|XP_004324597.1
☐	PREDICTED: cholinesterase isoform X2 [Chinchilla lanigera]	38.4	38.4	85%	0.062	92%	gi|533158556|XP_005393195.1
☐	PREDICTED: cholinesterase isoform X2 [Struthio camelus australis	38.4	38.4	85%	0.062	92%	gi|697458921|XP_009666837.1
☐	PREDICTED: cholinesterase isoform X4 [Monodelphis domestica]	38.4	38.4	85%	0.062	92%	gi|612048246|XP_007502328.1
☐	PREDICTED: cholinesterase isoform X3 [Monodelphis domestica]	38.4	38.4	85%	0.062	92%	gi|612048244|XP_007502327.1
☐	PREDICTED: cholinesterase isoform X4 [Pelodiscus sinensis]	38.4	38.4	85%	0.062	92%	gi|558163876|XP_006123483.1
☐	PREDICTED: cholinesterase-like [Physeter catodon]	38.4	38.4	85%	0.062	92%	gi|593755372|XP_007116545.1
☐	PREDICTED: cholinesterase isoform X2 [Chlorocebus sabaeus]	38.4	38.4	85%	0.063	92%	gi|635084156|XP_007970395.1
☐	PREDICTED: cholinesterase isoform X3 [Equus przewalskii]	38.4	38.4	85%	0.063	92%	gi|664725797|XP_008520037.1
☐	PREDICTED: cholinesterase isoform X3 [Pelodiscus sinensis]	38.4	38.4	85%	0.063	92%	gi|558163871|XP_006123482.1
☐	PREDICTED: cholinesterase isoform X1 [Monodelphis domestica]	38.4	38.4	85%	0.063	92%	gi|612048240|XP_007502325.1
☐	hypothetical protein EGK_11933 [Macaca mulatta]	38.4	38.4	85%	0.063	92%	gi|355559896|EHH16624.1
☐	PREDICTED: cholinesterase-like isoform X5 [Anas platyrhynchos]	38.4	38.4	85%	0.063	92%	gi|514757148|XP_005022245.1
☐	PREDICTED: cholinesterase isoform X2 [Cavia porcellus]	38.4	38.4	85%	0.063	92%	gi|514460083|XP_005003514.1
☐	PREDICTED: cholinesterase isoform X3 [Meleagris gallopavo]	38.4	38.4	85%	0.063	92%	gi|733903684|XP_010715271.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhyd	38.4	38.4	85%	0.063	92%	gi|116354|P21927.1
☐	PREDICTED: cholinesterase isoform X2 [Meleagris gallopavo]	38.4	38.4	85%	0.063	92%	gi|733903681|XP_010715270.1
☐	PREDICTED: cholinesterase [Erinaceus europaeus]	38.4	38.4	85%	0.063	92%	gi|617605262|XP_007523705.1
☐	PREDICTED: cholinesterase [Tauraco erythrolophus]	38.4	38.4	85%	0.063	92%	gi|701378853|XP_009987847.1

☐	PREDICTED: cholinesterase [Manacus vitellinus]	38.4	38.4	85%	0.063	92%	gi|675428698|XP_008928282.1
☐	PREDICTED: cholinesterase [Oryctolagus cuniculus]	38.4	38.4	85%	0.063	92%	gi|291400118|XP_002716414.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus dromedarius]	38.4	38.4	85%	0.063	92%	gi|744553709|XP_010974642.1
☐	PREDICTED: cholinesterase isoform X1 [Camelus dromedarius]	38.4	38.4	85%	0.063	92%	gi|744553706|XP_010974641.1
☐	PREDICTED: cholinesterase isoform X2 [Camelus bactrianus]	38.4	38.4	85%	0.063	92%	gi|743713601|XP_010950371.1
☐	PREDICTED: cholinesterase isoform X1 [Struthio camelus australis	38.4	38.4	85%	0.063	92%	gi|697458918|XP_009666836.1
☐	butyrylcholinesterase precursor [Macaca fascicularis]	38.4	38.4	85%	0.063	92%	gi|290795732|ADD64703.1
☐	cholinesterase precursor [Equus caballus]	38.4	38.4	85%	0.063	92%	gi|126352540|NP_001075319.1
☐	PREDICTED: cholinesterase-like [Elephantulus edwardii]	38.4	38.4	85%	0.063	92%	gi|585675683|XP_006890440.1
☐	PREDICTED: cholinesterase [Vicugna pacos]	38.4	38.4	85%	0.063	92%	gi|560956860|XP_006200907.1
☐	PREDICTED: cholinesterase [Camelus ferus]	38.4	38.4	85%	0.063	92%	gi|560915255|XP_006183885.1
☐	PREDICTED: cholinesterase [Macaca fascicularis]	38.4	38.4	85%	0.063	92%	gi|544412493|XP_005546353.1
☐	PREDICTED: cholinesterase isoform X1 [Chinchilla lanigera]	38.4	38.4	85%	0.063	92%	gi|533158554|XP_005393194.1
☐	PREDICTED: cholinesterase-like [Melopsittacus undulatus]	38.4	38.4	85%	0.063	92%	gi|527262631|XP_005149550.1
☐	PREDICTED: cholinesterase-like isoform X4 [Anas platyrhynchos]	38.4	38.4	85%	0.063	92%	gi|514757144|XP_005022244.1
☐	PREDICTED: cholinesterase-like [Trichechus manatus latirostris]	38.4	38.4	85%	0.063	92%	gi|471406477|XP_004384938.1
☐	PREDICTED: cholinesterase [Orcinus orca]	38.4	38.4	85%	0.063	92%	gi|466076197|XP_004283487.1
☐	Cholinesterase [Pteropus alecto]	38.4	38.4	85%	0.063	92%	gi|431915168|ELK15855.1
☐	PREDICTED: cholinesterase [Sarcophilus harrisii]	38.4	38.4	85%	0.063	92%	gi|395528220|XP_003766229.1
☐	PREDICTED: cholinesterase isoform X1 [Cavia porcellus]	38.4	38.4	85%	0.063	92%	gi|348567235|XP_003469406.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase-like [Maca	38.4	38.4	85%	0.063	92%	gi|297286482|XP_002808379.1
☐	PREDICTED: cholinesterase [Ornithorhynchus anatinus]	38.4	38.4	85%	0.063	92%	gi|149633332|XP_001505841.1
☐	PREDICTED: cholinesterase isoform X1 [Meleagris gallopavo]	38.4	38.4	85%	0.063	92%	gi|733903673|XP_010715267.1
☐	PREDICTED: cholinesterase [Mesitornis unicolor]	38.4	38.4	85%	0.063	92%	gi|704565301|XP_010183737.1
☐	PREDICTED: cholinesterase [Caprimulgus carolinensis]	38.4	38.4	85%	0.063	92%	gi|704284800|XP_010173273.1
☐	PREDICTED: cholinesterase [Eurypyga helias]	38.4	38.4	85%	0.063	92%	gi|704257918|XP_010150053.1
☐	PREDICTED: cholinesterase [Buceros rhinoceros silvestris]	38.4	38.4	85%	0.063	92%	gi|704196237|XP_010140664.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

cholinesterase precursor [Pan troglodytes]

Sequence ID: gi|343960913|dbj|BAK62046.1| **Length:** 494 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 373 to 386 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.2 bits(99)	3e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    RDDYTKAEEILSRS  14
            RD+YTKAEEILSRS
Sbjct  373  RDNYTKAEEILSRS  386
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By Tabun Analogue Ta5

Sequence ID: gi|237823652|pdb|2WIL|A **Length:** 529 **Number of Matches:** 1

▶ See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 453 to 466 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.2 bits(99)	3e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    RDDYTKAEEILSRS  14
            RD+YTKAEEILSRS
Sbjct  453  RDNYTKAEEILSRS  466
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylcholinesterase

Sequence ID: gi|393715367|pdb|4AQD|A **Length:** 531 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 455 to 468 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.2 bits(99)	3e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    RDDYTKAEEILSRS  14
            RD+YTKAEEILSRS
Sbjct  455  RDNYTKAEEILSRS  468
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

monomeric butyrylcholinesterase [synthetic construct]

Sequence ID: gi|388261124|gb|AFK25766.1| **Length:** 557 **Number of Matches:** 1

Related Information

Range 1: 481 to 494 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.2 bits(99)	3e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    RDDYTKAEEILSRS  14
            RD+YTKAEEILSRS
Sbjct  481  RDNYTKAEEILSRS  494
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Co-Crystallization Studies Of Full Length Recombinant Bche With Cocaine Offers Insights Into Cocaine Detoxification

Sequence ID: gi|328877250|pdb|3O9M|A **Length:** 574 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 453 to 466 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.2 bits(99)	3e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    RDDYTKAEEILSRS  14
            RD+YTKAEEILSRS
Sbjct  453  RDNYTKAEEILSRS  466
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - B926MR7C01R

Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

BCHE_RDNYTKAEEILSRS_NonMod

RID	B926MR7C01R (Expires on 01-14 09:54 am)		
Query ID	lcl|158420	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	14	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

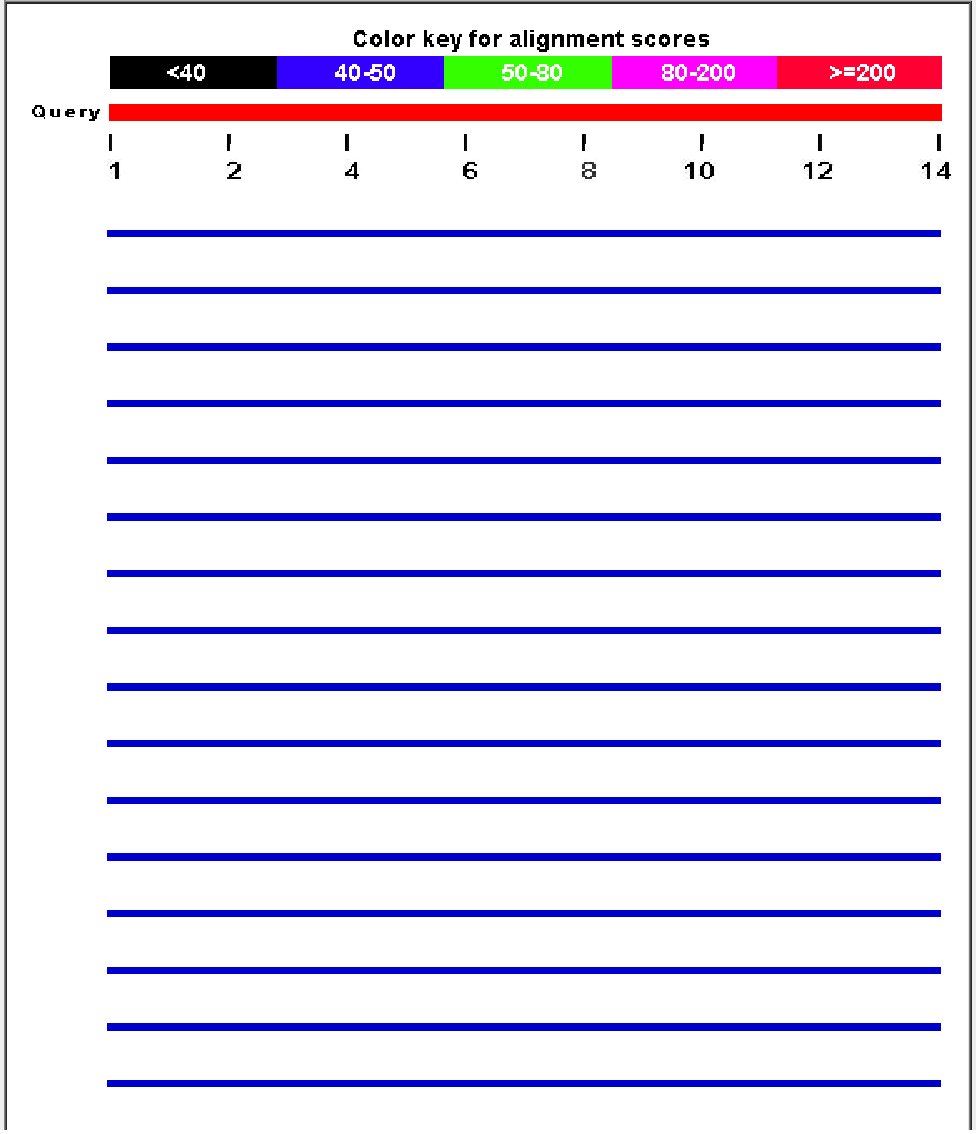
Graphic Summary

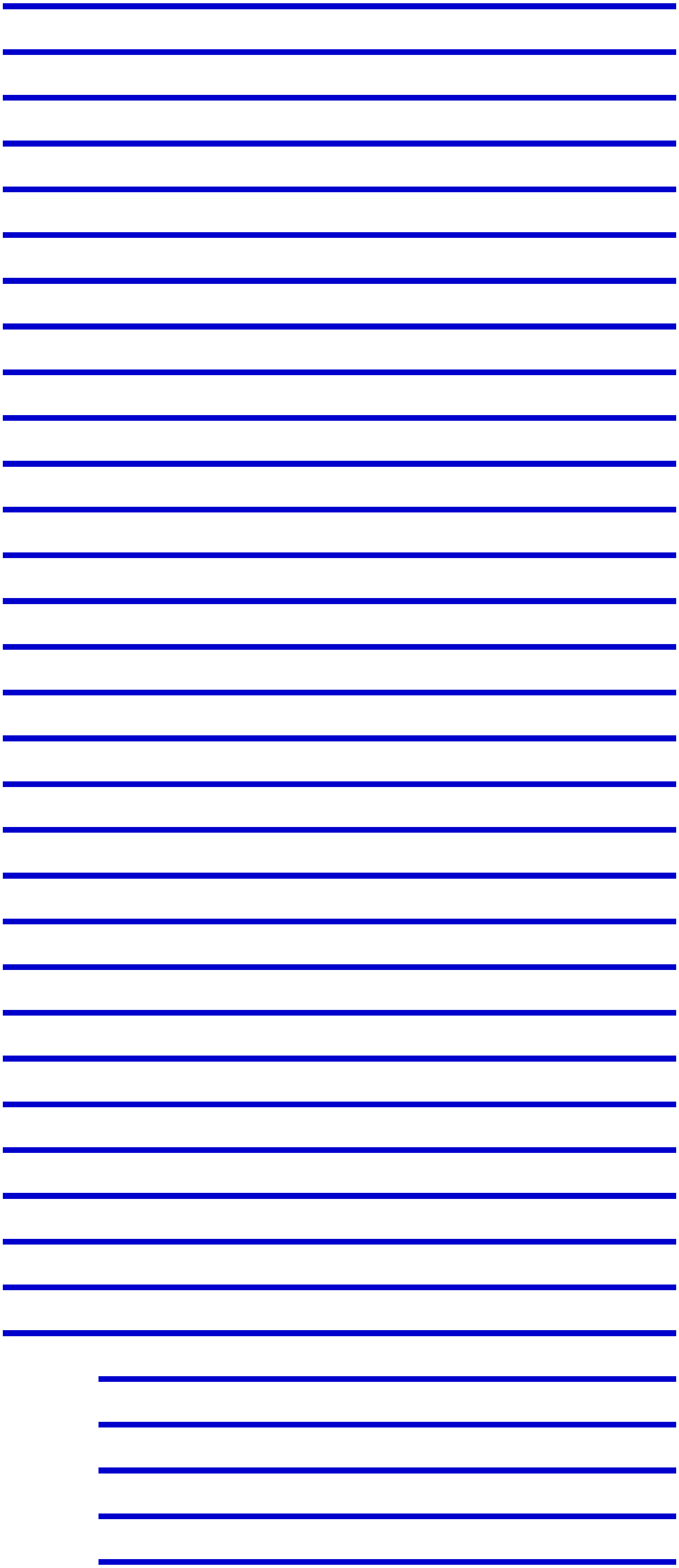
Show Conserved Domains

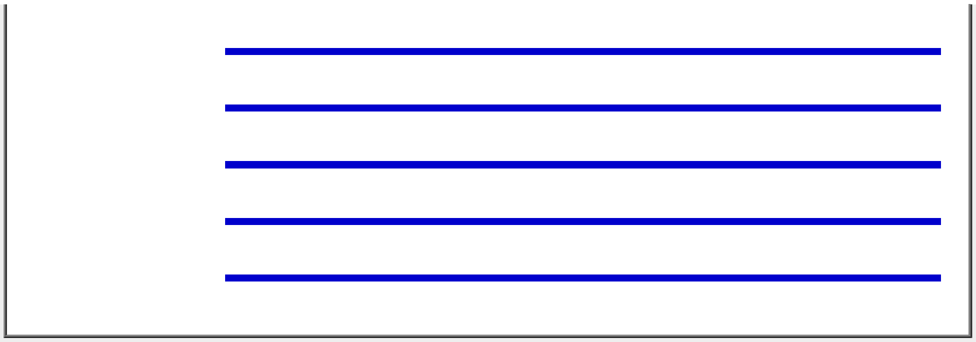
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	cholinesterase precursor [Pan troglodytes]	47.7	47.7	100%	5e-05	100%	gi|343960913|BAK62046.1
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	47.7	47.7	100%	5e-05	100%	gi|237823652|2WIL_A
☐	Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylchol	47.7	47.7	100%	5e-05	100%	gi|393715367|4AQD_A
☐	monomeric butyrylcholinesterase [synthetic construct]	47.7	47.7	100%	5e-05	100%	gi|388261124|AFK25766.1
☐	Chain A, Co-Crystallization Studies Of Full Length Recombinant Bc	47.7	47.7	100%	5e-05	100%	gi|328877250|3O9M_A
☐	butyrylcholinesterase p.Val204Asp splice variant [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|632795270|AHZ34327.1
☐	cholinesterase precursor [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|4557351|NP_000046.1
☐	unnamed protein product [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|158257558|BAF84752.1
☐	butyrylcholinesterase [synthetic construct]	47.7	47.7	100%	5e-05	100%	gi|260766471|ACX50257.1
☐	PREDICTED: cholinesterase [Gorilla gorilla gorilla]	47.7	47.7	100%	5e-05	100%	gi|426342776|XP_004038010.1
☐	PREDICTED: cholinesterase [Pan paniscus]	47.7	47.7	100%	5e-05	100%	gi|397493718|XP_003817746.1
☐	PREDICTED: cholinesterase isoform X1 [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|530375091|XP_005247742.1
☐	PREDICTED: cholinesterase [Pan troglodytes]	47.7	47.7	100%	5e-05	100%	gi|114590210|XP_516857.2
☐	PREDICTED: cholinesterase isoform X3 [Heterocephalus glaber]	45.2	45.2	100%	3e-04	93%	gi|512824498|XP_004880402.1
☐	PREDICTED: cholinesterase isoform X2 [Heterocephalus glaber]	45.2	45.2	100%	3e-04	93%	gi|512824494|XP_004880401.1
☐	PREDICTED: cholinesterase isoform X1 [Heterocephalus glaber]	45.2	45.2	100%	3e-04	93%	gi|512824490|XP_004880400.1
☐	cholinesterase precursor [Pongo abelii]	43.9	43.9	100%	9e-04	93%	gi|197097436|NP_001127509.1
☐	PREDICTED: cholinesterase isoform X1 [Pongo abelii]	43.9	43.9	100%	9e-04	93%	gi|686714306|XP_009237773.1
☐	PREDICTED: cholinesterase isoform X2 [Sus scrofa]	43.1	43.1	100%	0.002	93%	gi|545864567|XP_005670020.1
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholineste	43.1	43.1	100%	0.002	93%	gi|402550232|4AXB_A
☐	Chain A, X-Ray Structure Of Human Butyrylcholinesterase Inhibited	43.1	43.1	100%	0.002	93%	gi|326634060|2XQF_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	43.1	43.1	100%	0.002	93%	gi|258588213|2WSL_A
☐	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited I	43.1	43.1	100%	0.002	93%	gi|215794636|3DJY_A
☐	Chain A, Crystal Structure Of Human Butyryl Cholinesterase [Homo	43.1	43.1	100%	0.002	93%	gi|34810859|1P0I_A
☐	Chain A, Crystal Structure Of Soman-aged Human Butyrylcholineste	43.1	43.1	100%	0.002	93%	gi|402550237|4B0O_A
☐	Chain A, Structure Of Human Butyrylcholinesterase Inhibited By Cb	43.1	43.1	100%	0.002	93%	gi|340707403|2Y1K_A
☐	Chain A, G117h Mutant Of Human Butyrylcholinesterase In Comple	43.1	43.1	100%	0.002	93%	gi|313103512|2XMB_A
☐	Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By T	43.1	43.1	100%	0.002	93%	gi|237823648|2WIF_A
☐							

	Chain A, Nonaged Form Of Human Butyrylcholinesterase Inhibited	43.1	43.1	100%	0.002	93%	gi|237823647|2WID_A
☐	Chain A, Structure Of Human Butyrylcholinesterase In Complex Wit	43.1	43.1	100%	0.002	93%	gi|145579736|2J4C_A
☐	PREDICTED: cholinesterase-like isoform X2 [Mustela putorius furo]	43.1	43.1	100%	0.002	93%	gi|511910151|XP_004774476.1
☐	Chain A, Crystal Structure Of Recombinant Full Length Human Buty	43.1	43.1	100%	0.002	93%	gi|158429456|2PM8_A
☐	PREDICTED: cholinesterase [Nestor notabilis]	43.1	43.1	100%	0.002	93%	gi|701300599|XP_010010752.1
☐	PREDICTED: cholinesterase [Eptesicus fuscus]	43.1	43.1	100%	0.002	93%	gi|641703485|XP_008140478.1
☐	hypothetical protein PANDA_007095 [Ailuropoda melanoleuca]	43.1	43.1	100%	0.002	93%	gi|281337784|EFB13368.1
☐	PREDICTED: cholinesterase [Canis lupus familiaris]	43.1	43.1	100%	0.002	93%	gi|74003707|XP_545267.2
☐	PREDICTED: cholinesterase-like [Leptonychotes weddellii]	43.1	43.1	100%	0.002	93%	gi|585150385|XP_006727664.1
☐	PREDICTED: cholinesterase isoform X1 [Sus scrofa]	43.1	43.1	100%	0.002	93%	gi|335299867|XP_003358712.1
☐	PREDICTED: cholinesterase isoform X2 [Saimiri boliviensis bolivier	43.1	43.1	100%	0.002	93%	gi|725560928|XP_010334003.1
☐	PREDICTED: cholinesterase-like [Odobenus rosmarus divergens]	43.1	43.1	100%	0.002	93%	gi|472347065|XP_004393257.1
☐	PREDICTED: cholinesterase [Ursus maritimus]	43.1	43.1	100%	0.002	93%	gi|670999264|XP_008690527.1
☐	PREDICTED: cholinesterase-like isoform X1 [Mustela putorius furo]	43.1	43.1	100%	0.002	93%	gi|511910148|XP_004774475.1
☐	PREDICTED: cholinesterase isoform X1 [Saimiri boliviensis bolivier	43.1	43.1	100%	0.002	93%	gi|403265619|XP_003925023.1
☐	PREDICTED: cholinesterase-like [Ailuropoda melanoleuca]	43.1	43.1	100%	0.002	93%	gi|301766374|XP_002918607.1
☐	PREDICTED: cholinesterase isoform X2 [Loxodonta africana]	41.4	41.4	100%	0.006	93%	gi|731499961|XP_010594355.1
☐	PREDICTED: cholinesterase isoform X1 [Loxodonta africana]	41.4	41.4	100%	0.006	93%	gi|731499959|XP_003416305.2
☐	PREDICTED: cholinesterase [Balearica pavonina gibbericeps]	40.9	40.9	85%	0.009	100%	gi|723546565|XP_010296638.1
☐	PREDICTED: cholinesterase [Phaethon lepturus]	40.9	40.9	85%	0.009	100%	gi|723122346|XP_010287090.1
☐	PREDICTED: cholinesterase [Tyto alba]	40.9	40.9	85%	0.009	100%	gi|701367577|XP_009962519.1
☐	PREDICTED: cholinesterase [Gavia stellata]	40.9	40.9	85%	0.009	100%	gi|698412479|XP_009811650.1
☐	PREDICTED: cholinesterase [Cariama cristata]	40.9	40.9	85%	0.009	100%	gi|698406540|XP_009708153.1
☐	PREDICTED: cholinesterase [Phalacrocorax carbo]	40.9	40.9	85%	0.009	100%	gi|695141055|XP_009513025.1
☐	PREDICTED: cholinesterase [Merops nubicus]	40.9	40.9	85%	0.009	100%	gi|675619693|XP_008937822.1
☐	cholinesterase precursor [Camelus ferus]	40.9	40.9	85%	0.009	100%	gi|528762213|EPY81872.1
☐	PREDICTED: cholinesterase-like [Tursiops truncatus]	40.9	40.9	85%	0.009	100%	gi|470638951|XP_004324597.1
☐	PREDICTED: cholinesterase isoform X2 [Chinchilla lanigera]	40.9	40.9	85%	0.009	100%	gi|533158556|XP_005393195.1
☐	PREDICTED: cholinesterase isoform X2 [Struthio camelus australis	40.9	40.9	85%	0.009	100%	gi|697458921|XP_009666837.1
☐	PREDICTED: cholinesterase isoform X4 [Monodelphis domestica]	40.9	40.9	85%	0.009	100%	gi|612048246|XP_007502328.1
☐	PREDICTED: cholinesterase isoform X3 [Monodelphis domestica]	40.9	40.9	85%	0.009	100%	gi|612048244|XP_007502327.1
☐	PREDICTED: cholinesterase isoform X4 [Pelodiscus sinensis]	40.9	40.9	85%	0.009	100%	gi|558163876|XP_006123483.1
☐	PREDICTED: cholinesterase-like [Physeter catodon]	40.9	40.9	85%	0.009	100%	gi|593755372|XP_007116545.1
☐	PREDICTED: cholinesterase isoform X2 [Chlorocebus sabaeus]	40.9	40.9	85%	0.009	100%	gi|635084156|XP_007970395.1
☐	PREDICTED: cholinesterase isoform X3 [Equus przewalskii]	40.9	40.9	85%	0.009	100%	gi|664725797|XP_008520037.1
☐	PREDICTED: cholinesterase isoform X3 [Pelodiscus sinensis]	40.9	40.9	85%	0.009	100%	gi|558163871|XP_006123482.1
☐	PREDICTED: cholinesterase isoform X1 [Monodelphis domestica]	40.9	40.9	85%	0.009	100%	gi|612048240|XP_007502325.1
☐	hypothetical protein EGK_11933 [Macaca mulatta]	40.9	40.9	85%	0.009	100%	gi|355559896|EHH16624.1
☐	PREDICTED: cholinesterase-like isoform X5 [Anas platyrhynchos]	40.9	40.9	85%	0.009	100%	gi|514757148|XP_005022245.1
☐	PREDICTED: cholinesterase isoform X2 [Cavia porcellus]	40.9	40.9	85%	0.009	100%	gi|514460083|XP_005003514.1
☐	PREDICTED: cholinesterase isoform X3 [Meleagris gallopavo]	40.9	40.9	85%	0.009	100%	gi|733903684|XP_010715271.1
☐	RecName: Full=Cholinesterase; AltName: Full=Acylcholine acylhyd	40.9	40.9	85%	0.009	100%	gi|116354|P21927.1
☐	PREDICTED: cholinesterase isoform X2 [Meleagris gallopavo]	40.9	40.9	85%	0.009	100%	gi|733903681|XP_010715270.1
☐	PREDICTED: cholinesterase [Erinaceus europaeus]	40.9	40.9	85%	0.009	100%	gi|617605262|XP_007523705.1
☐	PREDICTED: cholinesterase [Tauraco erythrolophus]	40.9	40.9	85%	0.009	100%	gi|701378853|XP_009987847.1

☐	PREDICTED: cholinesterase [Manacus vitellinus]	40.9	40.9	85%	0.009	100%	gi|675428698|XP_008928282.1
☐	PREDICTED: cholinesterase [Oryctolagus cuniculus]	40.9	40.9	85%	0.009	100%	gi|291400118|XP_002716414.1
☐	PREDICTED: cholinesterase isoform X1 [Struthio camelus australis	40.9	40.9	85%	0.009	100%	gi|697458918|XP_009666836.1
☐	butyrylcholinesterase precursor [Macaca fascicularis]	40.9	40.9	85%	0.009	100%	gi|290795732|ADD64703.1
☐	cholinesterase precursor [Equus caballus]	40.9	40.9	85%	0.009	100%	gi|126352540|NP_001075319.1
☐	PREDICTED: cholinesterase-like [Elephantulus edwardii]	40.9	40.9	85%	0.009	100%	gi|585675683|XP_006890440.1
☐	PREDICTED: cholinesterase [Vicugna pacos]	40.9	40.9	85%	0.009	100%	gi|560956860|XP_006200907.1
☐	PREDICTED: cholinesterase [Camelus ferus]	40.9	40.9	85%	0.009	100%	gi|560915255|XP_006183885.1
☐	PREDICTED: cholinesterase [Macaca fascicularis]	40.9	40.9	85%	0.009	100%	gi|544412493|XP_005546353.1
☐	PREDICTED: cholinesterase isoform X1 [Chinchilla lanigera]	40.9	40.9	85%	0.009	100%	gi|533158554|XP_005393194.1
☐	PREDICTED: cholinesterase-like [Melopsittacus undulatus]	40.9	40.9	85%	0.009	100%	gi|527262631|XP_005149550.1
☐	PREDICTED: cholinesterase-like isoform X4 [Anas platyrhynchos]	40.9	40.9	85%	0.009	100%	gi|514757144|XP_005022244.1
☐	PREDICTED: cholinesterase-like [Trichechus manatus latirostris]	40.9	40.9	85%	0.009	100%	gi|471406477|XP_004384938.1
☐	PREDICTED: cholinesterase [Orcinus orca]	40.9	40.9	85%	0.009	100%	gi|466076197|XP_004283487.1
☐	Cholinesterase [Pteropus alecto]	40.9	40.9	85%	0.009	100%	gi|431915168|ELK15855.1
☐	PREDICTED: cholinesterase [Sarcophilus harrisii]	40.9	40.9	85%	0.009	100%	gi|395528220|XP_003766229.1
☐	PREDICTED: cholinesterase isoform X1 [Cavia porcellus]	40.9	40.9	85%	0.009	100%	gi|348567235|XP_003469406.1
☐	PREDICTED: LOW QUALITY PROTEIN: cholinesterase-like [Maca	40.9	40.9	85%	0.009	100%	gi|297286482|XP_002808379.1
☐	PREDICTED: cholinesterase [Ornithorhynchus anatinus]	40.9	40.9	85%	0.009	100%	gi|149633332|XP_001505841.1
☐	PREDICTED: cholinesterase isoform X1 [Meleagris gallopavo]	40.9	40.9	85%	0.009	100%	gi|733903673|XP_010715267.1
☐	PREDICTED: cholinesterase [Mesitornis unicolor]	40.9	40.9	85%	0.009	100%	gi|704565301|XP_010183737.1
☐	PREDICTED: cholinesterase [Caprimulgus carolinensis]	40.9	40.9	85%	0.009	100%	gi|704284800|XP_010173273.1
☐	PREDICTED: cholinesterase [Eurypyga helias]	40.9	40.9	85%	0.009	100%	gi|704257918|XP_010150053.1
☐	PREDICTED: cholinesterase [Buceros rhinoceros silvestris]	40.9	40.9	85%	0.009	100%	gi|704196237|XP_010140664.1
☐	PREDICTED: cholinesterase [Opisthocomus hoazin]	40.9	40.9	85%	0.009	100%	gi|700395426|XP_009938300.1
☐	PREDICTED: cholinesterase [Haliaeetus albicilla]	40.9	40.9	85%	0.009	100%	gi|700325936|XP_009929114.1
☐	PREDICTED: cholinesterase [Charadrius vociferus]	40.9	40.9	85%	0.009	100%	gi|699662024|XP_009882721.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

cholinesterase precursor [Pan troglodytes]

Sequence ID: gi|343960913|dbj|BAK62046.1| **Length:** 494 **Number of Matches:** 1

Range 1: 373 to 386 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	5e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    RDNYTKAEEILSRS  14
            RDNYTKAEEILSRS
Sbjct  373  RDNYTKAEEILSRS  386
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Aged Form Of Human Butyrylcholinesterase Inhibited By Tabun Analogue Ta5

Sequence ID: gi|237823652|pdb|2WIL|A **Length:** 529 **Number of Matches:** 1

▸ See 1 more title(s)

Range 1: 453 to 466 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	5e-05	14/14(100%)	14/14(100%)	0/14(0%)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

```
Query  1    RDNYTKAEEILSRS  14
            RDNYTKAEEILSRS
Sbjct  453  RDNYTKAEEILSRS  466
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of Fully Glycosylated Human Butyrylcholinesterase

Sequence ID: gi|393715367|pdb|4AQD|A **Length:** 531 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 455 to 468 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	5e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    RDNYTKAEEILSRS  14
            RDNYTKAEEILSRS
Sbjct  455  RDNYTKAEEILSRS  468
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

monomeric butyrylcholinesterase [synthetic construct]

Sequence ID: gi|388261124|gb|AFK25766.1| **Length:** 557 **Number of Matches:** 1

Range 1: 481 to 494 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	5e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    RDNYTKAEEILSRS  14
            RDNYTKAEEILSRS
Sbjct  481  RDNYTKAEEILSRS  494
```

Related Information

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Co-Crystallization Studies Of Full Length Recombinant Bche With Cocaine Offers Insights Into Cocaine Detoxification

Sequence ID: gi|328877250|pdb|3O9M|A **Length:** 574 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 453 to 466 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	5e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    RDNYTKAEEILSRS  14
            RDNYTKAEEILSRS
Sbjct  453  RDNYTKAEEILSRS  466
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BT2YC2WT013**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | You Tube How to read this page | Blast report description

BTD_KDVQIIVFPEDGIHGFDFTRT_Mod

RID BT2YC2WT013 (Expires on 01-20 11:45 am)

Query ID lcl|83420
Description None
Molecule type amino acid
Query Length 21

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

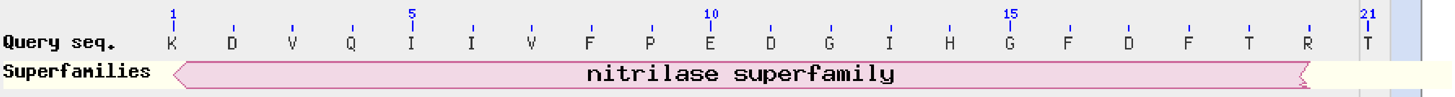
Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

New DELTA-BLAST a more sensitive protein-protein search Go

Graphic Summary

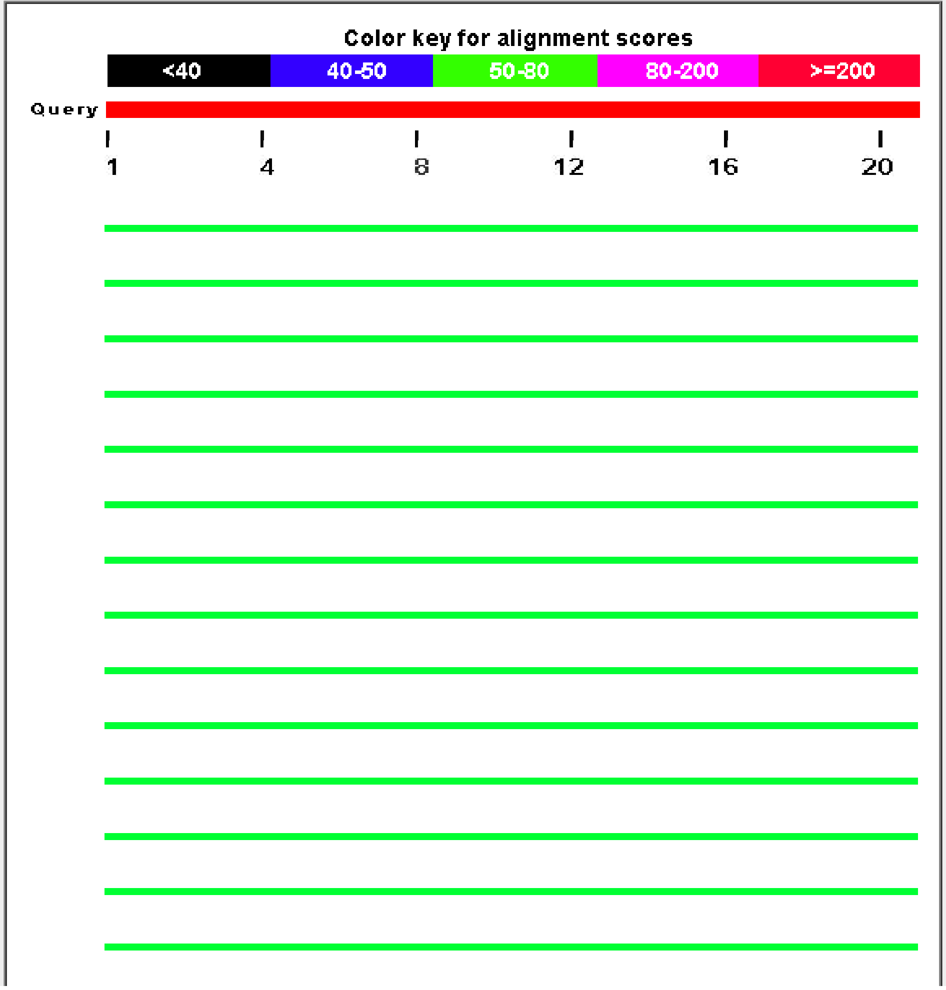
Show Conserved Domains

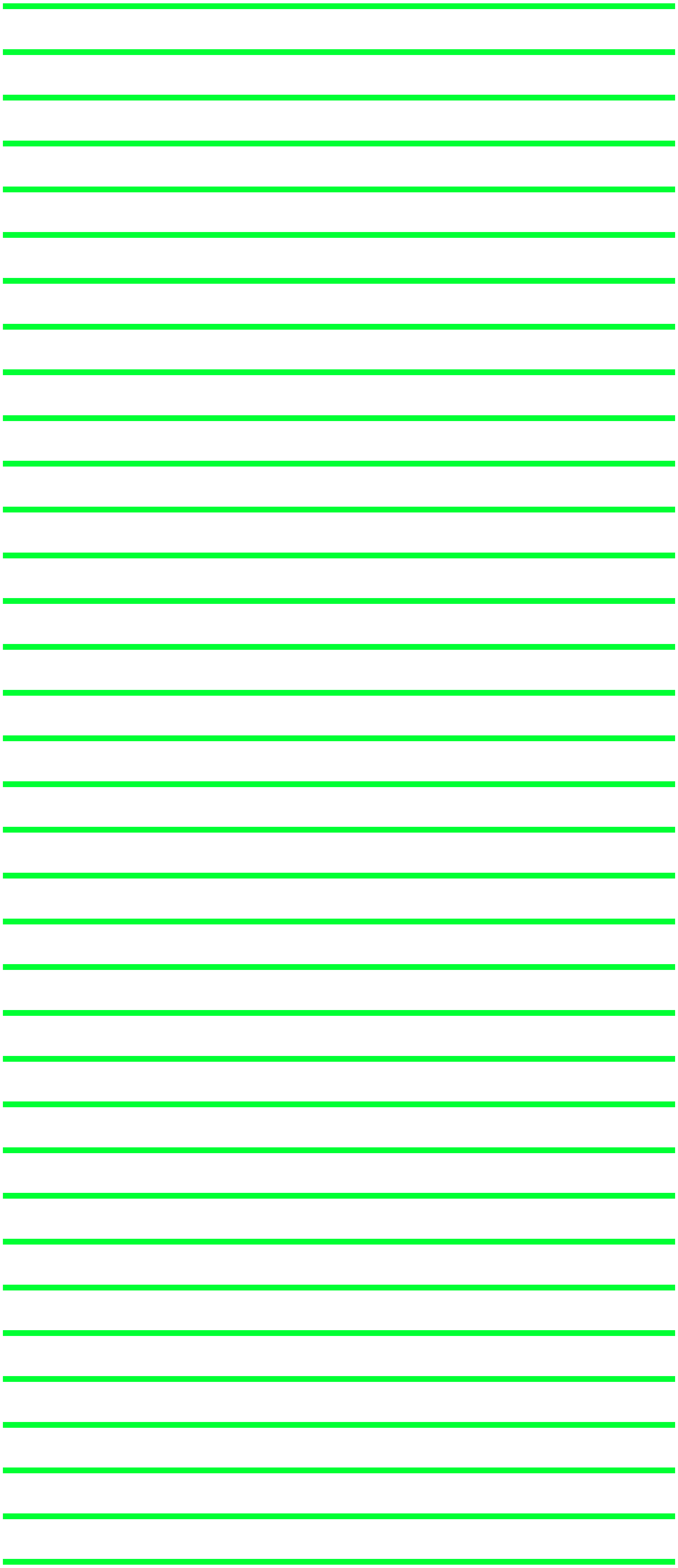
Putative conserved domains have been detected, click on the image below for detailed results.

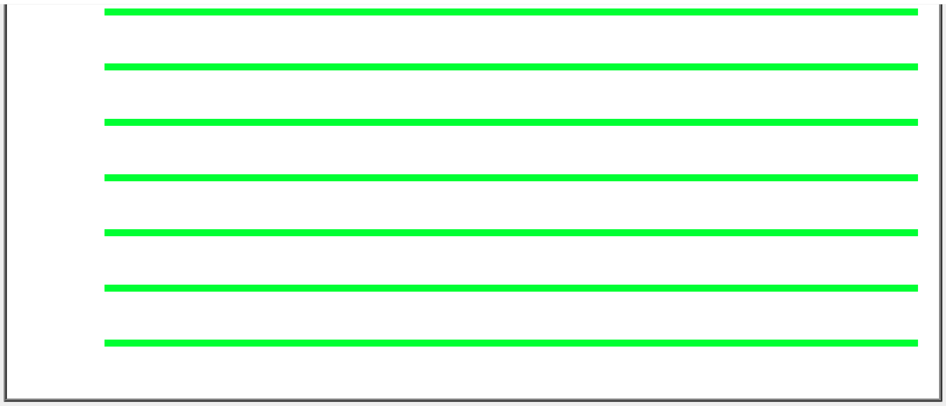


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	biotinidase, isoform CRA_c [Homo sapiens]	69.8	69.8	100%	3e-12	95%	gi|119584660|EAW64256.1
☐	biotinidase isoform 5 [Homo sapiens]	69.8	69.8	100%	3e-12	95%	gi|528524488|NP_001268655.1
☐	unnamed protein product [Homo sapiens]	69.8	69.8	100%	4e-12	95%	gi|221043776|BAH13565.1
☐	biotinidase isoform 4 precursor [Homo sapiens]	69.8	69.8	100%	4e-12	95%	gi|528524486|NP_001268654.1
☐	biotinidase precursor [Pan troglodytes]	69.8	69.8	100%	4e-12	95%	gi|697993457|NP_001289363.1
☐	PREDICTED: biotinidase isoform 1 [Gorilla gorilla gorilla]	69.8	69.8	100%	4e-12	95%	gi|426339607|XP_004033737.1
☐	PREDICTED: biotinidase isoform X2 [Pan troglodytes]	69.8	69.8	100%	4e-12	95%	gi|694900420|XP_009443239.1
☐	PREDICTED: biotinidase isoform X2 [Pan paniscus]	69.8	69.8	100%	4e-12	95%	gi|675784344|XP_008949921.1
☐	PREDICTED: biotinidase isoform 3 [Gorilla gorilla gorilla]	69.8	69.8	100%	4e-12	95%	gi|426339611|XP_004033739.1
☐	PREDICTED: biotinidase isoform 4 [Gorilla gorilla gorilla]	69.8	69.8	100%	4e-12	95%	gi|426339613|XP_004033740.1
☐	biotinidase isoform 3 [Homo sapiens]	69.8	69.8	100%	4e-12	95%	gi|4557373|NP_000051.1
☐	biotinidase isoform 1 [Homo sapiens]	69.8	69.8	100%	4e-12	95%	gi|528524481|NP_001268652.1
☐	biotinidase isoform 2 [Homo sapiens]	69.8	69.8	100%	4e-12	95%	gi|528524483|NP_001268653.1
☐	PREDICTED: biotinidase isoform 2 [Gorilla gorilla gorilla]	69.8	69.8	100%	4e-12	95%	gi|426339609|XP_004033738.1
☐	PREDICTED: biotinidase isoform X1 [Pan troglodytes]	69.8	69.8	100%	4e-12	95%	gi|410036604|XP_003950087.1
☐	PREDICTED: biotinidase isoform X1 [Pan paniscus]	69.8	69.8	100%	4e-12	95%	gi|397511808|XP_003826257.1
☐	PREDICTED: biotinidase-like isoform X10 [Chinchilla lanigera]	65.1	65.1	100%	2e-10	90%	gi|533146084|XP_005387502.1
☐	unnamed protein product [Macaca fascicularis]	65.1	65.1	100%	2e-10	90%	gi|90077268|BAE88314.1
☐	PREDICTED: biotinidase [Oryctolagus cuniculus]	65.1	65.1	100%	2e-10	90%	gi|655852029|XP_008264256.1
☐	PREDICTED: biotinidase [Nannospalax galili]	65.1	65.1	100%	2e-10	90%	gi|674081213|XP_008848205.1
☐	RecName: Full=Biotinidase; Short=Biotinase; Flags: Precursor	65.1	65.1	100%	2e-10	90%	gi|150421524|Q8CIF4.2
☐	PREDICTED: biotinidase [Rhinopithecus roxellana]	65.1	65.1	100%	2e-10	90%	gi|724960396|XP_010354361.1
☐	PREDICTED: biotinidase isoform X2 [Ursus maritimus]	65.1	65.1	100%	2e-10	90%	gi|670981874|XP_008707139.1
☐	PREDICTED: biotinidase [Galeopterus variegatus]	65.1	65.1	100%	2e-10	90%	gi|667288263|XP_008576771.1
☐	PREDICTED: biotinidase [Jaculus jaculus]	65.1	65.1	100%	2e-10	90%	gi|507555213|XP_004661377.1
☐	PREDICTED: biotinidase isoform X2 [Microtus ochrogaster]	65.1	65.1	100%	2e-10	90%	gi|532009812|XP_005348714.1
☐	PREDICTED: biotinidase isoform X2 [Peromyscus maniculatus	65.1	65.1	100%	2e-10	90%	gi|589967610|XP_006996306.1
☐	PREDICTED: biotinidase-like isoform X5 [Chinchilla lanigera]	65.1	65.1	100%	2e-10	90%	gi|533146074|XP_005387497.1

☐	PREDICTED: biotinidase [Mesocricetus auratus]	65.1	65.1	100%	2e-10	90%	gi|524955500|XP_005077724.1
☐	PREDICTED: biotinidase isoform X2 [Chlorocebus sabaeus]	65.1	65.1	100%	2e-10	90%	gi|635085523|XP_008007381.1
☐	PREDICTED: biotinidase isoform X2 [Physeter catodon]	65.1	65.1	100%	2e-10	90%	gi|593711507|XP_007102308.1
☐	PREDICTED: biotinidase isoform X4 [Canis lupus familiaris]	65.1	65.1	100%	2e-10	90%	gi|545538859|XP_005634450.1
☐	PREDICTED: biotinidase isoform X3 [Equus caballus]	65.1	65.1	100%	2e-10	90%	gi|545189350|XP_005600979.1
☐	PREDICTED: biotinidase isoform X2 [Macaca fascicularis]	65.1	65.1	100%	2e-10	90%	gi|544411158|XP_005545768.1
☐	PREDICTED: biotinidase isoform X1 [Cavia porcellus]	65.1	65.1	100%	2e-10	90%	gi|514481133|XP_003480063.2
☐	PREDICTED: biotinidase [Ceratotherium simum simum]	65.1	65.1	100%	2e-10	90%	gi|478490156|XP_004419451.1
☐	PREDICTED: biotinidase isoform 2 [Odobenus rosmarus diverg	65.1	65.1	100%	2e-10	90%	gi|472379495|XP_004409157.1
☐	PREDICTED: LOW QUALITY PROTEIN: biotinidase [Tursiops	65.1	65.1	100%	2e-10	90%	gi|470628904|XP_004321284.1
☐	PREDICTED: biotinidase [Orcinus orca]	65.1	65.1	100%	2e-10	90%	gi|466019817|XP_004271983.1
☐	PREDICTED: biotinidase isoform X3 [Saimiri boliviensis bolivie	65.1	65.1	100%	2e-10	90%	gi|725560828|XP_010333963.1
☐	PREDICTED: biotinidase isoform X2 [Papio anubis]	65.1	65.1	100%	2e-10	90%	gi|685527526|XP_009200021.1
☐	PREDICTED: biotinidase isoform X3 [Pongo abelii]	65.1	65.1	100%	2e-10	90%	gi|686713703|XP_009237577.1
☐	biotinidase precursor [Mus musculus]	65.1	65.1	100%	2e-10	90%	gi|13384648|NP_079571.1
☐	Biotinidase [Heterocephalus glaber]	65.1	65.1	100%	2e-10	90%	gi|351707565|EHB10484.1
☐	PREDICTED: biotinidase isoform X1 [Ursus maritimus]	65.1	65.1	100%	2e-10	90%	gi|670981872|XP_008707130.1
☐	PREDICTED: biotinidase [Equus przewalskii]	65.1	65.1	100%	2e-10	90%	gi|664753751|XP_008534346.1
☐	PREDICTED: biotinidase isoform X1 [Chlorocebus sabaeus]	65.1	65.1	100%	2e-10	90%	gi|635085521|XP_008007380.1
☐	PREDICTED: biotinidase isoform X1 [Felis catus]	65.1	65.1	100%	2e-10	90%	gi|587000359|XP_003992187.2
☐	PREDICTED: biotinidase isoform X2 [Felis catus]	65.1	65.1	100%	2e-10	90%	gi|587000357|XP_006936495.1
☐	PREDICTED: biotinidase isoform X3 [Leptonychotes weddellii]	65.1	65.1	100%	2e-10	90%	gi|585186600|XP_006744787.1
☐	PREDICTED: biotinidase isoform X2 [Leptonychotes weddellii]	65.1	65.1	100%	2e-10	90%	gi|585186598|XP_006744786.1
☐	PREDICTED: biotinidase isoform X3 [Canis lupus familiaris]	65.1	65.1	100%	2e-10	90%	gi|545538857|XP_005634449.1
☐	PREDICTED: biotinidase isoform X2 [Canis lupus familiaris]	65.1	65.1	100%	2e-10	90%	gi|545538855|XP_005634448.1
☐	PREDICTED: biotinidase isoform X2 [Equus caballus]	65.1	65.1	100%	2e-10	90%	gi|545189348|XP_005600978.1
☐	PREDICTED: biotinidase [Mustela putorius furo]	65.1	65.1	100%	2e-10	90%	gi|511908359|XP_004773614.1
☐	PREDICTED: biotinidase isoform 1 [Odobenus rosmarus diverg	65.1	65.1	100%	2e-10	90%	gi|472379493|XP_004409156.1
☐	PREDICTED: biotinidase [Trichechus manatus latirostris]	65.1	65.1	100%	2e-10	90%	gi|471407481|XP_004385327.1
☐	PREDICTED: biotinidase isoform X2 [Saimiri boliviensis bolivie	65.1	65.1	100%	2e-10	90%	gi|403265544|XP_003924991.1
☐	PREDICTED: biotinidase-like [Ailuropoda melanoleuca]	65.1	65.1	100%	2e-10	90%	gi|301759093|XP_002915396.1
☐	PREDICTED: biotinidase [Condylura cristata]	65.1	65.1	100%	2e-10	90%	gi|507976256|XP_004692357.1
☐	PREDICTED: biotinidase [Fukomys damarensis]	65.1	65.1	100%	2e-10	90%	gi|731285322|XP_010611073.1
☐	PREDICTED: biotinidase isoform X2 [Pongo abelii]	65.1	65.1	100%	2e-10	90%	gi|686713701|XP_009237576.1
☐	PREDICTED: biotinidase isoform X1 [Cricetulus griseus]	65.1	65.1	100%	2e-10	90%	gi|354465853|XP_003495391.1
☐	PREDICTED: biotinidase [Orycteropus afer afer]	65.1	65.1	100%	2e-10	90%	gi|634822252|XP_007934900.1
☐	PREDICTED: biotinidase isoform X1 [Physeter catodon]	65.1	65.1	100%	2e-10	90%	gi|593711505|XP_007102307.1
☐	PREDICTED: biotinidase-like isoform X1 [Chinchilla lanigera]	65.1	65.1	100%	2e-10	90%	gi|533146066|XP_005387493.1
☐	PREDICTED: biotinidase isoform X3 [Heterocephalus glaber]	65.1	65.1	100%	2e-10	90%	gi|512886961|XP_004896459.1
☐	PREDICTED: biotinidase isoform X1 [Leptonychotes weddellii]	65.1	65.1	100%	2e-10	90%	gi|585186596|XP_006744785.1
☐	PREDICTED: biotinidase isoform X1 [Canis lupus familiaris]	65.1	65.1	100%	2e-10	90%	gi|545538853|XP_005634447.1
☐	PREDICTED: biotinidase [Otolemur garnettii]	65.1	65.1	100%	2e-10	90%	gi|395816560|XP_003781769.1
☐	PREDICTED: biotinidase isoform X1 [Pongo abelii]	65.1	65.1	100%	2e-10	90%	gi|395734130|XP_003776360.1
☐	hypothetical protein EGM_11114 [Macaca fascicularis]	65.1	65.1	100%	2e-10	90%	gi|355747075|EHH51689.1
☐	hypothetical protein EGK_12122 [Macaca mulatta]	65.1	65.1	100%	2e-10	90%	gi|355560049|EHH16777.1
☐	PREDICTED: biotinidase isoform X1 [Microtus ochrogaster]	65.1	65.1	100%	2e-10	90%	gi|532009810|XP_005348713.1

☐	PREDICTED: biotinidase isoform X1 [Equus caballus]	65.1	65.1	100%	2e-10	90%	gi|545189346|XP_005600977.1
☐	PREDICTED: biotinidase isoform X2 [Cavia porcellus]	65.1	65.1	100%	2e-10	90%	gi|514481131|XP_005008361.1
☐	PREDICTED: biotinidase isoform X1 [Saimiri boliviensis bolivie	65.1	65.1	100%	2e-10	90%	gi|725560825|XP_010333962.1
☐	PREDICTED: biotinidase [Lipotes vexillifer]	65.1	65.1	100%	2e-10	90%	gi|602721076|XP_007470691.1
☐	PREDICTED: biotinidase isoform X1 [Heterocephalus glaber]	65.1	65.1	100%	2e-10	90%	gi|512886949|XP_004896457.1
☐	PREDICTED: biotinidase isoform X1 [Balaenoptera acutorostra	65.1	65.1	100%	2e-10	90%	gi|594624940|XP_007167058.1
☐	PREDICTED: biotinidase isoform X1 [Papio anubis]	65.1	65.1	100%	2e-10	90%	gi|685527524|XP_009200020.1
☐	PREDICTED: biotinidase isoform X1 [Macaca fascicularis]	65.1	65.1	100%	2e-10	90%	gi|544411156|XP_005545767.1
☐	PREDICTED: biotinidase isoform X3 [Balaenoptera acutorostra	65.1	65.1	100%	2e-10	90%	gi|594624944|XP_007167060.1
☐	PREDICTED: biotinidase-like [Octodon degus]	65.1	65.1	100%	2e-10	90%	gi|507646799|XP_004631734.1
☐	PREDICTED: biotinidase [Nomascus leucogenys]	63.4	63.4	90%	6e-10	95%	gi|332232450|XP_003265417.1
☐	PREDICTED: biotinidase isoform X2 [Cricetulus griseus]	63.4	63.4	90%	6e-10	95%	gi|625181248|XP_007632389.1
☐	PREDICTED: biotinidase isoform X1 [Peromyscus maniculatus	63.4	63.4	90%	6e-10	95%	gi|589967608|XP_006996305.1
☐	PREDICTED: biotinidase isoform X15 [Tupaia chinensis]	63.4	63.4	90%	6e-10	95%	gi|562886680|XP_006170761.1
☐	PREDICTED: biotinidase isoform X4 [Tupaia chinensis]	63.4	63.4	90%	6e-10	95%	gi|562886658|XP_006170750.1
☐	unnamed protein product [Mus musculus]	63.4	63.4	90%	6e-10	95%	gi|74183082|BAE22509.1
☐	PREDICTED: biotinidase [Panthera tigris altaica]	63.4	63.4	90%	6e-10	95%	gi|591322659|XP_007087428.1
☐	PREDICTED: biotinidase [Macaca mulatta]	63.4	63.4	90%	6e-10	95%	gi|297286947|XP_001083201.2
☐	PREDICTED: biotinidase isoform X3 [Tupaia chinensis]	63.4	63.4	90%	6e-10	95%	gi|562886656|XP_006170749.1
☐	Biotinidase [Fukomys damarensis]	63.4	63.4	90%	6e-10	95%	gi|676263045|KFO19807.1
☐	biotinidase [Cricetulus griseus]	63.4	63.4	90%	6e-10	95%	gi|537261432|ERE90059.1
☐	PREDICTED: biotinidase isoform X2 [Tupaia chinensis]	63.4	63.4	90%	6e-10	95%	gi|562886654|XP_006170748.1
☐	PREDICTED: biotinidase isoform X1 [Tupaia chinensis]	63.4	63.4	90%	6e-10	95%	gi|562886652|XP_006170747.1
☐	PREDICTED: biotinidase-like isoform X2 [Sus scrofa]	62.1	62.1	95%	2e-09	90%	gi|545860928|XP_005669335.1
☐	PREDICTED: biotinidase-like isoform X1 [Sus scrofa]	62.1	62.1	95%	2e-09	90%	gi|350590965|XP_003483176.1
☐	PREDICTED: biotinidase-like isoform X1 [Sus scrofa]	62.1	62.1	95%	2e-09	90%	gi|350590959|XP_003483174.1

⊖ Alignments

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biotinidase, isoform CRA_c [Homo sapiens]

Sequence ID: gi|119584660|gb|EAW64256.1| **Length:** 159 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 83 to 103 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.8 bits(157)	3e-12	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KDVQIIVFPEDGIHGFDFTRT  21
            KDVQIIVFPEDGIHGF+FTRT
Sbjct  83   KDVQIIVFPEDGIHGFNFTRT  103
```

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biotinidase isoform 5 [Homo sapiens]

Sequence ID: gi|528524488|ref|NP_001268655.1| **Length:** 179 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 103 to 123 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.8 bits(157)	3e-12	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KDVQIIVFPEDGIHGFDFTRT  21
            KDVQIIVFPEDGIHGF+FTRT
Sbjct  103  KDVQIIVFPEDGIHGFNFTRT  123
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221043776|dbj|BAH13565.1| **Length:** 523 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 83 to 103 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.8 bits(157)	4e-12	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KDVQIIVFPEDGIHGFDFTRT  21
            KDVQIIVFPEDGIHGF+FTRT
Sbjct  83   KDVQIIVFPEDGIHGFNFTRT  103
```

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biotinidase isoform 4 precursor [Homo sapiens]

Sequence ID: gi|528524486|ref|NP_001268654.1| **Length:** 523 **Number of Matches:** 1

▷ See 3 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 83 to 103 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.8 bits(157)	4e-12	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KDVQIIVFPEDGIHGFDFTRT  21
            KDVQIIVFPEDGIHGF+FTRT
Sbjct  83   KDVQIIVFPEDGIHGFNFTRT  103
```

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biotinidase precursor [Pan troglodytes]

Sequence ID: gi|697993457|ref|NP_001289363.1| **Length:** 523 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 83 to 103 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.8 bits(157)	4e-12	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KDVQIIVFPEDGIHGFDFTRT  21
            KDVQIIVFPEDGIHGF+FTRT
Sbjct  83   KDVQIIVFPEDGIHGFNFTRT  103
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

BTD_KDVQIIVFPEDGIHGFNFTRT_NonMod

RID B920AZP301R (Expires on 01-14 09:50 am)

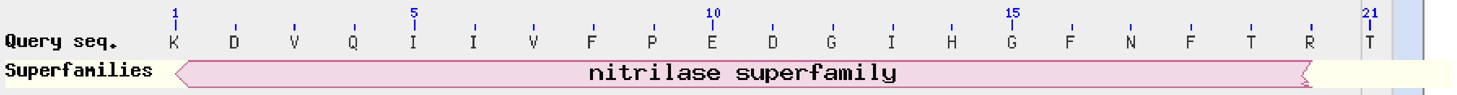
Query ID	lcl|84488	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	21		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

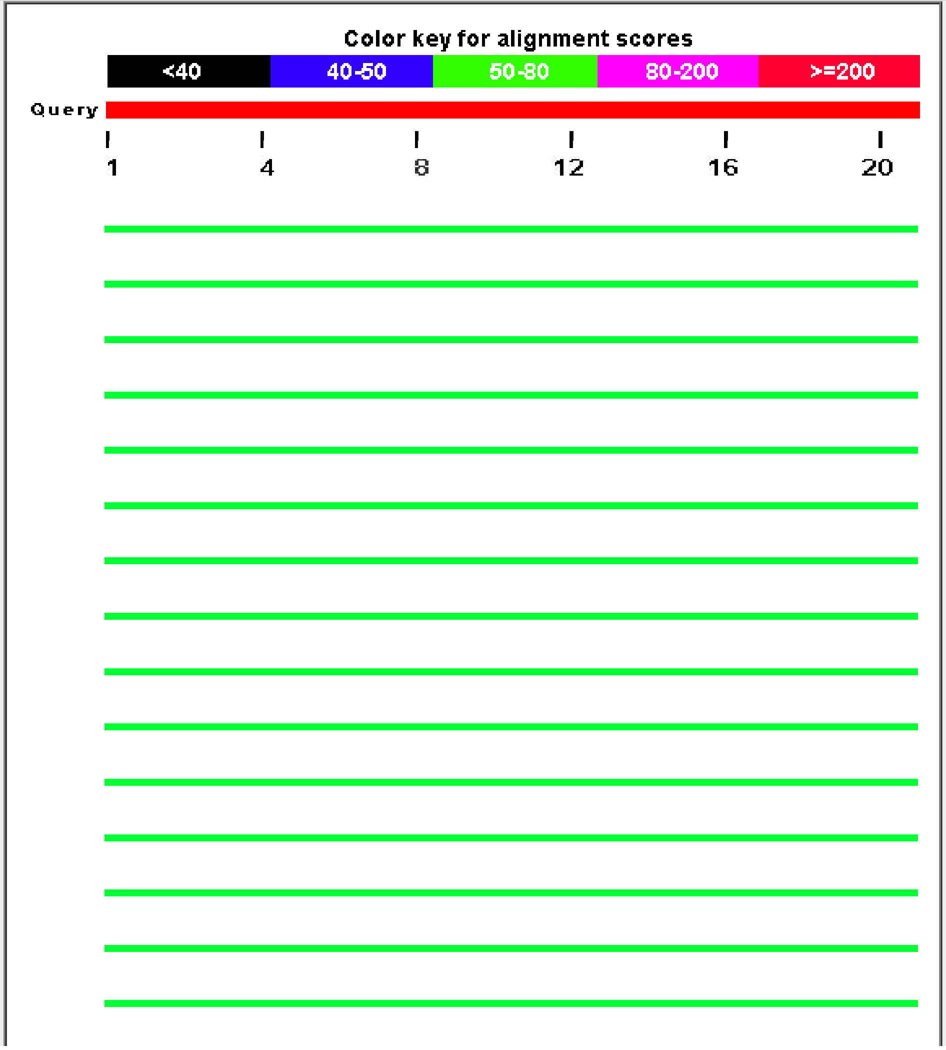
Show Conserved Domains

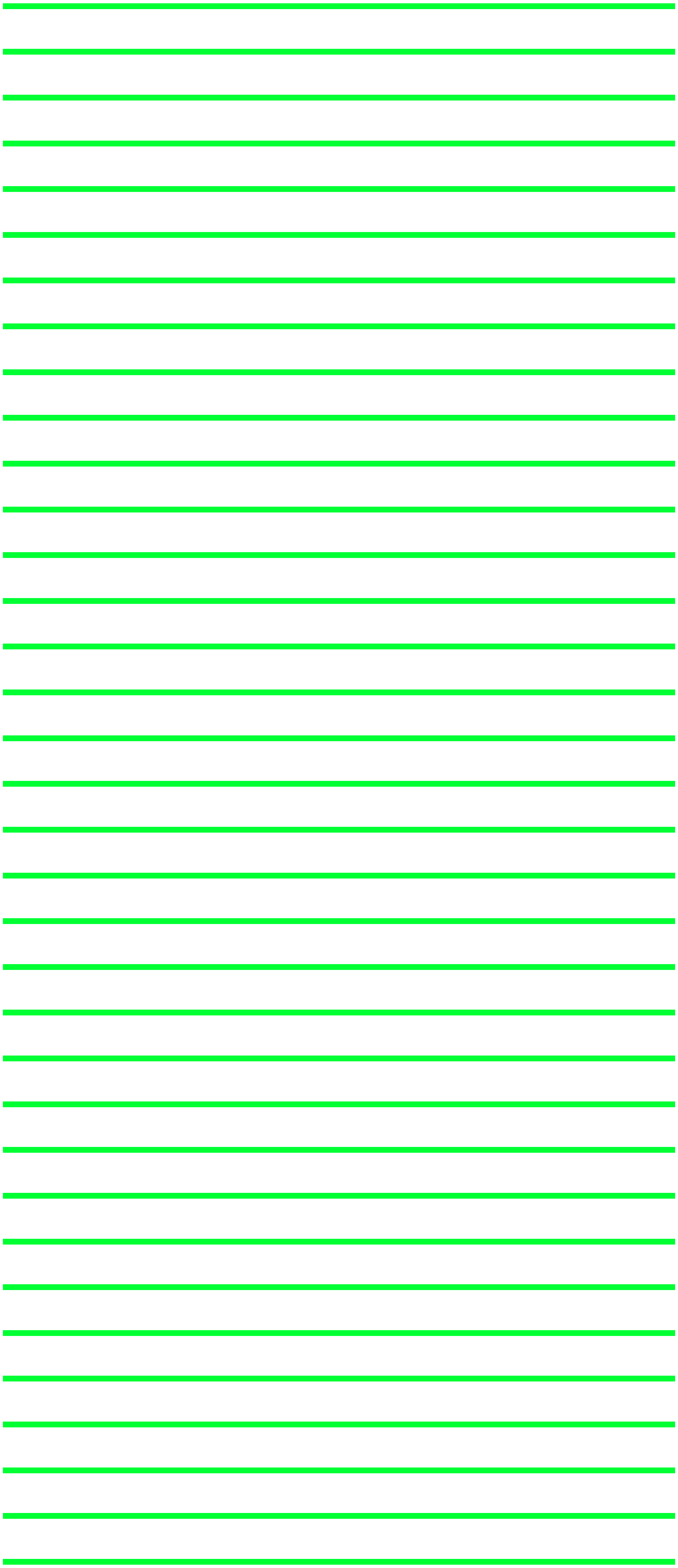
Putative conserved domains have been detected, click on the image below for detailed results.

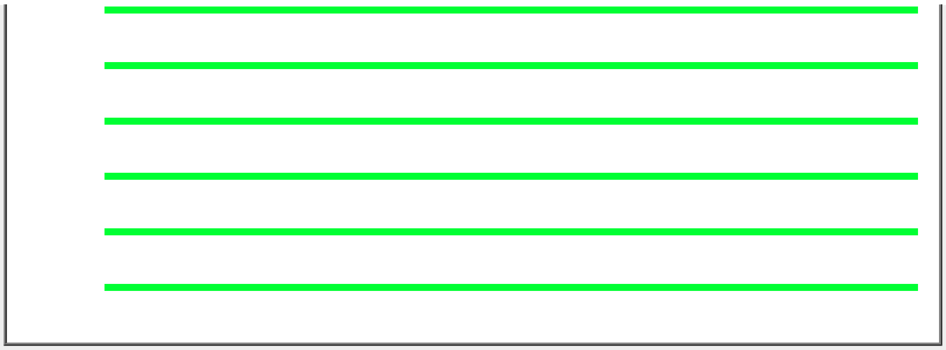


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	biotinidase, isoform CRA_c [Homo sapiens]	72.3	72.3	100%	3e-13	100%	gi|119584660|EAW64256.1
☐	biotinidase isoform 5 [Homo sapiens]	72.3	72.3	100%	3e-13	100%	gi|528524488|NP_001268655.1
☐	unnamed protein product [Homo sapiens]	72.3	72.3	100%	5e-13	100%	gi|221043776|BAH13565.1
☐	biotinidase isoform 4 precursor [Homo sapiens]	72.3	72.3	100%	5e-13	100%	gi|528524486|NP_001268654.1
☐	biotinidase precursor [Pan troglodytes]	72.3	72.3	100%	5e-13	100%	gi|697993457|NP_001289363.1
☐	PREDICTED: biotinidase isoform 1 [Gorilla gorilla gorilla]	72.3	72.3	100%	5e-13	100%	gi|426339607|XP_004033737.1
☐	PREDICTED: biotinidase isoform X2 [Pan troglodytes]	72.3	72.3	100%	5e-13	100%	gi|694900420|XP_009443239.1
☐	PREDICTED: biotinidase isoform X2 [Pan paniscus]	72.3	72.3	100%	5e-13	100%	gi|675784344|XP_008949921.1
☐	PREDICTED: biotinidase isoform 3 [Gorilla gorilla gorilla]	72.3	72.3	100%	5e-13	100%	gi|426339611|XP_004033739.1
☐	PREDICTED: biotinidase isoform 4 [Gorilla gorilla gorilla]	72.3	72.3	100%	5e-13	100%	gi|426339613|XP_004033740.1
☐	biotinidase isoform 3 [Homo sapiens]	72.3	72.3	100%	5e-13	100%	gi|4557373|NP_000051.1
☐	biotinidase isoform 1 [Homo sapiens]	72.3	72.3	100%	5e-13	100%	gi|528524481|NP_001268652.1
☐	biotinidase isoform 2 [Homo sapiens]	72.3	72.3	100%	5e-13	100%	gi|528524483|NP_001268653.1
☐	PREDICTED: biotinidase isoform 2 [Gorilla gorilla gorilla]	72.3	72.3	100%	5e-13	100%	gi|426339609|XP_004033738.1
☐	PREDICTED: biotinidase isoform X1 [Pan troglodytes]	72.3	72.3	100%	5e-13	100%	gi|410036604|XP_003950087.1
☐	PREDICTED: biotinidase isoform X1 [Pan paniscus]	72.3	72.3	100%	5e-13	100%	gi|397511808|XP_003826257.1
☐	PREDICTED: biotinidase-like isoform X10 [Chinchilla lanigera]	67.7	67.7	100%	2e-11	95%	gi|533146084|XP_005387502.1
☐	unnamed protein product [Macaca fascicularis]	67.7	67.7	100%	2e-11	95%	gi|90077268|BAE88314.1
☐	PREDICTED: biotinidase [Oryctolagus cuniculus]	67.7	67.7	100%	2e-11	95%	gi|655852029|XP_008264256.1
☐	PREDICTED: biotinidase [Nannospalax galili]	67.7	67.7	100%	2e-11	95%	gi|674081213|XP_008848205.1
☐	RecName: Full=Biotinidase; Short=Biotinase; Flags: Precursor [Mus	67.7	67.7	100%	2e-11	95%	gi|150421524|Q8CIF4.2
☐	PREDICTED: biotinidase [Rhinopithecus roxellana]	67.7	67.7	100%	2e-11	95%	gi|724960396|XP_010354361.1
☐	PREDICTED: biotinidase isoform X2 [Ursus maritimus]	67.7	67.7	100%	2e-11	95%	gi|670981874|XP_008707139.1
☐	PREDICTED: biotinidase [Galeopterus variegatus]	67.7	67.7	100%	2e-11	95%	gi|667288263|XP_008576771.1
☐	PREDICTED: biotinidase [Jaculus jaculus]	67.7	67.7	100%	2e-11	95%	gi|507555213|XP_004661377.1
☐	PREDICTED: biotinidase isoform X2 [Microtus ochrogaster]	67.7	67.7	100%	2e-11	95%	gi|532009812|XP_005348714.1
☐	PREDICTED: biotinidase isoform X2 [Peromyscus maniculatus bair	67.7	67.7	100%	2e-11	95%	gi|589967610|XP_006996306.1
☐	PREDICTED: biotinidase-like isoform X5 [Chinchilla lanigera]	67.7	67.7	100%	2e-11	95%	gi|533146074|XP_005387497.1
☐	PREDICTED: biotinidase [Mesocricetus auratus]	67.7	67.7	100%	2e-11	95%	gi|524955500|XP_005077724.1

☐	PREDICTED: biotinidase isoform X2 [Chlorocebus sabaeus]	67.7	67.7	100%	2e-11	95%	gi|635085523|XP_008007381.1
☐	PREDICTED: biotinidase isoform X2 [Physeter catodon]	67.7	67.7	100%	2e-11	95%	gi|593711507|XP_007102308.1
☐	PREDICTED: biotinidase isoform X4 [Canis lupus familiaris]	67.7	67.7	100%	2e-11	95%	gi|545538859|XP_005634450.1
☐	PREDICTED: biotinidase isoform X3 [Equus caballus]	67.7	67.7	100%	2e-11	95%	gi|545189350|XP_005600979.1
☐	PREDICTED: biotinidase isoform X2 [Macaca fascicularis]	67.7	67.7	100%	2e-11	95%	gi|544411158|XP_005545768.1
☐	PREDICTED: biotinidase isoform X1 [Cavia porcellus]	67.7	67.7	100%	2e-11	95%	gi|514481133|XP_003480063.2
☐	PREDICTED: biotinidase [Ceratotherium simum simum]	67.7	67.7	100%	2e-11	95%	gi|478490156|XP_004419451.1
☐	PREDICTED: biotinidase isoform 2 [Odobenus rosmarus divergens	67.7	67.7	100%	2e-11	95%	gi|472379495|XP_004409157.1
☐	PREDICTED: LOW QUALITY PROTEIN: biotinidase [Tursiops trunc	67.7	67.7	100%	2e-11	95%	gi|470628904|XP_004321284.1
☐	PREDICTED: biotinidase [Orcinus orca]	67.7	67.7	100%	2e-11	95%	gi|466019817|XP_004271983.1
☐	PREDICTED: biotinidase isoform X3 [Saimiri boliviensis boliviensis]	67.7	67.7	100%	2e-11	95%	gi|725560828|XP_010333963.1
☐	PREDICTED: biotinidase isoform X2 [Papio anubis]	67.7	67.7	100%	2e-11	95%	gi|685527526|XP_009200021.1
☐	PREDICTED: biotinidase isoform X3 [Pongo abelii]	67.7	67.7	100%	2e-11	95%	gi|686713703|XP_009237577.1
☐	biotinidase precursor [Mus musculus]	67.7	67.7	100%	2e-11	95%	gi|13384648|NP_079571.1
☐	Biotinidase [Heterocephalus glaber]	67.7	67.7	100%	2e-11	95%	gi|351707565|EHB10484.1
☐	PREDICTED: biotinidase isoform X1 [Ursus maritimus]	67.7	67.7	100%	2e-11	95%	gi|670981872|XP_008707130.1
☐	PREDICTED: biotinidase [Equus przewalskii]	67.7	67.7	100%	2e-11	95%	gi|664753751|XP_008534346.1
☐	PREDICTED: biotinidase isoform X1 [Chlorocebus sabaeus]	67.7	67.7	100%	2e-11	95%	gi|635085521|XP_008007380.1
☐	PREDICTED: biotinidase isoform X1 [Felis catus]	67.7	67.7	100%	2e-11	95%	gi|587000359|XP_003992187.2
☐	PREDICTED: biotinidase isoform X2 [Felis catus]	67.7	67.7	100%	2e-11	95%	gi|587000357|XP_006936495.1
☐	PREDICTED: biotinidase isoform X3 [Leptonychotes weddellii]	67.7	67.7	100%	2e-11	95%	gi|585186600|XP_006744787.1
☐	PREDICTED: biotinidase isoform X2 [Leptonychotes weddellii]	67.7	67.7	100%	2e-11	95%	gi|585186598|XP_006744786.1
☐	PREDICTED: biotinidase isoform X3 [Canis lupus familiaris]	67.7	67.7	100%	2e-11	95%	gi|545538857|XP_005634449.1
☐	PREDICTED: biotinidase isoform X2 [Canis lupus familiaris]	67.7	67.7	100%	2e-11	95%	gi|545538855|XP_005634448.1
☐	PREDICTED: biotinidase isoform X2 [Equus caballus]	67.7	67.7	100%	2e-11	95%	gi|545189348|XP_005600978.1
☐	PREDICTED: biotinidase [Mustela putorius furo]	67.7	67.7	100%	2e-11	95%	gi|511908359|XP_004773614.1
☐	PREDICTED: biotinidase isoform 1 [Odobenus rosmarus divergens	67.7	67.7	100%	2e-11	95%	gi|472379493|XP_004409156.1
☐	PREDICTED: biotinidase [Trichechus manatus latirostris]	67.7	67.7	100%	2e-11	95%	gi|471407481|XP_004385327.1
☐	PREDICTED: biotinidase isoform X2 [Saimiri boliviensis boliviensis]	67.7	67.7	100%	2e-11	95%	gi|403265544|XP_003924991.1
☐	PREDICTED: biotinidase-like [Ailuropoda melanoleuca]	67.7	67.7	100%	2e-11	95%	gi|301759093|XP_002915396.1
☐	PREDICTED: biotinidase [Condylura cristata]	67.7	67.7	100%	2e-11	95%	gi|507976256|XP_004692357.1
☐	PREDICTED: biotinidase [Fukomys damarensis]	67.7	67.7	100%	2e-11	95%	gi|731285322|XP_010611073.1
☐	PREDICTED: biotinidase isoform X2 [Pongo abelii]	67.7	67.7	100%	2e-11	95%	gi|686713701|XP_009237576.1
☐	PREDICTED: biotinidase isoform X1 [Cricetulus griseus]	67.7	67.7	100%	2e-11	95%	gi|354465853|XP_003495391.1
☐	PREDICTED: biotinidase [Orycteropus afer afer]	67.7	67.7	100%	2e-11	95%	gi|634822252|XP_007934900.1
☐	PREDICTED: biotinidase isoform X1 [Physeter catodon]	67.7	67.7	100%	2e-11	95%	gi|593711505|XP_007102307.1
☐	PREDICTED: biotinidase-like isoform X1 [Chinchilla lanigera]	67.7	67.7	100%	2e-11	95%	gi|533146066|XP_005387493.1
☐	PREDICTED: biotinidase isoform X3 [Heterocephalus glaber]	67.7	67.7	100%	2e-11	95%	gi|512886961|XP_004896459.1
☐	PREDICTED: biotinidase isoform X1 [Leptonychotes weddellii]	67.7	67.7	100%	2e-11	95%	gi|585186596|XP_006744785.1
☐	PREDICTED: biotinidase isoform X1 [Canis lupus familiaris]	67.7	67.7	100%	2e-11	95%	gi|545538853|XP_005634447.1
☐	PREDICTED: biotinidase [Otolemur garnettii]	67.7	67.7	100%	2e-11	95%	gi|395816560|XP_003781769.1
☐	PREDICTED: biotinidase isoform X1 [Pongo abelii]	67.7	67.7	100%	2e-11	95%	gi|395734130|XP_003776360.1
☐	hypothetical protein EGM_11114 [Macaca fascicularis]	67.7	67.7	100%	2e-11	95%	gi|355747075|EHH51689.1
☐	hypothetical protein EGK_12122 [Macaca mulatta]	67.7	67.7	100%	2e-11	95%	gi|355560049|EHH16777.1
☐	PREDICTED: biotinidase isoform X1 [Microtus ochrogaster]	67.7	67.7	100%	2e-11	95%	gi|532009810|XP_005348713.1
☐	PREDICTED: biotinidase isoform X1 [Equus caballus]	67.7	67.7	100%	2e-11	95%	gi|545189346|XP_005600977.1

☐	PREDICTED: biotinidase isoform X2 [Cavia porcellus]	67.7	67.7	100%	2e-11	95%	gi|514481131|XP_005008361.1
☐	PREDICTED: biotinidase isoform X1 [Saimiri boliviensis boliviensis]	67.7	67.7	100%	2e-11	95%	gi|725560825|XP_010333962.1
☐	PREDICTED: biotinidase [Lipotes vexillifer]	67.7	67.7	100%	2e-11	95%	gi|602721076|XP_007470691.1
☐	PREDICTED: biotinidase isoform X1 [Heterocephalus glaber]	67.7	67.7	100%	2e-11	95%	gi|512886949|XP_004896457.1
☐	PREDICTED: biotinidase isoform X1 [Balaenoptera acutorostrata sc	67.7	67.7	100%	2e-11	95%	gi|594624940|XP_007167058.1
☐	PREDICTED: biotinidase isoform X1 [Papio anubis]	67.7	67.7	100%	2e-11	95%	gi|685527524|XP_009200020.1
☐	PREDICTED: biotinidase isoform X1 [Macaca fascicularis]	67.7	67.7	100%	2e-11	95%	gi|544411156|XP_005545767.1
☐	PREDICTED: biotinidase isoform X3 [Balaenoptera acutorostrata sc	67.7	67.7	100%	2e-11	95%	gi|594624944|XP_007167060.1
☐	PREDICTED: biotinidase-like [Octodon degus]	67.7	67.7	100%	2e-11	95%	gi|507646799|XP_004631734.1
☐	PREDICTED: biotinidase [Nomascus leucogenys]	66.0	66.0	90%	7e-11	100%	gi|332232450|XP_003265417.1
☐	PREDICTED: biotinidase isoform X2 [Cricetulus griseus]	66.0	66.0	90%	7e-11	100%	gi|625181248|XP_007632389.1
☐	PREDICTED: biotinidase isoform X1 [Peromyscus maniculatus bair	66.0	66.0	90%	7e-11	100%	gi|589967608|XP_006996305.1
☐	PREDICTED: biotinidase isoform X15 [Tupaia chinensis]	66.0	66.0	90%	8e-11	100%	gi|562886680|XP_006170761.1
☐	PREDICTED: biotinidase isoform X4 [Tupaia chinensis]	66.0	66.0	90%	8e-11	100%	gi|562886658|XP_006170750.1
☐	unnamed protein product [Mus musculus]	66.0	66.0	90%	8e-11	100%	gi|74183082|BAE22509.1
☐	PREDICTED: biotinidase [Panthera tigris altaica]	66.0	66.0	90%	8e-11	100%	gi|591322659|XP_007087428.1
☐	PREDICTED: biotinidase [Macaca mulatta]	66.0	66.0	90%	8e-11	100%	gi|297286947|XP_001083201.2
☐	PREDICTED: biotinidase isoform X3 [Tupaia chinensis]	66.0	66.0	90%	8e-11	100%	gi|562886656|XP_006170749.1
☐	Biotinidase [Fukomys damarensis]	66.0	66.0	90%	8e-11	100%	gi|676263045|KFO19807.1
☐	biotinidase [Cricetulus griseus]	66.0	66.0	90%	8e-11	100%	gi|537261432|ERE90059.1
☐	PREDICTED: biotinidase isoform X2 [Tupaia chinensis]	66.0	66.0	90%	8e-11	100%	gi|562886654|XP_006170748.1
☐	PREDICTED: biotinidase isoform X1 [Tupaia chinensis]	66.0	66.0	90%	8e-11	100%	gi|562886652|XP_006170747.1
☐	PREDICTED: biotinidase-like isoform X2 [Sus scrofa]	64.7	64.7	95%	2e-10	95%	gi|545860928|XP_005669335.1
☐	PREDICTED: biotinidase-like isoform X2 [Sus scrofa]	64.7	64.7	95%	2e-10	95%	gi|545860909|XP_005669330.1
☐	PREDICTED: biotinidase isoform X1 [Myotis davidii]	64.7	64.7	95%	2e-10	95%	gi|584051114|XP_006770244.1

⊟ Alignments

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biotinidase, isoform CRA_c [Homo sapiens]

Sequence ID: gi|119584660|gb|EAW64256.1| **Length:** 159 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 83 to 103 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.3 bits(163)	3e-13	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KDVQIIVFPEDGIHGFNFTRT  21
            KDVQIIVFPEDGIHGFNFTRT
Sbjct  83   KDVQIIVFPEDGIHGFNFTRT  103
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

biotinidase isoform 5 [Homo sapiens]

Sequence ID: gi|528524488|ref|NP_001268655.1| **Length:** 179 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 103 to 123 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.3 bits(163)	3e-13	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KDVQIIVFPEDGIHGFNFTRT  21
            KDVQIIVFPEDGIHGFNFTRT
Sbjct  103  KDVQIIVFPEDGIHGFNFTRT  123
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221043776|dbj|BAH13565.1| **Length:** 523 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 83 to 103 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.3 bits(163)	5e-13	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KDVQIIVFPEDGIHGFNFTRT  21
            KDVQIIVFPEDGIHGFNFTRT
Sbjct  83   KDVQIIVFPEDGIHGFNFTRT  103
```

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biotinidase isoform 4 precursor [Homo sapiens]

Sequence ID: gi|528524486|ref|NP_001268654.1| **Length:** 523 **Number of Matches:** 1

▷ See 3 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 83 to 103 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.3 bits(163)	5e-13	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KDVQIIVFPEDGIHGFNFTRT  21
            KDVQIIVFPEDGIHGFNFTRT
Sbjct  83   KDVQIIVFPEDGIHGFNFTRT  103
```

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biotinidase precursor [Pan troglodytes]

Sequence ID: gi|697993457|ref|NP_001289363.1| **Length:** 523 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 83 to 103 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.3 bits(163)	5e-13	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KDVQIIVFPEDGIHGFNFTRT  21
            KDVQIIVFPEDGIHGFNFTRT
Sbjct  83   KDVQIIVFPEDGIHGFNFTRT  103
```

BLAST ®　*Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - BT2Z2RVD013

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit　Save Search Strategies　Formatting options　Download　How to read this page　Blast report description

BTD_KNPVGLIGAEDATGETDPSHSKF_Mod

RID BT2Z2RVD013 (Expires on 01-20 11:45 am)

Query ID	lcl|98063	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	23		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

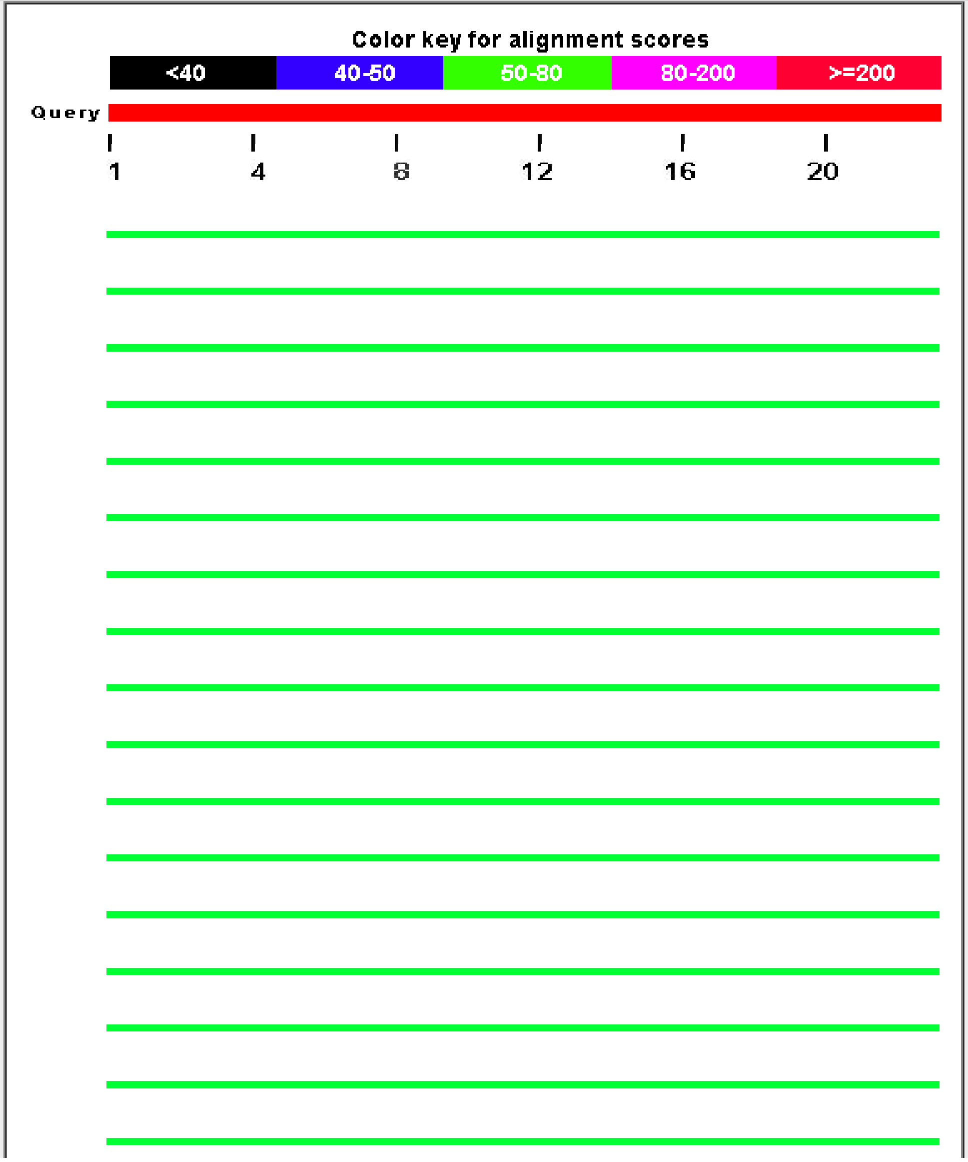
Graphic Summary

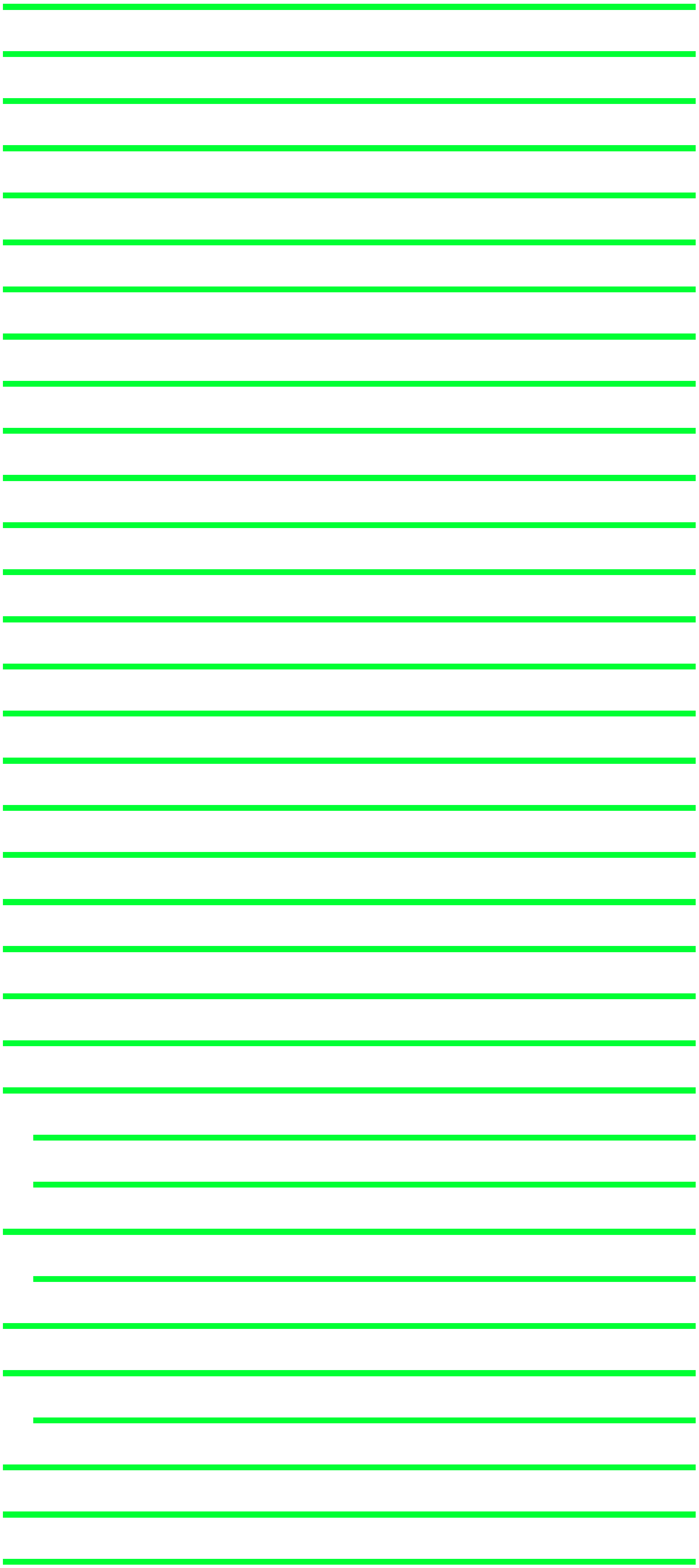
Show Conserved Domains

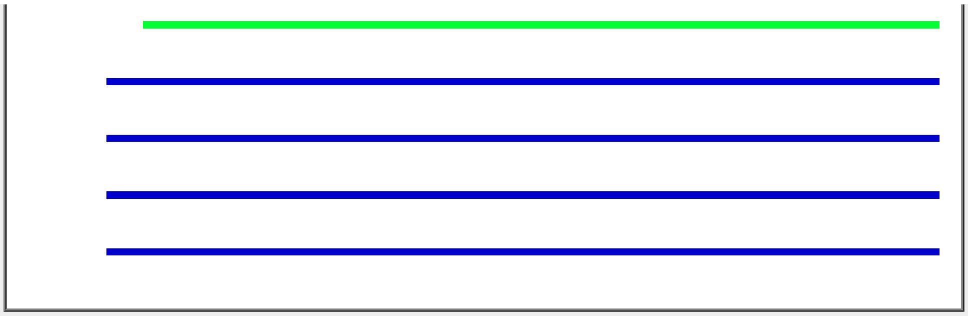
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: biotinidase [Nomascus leucogenys]	71.0	71.0	100%	2e-12	96%	gi|332232450|XP_003265417.1
☐	unnamed protein product [Macaca fascicularis]	71.0	71.0	100%	2e-12	96%	gi|90077268|BAE88314.1
☐	unnamed protein product [Homo sapiens]	71.0	71.0	100%	2e-12	96%	gi|221043776|BAH13565.1
☐	biotinidase isoform 4 precursor [Homo sapiens]	71.0	71.0	100%	2e-12	96%	gi|528524486|NP_001268654.1
☐	biotinidase precursor [Pan troglodytes]	71.0	71.0	100%	2e-12	96%	gi|697993457|NP_001289363.1
☐	PREDICTED: biotinidase isoform X2 [Chlorocebus sabaeus]	71.0	71.0	100%	2e-12	96%	gi|635085523|XP_008007381.1
☐	PREDICTED: biotinidase isoform X2 [Macaca fascicularis]	71.0	71.0	100%	2e-12	96%	gi|544411158|XP_005545768.1
☐	PREDICTED: biotinidase isoform X2 [Pan troglodytes]	71.0	71.0	100%	2e-12	96%	gi|694900420|XP_009443239.1
☐	PREDICTED: biotinidase isoform X2 [Pan paniscus]	71.0	71.0	100%	2e-12	96%	gi|675784344|XP_008949921.1
☐	PREDICTED: biotinidase isoform X3 [Pongo abelii]	71.0	71.0	100%	2e-12	96%	gi|686713703|XP_009237577.1
☐	PREDICTED: biotinidase isoform X1 [Chlorocebus sabaeus]	71.0	71.0	100%	2e-12	96%	gi|635085521|XP_008007380.1
☐	PREDICTED: biotinidase isoform X2 [Pongo abelii]	71.0	71.0	100%	2e-12	96%	gi|686713701|XP_009237576.1
☐	biotinidase isoform 3 [Homo sapiens]	71.0	71.0	100%	2e-12	96%	gi|4557373|NP_000051.1
☐	biotinidase isoform 1 [Homo sapiens]	71.0	71.0	100%	2e-12	96%	gi|528524481|NP_001268652.1
☐	biotinidase isoform 2 [Homo sapiens]	71.0	71.0	100%	2e-12	96%	gi|528524483|NP_001268653.1
☐	PREDICTED: biotinidase isoform X1 [Pan troglodytes]	71.0	71.0	100%	2e-12	96%	gi|410036604|XP_003950087.1
☐	PREDICTED: biotinidase isoform X1 [Pan paniscus]	71.0	71.0	100%	2e-12	96%	gi|397511808|XP_003826257.1
☐	PREDICTED: biotinidase isoform X1 [Pongo abelii]	71.0	71.0	100%	2e-12	96%	gi|395734130|XP_003776360.1
☐	hypothetical protein EGM_11114 [Macaca fascicularis]	71.0	71.0	100%	2e-12	96%	gi|355747075|EHH51689.1
☐	hypothetical protein EGK_12122 [Macaca mulatta]	71.0	71.0	100%	2e-12	96%	gi|355560049|EHH16777.1
☐	PREDICTED: biotinidase [Macaca mulatta]	71.0	71.0	100%	2e-12	96%	gi|297286947|XP_001083201.2
☐	PREDICTED: biotinidase isoform X1 [Macaca fascicularis]	71.0	71.0	100%	2e-12	96%	gi|544411156|XP_005545767.1
☐	PREDICTED: biotinidase isoform 1 [Gorilla gorilla gorilla]	68.5	68.5	100%	1e-11	91%	gi|426339607|XP_004033737.1
☐	PREDICTED: biotinidase isoform 3 [Gorilla gorilla gorilla]	68.5	68.5	100%	1e-11	91%	gi|426339611|XP_004033739.1
☐	PREDICTED: biotinidase isoform 4 [Gorilla gorilla gorilla]	68.5	68.5	100%	1e-11	91%	gi|426339613|XP_004033740.1
☐	PREDICTED: biotinidase isoform 2 [Gorilla gorilla gorilla]	68.5	68.5	100%	1e-11	91%	gi|426339609|XP_004033738.1
☐	PREDICTED: biotinidase [Rhinopithecus roxellana]	67.2	67.2	100%	4e-11	91%	gi|724960396|XP_010354361.1
☐	PREDICTED: biotinidase isoform X2 [Papio anubis]	63.4	63.4	100%	8e-10	87%	gi|685527526|XP_009200021.1
☐	PREDICTED: biotinidase isoform X1 [Papio anubis]	63.4	63.4	100%	8e-10	87%	gi|685527524|XP_009200020.1

☐	PREDICTED: biotinidase isoform X1 [Callithrix jacchus]	62.6	62.6	100%	1e-09	87%	gi|675740028|XP_008982107.1
☐	PREDICTED: biotinidase isoform X2 [Callithrix jacchus]	62.6	62.6	100%	1e-09	87%	gi|390476393|XP_002759736.2
☐	PREDICTED: biotinidase isoform X4 [Canis lupus familiaris]	54.9	54.9	100%	5e-07	78%	gi|545538859|XP_005634450.1
☐	PREDICTED: biotinidase isoform X3 [Canis lupus familiaris]	54.9	54.9	100%	5e-07	78%	gi|545538857|XP_005634449.1
☐	PREDICTED: biotinidase isoform X2 [Canis lupus familiaris]	54.9	54.9	100%	5e-07	78%	gi|545538855|XP_005634448.1
☐	PREDICTED: biotinidase isoform X1 [Canis lupus familiaris]	54.9	54.9	100%	5e-07	78%	gi|545538853|XP_005634447.1
☐	PREDICTED: biotinidase-like [Ictidomys tridecemlineatus]	54.5	54.5	100%	7e-07	78%	gi|532063189|XP_005317469.1
☐	PREDICTED: biotinidase isoform 2 [Odobenus rosmarus diverg	54.1	54.1	100%	1e-06	78%	gi|472379495|XP_004409157.1
☐	PREDICTED: biotinidase isoform X3 [Saimiri boliviensis bolivien	54.1	54.1	100%	1e-06	78%	gi|725560828|XP_010333963.1
☐	PREDICTED: biotinidase isoform 1 [Odobenus rosmarus diverg	54.1	54.1	100%	1e-06	78%	gi|472379493|XP_004409156.1
☐	PREDICTED: biotinidase isoform X2 [Saimiri boliviensis bolivien	54.1	54.1	100%	1e-06	78%	gi|403265544|XP_003924991.1
☐	PREDICTED: biotinidase isoform X1 [Saimiri boliviensis bolivien	54.1	54.1	100%	1e-06	78%	gi|725560825|XP_010333962.1
☐	PREDICTED: biotinidase isoform X1 [Felis catus]	53.7	53.7	95%	1e-06	77%	gi|587000359|XP_003992187.2
☐	PREDICTED: biotinidase isoform X2 [Felis catus]	53.7	53.7	95%	1e-06	77%	gi|587000357|XP_006936495.1
☐	PREDICTED: biotinidase [Ceratotherium simum simum]	52.0	52.0	100%	5e-06	74%	gi|478490156|XP_004419451.1
☐	PREDICTED: biotinidase [Mesocricetus auratus]	51.5	51.5	95%	7e-06	77%	gi|524955500|XP_005077724.1
☐	PREDICTED: biotinidase [Vicugna pacos]	51.1	51.1	100%	1e-05	74%	gi|560965913|XP_006205350.1
☐	PREDICTED: biotinidase [Jaculus jaculus]	50.7	50.7	100%	1e-05	74%	gi|507555213|XP_004661377.1
☐	PREDICTED: biotinidase isoform X2 [Microtus ochrogaster]	50.3	50.3	95%	2e-05	73%	gi|532009812|XP_005348714.1
☐	PREDICTED: biotinidase isoform X3 [Leptonychotes weddellii]	50.3	50.3	100%	2e-05	74%	gi|585186600|XP_006744787.1
☐	PREDICTED: biotinidase isoform X2 [Leptonychotes weddellii]	50.3	50.3	100%	2e-05	74%	gi|585186598|XP_006744786.1
☐	PREDICTED: biotinidase isoform X1 [Leptonychotes weddellii]	50.3	50.3	100%	2e-05	74%	gi|585186596|XP_006744785.1
☐	PREDICTED: biotinidase isoform X1 [Microtus ochrogaster]	50.3	50.3	95%	2e-05	73%	gi|532009810|XP_005348713.1
☐	biotinidase [Camelus ferus]	49.4	49.4	100%	3e-05	70%	gi|528756912|EPY76571.1
☐	PREDICTED: biotinidase isoform X2 [Camelus dromedarius]	49.4	49.4	100%	4e-05	70%	gi|744591359|XP_010987289.1
☐	PREDICTED: biotinidase isoform X2 [Camelus bactrianus]	49.4	49.4	100%	4e-05	70%	gi|743739779|XP_010964344.1
☐	PREDICTED: biotinidase [Camelus ferus]	49.4	49.4	100%	4e-05	70%	gi|560929390|XP_006190847.1
☐	PREDICTED: biotinidase isoform X1 [Camelus dromedarius]	49.4	49.4	100%	4e-05	70%	gi|744591356|XP_010987287.1
☐	PREDICTED: biotinidase isoform X1 [Camelus bactrianus]	49.4	49.4	100%	4e-05	70%	gi|743739777|XP_010964343.1
☐	PREDICTED: biotinidase [Panthera tigris altaica]	48.6	48.6	95%	7e-05	73%	gi|591322659|XP_007087428.1
☐	PREDICTED: biotinidase [Otolemur garnettii]	48.1	48.1	100%	9e-05	74%	gi|395816560|XP_003781769.1
☐	PREDICTED: biotinidase-like isoform X10 [Chinchilla lanigera]	47.7	47.7	100%	1e-04	70%	gi|533146084|XP_005387502.1
☐	PREDICTED: biotinidase-like isoform X5 [Chinchilla lanigera]	47.7	47.7	100%	1e-04	70%	gi|533146074|XP_005387497.1
☐	PREDICTED: biotinidase [Condylura cristata]	47.7	47.7	95%	1e-04	73%	gi|507976256|XP_004692357.1
☐	PREDICTED: biotinidase-like isoform X1 [Chinchilla lanigera]	47.7	47.7	100%	1e-04	70%	gi|533146066|XP_005387493.1
☐	PREDICTED: biotinidase [Trichechus manatus latirostris]	47.3	47.3	100%	2e-04	70%	gi|471407481|XP_004385327.1
☐	PREDICTED: biotinidase [Lipotes vexillifer]	47.3	47.3	100%	2e-04	74%	gi|602721076|XP_007470691.1
☐	PREDICTED: biotinidase isoform X1 [Balaenoptera acutorostra	47.3	47.3	100%	2e-04	74%	gi|594624940|XP_007167058.1
☐	PREDICTED: biotinidase isoform X3 [Balaenoptera acutorostra	47.3	47.3	100%	2e-04	74%	gi|594624944|XP_007167060.1
☐	PREDICTED: biotinidase isoform X3 [Equus caballus]	46.9	46.9	95%	2e-04	73%	gi|545189350|XP_005600979.1
☐	PREDICTED: biotinidase [Equus przewalskii]	46.9	46.9	95%	2e-04	73%	gi|664753751|XP_008534346.1
☐	PREDICTED: biotinidase isoform X2 [Equus caballus]	46.9	46.9	95%	2e-04	73%	gi|545189348|XP_005600978.1
☐	PREDICTED: biotinidase [Mustela putorius furo]	46.9	46.9	100%	2e-04	70%	gi|511908359|XP_004773614.1
☐	PREDICTED: biotinidase isoform X1 [Equus caballus]	46.9	46.9	95%	2e-04	73%	gi|545189346|XP_005600977.1
☐	PREDICTED: biotinidase isoform X2 [Ursus maritimus]	46.4	46.4	100%	3e-04	70%	gi|670981874|XP_008707139.1

☐	PREDICTED: biotinidase isoform X1 [Ursus maritimus]	46.4	46.4	100%	3e-04	70%	gi|670981872|XP_008707130.1
☐	PREDICTED: biotinidase [Fukomys damarensis]	46.4	46.4	100%	3e-04	70%	gi|731285322|XP_010611073.1
☐	Biotinidase [Fukomys damarensis]	46.4	46.4	100%	3e-04	70%	gi|676263045|KFO19807.1
☐	PREDICTED: biotinidase isoform X2 [Cricetulus griseus]	46.0	46.0	95%	4e-04	73%	gi|625181248|XP_007632389.1
☐	PREDICTED: biotinidase isoform X1 [Cricetulus griseus]	46.0	46.0	95%	4e-04	73%	gi|354465853|XP_003495391.1
☐	biotinidase [Cricetulus griseus]	46.0	46.0	95%	5e-04	73%	gi|537261432|ERE90059.1
☐	PREDICTED: biotinidase [Erinaceus europaeus]	45.6	45.6	95%	6e-04	68%	gi|617553342|XP_007530134.1
☐	PREDICTED: biotinidase [Galeopterus variegatus]	45.2	45.2	100%	8e-04	70%	gi|667288263|XP_008576771.1
☐	PREDICTED: LOW QUALITY PROTEIN: biotinidase [Tursiops	44.8	44.8	100%	0.001	70%	gi|470628904|XP_004321284.1
☐	PREDICTED: biotinidase [Orcinus orca]	44.8	44.8	100%	0.001	70%	gi|466019817|XP_004271983.1
☐	PREDICTED: biotinidase isoform X2 [Physeter catodon]	44.3	44.3	100%	0.002	70%	gi|593711507|XP_007102308.1
☐	PREDICTED: biotinidase isoform X1 [Physeter catodon]	44.3	44.3	100%	0.002	70%	gi|593711505|XP_007102307.1
☐	PREDICTED: biotinidase isoform X1 [Peromyscus maniculatus	43.5	43.5	95%	0.003	64%	gi|589967608|XP_006996305.1
☐	PREDICTED: biotinidase isoform X2 [Peromyscus maniculatus	43.5	43.5	95%	0.003	64%	gi|589967610|XP_006996306.1
☐	PREDICTED: biotinidase-like [Ailuropoda melanoleuca]	43.5	43.5	100%	0.003	70%	gi|301759093|XP_002915396.1
☐	hypothetical protein PANDA_003369 [Ailuropoda melanoleuca]	43.5	43.5	100%	0.003	70%	gi|281345880|EFB21464.1
☐	PREDICTED: biotinidase isoform X1 [Myotis lucifugus]	42.6	42.6	100%	0.005	70%	gi|558102610|XP_006083737.1
☐	PREDICTED: biotinidase isoform X3 [Myotis brandtii]	42.6	42.6	100%	0.005	70%	gi|554537982|XP_005863672.1
☐	PREDICTED: biotinidase isoform X2 [Myotis lucifugus]	42.6	42.6	100%	0.005	70%	gi|558102613|XP_006083738.1
☐	PREDICTED: biotinidase isoform X2 [Myotis brandtii]	42.6	42.6	100%	0.005	70%	gi|554537986|XP_005863671.1
☐	Biotinidase [Myotis brandtii]	42.6	42.6	100%	0.006	70%	gi|521024341|EPQ06129.1
☐	biotinidase, isoform CRA_a [Rattus norvegicus]	41.8	41.8	95%	0.010	64%	gi|149034168|EDL88938.1
☐	biotinidase, isoform CRA_c [Rattus norvegicus]	41.8	41.8	95%	0.010	64%	gi|149034170|EDL88940.1
☐	biotinidase precursor [Rattus norvegicus]	41.8	41.8	95%	0.010	64%	gi|58865670|NP_001012047.1
☐	PREDICTED: biotinidase isoform X2 [Rattus norvegicus]	41.8	41.8	95%	0.010	64%	gi|564387894|XP_006252671.1
☐	PREDICTED: biotinidase isoform X1 [Cavia porcellus]	41.4	41.4	100%	0.014	65%	gi|514481133|XP_003480063.2

⊟ Alignments

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PREDICTED: biotinidase [Nomascus leucogenys]

Sequence ID: gi|332232450|ref|XP_003265417.1| **Length:** 474 **Number of Matches:** 1

Range 1: 270 to 292 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
71.0 bits(160)	2e-12	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    KNPVGLIGAEDATGETDPSHSKF  23
            KNPVGLIGAE+ATGETDPSHSKF
Sbjct  270  KNPVGLIGAENATGETDPSHSKF  292
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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unnamed protein product [Macaca fascicularis]

Sequence ID: gi|90077268|dbj|BAE88314.1| **Length:** 493 **Number of Matches:** 1

Range 1: 323 to 345 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
71.0 bits(160)	2e-12	22/23(96%)	23/23(100%)	0/23(0%)

Related Information

Gene - associated gene details

```
Query  1    KNPVGLIGAEDATGETDPSHSKF  23
            KNPVGLIGAE+ATGETDPSHSKF
Sbjct  323  KNPVGLIGAENATGETDPSHSKF  345
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221043776|dbj|BAH13565.1| **Length:** 523 **Number of Matches:** 1

Range 1: 319 to 341 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
71.0 bits(160)	2e-12	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    KNPVGLIGAEDATGETDPSHSKF  23
            KNPVGLIGAE+ATGETDPSHSKF
Sbjct  319  KNPVGLIGAENATGETDPSHSKF  341
```

Related Information

Gene - associated gene details

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biotinidase isoform 4 precursor [Homo sapiens]

Sequence ID: gi|528524486|ref|NP_001268654.1| **Length:** 523 **Number of Matches:** 1

See 3 more title(s)

Range 1: 319 to 341 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
71.0 bits(160)	2e-12	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    KNPVGLIGAEDATGETDPSHSKF  23
            KNPVGLIGAE+ATGETDPSHSKF
Sbjct  319  KNPVGLIGAENATGETDPSHSKF  341
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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biotinidase precursor [Pan troglodytes]

Sequence ID: gi|697993457|ref|NP_001289363.1| **Length:** 523 **Number of Matches:** 1

See 1 more title(s)

Range 1: 319 to 341 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
71.0 bits(160)	2e-12	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    KNPVGLIGAEDATGETDPSHSKF  23
            KNPVGLIGAE+ATGETDPSHSKF
Sbjct  319  KNPVGLIGAENATGETDPSHSKF  341
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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NCBI/ BLAST/ blastp suite/ Formatting Results - BT38KVCN013

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   Formatting options   Download   How to read this page   Blast report description

BTD_KNPVGLIGAEDATGETDPSHSKFLKI_Mod

RID BT38KVCN013 (Expires on 01-20 11:50 am)

Query ID lcl|70574
Description None
Molecule type amino acid
Query Length 26

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

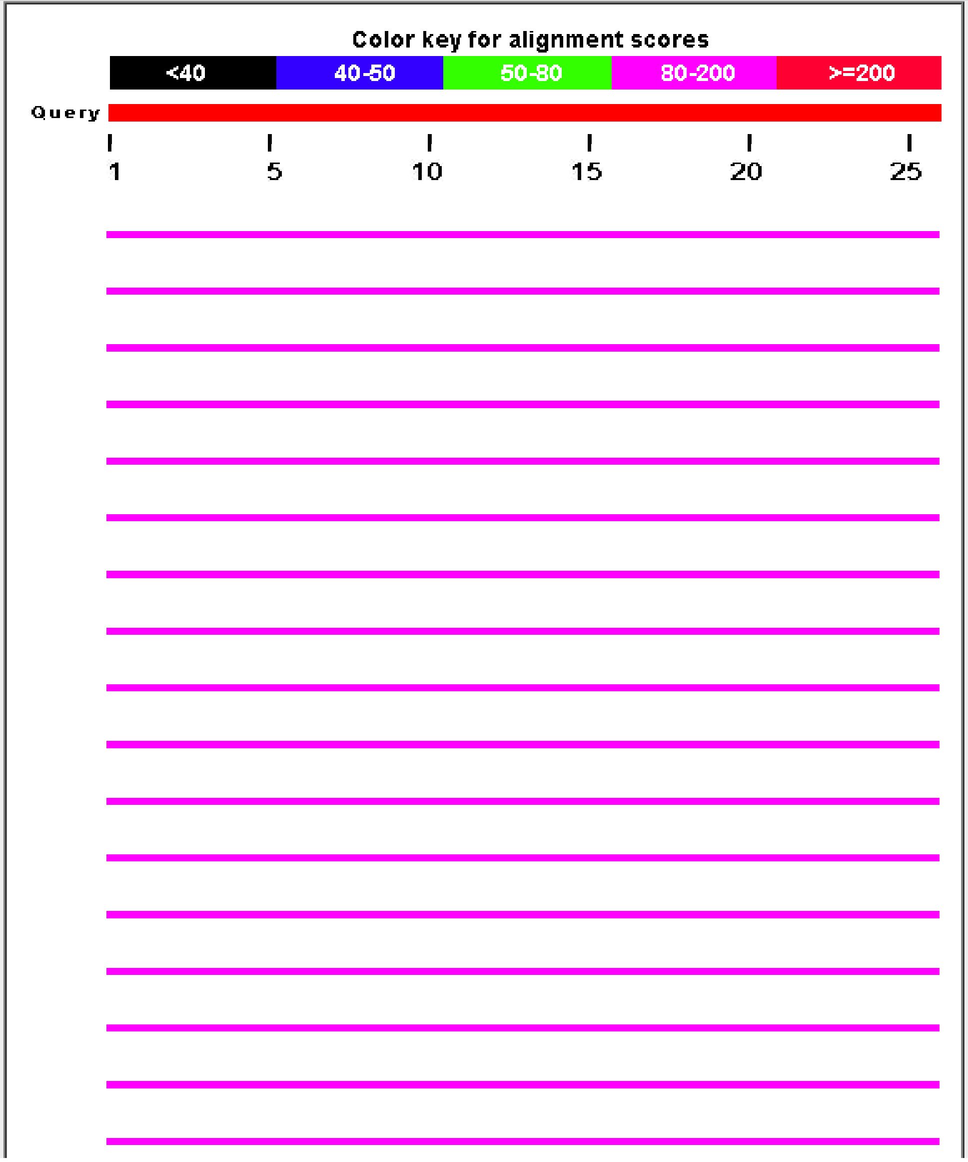
Graphic Summary

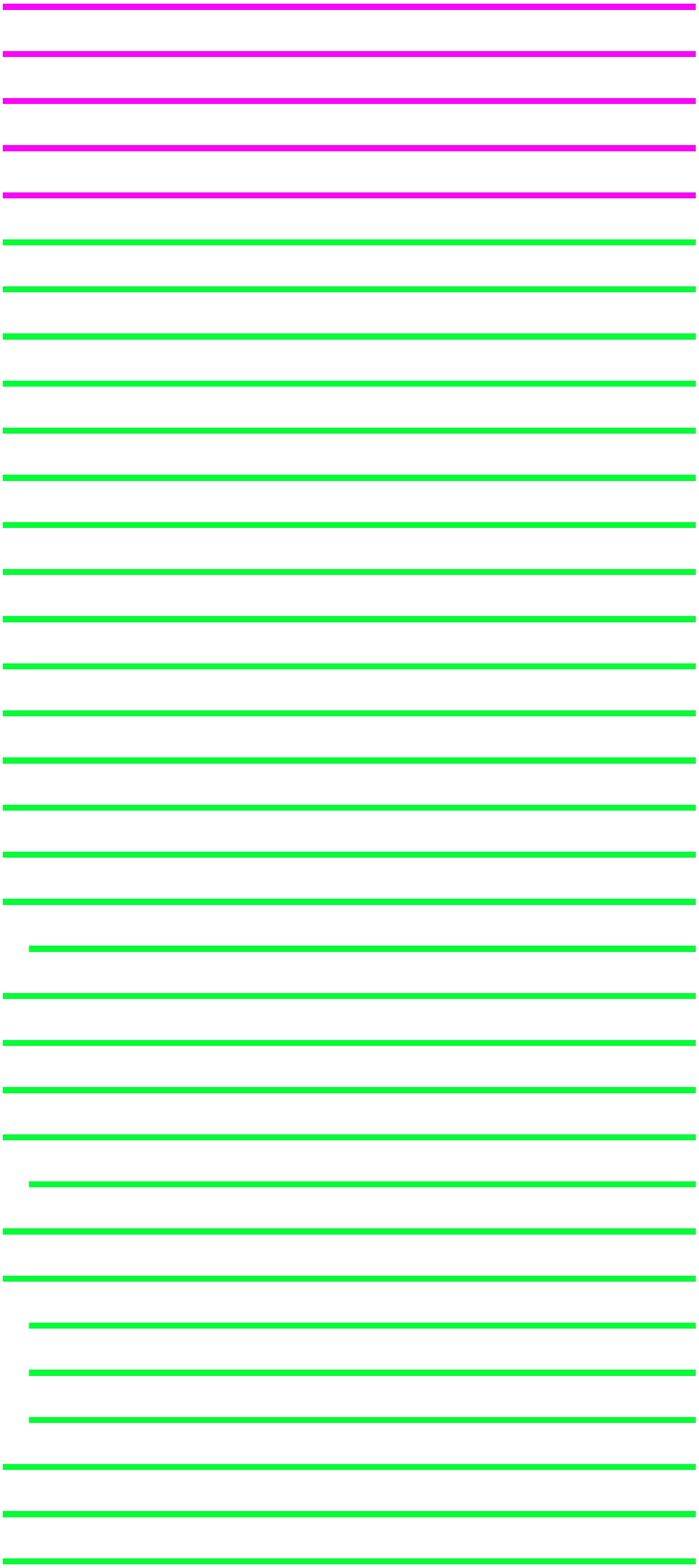
Show Conserved Domains

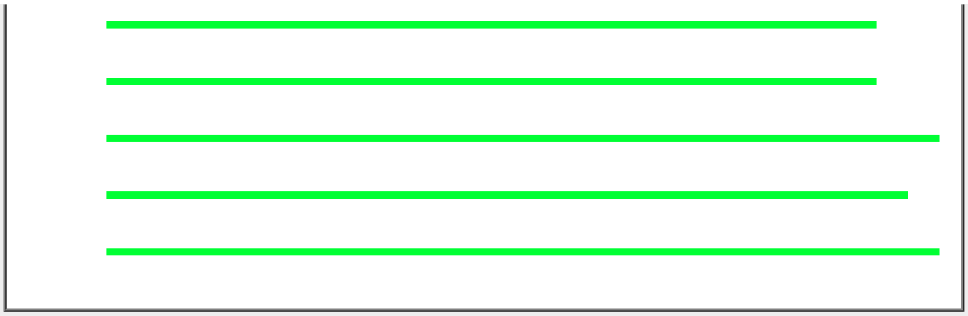
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: biotinidase [Nomascus leucogenys]	80.4	80.4	100%	2e-15	96%	gi|332232450|XP_003265417.1
☐	unnamed protein product [Macaca fascicularis]	80.4	80.4	100%	2e-15	96%	gi|90077268|BAE88314.1
☐	unnamed protein product [Homo sapiens]	80.4	80.4	100%	2e-15	96%	gi|221043776|BAH13565.1
☐	biotinidase isoform 4 precursor [Homo sapiens]	80.4	80.4	100%	2e-15	96%	gi|528524486|NP_001268654.1
☐	biotinidase precursor [Pan troglodytes]	80.4	80.4	100%	2e-15	96%	gi|697993457|NP_001289363.1
☐	PREDICTED: biotinidase isoform X2 [Chlorocebus sabaeus]	80.4	80.4	100%	2e-15	96%	gi|635085523|XP_008007381.1
☐	PREDICTED: biotinidase isoform X2 [Macaca fascicularis]	80.4	80.4	100%	2e-15	96%	gi|544411158|XP_005545768.1
☐	PREDICTED: biotinidase isoform X2 [Pan troglodytes]	80.4	80.4	100%	2e-15	96%	gi|694900420|XP_009443239.1
☐	PREDICTED: biotinidase isoform X2 [Pan paniscus]	80.4	80.4	100%	2e-15	96%	gi|675784344|XP_008949921.1
☐	PREDICTED: biotinidase isoform X3 [Pongo abelii]	80.4	80.4	100%	2e-15	96%	gi|686713703|XP_009237577.1
☐	PREDICTED: biotinidase isoform X1 [Chlorocebus sabaeus]	80.4	80.4	100%	2e-15	96%	gi|635085521|XP_008007380.1
☐	PREDICTED: biotinidase isoform X2 [Pongo abelii]	80.4	80.4	100%	2e-15	96%	gi|686713701|XP_009237576.1
☐	biotinidase isoform 3 [Homo sapiens]	80.4	80.4	100%	2e-15	96%	gi|4557373|NP_000051.1
☐	biotinidase isoform 1 [Homo sapiens]	80.4	80.4	100%	2e-15	96%	gi|528524481|NP_001268652.1
☐	biotinidase isoform 2 [Homo sapiens]	80.4	80.4	100%	2e-15	96%	gi|528524483|NP_001268653.1
☐	PREDICTED: biotinidase isoform X1 [Pan troglodytes]	80.4	80.4	100%	2e-15	96%	gi|410036604|XP_003950087.1
☐	PREDICTED: biotinidase isoform X1 [Pan paniscus]	80.4	80.4	100%	2e-15	96%	gi|397511808|XP_003826257.1
☐	PREDICTED: biotinidase isoform X1 [Pongo abelii]	80.4	80.4	100%	2e-15	96%	gi|395734130|XP_003776360.1
☐	hypothetical protein EGM_11114 [Macaca fascicularis]	80.4	80.4	100%	2e-15	96%	gi|355747075|EHH51689.1
☐	hypothetical protein EGK_12122 [Macaca mulatta]	80.4	80.4	100%	2e-15	96%	gi|355560049|EHH16777.1
☐	PREDICTED: biotinidase [Macaca mulatta]	80.4	80.4	100%	2e-15	96%	gi|297286947|XP_001083201.2
☐	PREDICTED: biotinidase isoform X1 [Macaca fascicularis]	80.4	80.4	100%	2e-15	96%	gi|544411156|XP_005545767.1
☐	PREDICTED: biotinidase isoform 1 [Gorilla gorilla gorilla]	77.8	77.8	100%	1e-14	92%	gi|426339607|XP_004033737.1
☐	PREDICTED: biotinidase isoform 3 [Gorilla gorilla gorilla]	77.8	77.8	100%	1e-14	92%	gi|426339611|XP_004033739.1
☐	PREDICTED: biotinidase isoform 4 [Gorilla gorilla gorilla]	77.8	77.8	100%	1e-14	92%	gi|426339613|XP_004033740.1
☐	PREDICTED: biotinidase isoform 2 [Gorilla gorilla gorilla]	77.8	77.8	100%	1e-14	92%	gi|426339609|XP_004033738.1
☐	PREDICTED: biotinidase [Rhinopithecus roxellana]	76.6	76.6	100%	4e-14	92%	gi|724960396|XP_010354361.1
☐	PREDICTED: biotinidase isoform X2 [Papio anubis]	72.7	72.7	100%	8e-13	88%	gi|685527526|XP_009200021.1
☐	PREDICTED: biotinidase isoform X1 [Papio anubis]	72.7	72.7	100%	8e-13	88%	gi|685527524|XP_009200020.1

☐	PREDICTED: biotinidase isoform X1 [Callithrix jacchus]	71.9	71.9	100%	1e-12	88%	gi|675740028|XP_008982107.1
☐	PREDICTED: biotinidase isoform X2 [Callithrix jacchus]	71.9	71.9	100%	1e-12	88%	gi|390476393|XP_002759736.2
☐	PREDICTED: biotinidase-like [Ictidomys tridecemlineatus]	63.8	63.8	100%	8e-10	81%	gi|532063189|XP_005317469.1
☐	PREDICTED: biotinidase isoform X3 [Saimiri boliviensis bolivie	63.4	63.4	100%	1e-09	81%	gi|725560828|XP_010333963.1
☐	PREDICTED: biotinidase isoform X2 [Saimiri boliviensis bolivie	63.4	63.4	100%	1e-09	81%	gi|403265544|XP_003924991.1
☐	PREDICTED: biotinidase isoform X1 [Saimiri boliviensis bolivie	63.4	63.4	100%	1e-09	81%	gi|725560825|XP_010333962.1
☐	PREDICTED: biotinidase [Ceratotherium simum simum]	61.3	61.3	100%	6e-09	77%	gi|478490156|XP_004419451.1
☐	PREDICTED: biotinidase [Vicugna pacos]	60.4	60.4	100%	1e-08	77%	gi|560965913|XP_006205350.1
☐	PREDICTED: biotinidase isoform X2 [Microtus ochrogaster]	59.6	59.6	96%	2e-08	76%	gi|532009812|XP_005348714.1
☐	PREDICTED: biotinidase isoform X4 [Canis lupus familiaris]	59.6	59.6	100%	2e-08	77%	gi|545538859|XP_005634450.1
☐	PREDICTED: biotinidase isoform X3 [Canis lupus familiaris]	59.6	59.6	100%	2e-08	77%	gi|545538857|XP_005634449.1
☐	PREDICTED: biotinidase isoform X2 [Canis lupus familiaris]	59.6	59.6	100%	2e-08	77%	gi|545538855|XP_005634448.1
☐	PREDICTED: biotinidase isoform X1 [Canis lupus familiaris]	59.6	59.6	100%	2e-08	77%	gi|545538853|XP_005634447.1
☐	PREDICTED: biotinidase isoform X1 [Microtus ochrogaster]	59.6	59.6	96%	2e-08	76%	gi|532009810|XP_005348713.1
☐	biotinidase [Camelus ferus]	58.7	58.7	100%	4e-08	73%	gi|528756912|EPY76571.1
☐	PREDICTED: biotinidase [Camelus ferus]	58.7	58.7	100%	4e-08	73%	gi|560929390|XP_006190847.1
☐	PREDICTED: biotinidase isoform X1 [Felis catus]	58.3	58.3	96%	5e-08	76%	gi|587000359|XP_003992187.2
☐	PREDICTED: biotinidase isoform X2 [Felis catus]	58.3	58.3	96%	5e-08	76%	gi|587000357|XP_006936495.1
☐	PREDICTED: biotinidase [Mesocricetus auratus]	57.9	57.9	96%	7e-08	76%	gi|524955500|XP_005077724.1
☐	PREDICTED: biotinidase [Otolemur garnettii]	57.5	57.5	100%	1e-07	77%	gi|395816560|XP_003781769.1
☐	PREDICTED: biotinidase-like isoform X10 [Chinchilla lanigera]	57.1	57.1	100%	1e-07	73%	gi|533146084|XP_005387502.1
☐	PREDICTED: biotinidase-like isoform X5 [Chinchilla lanigera]	57.1	57.1	100%	1e-07	73%	gi|533146074|XP_005387497.1
☐	PREDICTED: biotinidase isoform 2 [Odobenus rosmarus diverg	57.1	57.1	92%	1e-07	79%	gi|472379495|XP_004409157.1
☐	PREDICTED: biotinidase isoform 1 [Odobenus rosmarus diverg	57.1	57.1	92%	1e-07	79%	gi|472379493|XP_004409156.1
☐	PREDICTED: biotinidase-like isoform X1 [Chinchilla lanigera]	57.1	57.1	100%	1e-07	73%	gi|533146066|XP_005387493.1
☐	PREDICTED: biotinidase [Jaculus jaculus]	56.6	56.6	96%	2e-07	76%	gi|507555213|XP_004661377.1
☐	PREDICTED: biotinidase [Trichechus manatus latirostris]	56.6	56.6	100%	2e-07	73%	gi|471407481|XP_004385327.1
☐	PREDICTED: biotinidase [Lipotes vexillifer]	56.6	56.6	100%	2e-07	77%	gi|602721076|XP_007470691.1
☐	PREDICTED: biotinidase isoform X1 [Balaenoptera acutorostra	56.6	56.6	100%	2e-07	77%	gi|594624940|XP_007167058.1
☐	PREDICTED: biotinidase isoform X3 [Balaenoptera acutorostra	56.6	56.6	100%	2e-07	77%	gi|594624944|XP_007167060.1
☐	PREDICTED: biotinidase isoform X3 [Equus caballus]	56.2	56.2	96%	3e-07	76%	gi|545189350|XP_005600979.1
☐	PREDICTED: biotinidase [Equus przewalskii]	56.2	56.2	96%	3e-07	76%	gi|664753751|XP_008534346.1
☐	PREDICTED: biotinidase isoform X2 [Equus caballus]	56.2	56.2	96%	3e-07	76%	gi|545189348|XP_005600978.1
☐	PREDICTED: biotinidase isoform X1 [Equus caballus]	56.2	56.2	96%	3e-07	76%	gi|545189346|XP_005600977.1
☐	PREDICTED: biotinidase [Fukomys damarensis]	55.8	55.8	100%	4e-07	73%	gi|731285322|XP_010611073.1
☐	Biotinidase [Fukomys damarensis]	55.8	55.8	100%	4e-07	73%	gi|676263045|KFO19807.1
☐	PREDICTED: biotinidase isoform X2 [Cricetulus griseus]	55.4	55.4	96%	5e-07	76%	gi|625181248|XP_007632389.1
☐	PREDICTED: biotinidase isoform X1 [Cricetulus griseus]	55.4	55.4	96%	5e-07	76%	gi|354465853|XP_003495391.1
☐	biotinidase [Cricetulus griseus]	55.4	55.4	96%	5e-07	76%	gi|537261432|ERE90059.1
☐	PREDICTED: biotinidase [Erinaceus europaeus]	54.9	54.9	96%	7e-07	72%	gi|617553342|XP_007530134.1
☐	PREDICTED: biotinidase [Galeopterus variegatus]	54.5	54.5	100%	1e-06	73%	gi|667288263|XP_008576771.1
☐	PREDICTED: LOW QUALITY PROTEIN: biotinidase [Tursiops	54.1	54.1	100%	1e-06	73%	gi|470628904|XP_004321284.1
☐	PREDICTED: biotinidase [Orcinus orca]	54.1	54.1	100%	1e-06	73%	gi|466019817|XP_004271983.1
☐	PREDICTED: biotinidase isoform X2 [Physeter catodon]	53.7	53.7	100%	2e-06	73%	gi|593711507|XP_007102308.1
☐	PREDICTED: biotinidase [Condylura cristata]	53.7	53.7	92%	2e-06	75%	gi|507976256|XP_004692357.1

☐	PREDICTED: biotinidase isoform X1 [Physeter catodon]	53.7	53.7	100%	2e-06	73%	gi|593711505|XP_007102307.1
☐	PREDICTED: biotinidase [Panthera tigris altaica]	53.2	53.2	96%	3e-06	72%	gi|591322659|XP_007087428.1
☐	PREDICTED: biotinidase isoform X3 [Leptonychotes weddellii]	53.2	53.2	92%	3e-06	75%	gi|585186600|XP_006744787.1
☐	PREDICTED: biotinidase isoform X2 [Leptonychotes weddellii]	53.2	53.2	92%	3e-06	75%	gi|585186598|XP_006744786.1
☐	PREDICTED: biotinidase isoform X1 [Leptonychotes weddellii]	53.2	53.2	92%	3e-06	75%	gi|585186596|XP_006744785.1
☐	PREDICTED: biotinidase isoform X1 [Peromyscus maniculatus	52.8	52.8	96%	3e-06	68%	gi|589967608|XP_006996305.1
☐	PREDICTED: biotinidase isoform X2 [Peromyscus maniculatus	52.8	52.8	96%	4e-06	68%	gi|589967610|XP_006996306.1
☐	PREDICTED: biotinidase [Nannospalax galili]	50.3	50.3	100%	2e-05	69%	gi|674081213|XP_008848205.1
☐	Biotinidase [Heterocephalus glaber]	49.8	49.8	100%	3e-05	65%	gi|351707565|EHB10484.1
☐	PREDICTED: biotinidase [Mustela putorius furo]	49.8	49.8	92%	3e-05	71%	gi|511908359|XP_004773614.1
☐	PREDICTED: biotinidase isoform X3 [Heterocephalus glaber]	49.8	49.8	100%	3e-05	65%	gi|512886961|XP_004896459.1
☐	PREDICTED: biotinidase isoform X1 [Heterocephalus glaber]	49.8	49.8	100%	3e-05	65%	gi|512886949|XP_004896457.1
☐	PREDICTED: biotinidase isoform X2 [Ursus maritimus]	49.4	49.4	92%	4e-05	71%	gi|670981874|XP_008707139.1
☐	PREDICTED: biotinidase isoform X1 [Ursus maritimus]	49.4	49.4	92%	4e-05	71%	gi|670981872|XP_008707130.1
☐	biotinidase, isoform CRA_a [Rattus norvegicus]	48.6	48.6	96%	8e-05	64%	gi|149034168|EDL88938.1
☐	biotinidase, isoform CRA_c [Rattus norvegicus]	48.6	48.6	96%	8e-05	64%	gi|149034170|EDL88940.1
☐	biotinidase precursor [Rattus norvegicus]	48.6	48.6	96%	8e-05	64%	gi|58865670|NP_001012047.1
☐	PREDICTED: biotinidase isoform X1 [Myotis lucifugus]	48.6	48.6	96%	8e-05	72%	gi|558102610|XP_006083737.1
☐	PREDICTED: biotinidase isoform X3 [Myotis brandtii]	48.6	48.6	96%	8e-05	72%	gi|554537982|XP_005863672.1
☐	PREDICTED: biotinidase isoform X2 [Myotis lucifugus]	48.6	48.6	96%	8e-05	72%	gi|558102613|XP_006083738.1
☐	PREDICTED: biotinidase isoform X2 [Myotis brandtii]	48.6	48.6	96%	8e-05	72%	gi|554537986|XP_005863671.1
☐	PREDICTED: biotinidase isoform X2 [Rattus norvegicus]	48.6	48.6	96%	8e-05	64%	gi|564387894|XP_006252671.1
☐	Biotinidase [Myotis brandtii]	48.6	48.6	96%	8e-05	72%	gi|521024341|EPQ06129.1
☐	PREDICTED: biotinidase-like [Octodon degus]	46.9	46.9	96%	3e-04	72%	gi|507646799|XP_004631734.1
☐	PREDICTED: biotinidase [Loxodonta africana]	46.4	46.4	100%	4e-04	65%	gi|731510838|XP_010598778.1
☐	PREDICTED: biotinidase-like [Ailuropoda melanoleuca]	46.4	46.4	92%	4e-04	71%	gi|301759093|XP_002915396.1

⊟ Alignments

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PREDICTED: biotinidase [Nomascus leucogenys]

Sequence ID: gi|332232450|ref|XP_003265417.1| **Length:** 474 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 270 to 295 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	2e-15	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    KNPVGLIGAEDATGETDPSHSKFLKI  26
            KNPVGLIGAE+ATGETDPSHSKFLKI
Sbjct  270  KNPVGLIGAENATGETDPSHSKFLKI  295
```

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unnamed protein product [Macaca fascicularis]

Sequence ID: gi|90077268|dbj|BAE88314.1| **Length:** 493 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 323 to 348 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	2e-15	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    KNPVGLIGAEDATGETDPSHSKFLKI  26
            KNPVGLIGAE+ATGETDPSHSKFLKI
Sbjct  323  KNPVGLIGAENATGETDPSHSKFLKI  348
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221043776|dbj|BAH13565.1| **Length:** 523 **Number of Matches:** 1

Range 1: 319 to 344 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	2e-15	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    KNPVGLIGAEDATGETDPSHSKFLKI  26
            KNPVGLIGAE+ATGETDPSHSKFLKI
Sbjct  319  KNPVGLIGAENATGETDPSHSKFLKI  344
```

Related Information

Gene - associated gene details

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biotinidase isoform 4 precursor [Homo sapiens]

Sequence ID: gi|528524486|ref|NP_001268654.1| **Length:** 523 **Number of Matches:** 1

See 3 more title(s)

Range 1: 319 to 344 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	2e-15	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    KNPVGLIGAEDATGETDPSHSKFLKI  26
            KNPVGLIGAE+ATGETDPSHSKFLKI
Sbjct  319  KNPVGLIGAENATGETDPSHSKFLKI  344
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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biotinidase precursor [Pan troglodytes]

Sequence ID: gi|697993457|ref|NP_001289363.1| **Length:** 523 **Number of Matches:** 1

See 1 more title(s)

Range 1: 319 to 344 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	2e-15	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    KNPVGLIGAEDATGETDPSHSKFLKI  26
            KNPVGLIGAE+ATGETDPSHSKFLKI
Sbjct  319  KNPVGLIGAENATGETDPSHSKFLKI  344
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - B920RBN201R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

BTD_KNPVGLIGAENATGETDPSHSKF_NonMod

RID B920RBN201R (Expires on 01-14 09:51 am)

Query ID lcl|88991

Description None

Molecule type amino acid

Query Length 23

Database Name nr

Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects

Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

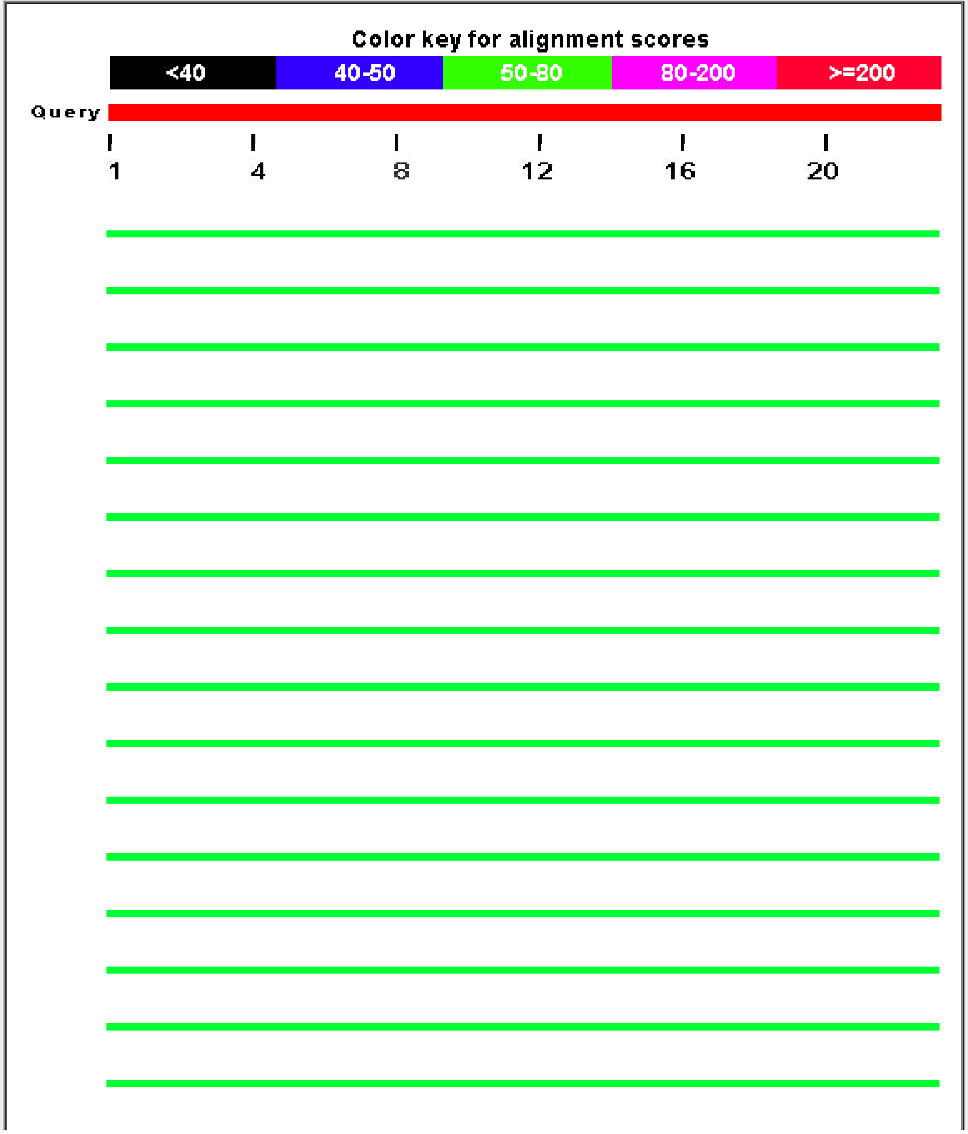
Graphic Summary

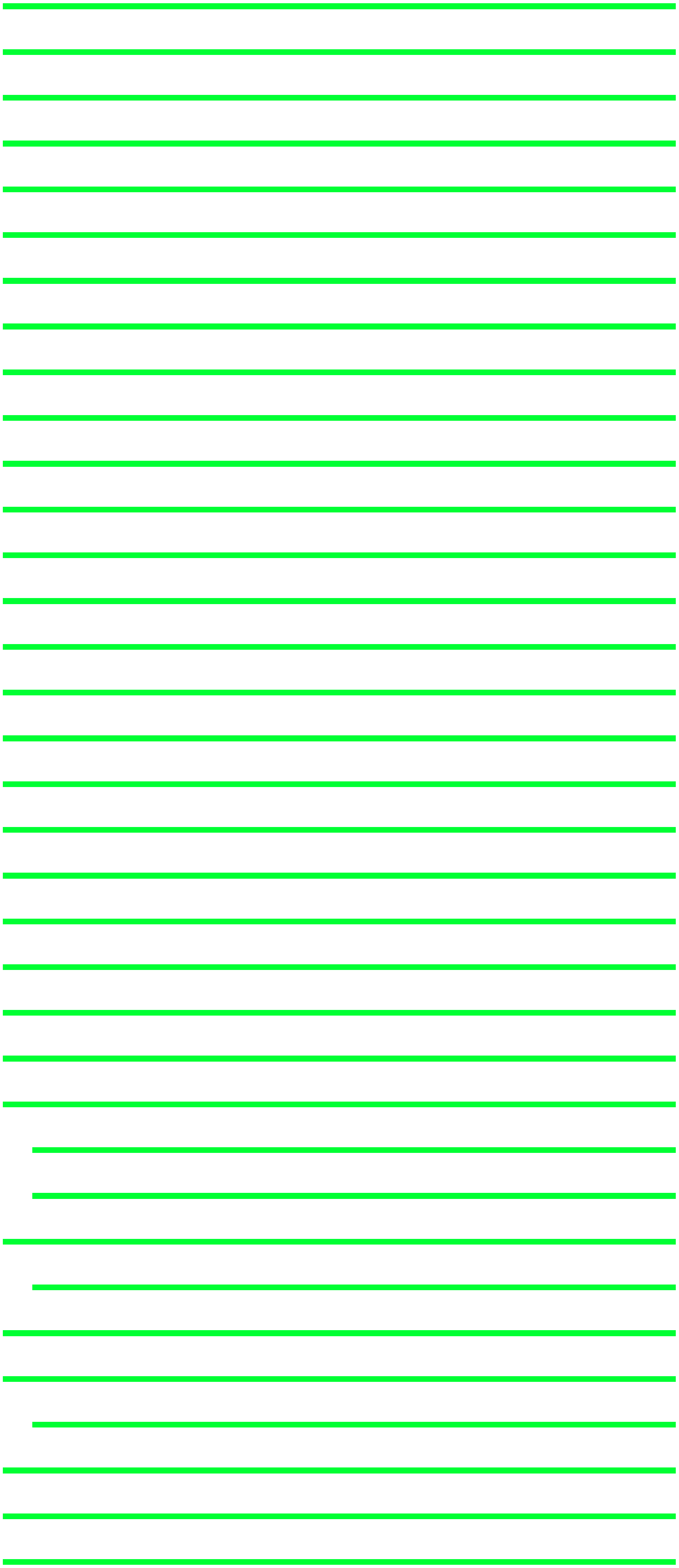
Show Conserved Domains

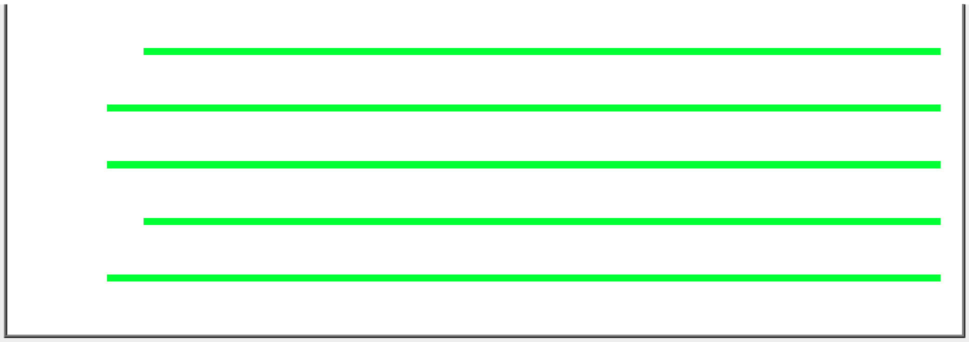
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: biotinidase [Nomascus leucogenys]	73.6	73.6	100%	2e-13	100%	gi|332232450|XP_003265417.1
☐	unnamed protein product [Macaca fascicularis]	73.6	73.6	100%	2e-13	100%	gi|90077268|BAE88314.1
☐	unnamed protein product [Homo sapiens]	73.6	73.6	100%	2e-13	100%	gi|221043776|BAH13565.1
☐	biotinidase isoform 4 precursor [Homo sapiens]	73.6	73.6	100%	2e-13	100%	gi|528524486|NP_001268654.1
☐	biotinidase precursor [Pan troglodytes]	73.6	73.6	100%	2e-13	100%	gi|697993457|NP_001289363.1
☐	PREDICTED: biotinidase isoform X2 [Chlorocebus sabaeus]	73.6	73.6	100%	2e-13	100%	gi|635085523|XP_008007381.1
☐	PREDICTED: biotinidase isoform X2 [Macaca fascicularis]	73.6	73.6	100%	2e-13	100%	gi|544411158|XP_005545768.1
☐	PREDICTED: biotinidase isoform X2 [Pan troglodytes]	73.6	73.6	100%	2e-13	100%	gi|694900420|XP_009443239.1
☐	PREDICTED: biotinidase isoform X2 [Pan paniscus]	73.6	73.6	100%	2e-13	100%	gi|675784344|XP_008949921.1
☐	PREDICTED: biotinidase isoform X3 [Pongo abelii]	73.6	73.6	100%	2e-13	100%	gi|686713703|XP_009237577.1
☐	PREDICTED: biotinidase isoform X1 [Chlorocebus sabaeus]	73.6	73.6	100%	2e-13	100%	gi|635085521|XP_008007380.1
☐	PREDICTED: biotinidase isoform X2 [Pongo abelii]	73.6	73.6	100%	2e-13	100%	gi|686713701|XP_009237576.1
☐	biotinidase isoform 3 [Homo sapiens]	73.6	73.6	100%	2e-13	100%	gi|4557373|NP_000051.1
☐	biotinidase isoform 1 [Homo sapiens]	73.6	73.6	100%	2e-13	100%	gi|528524481|NP_001268652.1
☐	biotinidase isoform 2 [Homo sapiens]	73.6	73.6	100%	2e-13	100%	gi|528524483|NP_001268653.1
☐	PREDICTED: biotinidase isoform X1 [Pan troglodytes]	73.6	73.6	100%	2e-13	100%	gi|410036604|XP_003950087.1
☐	PREDICTED: biotinidase isoform X1 [Pan paniscus]	73.6	73.6	100%	2e-13	100%	gi|397511808|XP_003826257.1
☐	PREDICTED: biotinidase isoform X1 [Pongo abelii]	73.6	73.6	100%	2e-13	100%	gi|395734130|XP_003776360.1
☐	hypothetical protein EGM_11114 [Macaca fascicularis]	73.6	73.6	100%	2e-13	100%	gi|355747075|EHH51689.1
☐	hypothetical protein EGK_12122 [Macaca mulatta]	73.6	73.6	100%	2e-13	100%	gi|355560049|EHH16777.1
☐	PREDICTED: biotinidase [Macaca mulatta]	73.6	73.6	100%	2e-13	100%	gi|297286947|XP_001083201.2
☐	PREDICTED: biotinidase isoform X1 [Macaca fascicularis]	73.6	73.6	100%	2e-13	100%	gi|544411156|XP_005545767.1
☐	PREDICTED: biotinidase isoform 1 [Gorilla gorilla gorilla]	71.0	71.0	100%	2e-12	96%	gi|426339607|XP_004033737.1
☐	PREDICTED: biotinidase isoform 3 [Gorilla gorilla gorilla]	71.0	71.0	100%	2e-12	96%	gi|426339611|XP_004033739.1
☐	PREDICTED: biotinidase isoform 4 [Gorilla gorilla gorilla]	71.0	71.0	100%	2e-12	96%	gi|426339613|XP_004033740.1
☐	PREDICTED: biotinidase isoform 2 [Gorilla gorilla gorilla]	71.0	71.0	100%	2e-12	96%	gi|426339609|XP_004033738.1
☐	PREDICTED: biotinidase [Rhinopithecus roxellana]	69.8	69.8	100%	5e-12	96%	gi|724960396|XP_010354361.1
☐	PREDICTED: biotinidase isoform X2 [Papio anubis]	66.0	66.0	100%	1e-10	91%	gi|685527526|XP_009200021.1
☐							

	PREDICTED: biotinidase isoform X1 [Papio anubis]	66.0	66.0	100%	1e-10	91%	gi|685527524|XP_009200020.1
☐	PREDICTED: biotinidase isoform X1 [Callithrix jacchus]	65.1	65.1	100%	2e-10	91%	gi|675740028|XP_008982107.1
☐	PREDICTED: biotinidase isoform X2 [Callithrix jacchus]	65.1	65.1	100%	2e-10	91%	gi|390476393|XP_002759736.2
☐	PREDICTED: biotinidase isoform X4 [Canis lupus familiaris]	57.5	57.5	100%	7e-08	83%	gi|545538859|XP_005634450.1
☐	PREDICTED: biotinidase isoform X3 [Canis lupus familiaris]	57.5	57.5	100%	7e-08	83%	gi|545538857|XP_005634449.1
☐	PREDICTED: biotinidase isoform X2 [Canis lupus familiaris]	57.5	57.5	100%	7e-08	83%	gi|545538855|XP_005634448.1
☐	PREDICTED: biotinidase isoform X1 [Canis lupus familiaris]	57.5	57.5	100%	7e-08	83%	gi|545538853|XP_005634447.1
☐	PREDICTED: biotinidase-like [Ictidomys tridecemlineatus]	57.1	57.1	100%	1e-07	83%	gi|532063189|XP_005317469.1
☐	PREDICTED: biotinidase isoform 2 [Odobenus rosmarus divergens	56.6	56.6	100%	1e-07	83%	gi|472379495|XP_004409157.1
☐	PREDICTED: biotinidase isoform X3 [Saimiri boliviensis boliviensis]	56.6	56.6	100%	1e-07	83%	gi|725560828|XP_010333963.1
☐	PREDICTED: biotinidase isoform 1 [Odobenus rosmarus divergens	56.6	56.6	100%	1e-07	83%	gi|472379493|XP_004409156.1
☐	PREDICTED: biotinidase isoform X2 [Saimiri boliviensis boliviensis]	56.6	56.6	100%	1e-07	83%	gi|403265544|XP_003924991.1
☐	PREDICTED: biotinidase isoform X1 [Saimiri boliviensis boliviensis]	56.6	56.6	100%	1e-07	83%	gi|725560825|XP_010333962.1
☐	PREDICTED: biotinidase isoform X1 [Felis catus]	56.2	56.2	95%	2e-07	82%	gi|587000359|XP_003992187.2
☐	PREDICTED: biotinidase isoform X2 [Felis catus]	56.2	56.2	95%	2e-07	82%	gi|587000357|XP_006936495.1
☐	PREDICTED: biotinidase [Ceratotherium simum simum]	54.5	54.5	100%	7e-07	78%	gi|478490156|XP_004419451.1
☐	PREDICTED: biotinidase [Mesocricetus auratus]	54.1	54.1	95%	1e-06	82%	gi|524955500|XP_005077724.1
☐	PREDICTED: biotinidase [Jaculus jaculus]	53.2	53.2	100%	2e-06	78%	gi|507555213|XP_004661377.1
☐	PREDICTED: biotinidase [Vicugna pacos]	52.8	52.8	100%	3e-06	74%	gi|560965913|XP_006205350.1
☐	PREDICTED: biotinidase isoform X2 [Microtus ochrogaster]	52.8	52.8	95%	3e-06	77%	gi|532009812|XP_005348714.1
☐	PREDICTED: biotinidase isoform X3 [Leptonychotes weddellii]	52.8	52.8	100%	3e-06	78%	gi|585186600|XP_006744787.1
☐	PREDICTED: biotinidase isoform X2 [Leptonychotes weddellii]	52.8	52.8	100%	3e-06	78%	gi|585186598|XP_006744786.1
☐	PREDICTED: biotinidase isoform X1 [Leptonychotes weddellii]	52.8	52.8	100%	3e-06	78%	gi|585186596|XP_006744785.1
☐	PREDICTED: biotinidase isoform X1 [Microtus ochrogaster]	52.8	52.8	95%	3e-06	77%	gi|532009810|XP_005348713.1
☐	biotinidase [Camelus ferus]	52.0	52.0	100%	5e-06	74%	gi|528756912|EPY76571.1
☐	PREDICTED: biotinidase [Camelus ferus]	52.0	52.0	100%	5e-06	74%	gi|560929390|XP_006190847.1
☐	PREDICTED: biotinidase [Panthera tigris altaica]	51.1	51.1	95%	9e-06	77%	gi|591322659|XP_007087428.1
☐	PREDICTED: biotinidase [Otolemur garnettii]	50.7	50.7	100%	1e-05	78%	gi|395816560|XP_003781769.1
☐	PREDICTED: biotinidase-like isoform X10 [Chinchilla lanigera]	50.3	50.3	100%	2e-05	74%	gi|533146084|XP_005387502.1
☐	PREDICTED: biotinidase-like isoform X5 [Chinchilla lanigera]	50.3	50.3	100%	2e-05	74%	gi|533146074|XP_005387497.1
☐	PREDICTED: biotinidase [Condylura cristata]	50.3	50.3	95%	2e-05	77%	gi|507976256|XP_004692357.1
☐	PREDICTED: biotinidase-like isoform X1 [Chinchilla lanigera]	50.3	50.3	100%	2e-05	74%	gi|533146066|XP_005387493.1
☐	PREDICTED: biotinidase [Trichechus manatus latirostris]	49.8	49.8	100%	2e-05	74%	gi|471407481|XP_004385327.1
☐	PREDICTED: biotinidase [Lipotes vexillifer]	49.8	49.8	100%	2e-05	78%	gi|602721076|XP_007470691.1
☐	PREDICTED: biotinidase isoform X1 [Balaenoptera acutorostrata sc	49.8	49.8	100%	2e-05	78%	gi|594624940|XP_007167058.1
☐	PREDICTED: biotinidase isoform X3 [Balaenoptera acutorostrata sc	49.8	49.8	100%	2e-05	78%	gi|594624944|XP_007167060.1
☐	PREDICTED: biotinidase isoform X3 [Equus caballus]	49.4	49.4	95%	3e-05	77%	gi|545189350|XP_005600979.1
☐	PREDICTED: biotinidase [Equus przewalskii]	49.4	49.4	95%	3e-05	77%	gi|664753751|XP_008534346.1
☐	PREDICTED: biotinidase isoform X2 [Equus caballus]	49.4	49.4	95%	3e-05	77%	gi|545189348|XP_005600978.1
☐	PREDICTED: biotinidase [Mustela putorius furo]	49.4	49.4	100%	3e-05	74%	gi|511908359|XP_004773614.1
☐	PREDICTED: biotinidase isoform X1 [Equus caballus]	49.4	49.4	95%	3e-05	77%	gi|545189346|XP_005600977.1
☐	PREDICTED: biotinidase isoform X2 [Ursus maritimus]	49.0	49.0	100%	5e-05	74%	gi|670981874|XP_008707139.1
☐	PREDICTED: biotinidase isoform X1 [Ursus maritimus]	49.0	49.0	100%	5e-05	74%	gi|670981872|XP_008707130.1
☐	PREDICTED: biotinidase [Fukomys damarensis]	49.0	49.0	100%	5e-05	74%	gi|731285322|XP_010611073.1
☐	Biotinidase [Fukomys damarensis]	49.0	49.0	100%	5e-05	74%	gi|676263045|KFO19807.1

☐	PREDICTED: biotinidase isoform X2 [Cricetulus griseus]	48.6	48.6	95%	6e-05	77%	gi|625181248|XP_007632389.1
☐	PREDICTED: biotinidase isoform X1 [Cricetulus griseus]	48.6	48.6	95%	6e-05	77%	gi|354465853|XP_003495391.1
☐	biotinidase [Cricetulus griseus]	48.6	48.6	95%	6e-05	77%	gi|537261432|ERE90059.1
☐	PREDICTED: biotinidase [Erinaceus europaeus]	48.1	48.1	95%	9e-05	73%	gi|617553342|XP_007530134.1
☐	PREDICTED: biotinidase [Galeopterus variegatus]	47.7	47.7	100%	1e-04	74%	gi|667288263|XP_008576771.1
☐	PREDICTED: LOW QUALITY PROTEIN: biotinidase [Tursiops trun	47.3	47.3	100%	2e-04	74%	gi|470628904|XP_004321284.1
☐	PREDICTED: biotinidase [Orcinus orca]	47.3	47.3	100%	2e-04	74%	gi|466019817|XP_004271983.1
☐	PREDICTED: biotinidase isoform X2 [Physeter catodon]	46.9	46.9	100%	2e-04	74%	gi|593711507|XP_007102308.1
☐	PREDICTED: biotinidase isoform X1 [Physeter catodon]	46.9	46.9	100%	2e-04	74%	gi|593711505|XP_007102307.1
☐	PREDICTED: biotinidase isoform X1 [Peromyscus maniculatus bair	46.0	46.0	95%	4e-04	68%	gi|589967608|XP_006996305.1
☐	PREDICTED: biotinidase isoform X2 [Peromyscus maniculatus bair	46.0	46.0	95%	4e-04	68%	gi|589967610|XP_006996306.1
☐	PREDICTED: biotinidase isoform X1 [Myotis lucifugus]	45.2	45.2	100%	8e-04	74%	gi|558102610|XP_006083737.1
☐	PREDICTED: biotinidase isoform X3 [Myotis brandtii]	45.2	45.2	100%	8e-04	74%	gi|554537982|XP_005863672.1
☐	PREDICTED: biotinidase isoform X2 [Myotis lucifugus]	45.2	45.2	100%	8e-04	74%	gi|558102613|XP_006083738.1
☐	PREDICTED: biotinidase isoform X2 [Myotis brandtii]	45.2	45.2	100%	8e-04	74%	gi|554537986|XP_005863671.1
☐	Biotinidase [Myotis brandtii]	45.2	45.2	100%	8e-04	74%	gi|521024341|EPQ06129.1
☐	PREDICTED: biotinidase-like [Ailuropoda melanoleuca]	44.8	44.8	100%	0.001	70%	gi|301759093|XP_002915396.1
☐	hypothetical protein PANDA_003369 [Ailuropoda melanoleuca]	44.8	44.8	100%	0.001	70%	gi|281345880|EFB21464.1
☐	biotinidase, isoform CRA_a [Rattus norvegicus]	44.3	44.3	95%	0.001	68%	gi|149034168|EDL88938.1
☐	biotinidase, isoform CRA_c [Rattus norvegicus]	44.3	44.3	95%	0.001	68%	gi|149034170|EDL88940.1
☐	biotinidase precursor [Rattus norvegicus]	44.3	44.3	95%	0.001	68%	gi|58865670|NP_001012047.1
☐	PREDICTED: biotinidase isoform X2 [Rattus norvegicus]	44.3	44.3	95%	0.001	68%	gi|564387894|XP_006252671.1
☐	PREDICTED: biotinidase isoform X1 [Cavia porcellus]	43.9	43.9	100%	0.002	70%	gi|514481133|XP_003480063.2
☐	PREDICTED: biotinidase isoform X2 [Cavia porcellus]	43.9	43.9	100%	0.002	70%	gi|514481131|XP_005008361.1
☐	PREDICTED: biotinidase [Nannospalax galili]	43.5	43.5	100%	0.003	70%	gi|674081213|XP_008848205.1
☐	Biotinidase [Heterocephalus glaber]	43.1	43.1	100%	0.004	65%	gi|351707565|EHB10484.1
☐	PREDICTED: biotinidase isoform X3 [Heterocephalus glaber]	43.1	43.1	100%	0.004	65%	gi|512886961|XP_004896459.1

⊟ Alignments

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PREDICTED: biotinidase [Nomascus leucogenys]

Sequence ID: gi|332232450|ref|XP_003265417.1| **Length:** 474 **Number of Matches:** 1

Range 1: 270 to 292 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.6 bits(166)	2e-13	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    KNPVGLIGAENATGETDPSHSKF  23
            KNPVGLIGAENATGETDPSHSKF
Sbjct  270  KNPVGLIGAENATGETDPSHSKF  292
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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unnamed protein product [Macaca fascicularis]

Sequence ID: gi|90077268|dbj|BAE88314.1| **Length:** 493 **Number of Matches:** 1

Range 1: 323 to 345 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.6 bits(166)	2e-13	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    KNPVGLIGAENATGETDPSHSKF  23
```

Related Information

Gene - associated gene details

```
             KNPVGLIGAENATGETDPSHSKF
Sbjct  323  KNPVGLIGAENATGETDPSHSKF  345
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221043776|dbj|BAH13565.1| **Length:** 523 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 319 to 341 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.6 bits(166)	2e-13	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    KNPVGLIGAENATGETDPSHSKF  23
            KNPVGLIGAENATGETDPSHSKF
Sbjct  319  KNPVGLIGAENATGETDPSHSKF  341
```

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biotinidase isoform 4 precursor [Homo sapiens]

Sequence ID: gi|528524486|ref|NP_001268654.1| **Length:** 523 **Number of Matches:** 1

See 3 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 319 to 341 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.6 bits(166)	2e-13	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    KNPVGLIGAENATGETDPSHSKF  23
            KNPVGLIGAENATGETDPSHSKF
Sbjct  319  KNPVGLIGAENATGETDPSHSKF  341
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

biotinidase precursor [Pan troglodytes]

Sequence ID: gi|697993457|ref|NP_001289363.1| **Length:** 523 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 319 to 341 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.6 bits(166)	2e-13	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    KNPVGLIGAENATGETDPSHSKF  23
            KNPVGLIGAENATGETDPSHSKF
Sbjct  319  KNPVGLIGAENATGETDPSHSKF  341
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ **Formatting Results - B9211R2A01R**

Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

BTD_KNPVGLIGAENATGETDPSHSKFLKI_NonMod

RID B9211R2A01R (Expires on 01-14 09:51 am)

Query ID	lcl|105458	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	26		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

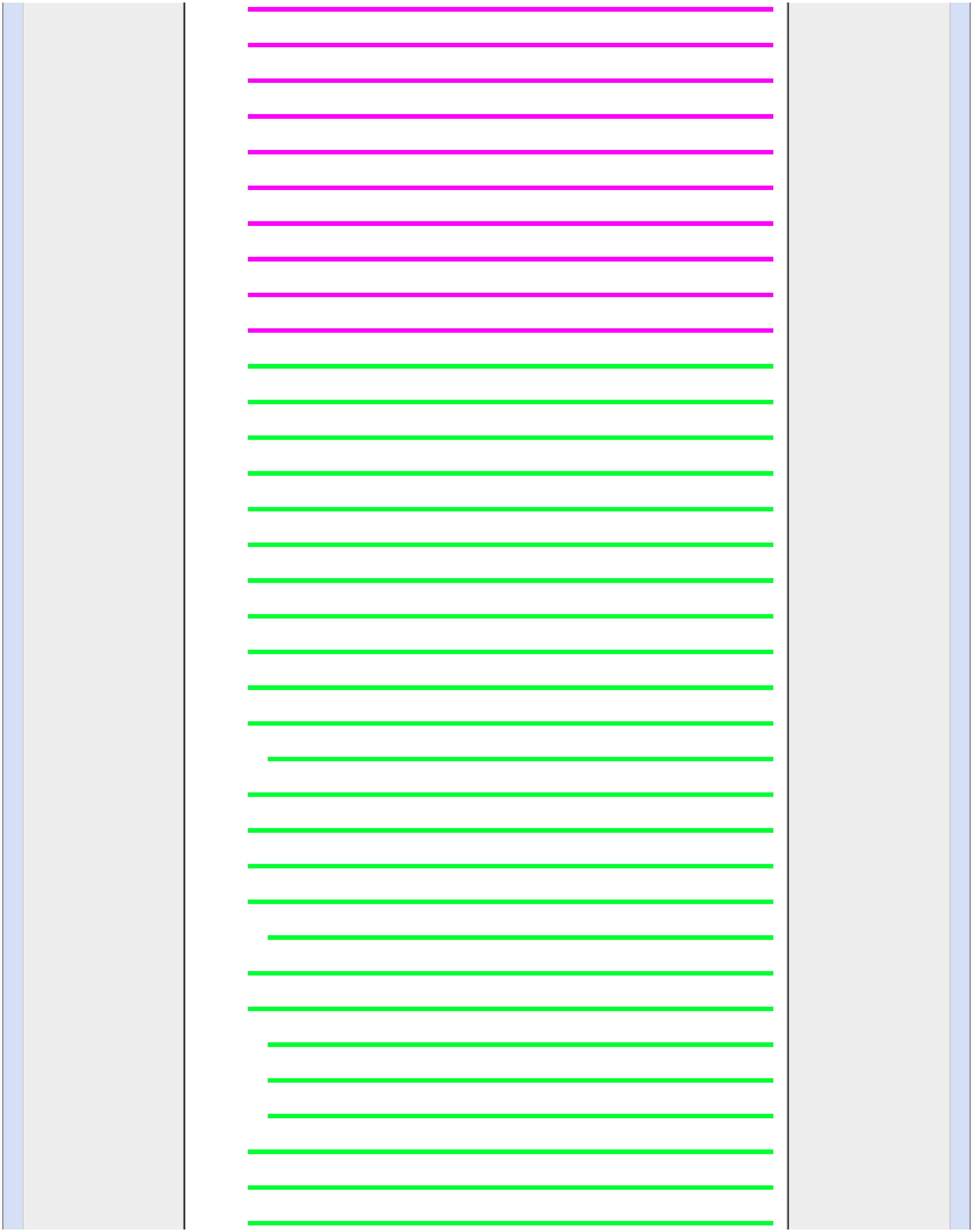
Graphic Summary

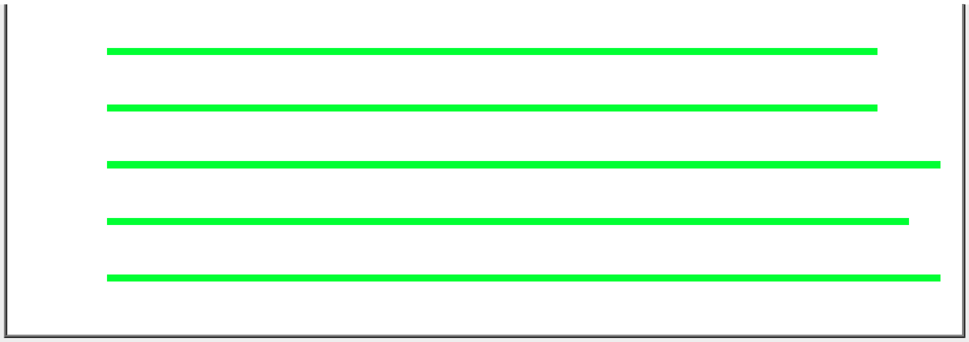
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: biotinidase [Nomascus leucogenys]	82.9	82.9	100%	2e-16	100%	gi|332232450|XP_003265417.1
☐	unnamed protein product [Macaca fascicularis]	82.9	82.9	100%	2e-16	100%	gi|90077268|BAE88314.1
☐	unnamed protein product [Homo sapiens]	82.9	82.9	100%	2e-16	100%	gi|221043776|BAH13565.1
☐	biotinidase isoform 4 precursor [Homo sapiens]	82.9	82.9	100%	2e-16	100%	gi|528524486|NP_001268654.1
☐	biotinidase precursor [Pan troglodytes]	82.9	82.9	100%	2e-16	100%	gi|697993457|NP_001289363.1
☐	PREDICTED: biotinidase isoform X2 [Chlorocebus sabaeus]	82.9	82.9	100%	2e-16	100%	gi|635085523|XP_008007381.1
☐	PREDICTED: biotinidase isoform X2 [Macaca fascicularis]	82.9	82.9	100%	2e-16	100%	gi|544411158|XP_005545768.1
☐	PREDICTED: biotinidase isoform X2 [Pan troglodytes]	82.9	82.9	100%	2e-16	100%	gi|694900420|XP_009443239.1
☐	PREDICTED: biotinidase isoform X2 [Pan paniscus]	82.9	82.9	100%	2e-16	100%	gi|675784344|XP_008949921.1
☐	PREDICTED: biotinidase isoform X3 [Pongo abelii]	82.9	82.9	100%	2e-16	100%	gi|686713703|XP_009237577.1
☐	PREDICTED: biotinidase isoform X1 [Chlorocebus sabaeus]	82.9	82.9	100%	2e-16	100%	gi|635085521|XP_008007380.1
☐	PREDICTED: biotinidase isoform X2 [Pongo abelii]	82.9	82.9	100%	2e-16	100%	gi|686713701|XP_009237576.1
☐	biotinidase isoform 3 [Homo sapiens]	82.9	82.9	100%	2e-16	100%	gi|4557373|NP_000051.1
☐	biotinidase isoform 1 [Homo sapiens]	82.9	82.9	100%	2e-16	100%	gi|528524481|NP_001268652.1
☐	biotinidase isoform 2 [Homo sapiens]	82.9	82.9	100%	2e-16	100%	gi|528524483|NP_001268653.1
☐	PREDICTED: biotinidase isoform X1 [Pan troglodytes]	82.9	82.9	100%	2e-16	100%	gi|410036604|XP_003950087.1
☐	PREDICTED: biotinidase isoform X1 [Pan paniscus]	82.9	82.9	100%	2e-16	100%	gi|397511808|XP_003826257.1
☐	PREDICTED: biotinidase isoform X1 [Pongo abelii]	82.9	82.9	100%	2e-16	100%	gi|395734130|XP_003776360.1
☐	hypothetical protein EGM_11114 [Macaca fascicularis]	82.9	82.9	100%	2e-16	100%	gi|355747075|EHH51689.1
☐	hypothetical protein EGK_12122 [Macaca mulatta]	82.9	82.9	100%	2e-16	100%	gi|355560049|EHH16777.1
☐	PREDICTED: biotinidase [Macaca mulatta]	82.9	82.9	100%	2e-16	100%	gi|297286947|XP_001083201.2
☐	PREDICTED: biotinidase isoform X1 [Macaca fascicularis]	82.9	82.9	100%	2e-16	100%	gi|544411156|XP_005545767.1
☐	PREDICTED: biotinidase isoform 1 [Gorilla gorilla gorilla]	80.4	80.4	100%	2e-15	96%	gi|426339607|XP_004033737.1
☐	PREDICTED: biotinidase isoform 3 [Gorilla gorilla gorilla]	80.4	80.4	100%	2e-15	96%	gi|426339611|XP_004033739.1
☐	PREDICTED: biotinidase isoform 4 [Gorilla gorilla gorilla]	80.4	80.4	100%	2e-15	96%	gi|426339613|XP_004033740.1
☐	PREDICTED: biotinidase isoform 2 [Gorilla gorilla gorilla]	80.4	80.4	100%	2e-15	96%	gi|426339609|XP_004033738.1
☐	PREDICTED: biotinidase [Rhinopithecus roxellana]	79.1	79.1	100%	5e-15	96%	gi|724960396|XP_010354361.1
☐	PREDICTED: biotinidase isoform X2 [Papio anubis]	75.3	75.3	100%	1e-13	92%	gi|685527526|XP_009200021.1
☐							

	PREDICTED: biotinidase isoform X1 [Papio anubis]	75.3	75.3	100%	1e-13	92%	gi|685527524|XP_009200020.1
☐	PREDICTED: biotinidase isoform X1 [Callithrix jacchus]	74.4	74.4	100%	2e-13	92%	gi|675740028|XP_008982107.1
☐	PREDICTED: biotinidase isoform X2 [Callithrix jacchus]	74.4	74.4	100%	2e-13	92%	gi|390476393|XP_002759736.2
☐	PREDICTED: biotinidase-like [Ictidomys tridecemlineatus]	66.4	66.4	100%	1e-10	85%	gi|532063189|XP_005317469.1
☐	PREDICTED: biotinidase isoform X3 [Saimiri boliviensis boliviensis]	66.0	66.0	100%	1e-10	85%	gi|725560828|XP_010333963.1
☐	PREDICTED: biotinidase isoform X2 [Saimiri boliviensis boliviensis]	66.0	66.0	100%	1e-10	85%	gi|403265544|XP_003924991.1
☐	PREDICTED: biotinidase isoform X1 [Saimiri boliviensis boliviensis]	66.0	66.0	100%	1e-10	85%	gi|725560825|XP_010333962.1
☐	PREDICTED: biotinidase [Ceratotherium simum simum]	63.8	63.8	100%	7e-10	81%	gi|478490156|XP_004419451.1
☐	PREDICTED: biotinidase [Vicugna pacos]	62.1	62.1	100%	3e-09	77%	gi|560965913|XP_006205350.1
☐	PREDICTED: biotinidase isoform X2 [Microtus ochrogaster]	62.1	62.1	96%	3e-09	80%	gi|532009812|XP_005348714.1
☐	PREDICTED: biotinidase isoform X4 [Canis lupus familiaris]	62.1	62.1	100%	3e-09	81%	gi|545538859|XP_005634450.1
☐	PREDICTED: biotinidase isoform X3 [Canis lupus familiaris]	62.1	62.1	100%	3e-09	81%	gi|545538857|XP_005634449.1
☐	PREDICTED: biotinidase isoform X2 [Canis lupus familiaris]	62.1	62.1	100%	3e-09	81%	gi|545538855|XP_005634448.1
☐	PREDICTED: biotinidase isoform X1 [Canis lupus familiaris]	62.1	62.1	100%	3e-09	81%	gi|545538853|XP_005634447.1
☐	PREDICTED: biotinidase isoform X1 [Microtus ochrogaster]	62.1	62.1	96%	3e-09	80%	gi|532009810|XP_005348713.1
☐	biotinidase [Camelus ferus]	61.3	61.3	100%	5e-09	77%	gi|528756912|EPY76571.1
☐	PREDICTED: biotinidase [Camelus ferus]	61.3	61.3	100%	5e-09	77%	gi|560929390|XP_006190847.1
☐	PREDICTED: biotinidase isoform X1 [Felis catus]	60.9	60.9	96%	7e-09	80%	gi|587000359|XP_003992187.2
☐	PREDICTED: biotinidase isoform X2 [Felis catus]	60.9	60.9	96%	7e-09	80%	gi|587000357|XP_006936495.1
☐	PREDICTED: biotinidase [Mesocricetus auratus]	60.4	60.4	96%	1e-08	80%	gi|524955500|XP_005077724.1
☐	PREDICTED: biotinidase [Otolemur garnettii]	60.0	60.0	100%	1e-08	81%	gi|395816560|XP_003781769.1
☐	PREDICTED: biotinidase-like isoform X10 [Chinchilla lanigera]	59.6	59.6	100%	2e-08	77%	gi|533146084|XP_005387502.1
☐	PREDICTED: biotinidase-like isoform X5 [Chinchilla lanigera]	59.6	59.6	100%	2e-08	77%	gi|533146074|XP_005387497.1
☐	PREDICTED: biotinidase isoform 2 [Odobenus rosmarus divergens	59.6	59.6	92%	2e-08	83%	gi|472379495|XP_004409157.1
☐	PREDICTED: biotinidase isoform 1 [Odobenus rosmarus divergens	59.6	59.6	92%	2e-08	83%	gi|472379493|XP_004409156.1
☐	PREDICTED: biotinidase-like isoform X1 [Chinchilla lanigera]	59.6	59.6	100%	2e-08	77%	gi|533146066|XP_005387493.1
☐	PREDICTED: biotinidase [Jaculus jaculus]	59.2	59.2	96%	3e-08	80%	gi|507555213|XP_004661377.1
☐	PREDICTED: biotinidase [Trichechus manatus latirostris]	59.2	59.2	100%	3e-08	77%	gi|471407481|XP_004385327.1
☐	PREDICTED: biotinidase [Lipotes vexillifer]	59.2	59.2	100%	3e-08	81%	gi|602721076|XP_007470691.1
☐	PREDICTED: biotinidase isoform X1 [Balaenoptera acutorostrata sc	59.2	59.2	100%	3e-08	81%	gi|594624940|XP_007167058.1
☐	PREDICTED: biotinidase isoform X3 [Balaenoptera acutorostrata sc	59.2	59.2	100%	3e-08	81%	gi|594624944|XP_007167060.1
☐	PREDICTED: biotinidase isoform X3 [Equus caballus]	58.7	58.7	96%	4e-08	80%	gi|545189350|XP_005600979.1
☐	PREDICTED: biotinidase [Equus przewalskii]	58.7	58.7	96%	4e-08	80%	gi|664753751|XP_008534346.1
☐	PREDICTED: biotinidase isoform X2 [Equus caballus]	58.7	58.7	96%	4e-08	80%	gi|545189348|XP_005600978.1
☐	PREDICTED: biotinidase isoform X1 [Equus caballus]	58.7	58.7	96%	4e-08	80%	gi|545189346|XP_005600977.1
☐	PREDICTED: biotinidase [Fukomys damarensis]	58.3	58.3	100%	5e-08	77%	gi|731285322|XP_010611073.1
☐	Biotinidase [Fukomys damarensis]	58.3	58.3	100%	5e-08	77%	gi|676263045|KFO19807.1
☐	PREDICTED: biotinidase isoform X2 [Cricetulus griseus]	57.9	57.9	96%	7e-08	80%	gi|625181248|XP_007632389.1
☐	PREDICTED: biotinidase isoform X1 [Cricetulus griseus]	57.9	57.9	96%	7e-08	80%	gi|354465853|XP_003495391.1
☐	biotinidase [Cricetulus griseus]	57.9	57.9	96%	7e-08	80%	gi|537261432|ERE90059.1
☐	PREDICTED: biotinidase [Erinaceus europaeus]	57.5	57.5	96%	1e-07	76%	gi|617553342|XP_007530134.1
☐	PREDICTED: biotinidase [Galeopterus variegatus]	57.1	57.1	100%	1e-07	77%	gi|667288263|XP_008576771.1
☐	PREDICTED: LOW QUALITY PROTEIN: biotinidase [Tursiops trunc	56.6	56.6	100%	2e-07	77%	gi|470628904|XP_004321284.1
☐	PREDICTED: biotinidase [Orcinus orca]	56.6	56.6	100%	2e-07	77%	gi|466019817|XP_004271983.1
☐	PREDICTED: biotinidase isoform X2 [Physeter catodon]	56.2	56.2	100%	3e-07	77%	gi|593711507|XP_007102308.1

☐	PREDICTED: biotinidase [Condylura cristata]	56.2	56.2	92%	3e-07	79%	gi|507976256|XP_004692357.1
☐	PREDICTED: biotinidase isoform X1 [Physeter catodon]	56.2	56.2	100%	3e-07	77%	gi|593711505|XP_007102307.1
☐	PREDICTED: biotinidase [Panthera tigris altaica]	55.8	55.8	96%	4e-07	76%	gi|591322659|XP_007087428.1
☐	PREDICTED: biotinidase isoform X3 [Leptonychotes weddellii]	55.8	55.8	92%	4e-07	79%	gi|585186600|XP_006744787.1
☐	PREDICTED: biotinidase isoform X2 [Leptonychotes weddellii]	55.8	55.8	92%	4e-07	79%	gi|585186598|XP_006744786.1
☐	PREDICTED: biotinidase isoform X1 [Leptonychotes weddellii]	55.8	55.8	92%	4e-07	79%	gi|585186596|XP_006744785.1
☐	PREDICTED: biotinidase isoform X1 [Peromyscus maniculatus bair	55.4	55.4	96%	5e-07	72%	gi|589967608|XP_006996305.1
☐	PREDICTED: biotinidase isoform X2 [Peromyscus maniculatus bair	55.4	55.4	96%	5e-07	72%	gi|589967610|XP_006996306.1
☐	PREDICTED: biotinidase [Nannospalax galili]	52.8	52.8	100%	3e-06	73%	gi|674081213|XP_008848205.1
☐	Biotinidase [Heterocephalus glaber]	52.4	52.4	100%	5e-06	69%	gi|351707565|EHB10484.1
☐	PREDICTED: biotinidase [Mustela putorius furo]	52.4	52.4	92%	5e-06	75%	gi|511908359|XP_004773614.1
☐	PREDICTED: biotinidase isoform X3 [Heterocephalus glaber]	52.4	52.4	100%	5e-06	69%	gi|512886961|XP_004896459.1
☐	PREDICTED: biotinidase isoform X1 [Heterocephalus glaber]	52.4	52.4	100%	5e-06	69%	gi|512886949|XP_004896457.1
☐	PREDICTED: biotinidase isoform X2 [Ursus maritimus]	52.0	52.0	92%	6e-06	75%	gi|670981874|XP_008707139.1
☐	PREDICTED: biotinidase isoform X1 [Ursus maritimus]	52.0	52.0	92%	6e-06	75%	gi|670981872|XP_008707130.1
☐	biotinidase, isoform CRA_a [Rattus norvegicus]	51.1	51.1	96%	1e-05	68%	gi|149034168|EDL88938.1
☐	biotinidase, isoform CRA_c [Rattus norvegicus]	51.1	51.1	96%	1e-05	68%	gi|149034170|EDL88940.1
☐	biotinidase precursor [Rattus norvegicus]	51.1	51.1	96%	1e-05	68%	gi|58865670|NP_001012047.1
☐	PREDICTED: biotinidase isoform X1 [Myotis lucifugus]	51.1	51.1	96%	1e-05	76%	gi|558102610|XP_006083737.1
☐	PREDICTED: biotinidase isoform X3 [Myotis brandtii]	51.1	51.1	96%	1e-05	76%	gi|554537982|XP_005863672.1
☐	PREDICTED: biotinidase isoform X2 [Myotis lucifugus]	51.1	51.1	96%	1e-05	76%	gi|558102613|XP_006083738.1
☐	PREDICTED: biotinidase isoform X2 [Myotis brandtii]	51.1	51.1	96%	1e-05	76%	gi|554537986|XP_005863671.1
☐	PREDICTED: biotinidase isoform X2 [Rattus norvegicus]	51.1	51.1	96%	1e-05	68%	gi|564387894|XP_006252671.1
☐	Biotinidase [Myotis brandtii]	51.1	51.1	96%	1e-05	76%	gi|521024341|EPQ06129.1
☐	PREDICTED: biotinidase-like [Octodon degus]	49.4	49.4	96%	4e-05	76%	gi|507646799|XP_004631734.1
☐	PREDICTED: biotinidase [Loxodonta africana]	49.0	49.0	100%	6e-05	69%	gi|731510838|XP_010598778.1
☐	PREDICTED: biotinidase [Orycteropus afer afer]	48.6	48.6	100%	8e-05	69%	gi|634822252|XP_007934900.1

Alignments

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PREDICTED: biotinidase [Nomascus leucogenys]

Sequence ID: gi|332232450|ref|XP_003265417.1| **Length:** 474 **Number of Matches:** 1

Range 1: 270 to 295 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.9 bits(188)	2e-16	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KNPVGLIGAENATGETDPSHSKFLKI  26
            KNPVGLIGAENATGETDPSHSKFLKI
Sbjct  270  KNPVGLIGAENATGETDPSHSKFLKI  295
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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unnamed protein product [Macaca fascicularis]

Sequence ID: gi|90077268|dbj|BAE88314.1| **Length:** 493 **Number of Matches:** 1

Range 1: 323 to 348 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.9 bits(188)	2e-16	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KNPVGLIGAENATGETDPSHSKFLKI  26
```

Related Information

Gene - associated gene details

```
                 KNPVGLIGAENATGETDPSHSKFLKI
Sbjct  323  KNPVGLIGAENATGETDPSHSKFLKI  348
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221043776|dbj|BAH13565.1| **Length:** 523 **Number of Matches:** 1

Range 1: 319 to 344 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.9 bits(188)	2e-16	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KNPVGLIGAENATGETDPSHSKFLKI  26
            KNPVGLIGAENATGETDPSHSKFLKI
Sbjct  319  KNPVGLIGAENATGETDPSHSKFLKI  344
```

Related Information

Gene - associated gene details

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biotinidase isoform 4 precursor [Homo sapiens]

Sequence ID: gi|528524486|ref|NP_001268654.1| **Length:** 523 **Number of Matches:** 1

▷ See 3 more title(s)

Range 1: 319 to 344 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.9 bits(188)	2e-16	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KNPVGLIGAENATGETDPSHSKFLKI  26
            KNPVGLIGAENATGETDPSHSKFLKI
Sbjct  319  KNPVGLIGAENATGETDPSHSKFLKI  344
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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biotinidase precursor [Pan troglodytes]

Sequence ID: gi|697993457|ref|NP_001289363.1| **Length:** 523 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 319 to 344 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.9 bits(188)	2e-16	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KNPVGLIGAENATGETDPSHSKFLKI  26
            KNPVGLIGAENATGETDPSHSKFLKI
Sbjct  319  KNPVGLIGAENATGETDPSHSKFLKI  344
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

BTD_KSHLIIAQVAKNPVGLIGAEDATGETDPSHSKF_Mod

RID BT3AEDCA013 (Expires on 01-20 11:51 am)

Query ID	lcl|6932	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	33		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

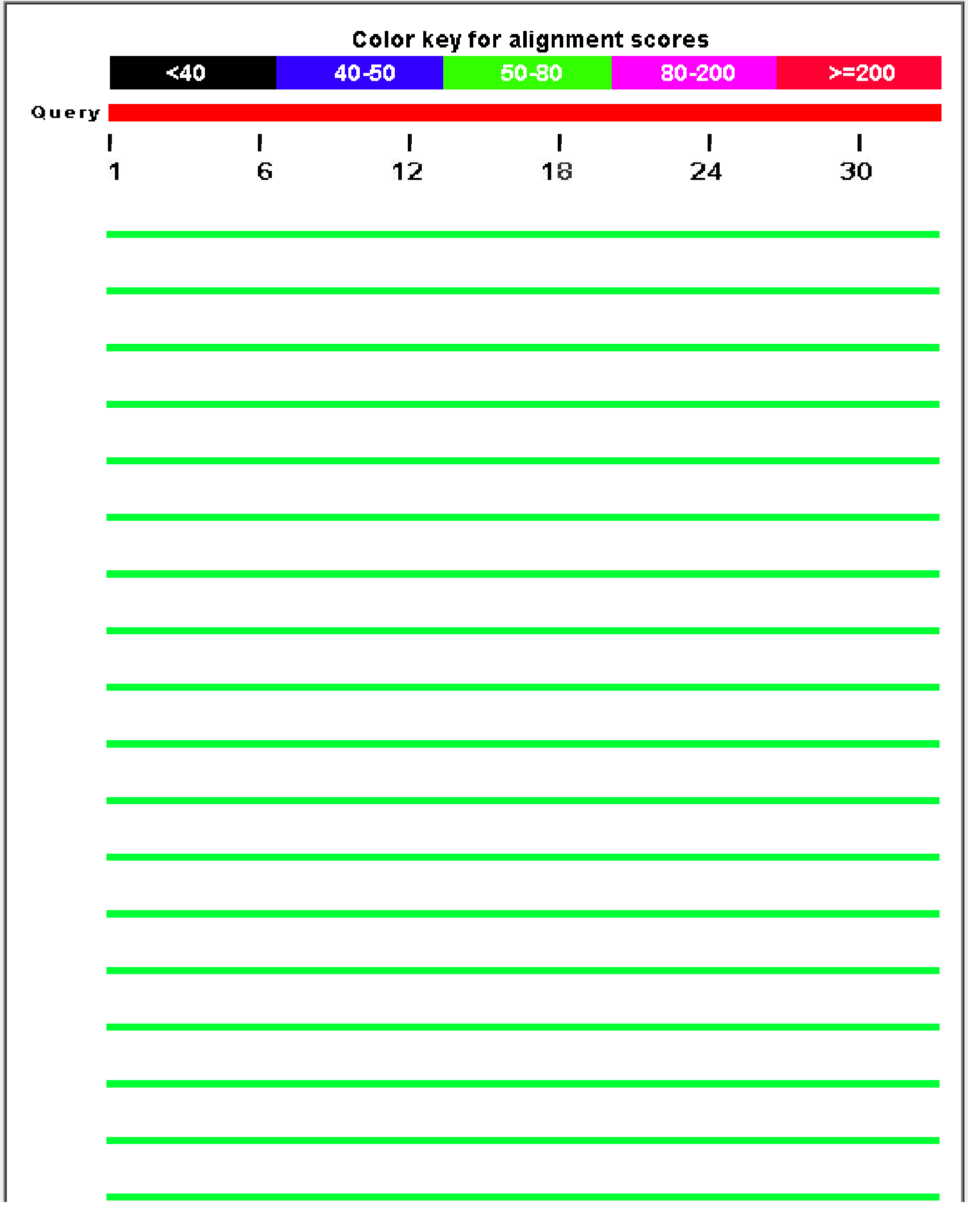
Graphic Summary

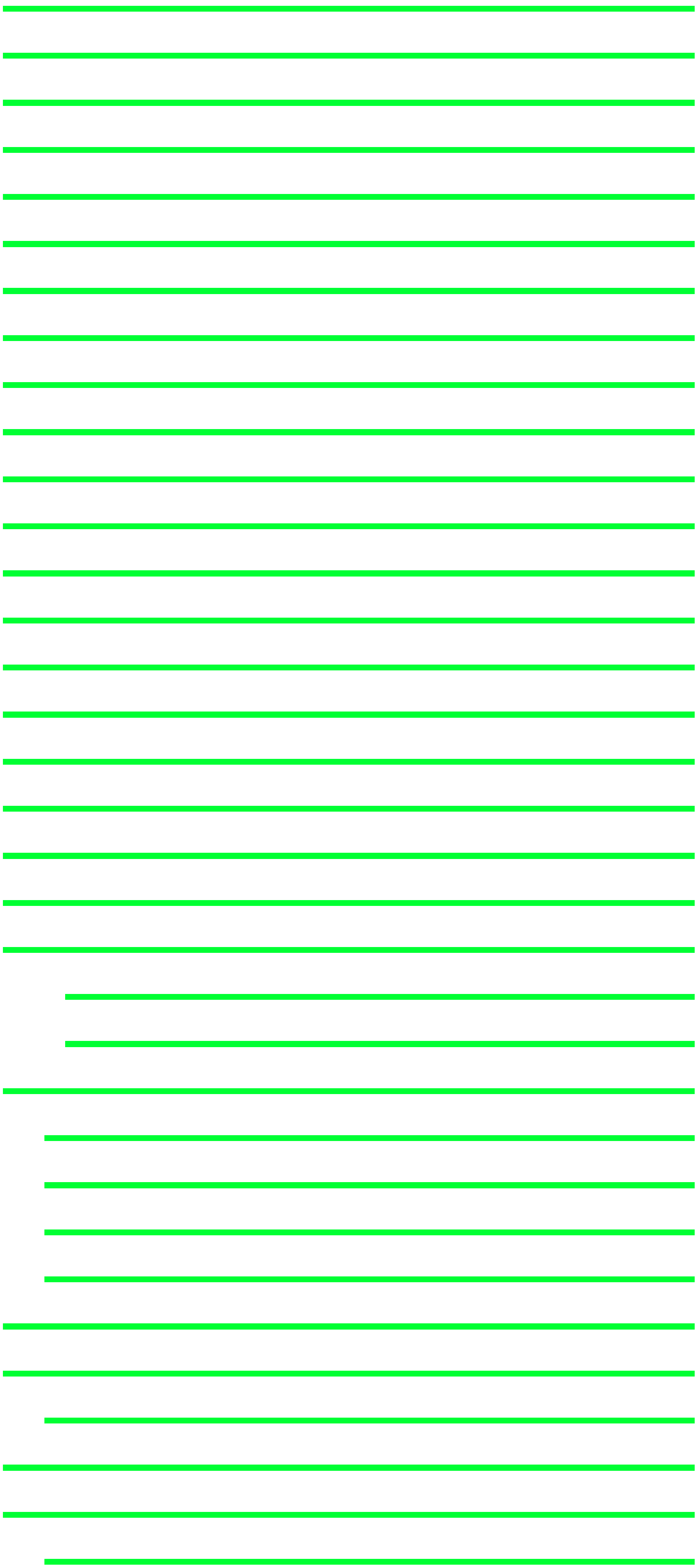
Show Conserved Domains

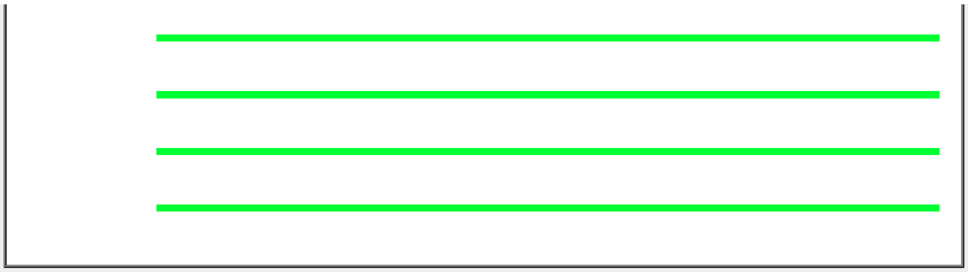
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: biotinidase [Nomascus leucogenys]	67.4	67.4	100%	8e-12	97%	gi|332232450|XP_003265417.1
☐	unnamed protein product [Homo sapiens]	67.4	67.4	100%	8e-12	97%	gi|221043776|BAH13565.1
☐	biotinidase isoform 4 precursor [Homo sapiens]	67.4	67.4	100%	8e-12	97%	gi|528524486|NP_001268654.1
☐	biotinidase precursor [Pan troglodytes]	67.4	67.4	100%	8e-12	97%	gi|697993457|NP_001289363.1
☐	PREDICTED: biotinidase isoform X2 [Pan troglodytes]	67.4	67.4	100%	9e-12	97%	gi|694900420|XP_009443239.1
☐	PREDICTED: biotinidase isoform X2 [Pan paniscus]	67.4	67.4	100%	9e-12	97%	gi|675784344|XP_008949921.1
☐	PREDICTED: biotinidase isoform X3 [Pongo abelii]	67.4	67.4	100%	9e-12	97%	gi|686713703|XP_009237577.1
☐	PREDICTED: biotinidase isoform X2 [Pongo abelii]	67.4	67.4	100%	9e-12	97%	gi|686713701|XP_009237576.1
☐	biotinidase isoform 3 [Homo sapiens]	67.4	67.4	100%	9e-12	97%	gi|4557373|NP_000051.1
☐	biotinidase isoform 1 [Homo sapiens]	67.4	67.4	100%	9e-12	97%	gi|528524481|NP_001268652.1
☐	biotinidase isoform 2 [Homo sapiens]	67.4	67.4	100%	9e-12	97%	gi|528524483|NP_001268653.1
☐	PREDICTED: biotinidase isoform X1 [Pan troglodytes]	67.4	67.4	100%	9e-12	97%	gi|410036604|XP_003950087.1
☐	PREDICTED: biotinidase isoform X1 [Pan paniscus]	67.4	67.4	100%	9e-12	97%	gi|397511808|XP_003826257.1
☐	PREDICTED: biotinidase isoform X1 [Pongo abelii]	67.4	67.4	100%	9e-12	97%	gi|395734130|XP_003776360.1
☐	PREDICTED: biotinidase isoform 1 [Gorilla gorilla gorilla]	67.0	67.0	100%	1e-11	94%	gi|426339607|XP_004033737.1
☐	PREDICTED: biotinidase isoform 3 [Gorilla gorilla gorilla]	67.0	67.0	100%	1e-11	94%	gi|426339611|XP_004033739.1
☐	PREDICTED: biotinidase isoform 4 [Gorilla gorilla gorilla]	67.0	67.0	100%	1e-11	94%	gi|426339613|XP_004033740.1
☐	PREDICTED: biotinidase isoform 2 [Gorilla gorilla gorilla]	67.0	67.0	100%	1e-11	94%	gi|426339609|XP_004033738.1
☐	unnamed protein product [Macaca fascicularis]	65.9	65.9	100%	3e-11	94%	gi|90077268|BAE88314.1
☐	PREDICTED: biotinidase isoform X2 [Macaca fascicularis]	65.9	65.9	100%	3e-11	94%	gi|544411158|XP_005545768.1
☐	hypothetical protein EGM_11114 [Macaca fascicularis]	65.9	65.9	100%	3e-11	94%	gi|355747075|EHH51689.1
☐	hypothetical protein EGK_12122 [Macaca mulatta]	65.9	65.9	100%	3e-11	94%	gi|355560049|EHH16777.1
☐	PREDICTED: biotinidase [Macaca mulatta]	65.9	65.9	100%	3e-11	94%	gi|297286947|XP_001083201.2
☐	PREDICTED: biotinidase isoform X1 [Macaca fascicularis]	65.9	65.9	100%	3e-11	94%	gi|544411156|XP_005545767.1
☐	PREDICTED: biotinidase isoform X2 [Chlorocebus sabaeus]	64.3	64.3	100%	1e-10	91%	gi|635085523|XP_008007381.1
☐	PREDICTED: biotinidase isoform X1 [Chlorocebus sabaeus]	64.3	64.3	100%	1e-10	91%	gi|635085521|XP_008007380.1
☐	PREDICTED: biotinidase [Rhinopithecus roxellana]	61.6	61.6	100%	9e-10	85%	gi|724960396|XP_010354361.1
☐	PREDICTED: biotinidase isoform X2 [Papio anubis]	60.5	60.5	100%	2e-09	85%	gi|685527526|XP_009200021.1
☐	PREDICTED: biotinidase isoform X1 [Papio anubis]	60.5	60.5	100%	3e-09	85%	gi|685527524|XP_009200020.1
☐	PREDICTED: biotinidase isoform X4 [Canis lupus familiaris]	58.5	58.5	100%	1e-08	79%	gi|545538859|XP_005634450.1

☐	PREDICTED: biotinidase isoform X3 [Canis lupus familiaris]	58.5	58.5	100%	1e-08	79%	gi|545538857|XP_005634449.1
☐	PREDICTED: biotinidase isoform X2 [Canis lupus familiaris]	58.5	58.5	100%	1e-08	79%	gi|545538855|XP_005634448.1
☐	PREDICTED: biotinidase isoform X1 [Canis lupus familiaris]	58.5	58.5	100%	1e-08	79%	gi|545538853|XP_005634447.1
☐	PREDICTED: biotinidase-like [Ictidomys tridecemlineatus]	58.2	58.2	100%	1e-08	79%	gi|532063189|XP_005317469.1
☐	PREDICTED: biotinidase [Ceratotherium simum simum]	58.2	58.2	100%	2e-08	79%	gi|478490156|XP_004419451.1
☐	PREDICTED: biotinidase isoform X3 [Equus caballus]	56.6	56.6	100%	5e-08	76%	gi|545189350|XP_005600979.1
☐	PREDICTED: biotinidase [Equus przewalskii]	56.6	56.6	100%	5e-08	76%	gi|664753751|XP_008534346.1
☐	PREDICTED: biotinidase isoform X2 [Equus caballus]	56.6	56.6	100%	5e-08	76%	gi|545189348|XP_005600978.1
☐	PREDICTED: biotinidase isoform X1 [Equus caballus]	56.6	56.6	100%	5e-08	76%	gi|545189346|XP_005600977.1
☐	PREDICTED: biotinidase isoform X1 [Callithrix jacchus]	55.8	55.8	90%	1e-07	90%	gi|675740028|XP_008982107.1
☐	PREDICTED: biotinidase isoform X2 [Callithrix jacchus]	55.8	55.8	90%	1e-07	90%	gi|390476393|XP_002759736.2
☐	PREDICTED: biotinidase [Vicugna pacos]	55.5	55.5	100%	1e-07	70%	gi|560965913|XP_006205350.1
☐	PREDICTED: biotinidase isoform 2 [Odobenus rosmarus diverg	55.5	55.5	93%	1e-07	84%	gi|472379495|XP_004409157.1
☐	PREDICTED: biotinidase isoform X1 [Felis catus]	55.5	55.5	93%	1e-07	81%	gi|587000359|XP_003992187.2
☐	PREDICTED: biotinidase isoform X2 [Felis catus]	55.5	55.5	93%	1e-07	81%	gi|587000357|XP_006936495.1
☐	PREDICTED: biotinidase isoform 1 [Odobenus rosmarus diverg	55.5	55.5	93%	1e-07	84%	gi|472379493|XP_004409156.1
☐	PREDICTED: biotinidase [Otolemur garnettii]	55.5	55.5	100%	1e-07	79%	gi|395816560|XP_003781769.1
☐	PREDICTED: biotinidase [Mustela putorius furo]	55.1	55.1	100%	2e-07	73%	gi|511908359|XP_004773614.1
☐	PREDICTED: biotinidase [Jaculus jaculus]	54.7	54.7	93%	2e-07	81%	gi|507555213|XP_004661377.1
☐	PREDICTED: biotinidase isoform X2 [Microtus ochrogaster]	54.7	54.7	100%	2e-07	73%	gi|532009812|XP_005348714.1
☐	PREDICTED: biotinidase isoform X1 [Microtus ochrogaster]	54.7	54.7	100%	3e-07	73%	gi|532009810|XP_005348713.1
☐	PREDICTED: biotinidase-like isoform X10 [Chinchilla lanigera]	54.3	54.3	93%	3e-07	77%	gi|533146084|XP_005387502.1
☐	PREDICTED: biotinidase-like isoform X5 [Chinchilla lanigera]	54.3	54.3	93%	3e-07	77%	gi|533146074|XP_005387497.1
☐	PREDICTED: biotinidase isoform X3 [Leptonychotes weddellii]	54.3	54.3	93%	3e-07	81%	gi|585186600|XP_006744787.1
☐	PREDICTED: biotinidase isoform X2 [Leptonychotes weddellii]	54.3	54.3	93%	3e-07	81%	gi|585186598|XP_006744786.1
☐	PREDICTED: biotinidase-like isoform X1 [Chinchilla lanigera]	54.3	54.3	93%	3e-07	77%	gi|533146066|XP_005387493.1
☐	PREDICTED: biotinidase isoform X1 [Leptonychotes weddellii]	54.3	54.3	93%	4e-07	81%	gi|585186596|XP_006744785.1
☐	biotinidase [Camelus ferus]	53.5	53.5	100%	5e-07	67%	gi|528756912|EPY76571.1
☐	PREDICTED: biotinidase [Panthera tigris altaica]	53.9	53.9	93%	5e-07	77%	gi|591322659|XP_007087428.1
☐	PREDICTED: biotinidase [Trichechus manatus latirostris]	53.9	53.9	100%	5e-07	70%	gi|471407481|XP_004385327.1
☐	PREDICTED: biotinidase [Fukomys damarensis]	53.9	53.9	100%	5e-07	73%	gi|731285322|XP_010611073.1
☐	PREDICTED: biotinidase [Lipotes vexillifer]	53.9	53.9	100%	5e-07	76%	gi|602721076|XP_007470691.1
☐	PREDICTED: biotinidase isoform X1 [Balaenoptera acutorostra	53.9	53.9	100%	5e-07	76%	gi|594624940|XP_007167058.1
☐	Biotinidase [Fukomys damarensis]	53.9	53.9	100%	5e-07	73%	gi|676263045|KFO19807.1
☐	PREDICTED: biotinidase isoform X3 [Balaenoptera acutorostra	53.9	53.9	100%	5e-07	76%	gi|594624944|XP_007167060.1
☐	PREDICTED: biotinidase isoform X2 [Camelus dromedarius]	53.5	53.5	100%	6e-07	67%	gi|744591359|XP_010987289.1
☐	PREDICTED: biotinidase isoform X2 [Camelus bactrianus]	53.5	53.5	100%	6e-07	67%	gi|743739779|XP_010964344.1
☐	PREDICTED: biotinidase isoform X2 [Ursus maritimus]	53.5	53.5	100%	6e-07	73%	gi|670981874|XP_008707139.1
☐	PREDICTED: biotinidase [Camelus ferus]	53.5	53.5	100%	6e-07	67%	gi|560929390|XP_006190847.1
☐	PREDICTED: LOW QUALITY PROTEIN: biotinidase [Tursiops	53.5	53.5	100%	6e-07	73%	gi|470628904|XP_004321284.1
☐	PREDICTED: biotinidase [Orcinus orca]	53.5	53.5	100%	6e-07	73%	gi|466019817|XP_004271983.1
☐	PREDICTED: biotinidase isoform X1 [Ursus maritimus]	53.5	53.5	100%	6e-07	73%	gi|670981872|XP_008707130.1
☐	PREDICTED: biotinidase isoform X1 [Camelus dromedarius]	53.5	53.5	100%	7e-07	67%	gi|744591356|XP_010987287.1
☐	PREDICTED: biotinidase isoform X1 [Camelus bactrianus]	53.5	53.5	100%	7e-07	67%	gi|743739777|XP_010964343.1
☐	PREDICTED: biotinidase [Galeopterus variegatus]	52.8	52.8	93%	1e-06	77%	gi|667288263|XP_008576771.1

☐	PREDICTED: biotinidase isoform X2 [Cricetulus griseus]	52.4	52.4	93%	1e-06	77%	gi|625181248|XP_007632389.1
☐	PREDICTED: biotinidase isoform X2 [Physeter catodon]	52.4	52.4	100%	2e-06	73%	gi|593711507|XP_007102308.1
☐	PREDICTED: biotinidase isoform X1 [Cricetulus griseus]	52.4	52.4	93%	2e-06	77%	gi|354465853|XP_003495391.1
☐	PREDICTED: biotinidase isoform X1 [Physeter catodon]	52.4	52.4	100%	2e-06	73%	gi|593711505|XP_007102307.1
☐	biotinidase [Cricetulus griseus]	52.4	52.4	93%	2e-06	77%	gi|537261432|ERE90059.1
☐	PREDICTED: biotinidase-like [Ailuropoda melanoleuca]	52.0	52.0	100%	2e-06	70%	gi|301759093|XP_002915396.1
☐	hypothetical protein PANDA_003369 [Ailuropoda melanoleuca]	52.0	52.0	100%	2e-06	70%	gi|281345880|EFB21464.1
☐	PREDICTED: biotinidase isoform X1 [Peromyscus maniculatus	51.2	51.2	100%	4e-06	70%	gi|589967608|XP_006996305.1
☐	PREDICTED: biotinidase [Nannospalax galili]	51.2	51.2	100%	4e-06	70%	gi|674081213|XP_008848205.1
☐	PREDICTED: biotinidase isoform X2 [Peromyscus maniculatus	51.2	51.2	100%	4e-06	70%	gi|589967610|XP_006996306.1
☐	PREDICTED: biotinidase [Mesocricetus auratus]	50.8	50.8	100%	6e-06	73%	gi|524955500|XP_005077724.1
☐	Biotinidase [Heterocephalus glaber]	50.4	50.4	100%	8e-06	67%	gi|351707565|EHB10484.1
☐	PREDICTED: biotinidase isoform X3 [Heterocephalus glaber]	50.4	50.4	100%	8e-06	67%	gi|512886961|XP_004896459.1
☐	PREDICTED: biotinidase isoform X1 [Heterocephalus glaber]	50.4	50.4	100%	8e-06	67%	gi|512886949|XP_004896457.1
☐	PREDICTED: biotinidase isoform X1 [Cavia porcellus]	50.1	50.1	100%	1e-05	67%	gi|514481133|XP_003480063.2
☐	PREDICTED: biotinidase isoform X2 [Cavia porcellus]	50.1	50.1	100%	1e-05	67%	gi|514481131|XP_005008361.1
☐	PREDICTED: biotinidase [Loxodonta africana]	49.3	49.3	100%	2e-05	61%	gi|731510838|XP_010598778.1
☐	TPA: biotinidase precursor [Bos taurus]	48.9	48.9	100%	3e-05	67%	gi|296490802|DAA32915.1
☐	biotinidase precursor [Bos taurus]	48.9	48.9	100%	3e-05	67%	gi|156121059|NP_001095676.1
☐	PREDICTED: biotinidase isoform X1 [Bos taurus]	48.9	48.9	100%	3e-05	67%	gi|528938459|XP_005202205.1
☐	PREDICTED: biotinidase [Erinaceus europaeus]	48.9	48.9	100%	3e-05	64%	gi|617553342|XP_007530134.1
☐	biotinidase, isoform CRA_a [Rattus norvegicus]	48.1	48.1	100%	4e-05	64%	gi|149034168|EDL88938.1
☐	biotinidase, isoform CRA_c [Rattus norvegicus]	48.1	48.1	100%	4e-05	64%	gi|149034170|EDL88940.1
☐	biotinidase precursor [Rattus norvegicus]	48.1	48.1	100%	5e-05	64%	gi|58865670|NP_001012047.1
☐	PREDICTED: biotinidase [Pteropus alecto]	48.1	48.1	93%	5e-05	71%	gi|586544408|XP_006907323.1

⊟ Alignments

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PREDICTED: biotinidase [Nomascus leucogenys]

Sequence ID: gi|332232450|ref|XP_003265417.1| **Length:** 474 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 260 to 292 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.4 bits(163)	8e-12	32/33(97%)	33/33(100%)	0/33(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAEDATGETDPSHSKF  33
            KSHLIIAQVAKNPVGLIGAE+ATGETDPSHSKF
Sbjct  260  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  292
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221043776|dbj|BAH13565.1| **Length:** 523 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 309 to 341 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.4 bits(163)	8e-12	32/33(97%)	33/33(100%)	0/33(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAEDATGETDPSHSKF  33
            KSHLIIAQVAKNPVGLIGAE+ATGETDPSHSKF
Sbjct  309  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  341
```

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biotinidase isoform 4 precursor [Homo sapiens]

Sequence ID: gi|528524486|ref|NP_001268654.1| **Length:** 523 **Number of Matches:** 1

See 3 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 309 to 341 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.4 bits(163)	8e-12	32/33(97%)	33/33(100%)	0/33(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAEDATGETDPSHSKF  33
            KSHLIIAQVAKNPVGLIGAE+ATGETDPSHSKF
Sbjct  309  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  341
```

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biotinidase precursor [Pan troglodytes]

Sequence ID: gi|697993457|ref|NP_001289363.1| **Length:** 523 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 309 to 341 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.4 bits(163)	8e-12	32/33(97%)	33/33(100%)	0/33(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAEDATGETDPSHSKF  33
            KSHLIIAQVAKNPVGLIGAE+ATGETDPSHSKF
Sbjct  309  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  341
```

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PREDICTED: biotinidase isoform X2 [Pan troglodytes]

Sequence ID: gi|694900420|ref|XP_009443239.1| **Length:** 527 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 313 to 345 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.4 bits(163)	9e-12	32/33(97%)	33/33(100%)	0/33(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAEDATGETDPSHSKF  33
            KSHLIIAQVAKNPVGLIGAE+ATGETDPSHSKF
Sbjct  313  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  345
```

BTD_KSHLIIAQVAKNPVGLIGAEDATGETDPSHSKFLKI_Mod

RID BT4XNGRP013 (Expires on 01-20 12:18 pm)

Query ID lcl|58007
Description None
Molecule type amino acid
Query Length 36

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

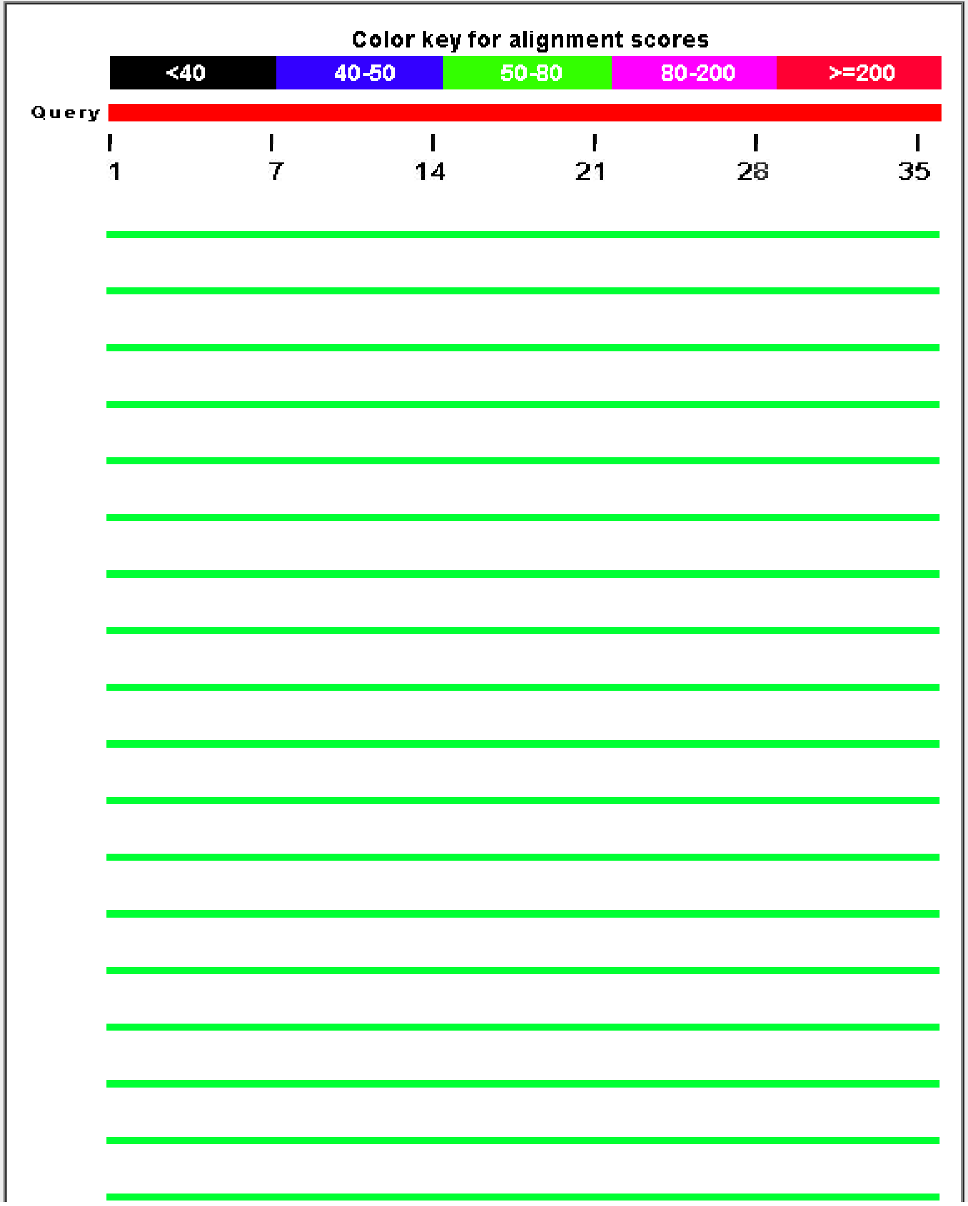
Graphic Summary

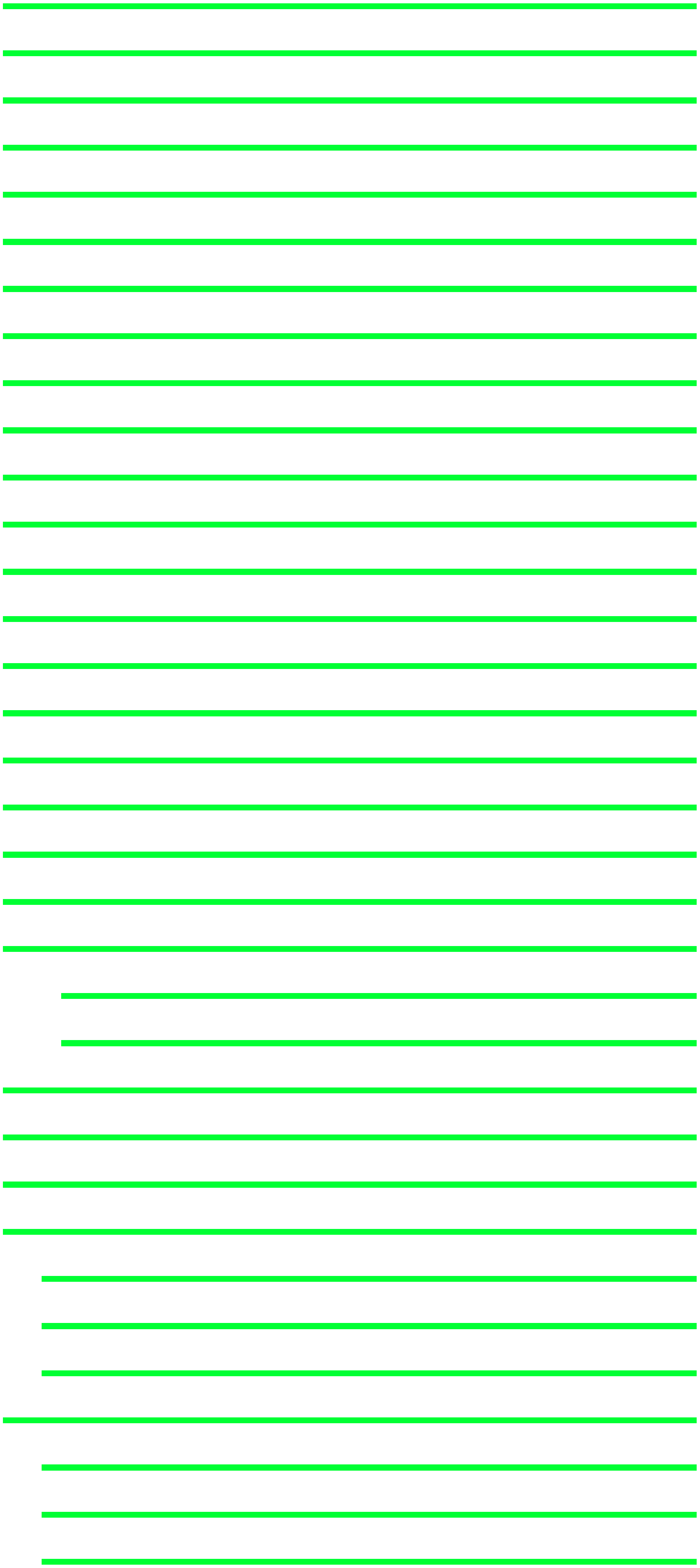
Show Conserved Domains

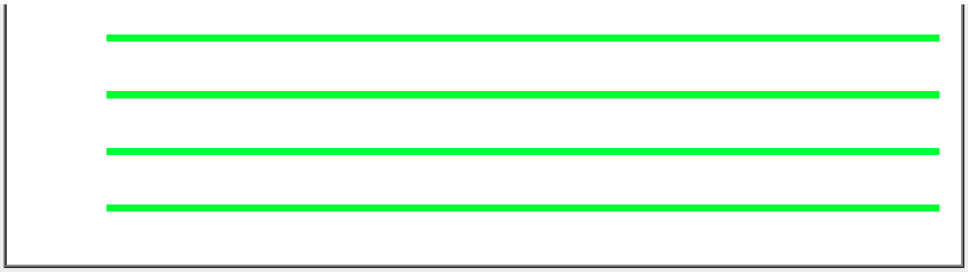
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: biotinidase [Nomascus leucogenys]	72.4	72.4	100%	1e-13	97%	gi|332232450|XP_003265417.1
☐	unnamed protein product [Homo sapiens]	72.4	72.4	100%	2e-13	97%	gi|221043776|BAH13565.1
☐	biotinidase isoform 4 precursor [Homo sapiens]	72.4	72.4	100%	2e-13	97%	gi|528524486|NP_001268654.1
☐	biotinidase precursor [Pan troglodytes]	72.4	72.4	100%	2e-13	97%	gi|697993457|NP_001289363.1
☐	PREDICTED: biotinidase isoform X2 [Pan troglodytes]	72.4	72.4	100%	2e-13	97%	gi|694900420|XP_009443239.1
☐	PREDICTED: biotinidase isoform X2 [Pan paniscus]	72.4	72.4	100%	2e-13	97%	gi|675784344|XP_008949921.1
☐	PREDICTED: biotinidase isoform X3 [Pongo abelii]	72.4	72.4	100%	2e-13	97%	gi|686713703|XP_009237577.1
☐	PREDICTED: biotinidase isoform X2 [Pongo abelii]	72.4	72.4	100%	2e-13	97%	gi|686713701|XP_009237576.1
☐	biotinidase isoform 3 [Homo sapiens]	72.4	72.4	100%	2e-13	97%	gi|4557373|NP_000051.1
☐	biotinidase isoform 1 [Homo sapiens]	72.4	72.4	100%	2e-13	97%	gi|528524481|NP_001268652.1
☐	biotinidase isoform 2 [Homo sapiens]	72.4	72.4	100%	2e-13	97%	gi|528524483|NP_001268653.1
☐	PREDICTED: biotinidase isoform X1 [Pan troglodytes]	72.4	72.4	100%	2e-13	97%	gi|410036604|XP_003950087.1
☐	PREDICTED: biotinidase isoform X1 [Pan paniscus]	72.4	72.4	100%	2e-13	97%	gi|397511808|XP_003826257.1
☐	PREDICTED: biotinidase isoform X1 [Pongo abelii]	72.4	72.4	100%	2e-13	97%	gi|395734130|XP_003776360.1
☐	PREDICTED: biotinidase isoform 1 [Gorilla gorilla gorilla]	72.0	72.0	100%	2e-13	94%	gi|426339607|XP_004033737.1
☐	PREDICTED: biotinidase isoform 3 [Gorilla gorilla gorilla]	72.0	72.0	100%	2e-13	94%	gi|426339611|XP_004033739.1
☐	PREDICTED: biotinidase isoform 4 [Gorilla gorilla gorilla]	72.0	72.0	100%	2e-13	94%	gi|426339613|XP_004033740.1
☐	PREDICTED: biotinidase isoform 2 [Gorilla gorilla gorilla]	72.0	72.0	100%	2e-13	94%	gi|426339609|XP_004033738.1
☐	unnamed protein product [Macaca fascicularis]	70.9	70.9	100%	5e-13	94%	gi|90077268|BAE88314.1
☐	PREDICTED: biotinidase isoform X2 [Macaca fascicularis]	70.9	70.9	100%	6e-13	94%	gi|544411158|XP_005545768.1
☐	hypothetical protein EGM_11114 [Macaca fascicularis]	70.9	70.9	100%	6e-13	94%	gi|355747075|EHH51689.1
☐	hypothetical protein EGK_12122 [Macaca mulatta]	70.9	70.9	100%	6e-13	94%	gi|355560049|EHH16777.1
☐	PREDICTED: biotinidase [Macaca mulatta]	70.9	70.9	100%	6e-13	94%	gi|297286947|XP_001083201.2
☐	PREDICTED: biotinidase isoform X1 [Macaca fascicularis]	70.9	70.9	100%	6e-13	94%	gi|544411156|XP_005545767.1
☐	PREDICTED: biotinidase isoform X2 [Chlorocebus sabaeus]	69.3	69.3	100%	2e-12	92%	gi|635085523|XP_008007381.1
☐	PREDICTED: biotinidase isoform X1 [Chlorocebus sabaeus]	69.3	69.3	100%	2e-12	92%	gi|635085521|XP_008007380.1
☐	PREDICTED: biotinidase [Rhinopithecus roxellana]	66.6	66.6	100%	2e-11	86%	gi|724960396|XP_010354361.1
☐	PREDICTED: biotinidase isoform X2 [Papio anubis]	65.5	65.5	100%	5e-11	86%	gi|685527526|XP_009200021.1
☐	PREDICTED: biotinidase isoform X1 [Papio anubis]	65.5	65.5	100%	5e-11	86%	gi|685527524|XP_009200020.1
☐	PREDICTED: biotinidase-like [Ictidomys tridecemlineatus]	63.2	63.2	100%	3e-10	81%	gi|532063189|XP_005317469.1

☐	PREDICTED: biotinidase [Ceratotherium simum simum]	63.2	63.2	100%	3e-10	81%	gi|478490156|XP_004419451.1
☐	PREDICTED: biotinidase isoform X4 [Canis lupus familiaris]	62.0	62.0	100%	8e-10	78%	gi|545538859|XP_005634450.1
☐	PREDICTED: biotinidase isoform X3 [Canis lupus familiaris]	62.0	62.0	100%	8e-10	78%	gi|545538857|XP_005634449.1
☐	PREDICTED: biotinidase isoform X2 [Canis lupus familiaris]	62.0	62.0	100%	8e-10	78%	gi|545538855|XP_005634448.1
☐	PREDICTED: biotinidase isoform X1 [Canis lupus familiaris]	62.0	62.0	100%	8e-10	78%	gi|545538853|XP_005634447.1
☐	PREDICTED: biotinidase isoform X3 [Equus caballus]	61.6	61.6	100%	1e-09	78%	gi|545189350|XP_005600979.1
☐	PREDICTED: biotinidase [Equus przewalskii]	61.6	61.6	100%	1e-09	78%	gi|664753751|XP_008534346.1
☐	PREDICTED: biotinidase isoform X2 [Equus caballus]	61.6	61.6	100%	1e-09	78%	gi|545189348|XP_005600978.1
☐	PREDICTED: biotinidase isoform X1 [Equus caballus]	61.6	61.6	100%	1e-09	78%	gi|545189346|XP_005600977.1
☐	PREDICTED: biotinidase isoform X1 [Callithrix jacchus]	60.8	60.8	91%	2e-09	91%	gi|675740028|XP_008982107.1
☐	PREDICTED: biotinidase isoform X2 [Callithrix jacchus]	60.8	60.8	91%	2e-09	91%	gi|390476393|XP_002759736.2
☐	PREDICTED: biotinidase [Vicugna pacos]	60.5	60.5	100%	3e-09	72%	gi|560965913|XP_006205350.1
☐	PREDICTED: biotinidase [Otolemur garnettii]	60.5	60.5	100%	3e-09	81%	gi|395816560|XP_003781769.1
☐	PREDICTED: biotinidase isoform X2 [Microtus ochrogaster]	59.7	59.7	100%	5e-09	75%	gi|532009812|XP_005348714.1
☐	PREDICTED: biotinidase isoform X1 [Microtus ochrogaster]	59.7	59.7	100%	5e-09	75%	gi|532009810|XP_005348713.1
☐	PREDICTED: biotinidase-like isoform X10 [Chinchilla lanigera]	59.3	59.3	94%	6e-09	79%	gi|533146084|XP_005387502.1
☐	PREDICTED: biotinidase-like isoform X5 [Chinchilla lanigera]	59.3	59.3	94%	7e-09	79%	gi|533146074|XP_005387497.1
☐	PREDICTED: biotinidase-like isoform X1 [Chinchilla lanigera]	59.3	59.3	94%	7e-09	79%	gi|533146066|XP_005387493.1
☐	biotinidase [Camelus ferus]	58.5	58.5	100%	9e-09	69%	gi|528756912|EPY76571.1
☐	PREDICTED: biotinidase [Jaculus jaculus]	58.9	58.9	94%	9e-09	79%	gi|507555213|XP_004661377.1
☐	PREDICTED: biotinidase isoform X1 [Felis catus]	58.9	58.9	94%	9e-09	79%	gi|587000359|XP_003992187.2
☐	PREDICTED: biotinidase isoform X2 [Felis catus]	58.9	58.9	94%	9e-09	79%	gi|587000357|XP_006936495.1
☐	PREDICTED: biotinidase [Trichechus manatus latirostris]	58.9	58.9	100%	9e-09	72%	gi|471407481|XP_004385327.1
☐	PREDICTED: biotinidase [Fukomys damarensis]	58.9	58.9	100%	9e-09	75%	gi|731285322|XP_010611073.1
☐	PREDICTED: biotinidase [Lipotes vexillifer]	58.9	58.9	100%	1e-08	78%	gi|602721076|XP_007470691.1
☐	PREDICTED: biotinidase isoform X1 [Balaenoptera acutorostra	58.9	58.9	100%	1e-08	78%	gi|594624940|XP_007167058.1
☐	Biotinidase [Fukomys damarensis]	58.9	58.9	100%	1e-08	75%	gi|676263045|KFO19807.1
☐	PREDICTED: biotinidase isoform X3 [Balaenoptera acutorostra	58.9	58.9	100%	1e-08	78%	gi|594624944|XP_007167060.1
☐	PREDICTED: biotinidase isoform X2 [Camelus dromedarius]	58.5	58.5	100%	1e-08	69%	gi|744591359|XP_010987289.1
☐	PREDICTED: biotinidase isoform X2 [Camelus bactrianus]	58.5	58.5	100%	1e-08	69%	gi|743739779|XP_010964344.1
☐	PREDICTED: biotinidase [Camelus ferus]	58.5	58.5	100%	1e-08	69%	gi|560929390|XP_006190847.1
☐	PREDICTED: LOW QUALITY PROTEIN: biotinidase [Tursiops	58.5	58.5	100%	1e-08	75%	gi|470628904|XP_004321284.1
☐	PREDICTED: biotinidase [Orcinus orca]	58.5	58.5	100%	1e-08	75%	gi|466019817|XP_004271983.1
☐	PREDICTED: biotinidase isoform X1 [Camelus dromedarius]	58.5	58.5	100%	1e-08	69%	gi|744591356|XP_010987287.1
☐	PREDICTED: biotinidase isoform X1 [Camelus bactrianus]	58.5	58.5	100%	1e-08	69%	gi|743739777|XP_010964343.1
☐	PREDICTED: biotinidase isoform 2 [Odobenus rosmarus diverg	58.2	58.2	94%	2e-08	79%	gi|472379495|XP_004409157.1
☐	PREDICTED: biotinidase isoform 1 [Odobenus rosmarus diverg	58.2	58.2	94%	2e-08	79%	gi|472379493|XP_004409156.1
☐	PREDICTED: biotinidase [Galeopterus variegatus]	57.8	57.8	94%	2e-08	79%	gi|667288263|XP_008576771.1
☐	PREDICTED: biotinidase [Mustela putorius furo]	57.8	57.8	100%	2e-08	69%	gi|511908359|XP_004773614.1
☐	PREDICTED: biotinidase isoform X2 [Cricetulus griseus]	57.4	57.4	94%	3e-08	79%	gi|625181248|XP_007632389.1
☐	PREDICTED: biotinidase isoform X2 [Physeter catodon]	57.4	57.4	100%	3e-08	75%	gi|593711507|XP_007102308.1
☐	PREDICTED: biotinidase [Panthera tigris altaica]	57.4	57.4	94%	3e-08	76%	gi|591322659|XP_007087428.1
☐	PREDICTED: biotinidase isoform X1 [Cricetulus griseus]	57.4	57.4	94%	3e-08	79%	gi|354465853|XP_003495391.1
☐	PREDICTED: biotinidase isoform X1 [Physeter catodon]	57.4	57.4	100%	3e-08	75%	gi|593711505|XP_007102307.1
☐	biotinidase [Cricetulus griseus]	57.4	57.4	94%	3e-08	79%	gi|537261432|ERE90059.1

☐	PREDICTED: biotinidase isoform X3 [Leptonychotes weddellii]	57.0	57.0	94%	4e-08	76%	gi|585186600|XP_006744787.1
☐	PREDICTED: biotinidase isoform X2 [Leptonychotes weddellii]	57.0	57.0	94%	4e-08	76%	gi|585186598|XP_006744786.1
☐	PREDICTED: biotinidase isoform X1 [Leptonychotes weddellii]	57.0	57.0	94%	5e-08	76%	gi|585186596|XP_006744785.1
☐	PREDICTED: biotinidase isoform X1 [Peromyscus maniculatus	56.2	56.2	100%	8e-08	72%	gi|589967608|XP_006996305.1
☐	PREDICTED: biotinidase [Nannospalax galili]	56.2	56.2	100%	8e-08	72%	gi|674081213|XP_008848205.1
☐	PREDICTED: biotinidase isoform X2 [Ursus maritimus]	56.2	56.2	100%	8e-08	69%	gi|670981874|XP_008707139.1
☐	PREDICTED: biotinidase isoform X2 [Peromyscus maniculatus	56.2	56.2	100%	8e-08	72%	gi|589967610|XP_006996306.1
☐	PREDICTED: biotinidase isoform X1 [Ursus maritimus]	56.2	56.2	100%	8e-08	69%	gi|670981872|XP_008707130.1
☐	Biotinidase [Heterocephalus glaber]	55.5	55.5	100%	2e-07	69%	gi|351707565|EHB10484.1
☐	PREDICTED: biotinidase isoform X3 [Heterocephalus glaber]	55.5	55.5	100%	2e-07	69%	gi|512886961|XP_004896459.1
☐	PREDICTED: biotinidase isoform X1 [Heterocephalus glaber]	55.5	55.5	100%	2e-07	69%	gi|512886949|XP_004896457.1
☐	PREDICTED: biotinidase [Mesocricetus auratus]	54.7	54.7	100%	3e-07	72%	gi|524955500|XP_005077724.1
☐	PREDICTED: biotinidase-like [Ailuropoda melanoleuca]	54.7	54.7	100%	3e-07	67%	gi|301759093|XP_002915396.1
☐	hypothetical protein PANDA_003369 [Ailuropoda melanoleuca]	54.7	54.7	100%	3e-07	67%	gi|281345880|EFB21464.1
☐	PREDICTED: biotinidase [Loxodonta africana]	54.3	54.3	100%	4e-07	64%	gi|731510838|XP_010598778.1
☐	PREDICTED: biotinidase [Erinaceus europaeus]	53.9	53.9	100%	6e-07	67%	gi|617553342|XP_007530134.1
☐	biotinidase, isoform CRA_a [Rattus norvegicus]	52.8	52.8	100%	1e-06	64%	gi|149034168|EDL88938.1
☐	biotinidase, isoform CRA_c [Rattus norvegicus]	52.8	52.8	100%	1e-06	64%	gi|149034170|EDL88940.1
☐	biotinidase precursor [Rattus norvegicus]	52.8	52.8	100%	1e-06	64%	gi|58865670|NP_001012047.1
☐	PREDICTED: biotinidase isoform X1 [Cavia porcellus]	52.8	52.8	100%	1e-06	64%	gi|514481133|XP_003480063.2
☐	PREDICTED: biotinidase isoform X2 [Rattus norvegicus]	52.8	52.8	100%	1e-06	64%	gi|564387894|XP_006252671.1
☐	PREDICTED: biotinidase isoform X2 [Cavia porcellus]	52.8	52.8	100%	1e-06	64%	gi|514481131|XP_005008361.1
☐	PREDICTED: biotinidase isoform X3 [Saimiri boliviensis bolivie	52.4	52.4	91%	2e-06	79%	gi|725560828|XP_010333963.1
☐	PREDICTED: biotinidase isoform X2 [Saimiri boliviensis bolivie	52.4	52.4	91%	2e-06	79%	gi|403265544|XP_003924991.1
☐	PREDICTED: biotinidase isoform X1 [Saimiri boliviensis bolivie	52.4	52.4	91%	2e-06	79%	gi|725560825|XP_010333962.1

Alignments

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PREDICTED: biotinidase [Nomascus leucogenys]

Sequence ID: gi|332232450|ref|XP_003265417.1| **Length:** 474 **Number of Matches:** 1

Range 1: 260 to 295 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.4 bits(176)	1e-13	35/36(97%)	36/36(100%)	0/36(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAEDATGETDPSHSKFLKI  36
            KSHLIIAQVAKNPVGLIGAE+ATGETDPSHSKFLKI
Sbjct  260  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  295
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221043776|dbj|BAH13565.1| **Length:** 523 **Number of Matches:** 1

Range 1: 309 to 344 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.4 bits(176)	2e-13	35/36(97%)	36/36(100%)	0/36(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAEDATGETDPSHSKFLKI  36
            KSHLIIAQVAKNPVGLIGAE+ATGETDPSHSKFLKI
Sbjct  309  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  344
```

Related Information

Gene - associated gene details

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biotinidase isoform 4 precursor [Homo sapiens]

Sequence ID: gi|528524486|ref|NP_001268654.1| **Length:** 523 **Number of Matches:** 1

See 3 more title(s)

Range 1: 309 to 344 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.4 bits(176)	2e-13	35/36(97%)	36/36(100%)	0/36(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAEDATGETDPSHSKFLKI  36
            KSHLIIAQVAKNPVGLIGAE+ATGETDPSHSKFLKI
Sbjct  309  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  344
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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biotinidase precursor [Pan troglodytes]

Sequence ID: gi|697993457|ref|NP_001289363.1| **Length:** 523 **Number of Matches:** 1

See 1 more title(s)

Range 1: 309 to 344 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.4 bits(176)	2e-13	35/36(97%)	36/36(100%)	0/36(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAEDATGETDPSHSKFLKI  36
            KSHLIIAQVAKNPVGLIGAE+ATGETDPSHSKFLKI
Sbjct  309  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  344
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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PREDICTED: biotinidase isoform X2 [Pan troglodytes]

Sequence ID: gi|694900420|ref|XP_009443239.1| **Length:** 527 **Number of Matches:** 1

See 1 more title(s)

Range 1: 313 to 348 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.4 bits(176)	2e-13	35/36(97%)	36/36(100%)	0/36(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAEDATGETDPSHSKFLKI  36
            KSHLIIAQVAKNPVGLIGAE+ATGETDPSHSKFLKI
Sbjct  313  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  348
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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NCBI/ BLAST/ blastp suite/ Formatting Results - B921BCE001R

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BTD_KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF_NonMod

RID B921BCE001R (Expires on 01-14 09:51 am)

Query ID	lcl|111602	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	33		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

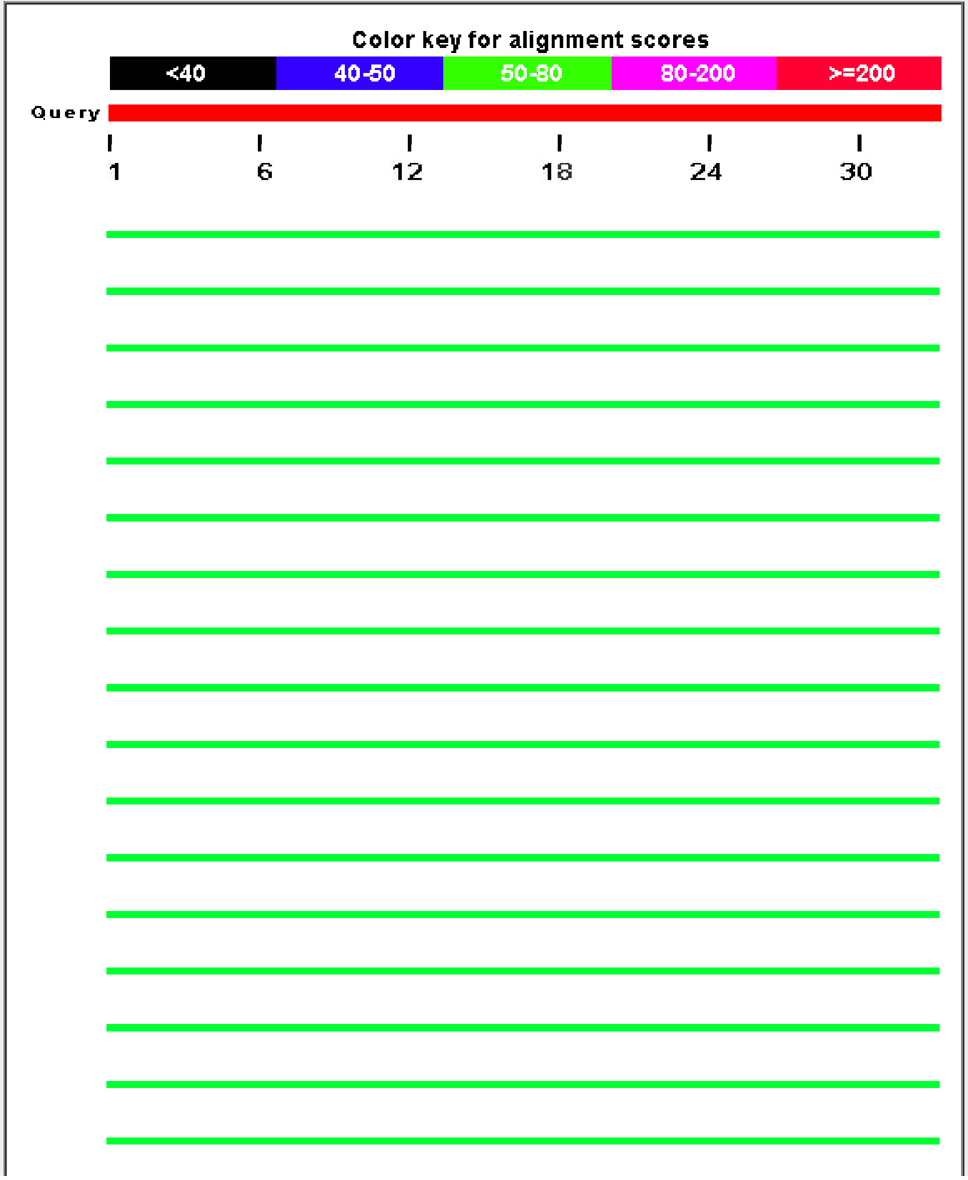
Graphic Summary

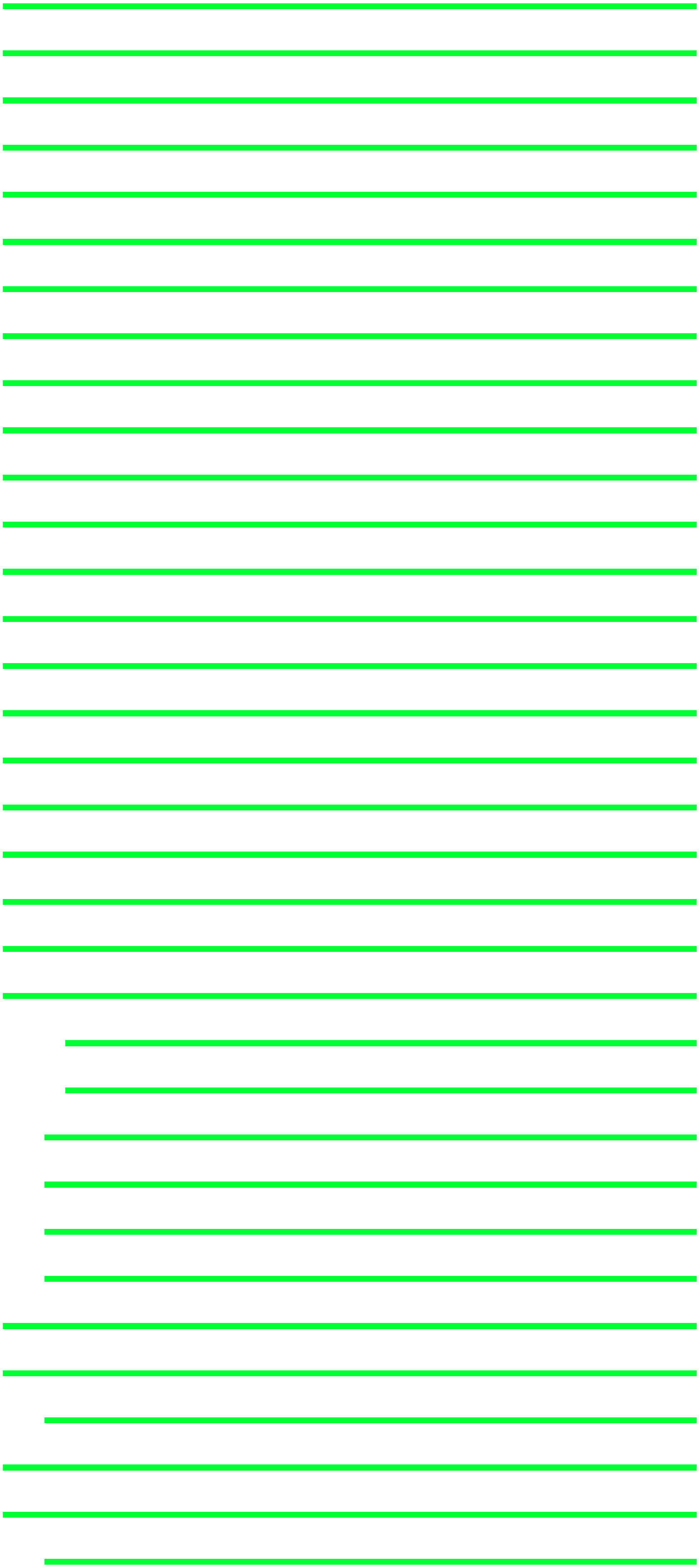
Show Conserved Domains

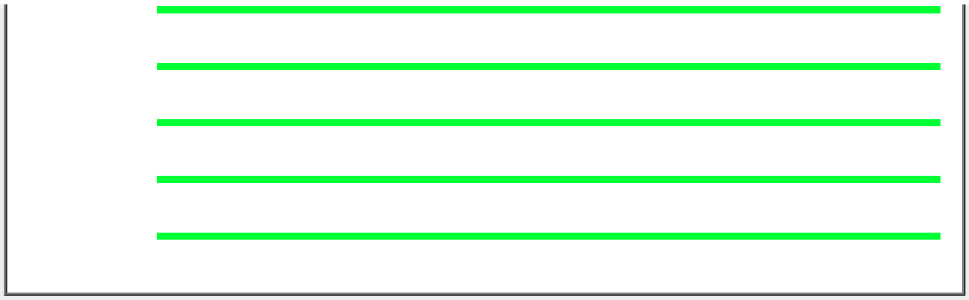
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: biotinidase [Nomascus leucogenys]	69.3	69.3	100%	1e-12	100%	gi|332232450|XP_003265417.1
☐	unnamed protein product [Homo sapiens]	69.3	69.3	100%	2e-12	100%	gi|221043776|BAH13565.1
☐	biotinidase isoform 4 precursor [Homo sapiens]	69.3	69.3	100%	2e-12	100%	gi|528524486|NP_001268654.1
☐	biotinidase precursor [Pan troglodytes]	69.3	69.3	100%	2e-12	100%	gi|697993457|NP_001289363.1
☐	PREDICTED: biotinidase isoform X2 [Pan troglodytes]	69.3	69.3	100%	2e-12	100%	gi|694900420|XP_009443239.1
☐	PREDICTED: biotinidase isoform X2 [Pan paniscus]	69.3	69.3	100%	2e-12	100%	gi|675784344|XP_008949921.1
☐	PREDICTED: biotinidase isoform X3 [Pongo abelii]	69.3	69.3	100%	2e-12	100%	gi|686713703|XP_009237577.1
☐	PREDICTED: biotinidase isoform X2 [Pongo abelii]	69.3	69.3	100%	2e-12	100%	gi|686713701|XP_009237576.1
☐	biotinidase isoform 3 [Homo sapiens]	69.3	69.3	100%	2e-12	100%	gi|4557373|NP_000051.1
☐	biotinidase isoform 1 [Homo sapiens]	69.3	69.3	100%	2e-12	100%	gi|528524481|NP_001268652.1
☐	biotinidase isoform 2 [Homo sapiens]	69.3	69.3	100%	2e-12	100%	gi|528524483|NP_001268653.1
☐	PREDICTED: biotinidase isoform X1 [Pan troglodytes]	69.3	69.3	100%	2e-12	100%	gi|410036604|XP_003950087.1
☐	PREDICTED: biotinidase isoform X1 [Pan paniscus]	69.3	69.3	100%	2e-12	100%	gi|397511808|XP_003826257.1
☐	PREDICTED: biotinidase isoform X1 [Pongo abelii]	69.3	69.3	100%	2e-12	100%	gi|395734130|XP_003776360.1
☐	PREDICTED: biotinidase isoform 1 [Gorilla gorilla gorilla]	68.9	68.9	100%	2e-12	97%	gi|426339607|XP_004033737.1
☐	PREDICTED: biotinidase isoform 3 [Gorilla gorilla gorilla]	68.9	68.9	100%	2e-12	97%	gi|426339611|XP_004033739.1
☐	PREDICTED: biotinidase isoform 4 [Gorilla gorilla gorilla]	68.9	68.9	100%	2e-12	97%	gi|426339613|XP_004033740.1
☐	PREDICTED: biotinidase isoform 2 [Gorilla gorilla gorilla]	68.9	68.9	100%	2e-12	97%	gi|426339609|XP_004033738.1
☐	unnamed protein product [Macaca fascicularis]	67.8	67.8	100%	5e-12	97%	gi|90077268|BAE88314.1
☐	PREDICTED: biotinidase isoform X2 [Macaca fascicularis]	67.8	67.8	100%	6e-12	97%	gi|544411158|XP_005545768.1
☐	hypothetical protein EGM_11114 [Macaca fascicularis]	67.8	67.8	100%	6e-12	97%	gi|355747075|EHH51689.1
☐	hypothetical protein EGK_12122 [Macaca mulatta]	67.8	67.8	100%	6e-12	97%	gi|355560049|EHH16777.1
☐	PREDICTED: biotinidase [Macaca mulatta]	67.8	67.8	100%	6e-12	97%	gi|297286947|XP_001083201.2
☐	PREDICTED: biotinidase isoform X1 [Macaca fascicularis]	67.8	67.8	100%	6e-12	97%	gi|544411156|XP_005545767.1
☐	PREDICTED: biotinidase isoform X2 [Chlorocebus sabaeus]	66.2	66.2	100%	2e-11	94%	gi|635085523|XP_008007381.1
☐	PREDICTED: biotinidase isoform X1 [Chlorocebus sabaeus]	66.2	66.2	100%	2e-11	94%	gi|635085521|XP_008007380.1
☐	PREDICTED: biotinidase [Rhinopithecus roxellana]	63.5	63.5	100%	2e-10	88%	gi|724960396|XP_010354361.1
☐	PREDICTED: biotinidase isoform X2 [Papio anubis]	62.4	62.4	100%	5e-10	88%	gi|685527526|XP_009200021.1
☐	PREDICTED: biotinidase isoform X1 [Papio anubis]	62.4	62.4	100%	5e-10	88%	gi|685527524|XP_009200020.1
☐							

	PREDICTED: biotinidase isoform X4 [Canis lupus familiaris]	60.5	60.5	100%	2e-09	82%	gi|545538859|XP_005634450.1
☐	PREDICTED: biotinidase isoform X3 [Canis lupus familiaris]	60.5	60.5	100%	2e-09	82%	gi|545538857|XP_005634449.1
☐	PREDICTED: biotinidase isoform X2 [Canis lupus familiaris]	60.5	60.5	100%	2e-09	82%	gi|545538855|XP_005634448.1
☐	PREDICTED: biotinidase isoform X1 [Canis lupus familiaris]	60.5	60.5	100%	2e-09	82%	gi|545538853|XP_005634447.1
☐	PREDICTED: biotinidase-like [Ictidomys tridecemlineatus]	60.1	60.1	100%	3e-09	82%	gi|532063189|XP_005317469.1
☐	PREDICTED: biotinidase [Ceratotherium simum simum]	60.1	60.1	100%	3e-09	82%	gi|478490156|XP_004419451.1
☐	PREDICTED: biotinidase isoform X3 [Equus caballus]	58.5	58.5	100%	1e-08	79%	gi|545189350|XP_005600979.1
☐	PREDICTED: biotinidase [Equus przewalskii]	58.5	58.5	100%	1e-08	79%	gi|664753751|XP_008534346.1
☐	PREDICTED: biotinidase isoform X2 [Equus caballus]	58.5	58.5	100%	1e-08	79%	gi|545189348|XP_005600978.1
☐	PREDICTED: biotinidase isoform X1 [Equus caballus]	58.5	58.5	100%	1e-08	79%	gi|545189346|XP_005600977.1
☐	PREDICTED: biotinidase isoform X1 [Callithrix jacchus]	57.8	57.8	90%	2e-08	93%	gi|675740028|XP_008982107.1
☐	PREDICTED: biotinidase isoform X2 [Callithrix jacchus]	57.8	57.8	90%	2e-08	93%	gi|390476393|XP_002759736.2
☐	PREDICTED: biotinidase isoform 2 [Odobenus rosmarus divergens	57.4	57.4	93%	3e-08	87%	gi|472379495|XP_004409157.1
☐	PREDICTED: biotinidase isoform X1 [Felis catus]	57.4	57.4	93%	3e-08	84%	gi|587000359|XP_003992187.2
☐	PREDICTED: biotinidase isoform X2 [Felis catus]	57.4	57.4	93%	3e-08	84%	gi|587000357|XP_006936495.1
☐	PREDICTED: biotinidase isoform 1 [Odobenus rosmarus divergens	57.4	57.4	93%	3e-08	87%	gi|472379493|XP_004409156.1
☐	PREDICTED: biotinidase [Otolemur garnettii]	57.4	57.4	100%	3e-08	82%	gi|395816560|XP_003781769.1
☐	PREDICTED: biotinidase [Mustela putorius furo]	57.0	57.0	100%	4e-08	76%	gi|511908359|XP_004773614.1
☐	PREDICTED: biotinidase [Jaculus jaculus]	56.6	56.6	93%	5e-08	84%	gi|507555213|XP_004661377.1
☐	PREDICTED: biotinidase isoform X2 [Microtus ochrogaster]	56.6	56.6	100%	5e-08	76%	gi|532009812|XP_005348714.1
☐	PREDICTED: biotinidase isoform X1 [Microtus ochrogaster]	56.6	56.6	100%	5e-08	76%	gi|532009810|XP_005348713.1
☐	PREDICTED: biotinidase-like isoform X10 [Chinchilla lanigera]	56.2	56.2	93%	6e-08	81%	gi|533146084|XP_005387502.1
☐	PREDICTED: biotinidase-like isoform X5 [Chinchilla lanigera]	56.2	56.2	93%	7e-08	81%	gi|533146074|XP_005387497.1
☐	PREDICTED: biotinidase isoform X3 [Leptonychotes weddellii]	56.2	56.2	93%	7e-08	84%	gi|585186600|XP_006744787.1
☐	PREDICTED: biotinidase isoform X2 [Leptonychotes weddellii]	56.2	56.2	93%	7e-08	84%	gi|585186598|XP_006744786.1
☐	PREDICTED: biotinidase-like isoform X1 [Chinchilla lanigera]	56.2	56.2	93%	7e-08	81%	gi|533146066|XP_005387493.1
☐	PREDICTED: biotinidase isoform X1 [Leptonychotes weddellii]	56.2	56.2	93%	7e-08	84%	gi|585186596|XP_006744785.1
☐	biotinidase [Camelus ferus]	55.5	55.5	100%	9e-08	70%	gi|528756912|EPY76571.1
☐	PREDICTED: biotinidase [Vicugna pacos]	55.8	55.8	100%	9e-08	70%	gi|560965913|XP_006205350.1
☐	PREDICTED: biotinidase [Panthera tigris altaica]	55.8	55.8	93%	9e-08	81%	gi|591322659|XP_007087428.1
☐	PREDICTED: biotinidase [Trichechus manatus latirostris]	55.8	55.8	100%	9e-08	73%	gi|471407481|XP_004385327.1
☐	PREDICTED: biotinidase [Fukomys damarensis]	55.8	55.8	100%	9e-08	76%	gi|731285322|XP_010611073.1
☐	PREDICTED: biotinidase [Lipotes vexillifer]	55.8	55.8	100%	1e-07	79%	gi|602721076|XP_007470691.1
☐	PREDICTED: biotinidase isoform X1 [Balaenoptera acutorostrata sc	55.8	55.8	100%	1e-07	79%	gi|594624940|XP_007167058.1
☐	Biotinidase [Fukomys damarensis]	55.8	55.8	100%	1e-07	76%	gi|676263045|KFO19807.1
☐	PREDICTED: biotinidase isoform X3 [Balaenoptera acutorostrata sc	55.8	55.8	100%	1e-07	79%	gi|594624944|XP_007167060.1
☐	PREDICTED: biotinidase isoform X2 [Ursus maritimus]	55.5	55.5	100%	1e-07	76%	gi|670981874|XP_008707139.1
☐	PREDICTED: biotinidase [Camelus ferus]	55.5	55.5	100%	1e-07	70%	gi|560929390|XP_006190847.1
☐	PREDICTED: LOW QUALITY PROTEIN: biotinidase [Tursiops trunc	55.5	55.5	100%	1e-07	76%	gi|470628904|XP_004321284.1
☐	PREDICTED: biotinidase [Orcinus orca]	55.5	55.5	100%	1e-07	76%	gi|466019817|XP_004271983.1
☐	PREDICTED: biotinidase isoform X1 [Ursus maritimus]	55.5	55.5	100%	1e-07	76%	gi|670981872|XP_008707130.1
☐	PREDICTED: biotinidase [Galeopterus variegatus]	54.7	54.7	93%	2e-07	81%	gi|667288263|XP_008576771.1
☐	PREDICTED: biotinidase isoform X2 [Cricetulus griseus]	54.3	54.3	93%	3e-07	81%	gi|625181248|XP_007632389.1
☐	PREDICTED: biotinidase isoform X2 [Physeter catodon]	54.3	54.3	100%	3e-07	76%	gi|593711507|XP_007102308.1
☐	PREDICTED: biotinidase isoform X1 [Cricetulus griseus]	54.3	54.3	93%	3e-07	81%	gi|354465853|XP_003495391.1

☐	PREDICTED: biotinidase isoform X1 [Physeter catodon]	54.3	54.3	100%	3e-07	76%	gi|593711505|XP_007102307.1
☐	biotinidase [Cricetulus griseus]	54.3	54.3	93%	3e-07	81%	gi|537261432|ERE90059.1
☐	PREDICTED: biotinidase isoform X1 [Peromyscus maniculatus bair	53.1	53.1	100%	8e-07	73%	gi|589967608|XP_006996305.1
☐	PREDICTED: biotinidase [Nannospalax galili]	53.1	53.1	100%	8e-07	73%	gi|674081213|XP_008848205.1
☐	PREDICTED: biotinidase isoform X2 [Peromyscus maniculatus bair	53.1	53.1	100%	8e-07	73%	gi|589967610|XP_006996306.1
☐	PREDICTED: biotinidase [Mesocricetus auratus]	52.8	52.8	100%	1e-06	76%	gi|524955500|XP_005077724.1
☐	Biotinidase [Heterocephalus glaber]	52.4	52.4	100%	2e-06	70%	gi|351707565|EHB10484.1
☐	PREDICTED: biotinidase-like [Ailuropoda melanoleuca]	52.4	52.4	100%	2e-06	70%	gi|301759093|XP_002915396.1
☐	hypothetical protein PANDA_003369 [Ailuropoda melanoleuca]	52.4	52.4	100%	2e-06	70%	gi|281345880|EFB21464.1
☐	PREDICTED: biotinidase isoform X3 [Heterocephalus glaber]	52.4	52.4	100%	2e-06	70%	gi|512886961|XP_004896459.1
☐	PREDICTED: biotinidase isoform X1 [Heterocephalus glaber]	52.4	52.4	100%	2e-06	70%	gi|512886949|XP_004896457.1
☐	PREDICTED: biotinidase isoform X1 [Cavia porcellus]	52.0	52.0	100%	2e-06	70%	gi|514481133|XP_003480063.2
☐	PREDICTED: biotinidase isoform X2 [Cavia porcellus]	52.0	52.0	100%	2e-06	70%	gi|514481131|XP_005008361.1
☐	PREDICTED: biotinidase [Loxodonta africana]	51.2	51.2	100%	4e-06	64%	gi|731510838|XP_010598778.1
☐	TPA: biotinidase precursor [Bos taurus]	50.8	50.8	100%	5e-06	70%	gi|296490802|DAA32915.1
☐	biotinidase precursor [Bos taurus]	50.8	50.8	100%	5e-06	70%	gi|156121059|NP_001095676.1
☐	PREDICTED: biotinidase isoform X1 [Bos taurus]	50.8	50.8	100%	5e-06	70%	gi|528938459|XP_005202205.1
☐	PREDICTED: biotinidase [Erinaceus europaeus]	50.8	50.8	100%	6e-06	67%	gi|617553342|XP_007530134.1
☐	biotinidase, isoform CRA_a [Rattus norvegicus]	50.1	50.1	100%	8e-06	67%	gi|149034168|EDL88938.1
☐	biotinidase, isoform CRA_c [Rattus norvegicus]	50.1	50.1	100%	8e-06	67%	gi|149034170|EDL88940.1
☐	biotinidase precursor [Rattus norvegicus]	50.1	50.1	100%	1e-05	67%	gi|58865670|NP_001012047.1
☐	PREDICTED: biotinidase [Pteropus alecto]	50.1	50.1	93%	1e-05	74%	gi|586544408|XP_006907323.1
☐	PREDICTED: biotinidase isoform X2 [Capra hircus]	50.1	50.1	100%	1e-05	67%	gi|548452663|XP_005675772.1
☐	PREDICTED: biotinidase isoform X2 [Rattus norvegicus]	50.1	50.1	100%	1e-05	67%	gi|564387894|XP_006252671.1
☐	PREDICTED: biotinidase [Ovis aries]	50.1	50.1	100%	1e-05	67%	gi|426219576|XP_004003996.1
☐	PREDICTED: biotinidase isoform X1 [Capra hircus]	50.1	50.1	100%	1e-05	67%	gi|548452657|XP_005675771.1

Alignments

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PREDICTED: biotinidase [Nomascus leucogenys]

Sequence ID: gi|332232450|ref|XP_003265417.1| **Length:** 474 **Number of Matches:** 1

Range 1: 260 to 292 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.3 bits(168)	1e-12	33/33(100%)	33/33(100%)	0/33(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  33
            KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF
Sbjct  260  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  292
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221043776|dbj|BAH13565.1| **Length:** 523 **Number of Matches:** 1

Range 1: 309 to 341 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.3 bits(168)	2e-12	33/33(100%)	33/33(100%)	0/33(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  33
            KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF
Sbjct  309  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  341
```

Related Information

Gene - associated gene details

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biotinidase isoform 4 precursor [Homo sapiens]

Sequence ID: gi|528524486|ref|NP_001268654.1| **Length:** 523 **Number of Matches:** 1

▷ See 3 more title(s)

Range 1: 309 to 341 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.3 bits(168)	2e-12	33/33(100%)	33/33(100%)	0/33(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  33
            KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF
Sbjct  309  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  341
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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biotinidase precursor [Pan troglodytes]

Sequence ID: gi|697993457|ref|NP_001289363.1| **Length:** 523 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 309 to 341 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.3 bits(168)	2e-12	33/33(100%)	33/33(100%)	0/33(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  33
            KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF
Sbjct  309  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  341
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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PREDICTED: biotinidase isoform X2 [Pan troglodytes]

Sequence ID: gi|694900420|ref|XP_009443239.1| **Length:** 527 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 313 to 345 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.3 bits(168)	2e-12	33/33(100%)	33/33(100%)	0/33(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  33
            KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF
Sbjct  313  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKF  345
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - B921P7NN01R

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

BTD_KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI_NonMod

RID	B921P7NN01R (Expires on 01-14 09:51 am)
Query ID	lcl|97019
Description	None
Molecule type	amino acid
Query Length	36
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

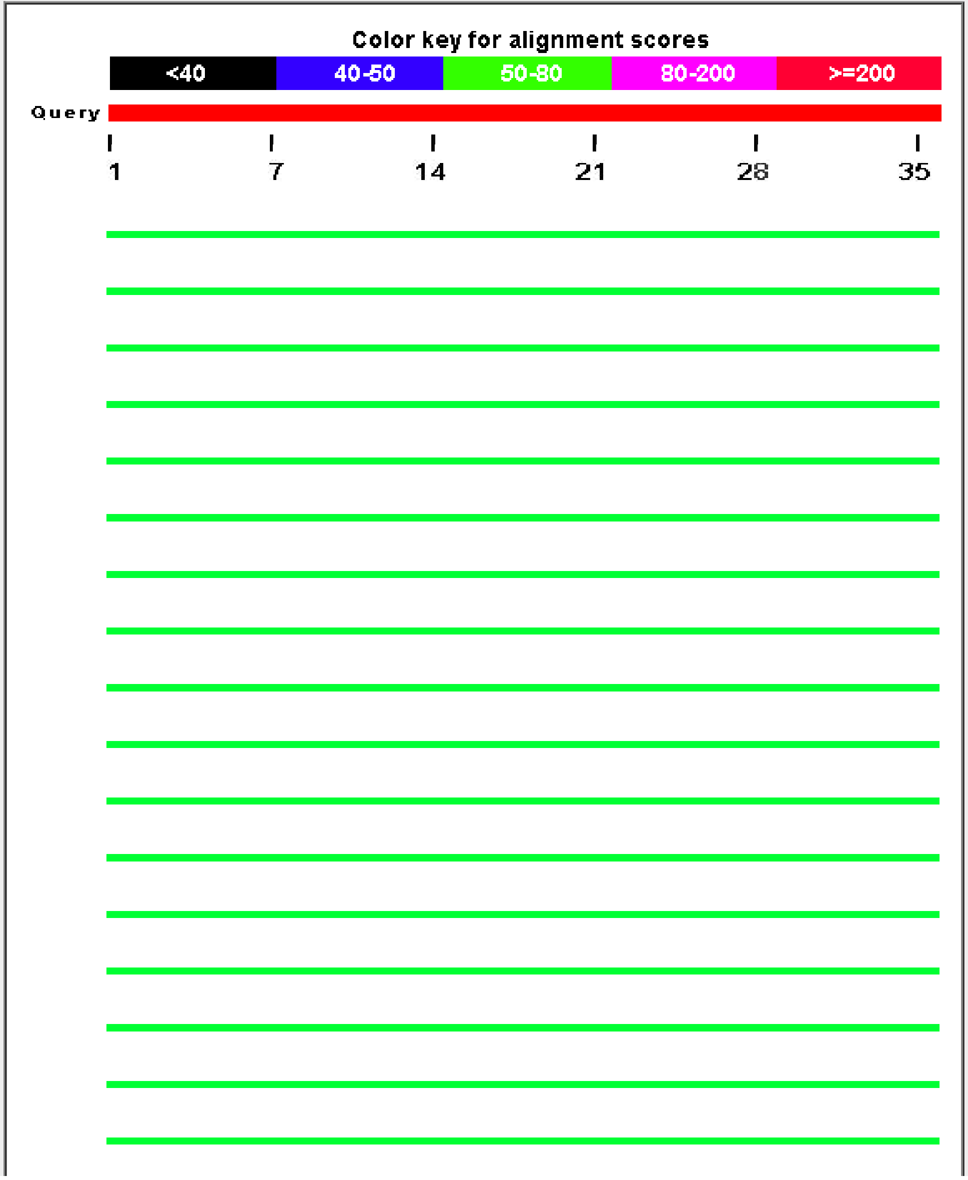
Graphic Summary

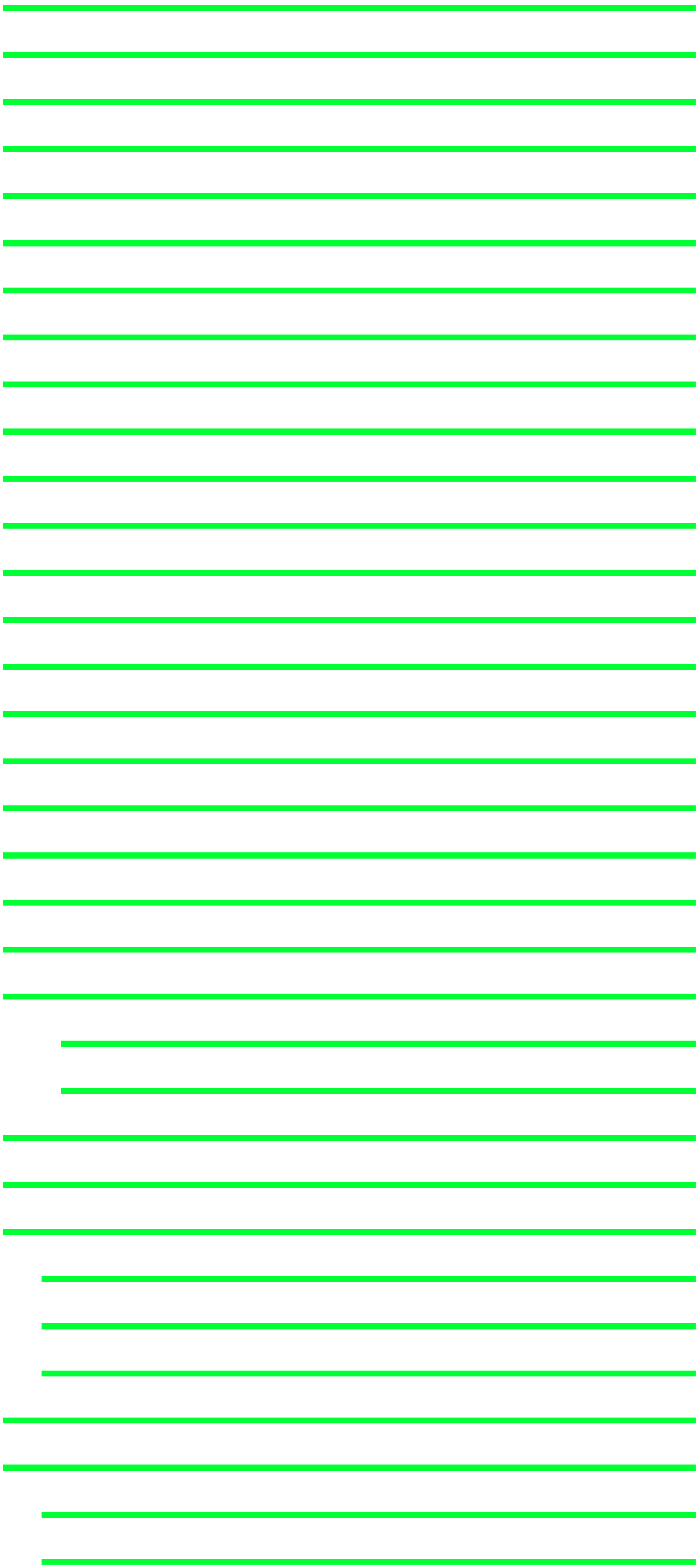
Show Conserved Domains

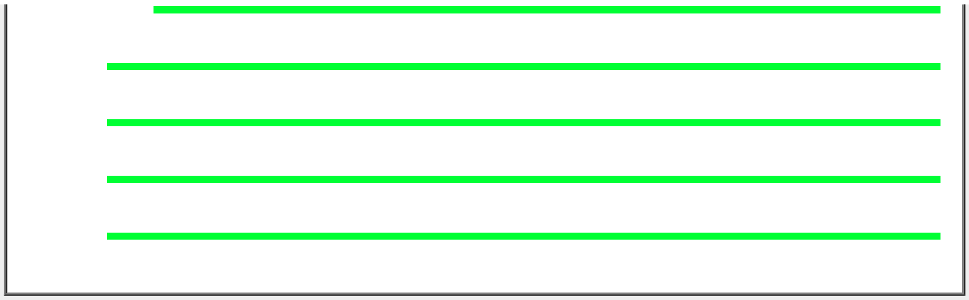
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: biotinidase [Nomascus leucogenys]	74.3	74.3	100%	3e-14	100%	gi|332232450|XP_003265417.1
☐	unnamed protein product [Homo sapiens]	74.3	74.3	100%	3e-14	100%	gi|221043776|BAH13565.1
☐	biotinidase isoform 4 precursor [Homo sapiens]	74.3	74.3	100%	3e-14	100%	gi|528524486|NP_001268654.1
☐	biotinidase precursor [Pan troglodytes]	74.3	74.3	100%	3e-14	100%	gi|697993457|NP_001289363.1
☐	PREDICTED: biotinidase isoform X2 [Pan troglodytes]	74.3	74.3	100%	3e-14	100%	gi|694900420|XP_009443239.1
☐	PREDICTED: biotinidase isoform X2 [Pan paniscus]	74.3	74.3	100%	3e-14	100%	gi|675784344|XP_008949921.1
☐	PREDICTED: biotinidase isoform X3 [Pongo abelii]	74.3	74.3	100%	3e-14	100%	gi|686713703|XP_009237577.1
☐	PREDICTED: biotinidase isoform X2 [Pongo abelii]	74.3	74.3	100%	3e-14	100%	gi|686713701|XP_009237576.1
☐	biotinidase isoform 3 [Homo sapiens]	74.3	74.3	100%	3e-14	100%	gi|4557373|NP_000051.1
☐	biotinidase isoform 1 [Homo sapiens]	74.3	74.3	100%	3e-14	100%	gi|528524481|NP_001268652.1
☐	biotinidase isoform 2 [Homo sapiens]	74.3	74.3	100%	3e-14	100%	gi|528524483|NP_001268653.1
☐	PREDICTED: biotinidase isoform X1 [Pan troglodytes]	74.3	74.3	100%	3e-14	100%	gi|410036604|XP_003950087.1
☐	PREDICTED: biotinidase isoform X1 [Pan paniscus]	74.3	74.3	100%	3e-14	100%	gi|397511808|XP_003826257.1
☐	PREDICTED: biotinidase isoform X1 [Pongo abelii]	74.3	74.3	100%	3e-14	100%	gi|395734130|XP_003776360.1
☐	PREDICTED: biotinidase isoform 1 [Gorilla gorilla gorilla]	73.9	73.9	100%	4e-14	97%	gi|426339607|XP_004033737.1
☐	PREDICTED: biotinidase isoform 3 [Gorilla gorilla gorilla]	73.9	73.9	100%	5e-14	97%	gi|426339611|XP_004033739.1
☐	PREDICTED: biotinidase isoform 4 [Gorilla gorilla gorilla]	73.9	73.9	100%	5e-14	97%	gi|426339613|XP_004033740.1
☐	PREDICTED: biotinidase isoform 2 [Gorilla gorilla gorilla]	73.9	73.9	100%	5e-14	97%	gi|426339609|XP_004033738.1
☐	unnamed protein product [Macaca fascicularis]	72.8	72.8	100%	1e-13	97%	gi|90077268|BAE88314.1
☐	PREDICTED: biotinidase isoform X2 [Macaca fascicularis]	72.8	72.8	100%	1e-13	97%	gi|544411158|XP_005545768.1
☐	hypothetical protein EGM_11114 [Macaca fascicularis]	72.8	72.8	100%	1e-13	97%	gi|355747075|EHH51689.1
☐	hypothetical protein EGK_12122 [Macaca mulatta]	72.8	72.8	100%	1e-13	97%	gi|355560049|EHH16777.1
☐	PREDICTED: biotinidase [Macaca mulatta]	72.8	72.8	100%	1e-13	97%	gi|297286947|XP_001083201.2
☐	PREDICTED: biotinidase isoform X1 [Macaca fascicularis]	72.8	72.8	100%	1e-13	97%	gi|544411156|XP_005545767.1
☐	PREDICTED: biotinidase isoform X2 [Chlorocebus sabaeus]	71.2	71.2	100%	4e-13	94%	gi|635085523|XP_008007381.1
☐	PREDICTED: biotinidase isoform X1 [Chlorocebus sabaeus]	71.2	71.2	100%	4e-13	94%	gi|635085521|XP_008007380.1
☐	PREDICTED: biotinidase [Rhinopithecus roxellana]	68.6	68.6	100%	4e-12	89%	gi|724960396|XP_010354361.1
☐	PREDICTED: biotinidase isoform X2 [Papio anubis]	67.4	67.4	100%	9e-12	89%	gi|685527526|XP_009200021.1
☐	PREDICTED: biotinidase isoform X1 [Papio anubis]	67.4	67.4	100%	1e-11	89%	gi|685527524|XP_009200020.1
☐							

	PREDICTED: biotinidase-like [Ictidomys tridecemlineatus]	65.1	65.1	100%	5e-11	83%	gi|532063189|XP_005317469.1
☐	PREDICTED: biotinidase [Ceratotherium simum simum]	65.1	65.1	100%	6e-11	83%	gi|478490156|XP_004419451.1
☐	PREDICTED: biotinidase isoform X4 [Canis lupus familiaris]	63.9	63.9	100%	2e-10	81%	gi|545538859|XP_005634450.1
☐	PREDICTED: biotinidase isoform X3 [Canis lupus familiaris]	63.9	63.9	100%	2e-10	81%	gi|545538857|XP_005634449.1
☐	PREDICTED: biotinidase isoform X2 [Canis lupus familiaris]	63.9	63.9	100%	2e-10	81%	gi|545538855|XP_005634448.1
☐	PREDICTED: biotinidase isoform X1 [Canis lupus familiaris]	63.9	63.9	100%	2e-10	81%	gi|545538853|XP_005634447.1
☐	PREDICTED: biotinidase isoform X3 [Equus caballus]	63.5	63.5	100%	2e-10	81%	gi|545189350|XP_005600979.1
☐	PREDICTED: biotinidase [Equus przewalskii]	63.5	63.5	100%	2e-10	81%	gi|664753751|XP_008534346.1
☐	PREDICTED: biotinidase isoform X2 [Equus caballus]	63.5	63.5	100%	2e-10	81%	gi|545189348|XP_005600978.1
☐	PREDICTED: biotinidase isoform X1 [Equus caballus]	63.5	63.5	100%	2e-10	81%	gi|545189346|XP_005600977.1
☐	PREDICTED: biotinidase isoform X1 [Callithrix jacchus]	62.8	62.8	91%	4e-10	94%	gi|675740028|XP_008982107.1
☐	PREDICTED: biotinidase isoform X2 [Callithrix jacchus]	62.8	62.8	91%	4e-10	94%	gi|390476393|XP_002759736.2
☐	PREDICTED: biotinidase [Otolemur garnettii]	62.4	62.4	100%	6e-10	83%	gi|395816560|XP_003781769.1
☐	PREDICTED: biotinidase isoform X2 [Microtus ochrogaster]	61.6	61.6	100%	1e-09	78%	gi|532009812|XP_005348714.1
☐	PREDICTED: biotinidase isoform X1 [Microtus ochrogaster]	61.6	61.6	100%	1e-09	78%	gi|532009810|XP_005348713.1
☐	PREDICTED: biotinidase-like isoform X10 [Chinchilla lanigera]	61.2	61.2	94%	1e-09	82%	gi|533146084|XP_005387502.1
☐	PREDICTED: biotinidase-like isoform X5 [Chinchilla lanigera]	61.2	61.2	94%	1e-09	82%	gi|533146074|XP_005387497.1
☐	PREDICTED: biotinidase-like isoform X1 [Chinchilla lanigera]	61.2	61.2	94%	1e-09	82%	gi|533146066|XP_005387493.1
☐	biotinidase [Camelus ferus]	60.5	60.5	100%	2e-09	72%	gi|528756912|EPY76571.1
☐	PREDICTED: biotinidase [Vicugna pacos]	60.8	60.8	100%	2e-09	72%	gi|560965913|XP_006205350.1
☐	PREDICTED: biotinidase [Jaculus jaculus]	60.8	60.8	94%	2e-09	82%	gi|507555213|XP_004661377.1
☐	PREDICTED: biotinidase isoform X1 [Felis catus]	60.8	60.8	94%	2e-09	82%	gi|587000359|XP_003992187.2
☐	PREDICTED: biotinidase isoform X2 [Felis catus]	60.8	60.8	94%	2e-09	82%	gi|587000357|XP_006936495.1
☐	PREDICTED: biotinidase [Trichechus manatus latirostris]	60.8	60.8	100%	2e-09	75%	gi|471407481|XP_004385327.1
☐	PREDICTED: biotinidase [Fukomys damarensis]	60.8	60.8	100%	2e-09	78%	gi|731285322|XP_010611073.1
☐	PREDICTED: biotinidase [Lipotes vexillifer]	60.8	60.8	100%	2e-09	81%	gi|602721076|XP_007470691.1
☐	PREDICTED: biotinidase isoform X1 [Balaenoptera acutorostrata sc	60.8	60.8	100%	2e-09	81%	gi|594624940|XP_007167058.1
☐	Biotinidase [Fukomys damarensis]	60.8	60.8	100%	2e-09	78%	gi|676263045|KFO19807.1
☐	PREDICTED: biotinidase isoform X3 [Balaenoptera acutorostrata sc	60.8	60.8	100%	2e-09	81%	gi|594624944|XP_007167060.1
☐	PREDICTED: biotinidase [Camelus ferus]	60.5	60.5	100%	3e-09	72%	gi|560929390|XP_006190847.1
☐	PREDICTED: LOW QUALITY PROTEIN: biotinidase [Tursiops trunc	60.5	60.5	100%	3e-09	78%	gi|470628904|XP_004321284.1
☐	PREDICTED: biotinidase [Orcinus orca]	60.5	60.5	100%	3e-09	78%	gi|466019817|XP_004271983.1
☐	PREDICTED: biotinidase isoform 2 [Odobenus rosmarus divergens	60.1	60.1	94%	3e-09	82%	gi|472379495|XP_004409157.1
☐	PREDICTED: biotinidase isoform 1 [Odobenus rosmarus divergens	60.1	60.1	94%	3e-09	82%	gi|472379493|XP_004409156.1
☐	PREDICTED: biotinidase [Galeopterus variegatus]	59.7	59.7	94%	5e-09	82%	gi|667288263|XP_008576771.1
☐	PREDICTED: biotinidase [Mustela putorius furo]	59.7	59.7	100%	5e-09	72%	gi|511908359|XP_004773614.1
☐	PREDICTED: biotinidase isoform X2 [Cricetulus griseus]	59.3	59.3	94%	6e-09	82%	gi|625181248|XP_007632389.1
☐	PREDICTED: biotinidase isoform X2 [Physeter catodon]	59.3	59.3	100%	6e-09	78%	gi|593711507|XP_007102308.1
☐	PREDICTED: biotinidase [Panthera tigris altaica]	59.3	59.3	94%	7e-09	79%	gi|591322659|XP_007087428.1
☐	PREDICTED: biotinidase isoform X1 [Cricetulus griseus]	59.3	59.3	94%	7e-09	82%	gi|354465853|XP_003495391.1
☐	PREDICTED: biotinidase isoform X1 [Physeter catodon]	59.3	59.3	100%	7e-09	78%	gi|593711505|XP_007102307.1
☐	biotinidase [Cricetulus griseus]	59.3	59.3	94%	7e-09	82%	gi|537261432|ERE90059.1
☐	PREDICTED: biotinidase isoform X3 [Leptonychotes weddellii]	58.9	58.9	94%	9e-09	79%	gi|585186600|XP_006744787.1
☐	PREDICTED: biotinidase isoform X2 [Leptonychotes weddellii]	58.9	58.9	94%	9e-09	79%	gi|585186598|XP_006744786.1
☐	PREDICTED: biotinidase isoform X1 [Leptonychotes weddellii]	58.9	58.9	94%	9e-09	79%	gi|585186596|XP_006744785.1

☐ PREDICTED: biotinidase isoform X1 [Peromyscus maniculatus bair	58.2	58.2	100%	2e-08	75%	gi|589967608|XP_006996305.1
☐ PREDICTED: biotinidase [Nannospalax galili]	58.2	58.2	100%	2e-08	75%	gi|674081213|XP_008848205.1
☐ PREDICTED: biotinidase isoform X2 [Ursus maritimus]	58.2	58.2	100%	2e-08	72%	gi|670981874|XP_008707139.1
☐ PREDICTED: biotinidase isoform X2 [Peromyscus maniculatus bair	58.2	58.2	100%	2e-08	75%	gi|589967610|XP_006996306.1
☐ PREDICTED: biotinidase isoform X1 [Ursus maritimus]	58.2	58.2	100%	2e-08	72%	gi|670981872|XP_008707130.1
☐ Biotinidase [Heterocephalus glaber]	57.4	57.4	100%	3e-08	72%	gi|351707565|EHB10484.1
☐ PREDICTED: biotinidase isoform X3 [Heterocephalus glaber]	57.4	57.4	100%	3e-08	72%	gi|512886961|XP_004896459.1
☐ PREDICTED: biotinidase isoform X1 [Heterocephalus glaber]	57.4	57.4	100%	3e-08	72%	gi|512886949|XP_004896457.1
☐ PREDICTED: biotinidase [Mesocricetus auratus]	56.6	56.6	100%	6e-08	75%	gi|524955500|XP_005077724.1
☐ PREDICTED: biotinidase [Loxodonta africana]	56.2	56.2	100%	8e-08	67%	gi|731510838|XP_010598778.1
☐ PREDICTED: biotinidase [Erinaceus europaeus]	55.8	55.8	100%	1e-07	69%	gi|617553342|XP_007530134.1
☐ PREDICTED: biotinidase-like [Ailuropoda melanoleuca]	55.1	55.1	100%	2e-07	67%	gi|301759093|XP_002915396.1
☐ hypothetical protein PANDA_003369 [Ailuropoda melanoleuca]	55.1	55.1	100%	2e-07	67%	gi|281345880|EFB21464.1
☐ biotinidase, isoform CRA_a [Rattus norvegicus]	54.7	54.7	100%	2e-07	67%	gi|149034168|EDL88938.1
☐ biotinidase, isoform CRA_c [Rattus norvegicus]	54.7	54.7	100%	2e-07	67%	gi|149034170|EDL88940.1
☐ biotinidase precursor [Rattus norvegicus]	54.7	54.7	100%	3e-07	67%	gi|58865670|NP_001012047.1
☐ PREDICTED: biotinidase isoform X1 [Cavia porcellus]	54.7	54.7	100%	3e-07	67%	gi|514481133|XP_003480063.2
☐ PREDICTED: biotinidase isoform X2 [Rattus norvegicus]	54.7	54.7	100%	3e-07	67%	gi|564387894|XP_006252671.1
☐ PREDICTED: biotinidase isoform X2 [Cavia porcellus]	54.7	54.7	100%	3e-07	67%	gi|514481131|XP_005008361.1
☐ PREDICTED: biotinidase isoform X3 [Saimiri boliviensis boliviensis]	54.3	54.3	91%	4e-07	82%	gi|725560828|XP_010333963.1
☐ PREDICTED: biotinidase isoform X2 [Saimiri boliviensis boliviensis]	54.3	54.3	91%	4e-07	82%	gi|403265544|XP_003924991.1
☐ PREDICTED: biotinidase isoform X1 [Saimiri boliviensis boliviensis]	54.3	54.3	91%	4e-07	82%	gi|725560825|XP_010333962.1
☐ PREDICTED: biotinidase isoform X1 [Mus musculus]	53.9	53.9	100%	4e-07	72%	gi|568987712|XP_006519092.1
☐ RecName: Full=Biotinidase; Short=Biotinase; Flags: Precursor [Mus	53.9	53.9	100%	5e-07	72%	gi|150421524|Q8CIF4.2
☐ unnamed protein product [Mus musculus]	53.9	53.9	100%	5e-07	72%	gi|74183082|BAE22509.1
☐ biotinidase precursor [Mus musculus]	53.9	53.9	100%	5e-07	72%	gi|13384648|NP_079571.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: biotinidase [Nomascus leucogenys]

Sequence ID: gi|332232450|ref|XP_003265417.1| **Length:** 474 **Number of Matches:** 1

Range 1: 260 to 295 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
74.3 bits(181)	3e-14	36/36(100%)	36/36(100%)	0/36(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  36
            KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI
Sbjct  260  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  295
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221043776|dbj|BAH13565.1| **Length:** 523 **Number of Matches:** 1

Range 1: 309 to 344 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
74.3 bits(181)	3e-14	36/36(100%)	36/36(100%)	0/36(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  36
            KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI
Sbjct  309  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  344
```

Related Information

Gene - associated gene details

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biotinidase isoform 4 precursor [Homo sapiens]

Sequence ID: gi|528524486|ref|NP_001268654.1| **Length:** 523 **Number of Matches:** 1

See 3 more title(s)

Range 1: 309 to 344 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
74.3 bits(181)	3e-14	36/36(100%)	36/36(100%)	0/36(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  36
            KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI
Sbjct  309  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  344
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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biotinidase precursor [Pan troglodytes]

Sequence ID: gi|697993457|ref|NP_001289363.1| **Length:** 523 **Number of Matches:** 1

See 1 more title(s)

Range 1: 309 to 344 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
74.3 bits(181)	3e-14	36/36(100%)	36/36(100%)	0/36(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  36
            KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI
Sbjct  309  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  344
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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PREDICTED: biotinidase isoform X2 [Pan troglodytes]

Sequence ID: gi|694900420|ref|XP_009443239.1| **Length:** 527 **Number of Matches:** 1

See 1 more title(s)

Range 1: 313 to 348 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
74.3 bits(181)	3e-14	36/36(100%)	36/36(100%)	0/36(0%)

```
Query  1    KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  36
            KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI
Sbjct  313  KSHLIIAQVAKNPVGLIGAENATGETDPSHSKFLKI  348
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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NCBI/ BLAST/ blastp suite/ Formatting Results - BT4F1XB1013

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit　Save Search Strategies　Formatting options　Download　How to read this page　Blast report description

BTD_KWNVNAPPTFHSEMMYDDFTLVPVWGKE_Mod

RID BT4F1XB1013 (Expires on 01-20 12:10 pm)

Query ID lcl|19040
Description None
Molecule type amino acid
Query Length 28

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

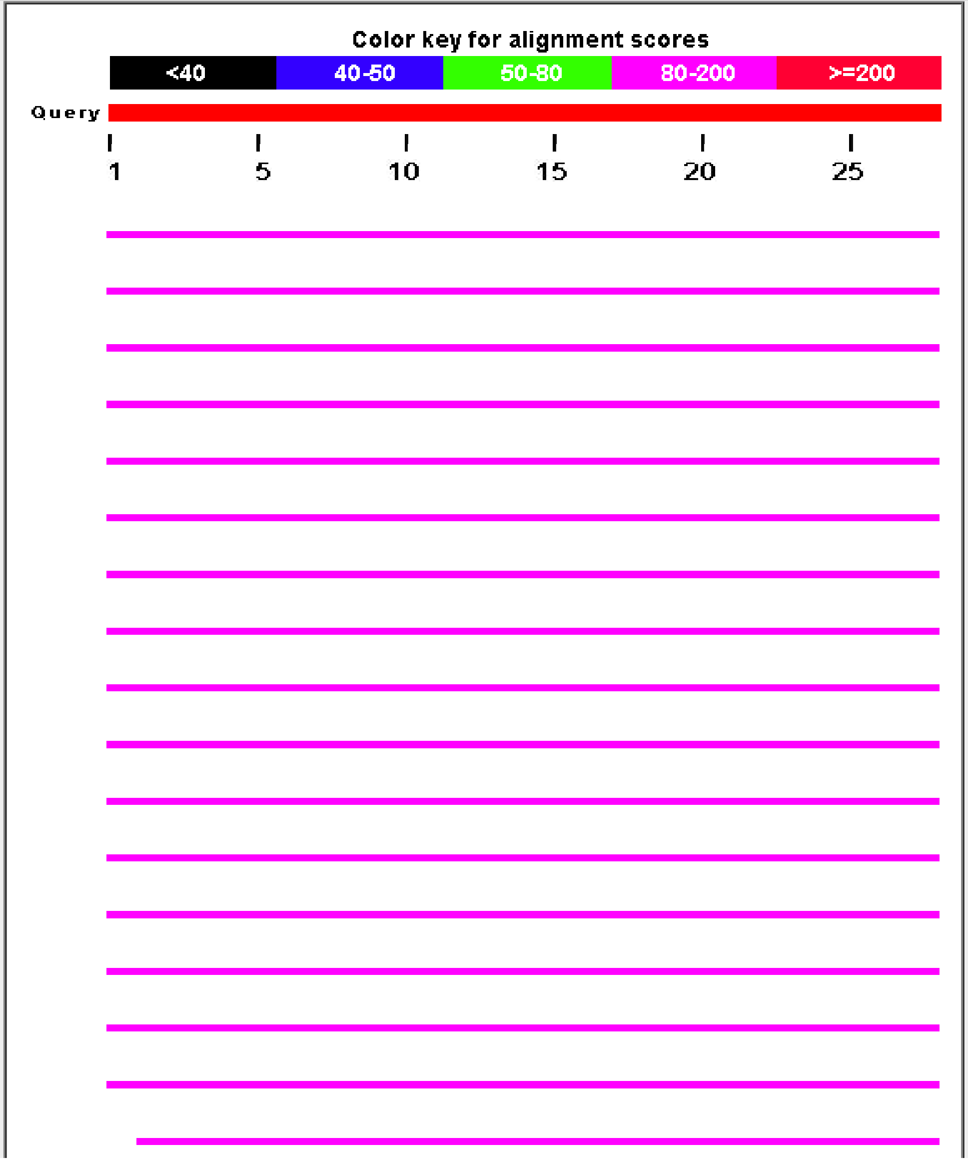
Graphic Summary

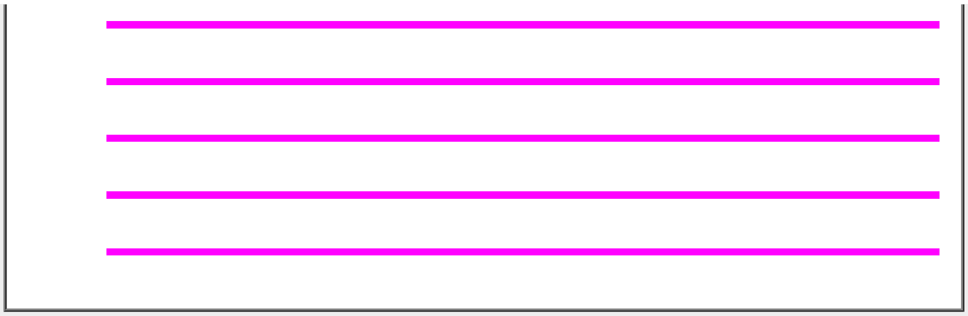
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: biotinidase [Nomascus leucogenys]	98.6	98.6	100%	1e-21	96%	gi|332232450|XP_003265417.1
☐	unnamed protein product [Homo sapiens]	98.6	98.6	100%	1e-21	96%	gi|221043776|BAH13565.1
☐	biotinidase isoform 4 precursor [Homo sapiens]	98.6	98.6	100%	1e-21	96%	gi|528524486|NP_001268654.1
☐	biotinidase precursor [Pan troglodytes]	98.6	98.6	100%	1e-21	96%	gi|697993457|NP_001289363.1
☐	PREDICTED: biotinidase isoform 1 [Gorilla gorilla gorilla]	98.6	98.6	100%	1e-21	96%	gi|426339607|XP_004033737.1
☐	PREDICTED: biotinidase isoform X2 [Pan troglodytes]	98.6	98.6	100%	1e-21	96%	gi|694900420|XP_009443239.1
☐	PREDICTED: biotinidase isoform X2 [Pan paniscus]	98.6	98.6	100%	1e-21	96%	gi|675784344|XP_008949921.1
☐	PREDICTED: biotinidase isoform 3 [Gorilla gorilla gorilla]	98.6	98.6	100%	1e-21	96%	gi|426339611|XP_004033739.1
☐	PREDICTED: biotinidase isoform 4 [Gorilla gorilla gorilla]	98.6	98.6	100%	1e-21	96%	gi|426339613|XP_004033740.1
☐	biotinidase isoform 3 [Homo sapiens]	98.6	98.6	100%	1e-21	96%	gi|4557373|NP_000051.1
☐	biotinidase isoform 1 [Homo sapiens]	98.6	98.6	100%	1e-21	96%	gi|528524481|NP_001268652.1
☐	biotinidase isoform 2 [Homo sapiens]	98.6	98.6	100%	1e-21	96%	gi|528524483|NP_001268653.1
☐	PREDICTED: biotinidase isoform 2 [Gorilla gorilla gorilla]	98.6	98.6	100%	1e-21	96%	gi|426339609|XP_004033738.1
☐	PREDICTED: biotinidase isoform X1 [Pan troglodytes]	98.6	98.6	100%	1e-21	96%	gi|410036604|XP_003950087.1
☐	PREDICTED: biotinidase isoform X1 [Pan paniscus]	98.6	98.6	100%	1e-21	96%	gi|397511808|XP_003826257.1
☐	PREDICTED: biotinidase [Jaculus jaculus]	96.5	96.5	100%	7e-21	93%	gi|507555213|XP_004661377.1
☐	PREDICTED: biotinidase isoform X3 [Pongo abelii]	95.6	95.6	96%	1e-20	96%	gi|686713703|XP_009237577.1
☐	PREDICTED: biotinidase isoform X2 [Pongo abelii]	95.6	95.6	96%	1e-20	96%	gi|686713701|XP_009237576.1
☐	PREDICTED: biotinidase isoform X1 [Pongo abelii]	95.6	95.6	96%	1e-20	96%	gi|395734130|XP_003776360.1
☐	PREDICTED: biotinidase isoform X2 [Cricetulus griseus]	95.2	95.2	100%	2e-20	93%	gi|625181248|XP_007632389.1
☐	PREDICTED: biotinidase isoform X1 [Peromyscus maniculatus	95.2	95.2	100%	2e-20	93%	gi|589967608|XP_006996305.1
☐	unnamed protein product [Macaca fascicularis]	95.2	95.2	100%	2e-20	93%	gi|90077268|BAE88314.1
☐	PREDICTED: biotinidase [Galeopterus variegatus]	95.2	95.2	100%	2e-20	93%	gi|667288263|XP_008576771.1
☐	PREDICTED: biotinidase isoform X2 [Microtus ochrogaster]	95.2	95.2	100%	2e-20	93%	gi|532009812|XP_005348714.1
☐	PREDICTED: biotinidase isoform X2 [Peromyscus maniculatus	95.2	95.2	100%	2e-20	93%	gi|589967610|XP_006996306.1
☐	PREDICTED: biotinidase isoform X2 [Chlorocebus sabaeus]	95.2	95.2	100%	2e-20	93%	gi|635085523|XP_008007381.1
☐	PREDICTED: biotinidase isoform X2 [Macaca fascicularis]	95.2	95.2	100%	2e-20	93%	gi|544411158|XP_005545768.1
☐	PREDICTED: biotinidase isoform X2 [Papio anubis]	95.2	95.2	100%	2e-20	93%	gi|685527526|XP_009200021.1
☐	PREDICTED: biotinidase isoform X1 [Chlorocebus sabaeus]	95.2	95.2	100%	2e-20	93%	gi|635085521|XP_008007380.1

☐	PREDICTED: biotinidase [Mustela putorius furo]	95.2	95.2	100%	2e-20	93%	gi|511908359|XP_004773614.1
☐	PREDICTED: biotinidase isoform X1 [Cricetulus griseus]	95.2	95.2	100%	2e-20	93%	gi|354465853|XP_003495391.1
☐	PREDICTED: biotinidase [Orycteropus afer afer]	95.2	95.2	100%	2e-20	93%	gi|634822252|XP_007934900.1
☐	hypothetical protein EGM_11114 [Macaca fascicularis]	95.2	95.2	100%	2e-20	93%	gi|355747075|EHH51689.1
☐	hypothetical protein EGK_12122 [Macaca mulatta]	95.2	95.2	100%	2e-20	93%	gi|355560049|EHH16777.1
☐	PREDICTED: biotinidase isoform X1 [Microtus ochrogaster]	95.2	95.2	100%	2e-20	93%	gi|532009810|XP_005348713.1
☐	PREDICTED: biotinidase [Macaca mulatta]	95.2	95.2	100%	2e-20	93%	gi|297286947|XP_001083201.2
☐	PREDICTED: biotinidase isoform X1 [Papio anubis]	95.2	95.2	100%	2e-20	93%	gi|685527524|XP_009200020.1
☐	PREDICTED: biotinidase isoform X1 [Macaca fascicularis]	95.2	95.2	100%	2e-20	93%	gi|544411156|XP_005545767.1
☐	biotinidase [Cricetulus griseus]	95.2	95.2	100%	2e-20	93%	gi|537261432|ERE90059.1
☐	biotinidase, isoform CRA_a [Rattus norvegicus]	94.8	94.8	100%	3e-20	93%	gi|149034168|EDL88938.1
☐	biotinidase, isoform CRA_c [Rattus norvegicus]	94.8	94.8	100%	3e-20	93%	gi|149034170|EDL88940.1
☐	PREDICTED: biotinidase isoform X2 [Rattus norvegicus]	94.8	94.8	100%	3e-20	93%	gi|564387894|XP_006252671.1
☐	PREDICTED: biotinidase [Chrysochloris asiatica]	93.1	93.1	100%	1e-19	89%	gi|586456511|XP_006840071.1
☐	PREDICTED: biotinidase-like [Ictidomys tridecemlineatus]	92.7	92.7	100%	1e-19	89%	gi|532063189|XP_005317469.1
☐	PREDICTED: biotinidase isoform X4 [Canis lupus familiaris]	91.8	91.8	100%	3e-19	89%	gi|545538859|XP_005634450.1
☐	PREDICTED: LOW QUALITY PROTEIN: biotinidase [Tursiops	91.8	91.8	100%	3e-19	89%	gi|470628904|XP_004321284.1
☐	PREDICTED: biotinidase [Orcinus orca]	91.8	91.8	100%	3e-19	89%	gi|466019817|XP_004271983.1
☐	PREDICTED: biotinidase isoform X3 [Canis lupus familiaris]	91.8	91.8	100%	3e-19	89%	gi|545538857|XP_005634449.1
☐	PREDICTED: biotinidase isoform X2 [Canis lupus familiaris]	91.8	91.8	100%	3e-19	89%	gi|545538855|XP_005634448.1
☐	PREDICTED: biotinidase isoform X1 [Canis lupus familiaris]	91.8	91.8	100%	3e-19	89%	gi|545538853|XP_005634447.1
☐	PREDICTED: biotinidase isoform X1 [Mus musculus]	91.0	91.0	100%	5e-19	89%	gi|568987712|XP_006519092.1
☐	RecName: Full=Biotinidase; Short=Biotinase; Flags: Precursor	91.0	91.0	100%	6e-19	89%	gi|150421524|Q8CIF4.2
☐	PREDICTED: biotinidase [Rhinopithecus roxellana]	91.0	91.0	100%	6e-19	89%	gi|724960396|XP_010354361.1
☐	unnamed protein product [Mus musculus]	91.0	91.0	100%	6e-19	89%	gi|74183082|BAE22509.1
☐	biotinidase precursor [Mus musculus]	91.0	91.0	100%	6e-19	89%	gi|13384648|NP_079571.1
☐	PREDICTED: biotinidase isoform X2 [Physeter catodon]	90.6	90.6	100%	8e-19	89%	gi|593711507|XP_007102308.1
☐	PREDICTED: biotinidase isoform X1 [Physeter catodon]	90.6	90.6	100%	8e-19	89%	gi|593711505|XP_007102307.1
☐	PREDICTED: biotinidase [Lipotes vexillifer]	90.6	90.6	100%	8e-19	89%	gi|602721076|XP_007470691.1
☐	PREDICTED: biotinidase isoform X1 [Balaenoptera acutorostra	90.6	90.6	100%	8e-19	89%	gi|594624940|XP_007167058.1
☐	PREDICTED: biotinidase isoform X3 [Balaenoptera acutorostra	90.6	90.6	100%	8e-19	89%	gi|594624944|XP_007167060.1
☐	PREDICTED: biotinidase isoform X3 [Equus caballus]	90.1	90.1	100%	1e-18	89%	gi|545189350|XP_005600979.1
☐	PREDICTED: biotinidase [Equus przewalskii]	90.1	180	100%	1e-18	89%	gi|664753751|XP_008534346.1
☐	PREDICTED: biotinidase isoform X2 [Equus caballus]	90.1	90.1	100%	1e-18	89%	gi|545189348|XP_005600978.1
☐	PREDICTED: biotinidase isoform X1 [Equus caballus]	90.1	90.1	100%	1e-18	89%	gi|545189346|XP_005600977.1
☐	PREDICTED: biotinidase [Erinaceus europaeus]	89.3	89.3	96%	2e-18	89%	gi|617553342|XP_007530134.1
☐	PREDICTED: biotinidase [Otolemur garnettii]	88.4	88.4	96%	4e-18	89%	gi|395816560|XP_003781769.1
☐	PREDICTED: biotinidase [Panthera tigris altaica]	88.0	88.0	100%	6e-18	86%	gi|591322659|XP_007087428.1
☐	PREDICTED: biotinidase isoform X1 [Felis catus]	88.0	88.0	100%	6e-18	86%	gi|587000359|XP_003992187.2
☐	PREDICTED: biotinidase isoform X2 [Felis catus]	88.0	88.0	100%	6e-18	86%	gi|587000357|XP_006936495.1
☐	PREDICTED: biotinidase [Mesocricetus auratus]	87.6	87.6	100%	8e-18	86%	gi|524955500|XP_005077724.1
☐	PREDICTED: biotinidase [Nannospalax galili]	86.7	86.7	100%	2e-17	86%	gi|674081213|XP_008848205.1
☐	PREDICTED: biotinidase isoform X2 [Ursus maritimus]	86.7	86.7	92%	2e-17	92%	gi|670981874|XP_008707139.1
☐	PREDICTED: biotinidase isoform 2 [Odobenus rosmarus diverg	86.7	86.7	96%	2e-17	89%	gi|472379495|XP_004409157.1
☐	PREDICTED: biotinidase isoform X1 [Ursus maritimus]	86.7	86.7	92%	2e-17	92%	gi|670981872|XP_008707130.1

☐	PREDICTED: biotinidase isoform X3 [Leptonychotes weddellii]	86.7	86.7	96%	2e-17	89%	gi|585186600|XP_006744787.1
☐	PREDICTED: biotinidase isoform X2 [Leptonychotes weddellii]	86.7	86.7	96%	2e-17	89%	gi|585186598|XP_006744786.1
☐	PREDICTED: biotinidase isoform 1 [Odobenus rosmarus diverg	86.7	86.7	96%	2e-17	89%	gi|472379493|XP_004409156.1
☐	PREDICTED: biotinidase isoform X1 [Leptonychotes weddellii]	86.7	86.7	96%	2e-17	89%	gi|585186596|XP_006744785.1
☐	PREDICTED: biotinidase [Ceratotherium simum simum]	86.3	86.3	100%	2e-17	86%	gi|478490156|XP_004419451.1
☐	PREDICTED: biotinidase isoform X3 [Saimiri boliviensis bolivie	85.9	85.9	100%	3e-17	89%	gi|725560828|XP_010333963.1
☐	PREDICTED: biotinidase isoform X2 [Saimiri boliviensis bolivie	85.9	85.9	100%	3e-17	89%	gi|403265544|XP_003924991.1
☐	PREDICTED: biotinidase isoform X1 [Saimiri boliviensis bolivie	85.9	85.9	100%	3e-17	89%	gi|725560825|XP_010333962.1
☐	PREDICTED: biotinidase [Echinops telfairi]	85.5	85.5	96%	4e-17	85%	gi|507651259|XP_004704067.1
☐	PREDICTED: biotinidase isoform X1 [Callithrix jacchus]	82.1	82.1	100%	6e-16	86%	gi|675740028|XP_008982107.1
☐	PREDICTED: biotinidase isoform X2 [Callithrix jacchus]	82.1	82.1	100%	6e-16	86%	gi|390476393|XP_002759736.2
☐	Biotinidase [Myotis davidii]	81.7	81.7	96%	9e-16	81%	gi|432092959|ELK25317.1
☐	PREDICTED: biotinidase isoform X1 [Myotis davidii]	81.7	81.7	96%	9e-16	81%	gi|584051114|XP_006770244.1
☐	PREDICTED: biotinidase isoform X1 [Myotis lucifugus]	81.7	81.7	96%	9e-16	81%	gi|558102610|XP_006083737.1
☐	PREDICTED: biotinidase isoform X3 [Myotis brandtii]	81.7	81.7	96%	9e-16	81%	gi|554537982|XP_005863672.1
☐	PREDICTED: biotinidase [Loxodonta africana]	81.7	81.7	100%	9e-16	79%	gi|731510838|XP_010598778.1
☐	PREDICTED: biotinidase isoform X2 [Myotis lucifugus]	81.7	81.7	96%	9e-16	81%	gi|558102613|XP_006083738.1
☐	PREDICTED: biotinidase isoform X2 [Myotis brandtii]	81.7	81.7	96%	9e-16	81%	gi|554537986|XP_005863671.1
☐	Biotinidase [Myotis brandtii]	81.7	81.7	96%	9e-16	81%	gi|521024341|EPQ06129.1
☐	PREDICTED: biotinidase [Trichechus manatus latirostris]	80.4	80.4	100%	2e-15	82%	gi|471407481|XP_004385327.1
☐	PREDICTED: biotinidase-like [Ailuropoda melanoleuca]	80.0	80.0	92%	3e-15	85%	gi|301759093|XP_002915396.1
☐	hypothetical protein PANDA_003369 [Ailuropoda melanoleuca]	80.0	80.0	92%	3e-15	85%	gi|281345880|EFB21464.1
☐	PREDICTED: biotinidase-like [Sus scrofa]	79.5	79.5	92%	4e-15	85%	gi|350590963|XP_003132114.3
☐	PREDICTED: biotinidase-like isoform X2 [Sus scrofa]	79.5	79.5	92%	5e-15	85%	gi|545860928|XP_005669335.1
☐	PREDICTED: biotinidase-like isoform X2 [Sus scrofa]	79.5	79.5	92%	5e-15	85%	gi|545860909|XP_005669330.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: biotinidase [Nomascus leucogenys]

Sequence ID: gi|332232450|ref|XP_003265417.1| **Length:** 474 **Number of Matches:** 1

Range 1: 316 to 343 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
98.6 bits(225)	1e-21	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    KWNVNAPPTFHSEMMYDDFTLVPVWGKE  28
            KWNVNAPPTFHSEMMYD+FTLVPVWGKE
Sbjct  316  KWNVNAPPTFHSEMMYDNFTLVPVWGKE  343
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221043776|dbj|BAH13565.1| **Length:** 523 **Number of Matches:** 1

Range 1: 365 to 392 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
98.6 bits(225)	1e-21	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    KWNVNAPPTFHSEMMYDDFTLVPVWGKE  28
            KWNVNAPPTFHSEMMYD+FTLVPVWGKE
Sbjct  365  KWNVNAPPTFHSEMMYDNFTLVPVWGKE  392
```

Related Information

Gene - associated gene details

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biotinidase isoform 4 precursor [Homo sapiens]

Sequence ID: gi|528524486|ref|NP_001268654.1| **Length:** 523 **Number of Matches:** 1

▷ See 3 more title(s)

Range 1: 365 to 392 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
98.6 bits(225)	1e-21	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    KWNVNAPPTFHSEMMYDDFTLVPVWGKE  28
            KWNVNAPPTFHSEMMYD+FTLVPVWGKE
Sbjct  365  KWNVNAPPTFHSEMMYDNFTLVPVWGKE  392
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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biotinidase precursor [Pan troglodytes]

Sequence ID: gi|697993457|ref|NP_001289363.1| **Length:** 523 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 365 to 392 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
98.6 bits(225)	1e-21	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    KWNVNAPPTFHSEMMYDDFTLVPVWGKE  28
            KWNVNAPPTFHSEMMYD+FTLVPVWGKE
Sbjct  365  KWNVNAPPTFHSEMMYDNFTLVPVWGKE  392
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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PREDICTED: biotinidase isoform 1 [Gorilla gorilla gorilla]

Sequence ID: gi|426339607|ref|XP_004033737.1| **Length:** 527 **Number of Matches:** 1

Range 1: 369 to 396 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
98.6 bits(225)	1e-21	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    KWNVNAPPTFHSEMMYDDFTLVPVWGKE  28
            KWNVNAPPTFHSEMMYD+FTLVPVWGKE
Sbjct  369  KWNVNAPPTFHSEMMYDNFTLVPVWGKE  396
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

BTD_KWNVNAPPTFHSEMMYDNFTLVPVWGKE_NonMod

RID B929UX6F01R (Expires on 01-14 09:55 am)

Query ID lcl|189320
Description None
Molecule type amino acid
Query Length 28

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

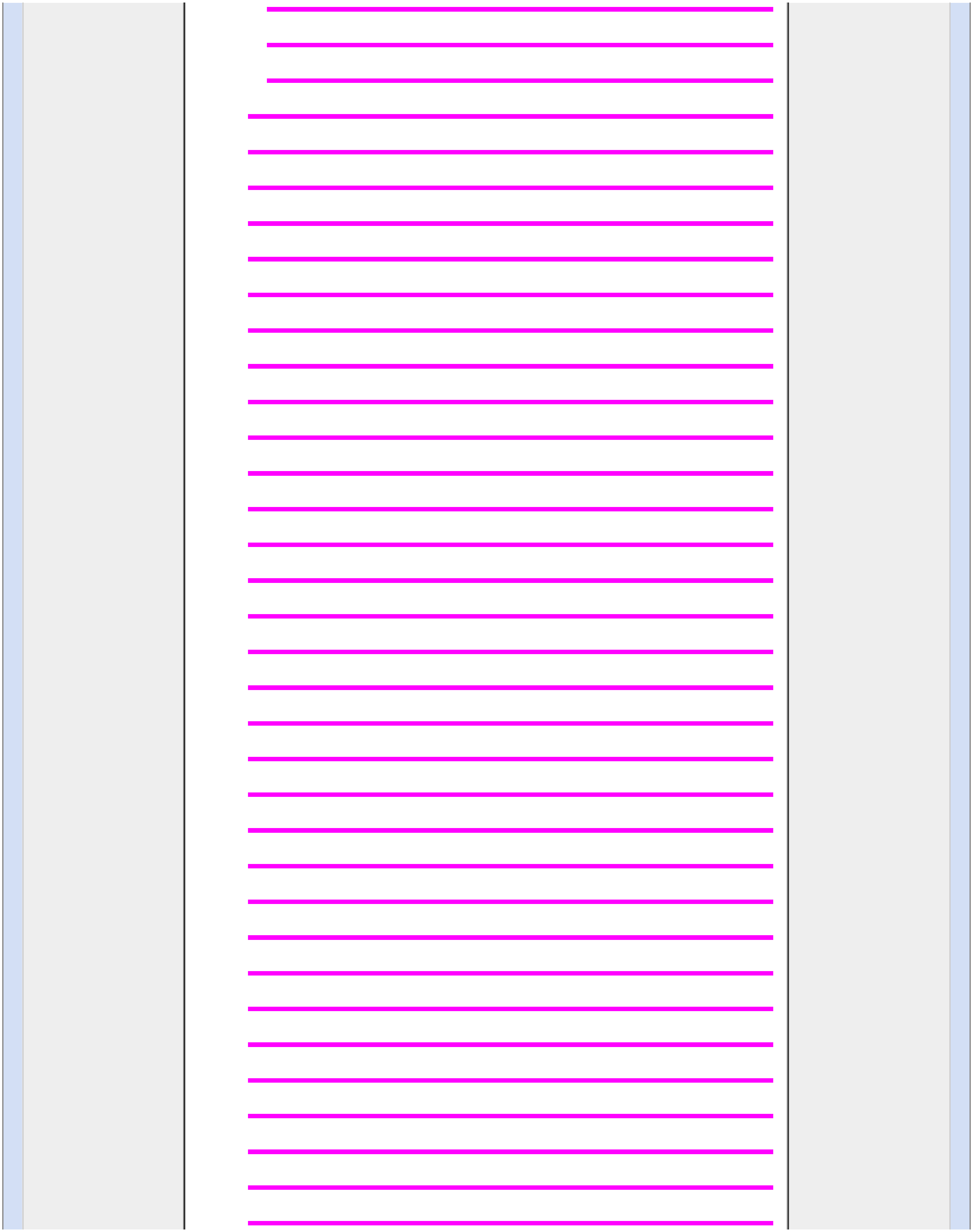
Graphic Summary

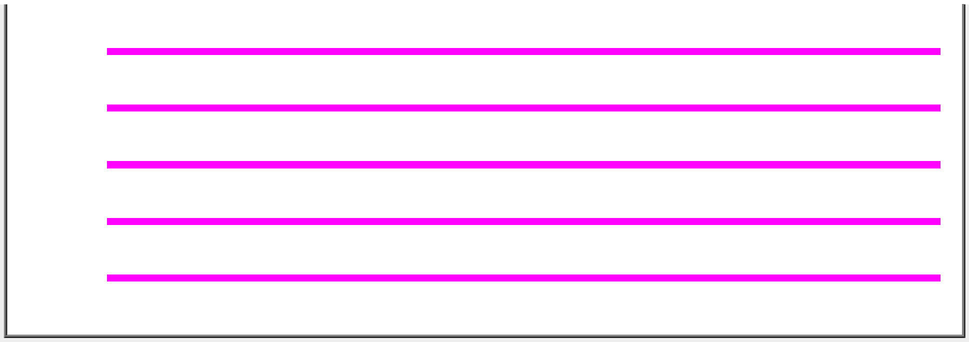
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: biotinidase [Nomascus leucogenys]	101	101	100%	2e-22	100%	gi|332232450|XP_003265417.1
☐	unnamed protein product [Homo sapiens]	101	101	100%	2e-22	100%	gi|221043776|BAH13565.1
☐	biotinidase isoform 4 precursor [Homo sapiens]	101	101	100%	2e-22	100%	gi|528524486|NP_001268654.1
☐	biotinidase precursor [Pan troglodytes]	101	101	100%	2e-22	100%	gi|697993457|NP_001289363.1
☐	PREDICTED: biotinidase isoform 1 [Gorilla gorilla gorilla]	101	101	100%	2e-22	100%	gi|426339607|XP_004033737.1
☐	PREDICTED: biotinidase isoform X2 [Pan troglodytes]	101	101	100%	2e-22	100%	gi|694900420|XP_009443239.1
☐	PREDICTED: biotinidase isoform X2 [Pan paniscus]	101	101	100%	2e-22	100%	gi|675784344|XP_008949921.1
☐	PREDICTED: biotinidase isoform 3 [Gorilla gorilla gorilla]	101	101	100%	2e-22	100%	gi|426339611|XP_004033739.1
☐	PREDICTED: biotinidase isoform 4 [Gorilla gorilla gorilla]	101	101	100%	2e-22	100%	gi|426339613|XP_004033740.1
☐	biotinidase isoform 3 [Homo sapiens]	101	101	100%	2e-22	100%	gi|4557373|NP_000051.1
☐	biotinidase isoform 1 [Homo sapiens]	101	101	100%	2e-22	100%	gi|528524481|NP_001268652.1
☐	biotinidase isoform 2 [Homo sapiens]	101	101	100%	2e-22	100%	gi|528524483|NP_001268653.1
☐	PREDICTED: biotinidase isoform 2 [Gorilla gorilla gorilla]	101	101	100%	2e-22	100%	gi|426339609|XP_004033738.1
☐	PREDICTED: biotinidase isoform X1 [Pan troglodytes]	101	101	100%	2e-22	100%	gi|410036604|XP_003950087.1
☐	PREDICTED: biotinidase isoform X1 [Pan paniscus]	101	101	100%	2e-22	100%	gi|397511808|XP_003826257.1
☐	PREDICTED: biotinidase [Jaculus jaculus]	99.0	99.0	100%	9e-22	96%	gi|507555213|XP_004661377.1
☐	PREDICTED: biotinidase isoform X3 [Pongo abelii]	98.2	98.2	96%	2e-21	100%	gi|686713703|XP_009237577.1
☐	PREDICTED: biotinidase isoform X2 [Pongo abelii]	98.2	98.2	96%	2e-21	100%	gi|686713701|XP_009237576.1
☐	PREDICTED: biotinidase isoform X1 [Pongo abelii]	98.2	98.2	96%	2e-21	100%	gi|395734130|XP_003776360.1
☐	PREDICTED: biotinidase isoform X2 [Cricetulus griseus]	97.8	97.8	100%	2e-21	96%	gi|625181248|XP_007632389.1
☐	PREDICTED: biotinidase isoform X1 [Peromyscus maniculatus bair	97.8	97.8	100%	2e-21	96%	gi|589967608|XP_006996305.1
☐	unnamed protein product [Macaca fascicularis]	97.8	97.8	100%	2e-21	96%	gi|90077268|BAE88314.1
☐	PREDICTED: biotinidase [Galeopterus variegatus]	97.8	97.8	100%	2e-21	96%	gi|667288263|XP_008576771.1
☐	PREDICTED: biotinidase isoform X2 [Microtus ochrogaster]	97.8	97.8	100%	2e-21	96%	gi|532009812|XP_005348714.1
☐	PREDICTED: biotinidase isoform X2 [Peromyscus maniculatus bair	97.8	97.8	100%	2e-21	96%	gi|589967610|XP_006996306.1
☐	PREDICTED: biotinidase isoform X2 [Chlorocebus sabaeus]	97.8	97.8	100%	3e-21	96%	gi|635085523|XP_008007381.1
☐	PREDICTED: biotinidase isoform X2 [Macaca fascicularis]	97.8	97.8	100%	3e-21	96%	gi|544411158|XP_005545768.1
☐	PREDICTED: biotinidase isoform X2 [Papio anubis]	97.8	97.8	100%	3e-21	96%	gi|685527526|XP_009200021.1
☐							

	PREDICTED: biotinidase isoform X1 [Chlorocebus sabaeus]	97.8	97.8	100%	3e-21	96%	gi|635085521|XP_008007380.1
☐	PREDICTED: biotinidase [Mustela putorius furo]	97.8	97.8	100%	3e-21	96%	gi|511908359|XP_004773614.1
☐	PREDICTED: biotinidase isoform X1 [Cricetulus griseus]	97.8	97.8	100%	3e-21	96%	gi|354465853|XP_003495391.1
☐	PREDICTED: biotinidase [Orycteropus afer afer]	97.8	97.8	100%	3e-21	96%	gi|634822252|XP_007934900.1
☐	hypothetical protein EGM_11114 [Macaca fascicularis]	97.8	97.8	100%	3e-21	96%	gi|355747075|EHH51689.1
☐	hypothetical protein EGK_12122 [Macaca mulatta]	97.8	97.8	100%	3e-21	96%	gi|355560049|EHH16777.1
☐	PREDICTED: biotinidase isoform X1 [Microtus ochrogaster]	97.8	97.8	100%	3e-21	96%	gi|532009810|XP_005348713.1
☐	PREDICTED: biotinidase [Macaca mulatta]	97.8	97.8	100%	3e-21	96%	gi|297286947|XP_001083201.2
☐	PREDICTED: biotinidase isoform X1 [Papio anubis]	97.8	97.8	100%	3e-21	96%	gi|685527524|XP_009200020.1
☐	PREDICTED: biotinidase isoform X1 [Macaca fascicularis]	97.8	97.8	100%	3e-21	96%	gi|544411156|XP_005545767.1
☐	biotinidase [Cricetulus griseus]	97.8	97.8	100%	3e-21	96%	gi|537261432|ERE90059.1
☐	biotinidase, isoform CRA_a [Rattus norvegicus]	97.3	97.3	100%	3e-21	96%	gi|149034168|EDL88938.1
☐	biotinidase, isoform CRA_c [Rattus norvegicus]	97.3	97.3	100%	3e-21	96%	gi|149034170|EDL88940.1
☐	biotinidase precursor [Rattus norvegicus]	97.3	97.3	100%	3e-21	96%	gi|58865670|NP_001012047.1
☐	PREDICTED: biotinidase isoform X2 [Rattus norvegicus]	97.3	97.3	100%	4e-21	96%	gi|564387894|XP_006252671.1
☐	PREDICTED: biotinidase [Chrysochloris asiatica]	95.6	95.6	100%	1e-20	93%	gi|586456511|XP_006840071.1
☐	PREDICTED: biotinidase-like [Ictidomys tridecemlineatus]	95.2	95.2	100%	2e-20	93%	gi|532063189|XP_005317469.1
☐	PREDICTED: biotinidase isoform X4 [Canis lupus familiaris]	94.4	94.4	100%	4e-20	93%	gi|545538859|XP_005634450.1
☐	PREDICTED: LOW QUALITY PROTEIN: biotinidase [Tursiops trunc	94.4	94.4	100%	4e-20	93%	gi|470628904|XP_004321284.1
☐	PREDICTED: biotinidase [Orcinus orca]	94.4	94.4	100%	4e-20	93%	gi|466019817|XP_004271983.1
☐	PREDICTED: biotinidase isoform X3 [Canis lupus familiaris]	94.4	94.4	100%	4e-20	93%	gi|545538857|XP_005634449.1
☐	PREDICTED: biotinidase isoform X2 [Canis lupus familiaris]	94.4	94.4	100%	4e-20	93%	gi|545538855|XP_005634448.1
☐	PREDICTED: biotinidase isoform X1 [Canis lupus familiaris]	94.4	94.4	100%	4e-20	93%	gi|545538853|XP_005634447.1
☐	PREDICTED: biotinidase isoform X1 [Mus musculus]	93.5	93.5	100%	7e-20	93%	gi|568987712|XP_006519092.1
☐	RecName: Full=Biotinidase; Short=Biotinase; Flags: Precursor [Mus	93.5	93.5	100%	7e-20	93%	gi|150421524|Q8CIF4.2
☐	PREDICTED: biotinidase [Rhinopithecus roxellana]	93.5	93.5	100%	7e-20	93%	gi|724960396|XP_010354361.1
☐	unnamed protein product [Mus musculus]	93.5	93.5	100%	7e-20	93%	gi|74183082|BAE22509.1
☐	biotinidase precursor [Mus musculus]	93.5	93.5	100%	7e-20	93%	gi|13384648|NP_079571.1
☐	PREDICTED: biotinidase isoform X2 [Physeter catodon]	93.1	93.1	100%	1e-19	93%	gi|593711507|XP_007102308.1
☐	PREDICTED: biotinidase isoform X1 [Physeter catodon]	93.1	93.1	100%	1e-19	93%	gi|593711505|XP_007102307.1
☐	PREDICTED: biotinidase [Lipotes vexillifer]	93.1	93.1	100%	1e-19	93%	gi|602721076|XP_007470691.1
☐	PREDICTED: biotinidase isoform X1 [Balaenoptera acutorostrata sc	93.1	93.1	100%	1e-19	93%	gi|594624940|XP_007167058.1
☐	PREDICTED: biotinidase isoform X3 [Balaenoptera acutorostrata sc	93.1	93.1	100%	1e-19	93%	gi|594624944|XP_007167060.1
☐	PREDICTED: biotinidase isoform X3 [Equus caballus]	92.7	92.7	100%	1e-19	93%	gi|545189350|XP_005600979.1
☐	PREDICTED: biotinidase [Equus przewalskii]	92.7	92.7	100%	1e-19	93%	gi|664753751|XP_008534346.1
☐	PREDICTED: biotinidase isoform X2 [Equus caballus]	92.7	92.7	100%	1e-19	93%	gi|545189348|XP_005600978.1
☐	PREDICTED: biotinidase isoform X1 [Equus caballus]	92.7	92.7	100%	1e-19	93%	gi|545189346|XP_005600977.1
☐	PREDICTED: biotinidase [Erinaceus europaeus]	91.8	91.8	96%	3e-19	93%	gi|617553342|XP_007530134.1
☐	PREDICTED: biotinidase [Otolemur garnettii]	91.0	91.0	96%	5e-19	93%	gi|395816560|XP_003781769.1
☐	PREDICTED: biotinidase [Panthera tigris altaica]	90.6	90.6	100%	8e-19	89%	gi|591322659|XP_007087428.1
☐	PREDICTED: biotinidase isoform X1 [Felis catus]	90.6	90.6	100%	8e-19	89%	gi|587000359|XP_003992187.2
☐	PREDICTED: biotinidase isoform X2 [Felis catus]	90.6	90.6	100%	8e-19	89%	gi|587000357|XP_006936495.1
☐	PREDICTED: biotinidase [Mesocricetus auratus]	90.1	90.1	100%	1e-18	89%	gi|524955500|XP_005077724.1
☐	PREDICTED: biotinidase [Nannospalax galili]	89.3	89.3	100%	2e-18	89%	gi|674081213|XP_008848205.1
☐	PREDICTED: biotinidase isoform X2 [Ursus maritimus]	89.3	89.3	92%	2e-18	96%	gi|670981874|XP_008707139.1

☐	PREDICTED: biotinidase isoform X1 [Ursus maritimus]	89.3	89.3	92%	2e-18	96%	gi|670981872|XP_008707130.1
☐	PREDICTED: biotinidase [Ceratotherium simum simum]	88.9	88.9	100%	3e-18	89%	gi|478490156|XP_004419451.1
☐	PREDICTED: biotinidase isoform 2 [Odobenus rosmarus divergens	88.4	88.4	96%	4e-18	89%	gi|472379495|XP_004409157.1
☐	PREDICTED: biotinidase isoform X3 [Saimiri boliviensis boliviensis]	88.4	88.4	100%	4e-18	93%	gi|725560828|XP_010333963.1
☐	PREDICTED: biotinidase isoform X3 [Leptonychotes weddellii]	88.4	88.4	96%	4e-18	89%	gi|585186600|XP_006744787.1
☐	PREDICTED: biotinidase isoform X2 [Leptonychotes weddellii]	88.4	88.4	96%	4e-18	89%	gi|585186598|XP_006744786.1
☐	PREDICTED: biotinidase isoform 1 [Odobenus rosmarus divergens	88.4	88.4	96%	4e-18	89%	gi|472379493|XP_004409156.1
☐	PREDICTED: biotinidase isoform X2 [Saimiri boliviensis boliviensis]	88.4	88.4	100%	4e-18	93%	gi|403265544|XP_003924991.1
☐	PREDICTED: biotinidase isoform X1 [Leptonychotes weddellii]	88.4	88.4	96%	4e-18	89%	gi|585186596|XP_006744785.1
☐	PREDICTED: biotinidase isoform X1 [Saimiri boliviensis boliviensis]	88.4	88.4	100%	4e-18	93%	gi|725560825|XP_010333962.1
☐	PREDICTED: biotinidase [Echinops telfairi]	88.0	88.0	96%	6e-18	89%	gi|507651259|XP_004704067.1
☐	PREDICTED: biotinidase isoform X1 [Callithrix jacchus]	84.6	84.6	100%	8e-17	89%	gi|675740028|XP_008982107.1
☐	PREDICTED: biotinidase isoform X2 [Callithrix jacchus]	84.6	84.6	100%	8e-17	89%	gi|390476393|XP_002759736.2
☐	Biotinidase [Myotis davidii]	84.2	84.2	96%	1e-16	85%	gi|432092959|ELK25317.1
☐	PREDICTED: biotinidase isoform X1 [Myotis davidii]	84.2	84.2	96%	1e-16	85%	gi|584051114|XP_006770244.1
☐	PREDICTED: biotinidase isoform X1 [Myotis lucifugus]	84.2	84.2	96%	1e-16	85%	gi|558102610|XP_006083737.1
☐	PREDICTED: biotinidase isoform X3 [Myotis brandtii]	84.2	84.2	96%	1e-16	85%	gi|554537982|XP_005863672.1
☐	PREDICTED: biotinidase [Loxodonta africana]	84.2	84.2	100%	1e-16	82%	gi|731510838|XP_010598778.1
☐	PREDICTED: biotinidase isoform X2 [Myotis lucifugus]	84.2	84.2	96%	1e-16	85%	gi|558102613|XP_006083738.1
☐	PREDICTED: biotinidase isoform X2 [Myotis brandtii]	84.2	84.2	96%	1e-16	85%	gi|554537986|XP_005863671.1
☐	Biotinidase [Myotis brandtii]	84.2	84.2	96%	1e-16	85%	gi|521024341|EPQ06129.1
☐	PREDICTED: biotinidase [Trichechus manatus latirostris]	82.9	82.9	100%	3e-16	86%	gi|471407481|XP_004385327.1
☐	PREDICTED: biotinidase-like [Ailuropoda melanoleuca]	82.5	82.5	92%	4e-16	88%	gi|301759093|XP_002915396.1
☐	hypothetical protein PANDA_003369 [Ailuropoda melanoleuca]	82.5	82.5	92%	4e-16	88%	gi|281345880|EFB21464.1
☐	PREDICTED: biotinidase-like [Sus scrofa]	82.1	82.1	92%	6e-16	88%	gi|350590963|XP_003132114.3
☐	PREDICTED: biotinidase-like isoform X2 [Sus scrofa]	82.1	82.1	92%	6e-16	88%	gi|545860928|XP_005669335.1
☐	PREDICTED: biotinidase-like isoform X2 [Sus scrofa]	82.1	82.1	92%	6e-16	88%	gi|545860909|XP_005669330.1

Alignments

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PREDICTED: biotinidase [Nomascus leucogenys]

Sequence ID: gi|332232450|ref|XP_003265417.1| **Length:** 474 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 316 to 343 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
101 bits(231)	2e-22	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    KWNVNAPPTFHSEMMYDNFTLVPVWGKE  28
            KWNVNAPPTFHSEMMYDNFTLVPVWGKE
Sbjct  316  KWNVNAPPTFHSEMMYDNFTLVPVWGKE  343
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: gi|221043776|dbj|BAH13565.1| **Length:** 523 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 365 to 392 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
101 bits(231)	2e-22	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    KWNVNAPPTFHSEMMYDNFTLVPVWGKE  28
```

```
               KWNVNAPPTFHSEMMYDNFTLVPVWGKE
Sbjct  365  KWNVNAPPTFHSEMMYDNFTLVPVWGKE  392
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

biotinidase isoform 4 precursor [Homo sapiens]

Sequence ID: gi|528524486|ref|NP_001268654.1| **Length:** 523 **Number of Matches:** 1

▷ See 3 more title(s)

Range 1: 365 to 392 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
101 bits(231)	2e-22	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    KWNVNAPPTFHSEMMYDNFTLVPVWGKE  28
            KWNVNAPPTFHSEMMYDNFTLVPVWGKE
Sbjct  365  KWNVNAPPTFHSEMMYDNFTLVPVWGKE  392
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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biotinidase precursor [Pan troglodytes]

Sequence ID: gi|697993457|ref|NP_001289363.1| **Length:** 523 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 365 to 392 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
101 bits(231)	2e-22	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    KWNVNAPPTFHSEMMYDNFTLVPVWGKE  28
            KWNVNAPPTFHSEMMYDNFTLVPVWGKE
Sbjct  365  KWNVNAPPTFHSEMMYDNFTLVPVWGKE  392
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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PREDICTED: biotinidase isoform 1 [Gorilla gorilla gorilla]

Sequence ID: gi|426339607|ref|XP_004033737.1| **Length:** 527 **Number of Matches:** 1

Range 1: 369 to 396 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
101 bits(231)	2e-22	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    KWNVNAPPTFHSEMMYDNFTLVPVWGKE  28
            KWNVNAPPTFHSEMMYDNFTLVPVWGKE
Sbjct  369  KWNVNAPPTFHSEMMYDNFTLVPVWGKE  396
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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C1RL_KDRQDGEEVLQCMPVCGRPVTPIAQDQTTLGSSRA_Mod

RID BTF5TH39013 (Expires on 01-20 15:13 pm)

Query ID	lcl|4241	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	35		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

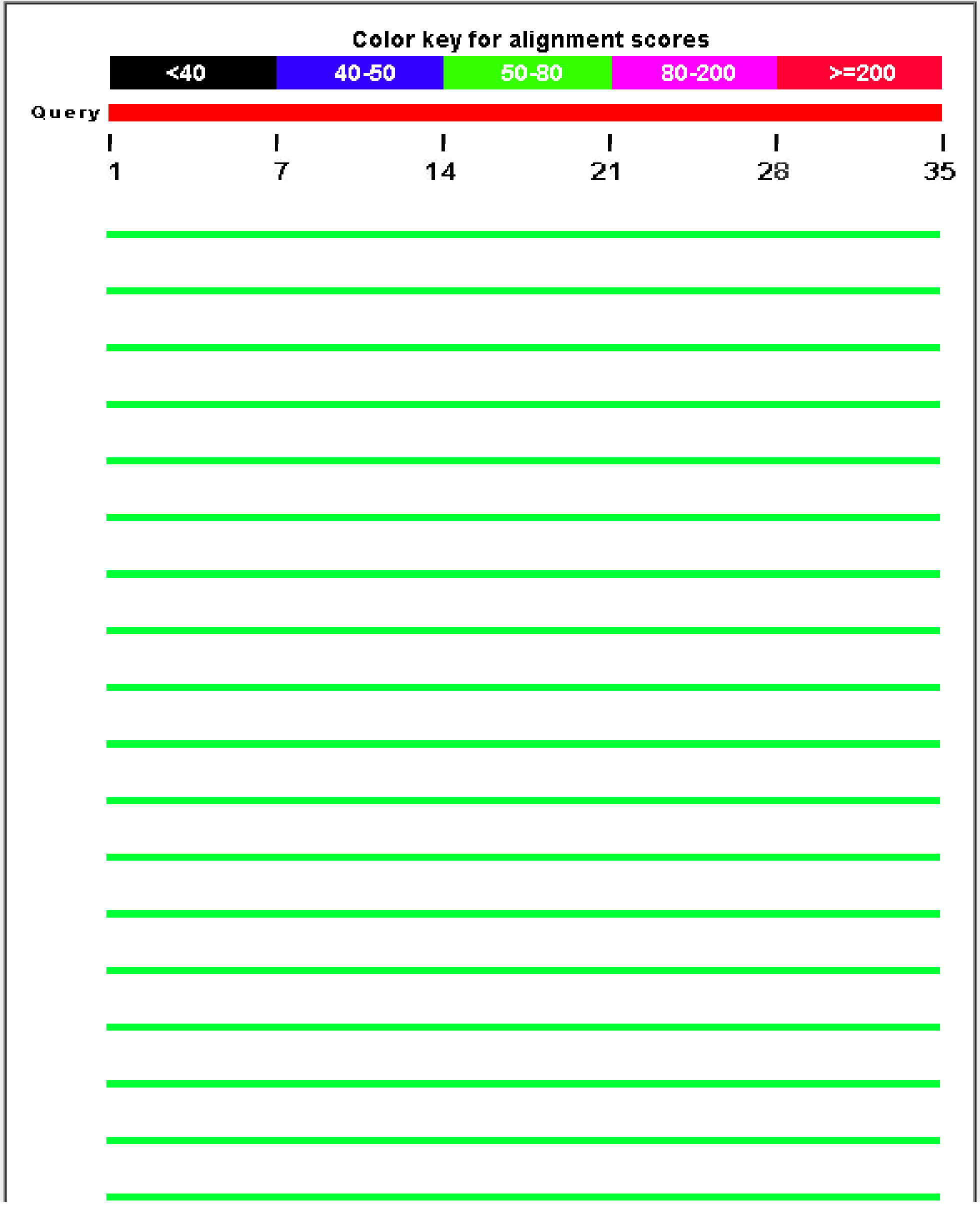
Graphic Summary

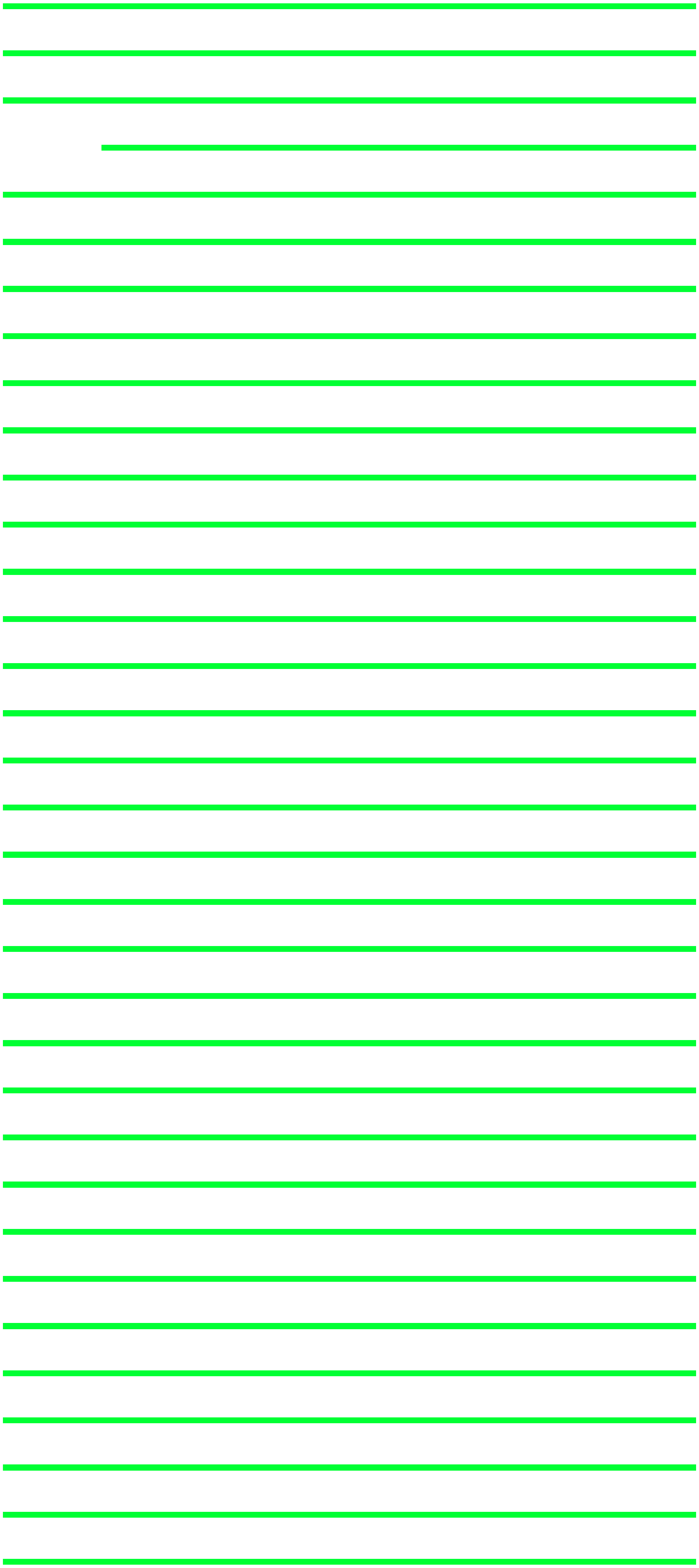
Show Conserved Domains

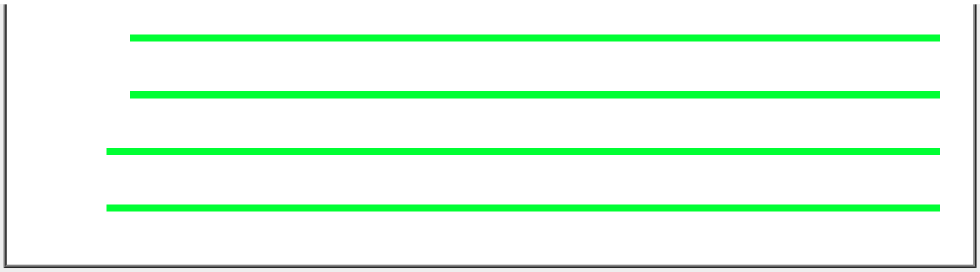
No putative conserved domains have been detected

Distribution of 104 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	complement C1r subcomponent-like protein isoform 2 precurso	73.9	73.9	100%	3e-14	97%	gi|663071006|NP_001284569.1
☐	PREDICTED: complement C1r subcomponent-like protein isofo	73.9	73.9	100%	3e-14	97%	gi|441670266|XP_004092185.1
☐	PREDICTED: complement C1r subcomponent-like protein isofo	73.9	73.9	100%	4e-14	97%	gi|332249352|XP_003273827.1
☐	complement C1r subcomponent-like protein isoform 1 precurso	73.9	73.9	100%	4e-14	97%	gi|289547636|NP_057630.2
☐	PREDICTED: complement C1r subcomponent-like protein isofo	73.9	73.9	100%	4e-14	97%	gi|114643162|XP_001163902.1
☐	complement component 1, r subcomponent-like precursor varia	73.9	73.9	100%	4e-14	97%	gi|62897163|BAD96522.1
☐	complement C1r-like proteinase precursor [Homo sapiens]	73.9	73.9	100%	4e-14	97%	gi|7271475|AAF44349.1
☐	PREDICTED: complement C1r subcomponent-like protein isofo	73.9	73.9	100%	4e-14	97%	gi|441670263|XP_004092184.1
☐	PREDICTED: complement C1r subcomponent-like protein isofo	73.9	73.9	100%	4e-14	97%	gi|675757427|XP_008971903.1
☐	PREDICTED: complement C1r subcomponent-like protein [Gor	71.6	71.6	100%	3e-13	94%	gi|426371473|XP_004052671.1
☐	unnamed protein product [Homo sapiens]	70.9	70.9	100%	4e-13	94%	gi|10436374|BAB14819.1
☐	PREDICTED: complement C1r subcomponent-like protein [Mac	70.9	70.9	100%	5e-13	94%	gi|544469176|XP_005570609.1
☐	PREDICTED: complement C1r subcomponent-like protein isofo	70.9	70.9	100%	5e-13	94%	gi|402884997|XP_003905955.1
☐	Complement C1r subcomponent-like protein [Macaca fascicula	70.9	70.9	100%	5e-13	94%	gi|355785846|EHH66029.1
☐	PREDICTED: complement C1r subcomponent-like protein isofo	70.9	70.9	100%	5e-13	94%	gi|685570876|XP_009178379.1
☐	Complement C1r subcomponent-like protein [Macaca mulatta]	69.3	69.3	100%	2e-12	91%	gi|355563948|EHH20448.1
☐	PREDICTED: complement C1r subcomponent-like protein [Chl	68.6	68.6	100%	3e-12	91%	gi|635063155|XP_007965642.1
☐	PREDICTED: complement C1r subcomponent-like protein [Call	63.9	63.9	100%	1e-10	83%	gi|675677706|XP_009001758.1
☐	PREDICTED: complement C1r subcomponent-like protein [Gal	62.8	62.8	100%	4e-10	80%	gi|667290276|XP_008577472.1
☐	PREDICTED: complement C1r subcomponent-like protein [Oto	61.6	61.6	100%	1e-09	77%	gi|395847725|XP_003796517.1
☐	PREDICTED: complement C1r subcomponent-like protein [Och	59.3	59.3	100%	6e-09	77%	gi|504173912|XP_004596521.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subc	58.5	58.5	85%	7e-09	90%	gi|686739538|XP_009245669.1
☐	PREDICTED: complement C1r subcomponent-like protein isofo	57.4	57.4	100%	2e-08	74%	gi|671039595|XP_008681740.1
☐	PREDICTED: complement C1r subcomponent-like protein isofo	57.4	57.4	100%	3e-08	74%	gi|671039593|XP_008681739.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subc	57.0	57.0	100%	4e-08	71%	gi|532105686|XP_005338428.1
☐	C1r-like protein [Mus musculus]	56.2	56.2	100%	4e-08	69%	gi|30842778|AAP41416.1
☐	complement C1r subcomponent-like protein precursor [Rattus r	56.6	56.6	100%	5e-08	71%	gi|50657416|NP_001002804.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subc	56.6	56.6	100%	5e-08	71%	gi|674104757|XP_008823575.1
☐	complement component 1, r subcomponent-like [Rattus norveg	56.6	56.6	100%	5e-08	71%	gi|149049502|EDM01956.1
☐	C1r-like protein [Mus musculus]	56.2	56.2	100%	7e-08	69%	gi|30842780|AAP41417.1

☐	complement component 1, r subcomponent-like [Mus musculus	56.2	56.2	100%	7e-08	69%	gi|148667322|EDK99738.1
☐	unnamed protein product [Mus musculus]	56.2	56.2	100%	7e-08	69%	gi|74225714|BAE21686.1
☐	complement C1r subcomponent-like protein precursor [Mus mu	56.2	56.2	100%	7e-08	69%	gi|269973899|NP_851989.3
☐	PREDICTED: complement C1r subcomponent-like protein [Lep	55.5	55.5	100%	1e-07	71%	gi|585171947|XP_006737937.1
☐	PREDICTED: complement C1r subcomponent-like protein [Odc	55.5	55.5	100%	1e-07	71%	gi|472376494|XP_004407682.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subc	55.5	55.5	100%	1e-07	69%	gi|560977345|XP_006210952.1
☐	Complement C1r subcomponent-like protein [Tupaia chinensis]	55.1	55.1	100%	2e-07	71%	gi|444510890|ELV09737.1
☐	PREDICTED: complement C1r subcomponent-like protein isofc	55.1	55.1	100%	2e-07	71%	gi|291392803|XP_002712893.1
☐	PREDICTED: complement C1r subcomponent-like protein isofc	55.1	55.1	100%	2e-07	71%	gi|655831423|XP_008257993.1
☐	PREDICTED: complement C1r subcomponent-like protein isofc	54.7	54.7	100%	2e-07	66%	gi|743695633|XP_010961963.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subc	55.1	55.1	100%	2e-07	71%	gi|562886979|XP_006170901.1
☐	PREDICTED: complement C1r subcomponent-like protein isofc	54.7	54.7	100%	3e-07	66%	gi|743695635|XP_010962042.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subc	54.7	54.7	100%	3e-07	66%	gi|560893125|XP_006173072.1
☐	PREDICTED: complement C1r subcomponent-like protein isofc	54.7	54.7	100%	3e-07	66%	gi|743695631|XP_010961901.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subc	54.7	54.7	100%	3e-07	71%	gi|507697361|XP_004643633.1
☐	complement C1r subcomponent-like protein [Camelus ferus]	54.7	54.7	100%	3e-07	66%	gi|528770117|EPY89776.1
☐	PREDICTED: complement C1r subcomponent-like protein [Elep	53.9	53.9	100%	5e-07	69%	gi|585679250|XP_006891411.1
☐	Complement C1r subcomponent-like protein [Cricetulus griseus	53.5	53.5	100%	5e-07	71%	gi|344242458|EGV98561.1
☐	PREDICTED: complement C1r subcomponent-like protein isofc	53.5	53.5	100%	6e-07	71%	gi|354467327|XP_003496121.1
☐	PREDICTED: complement C1r subcomponent-like protein [Cera	53.5	53.5	100%	7e-07	69%	gi|478529432|XP_004438886.1
☐	PREDICTED: complement C1r subcomponent-like protein [Tric	53.5	53.5	100%	8e-07	69%	gi|471411548|XP_004387327.1
☐	complement C1r-A subcomponent [Cricetulus griseus]	53.5	96.3	100%	1e-06	71%	gi|537136510|ERE66562.1
☐	PREDICTED: complement C1r subcomponent-like protein isofc	52.8	52.8	97%	1e-06	71%	gi|533127501|XP_005378915.1
☐	PREDICTED: complement C1r subcomponent-like protein isofc	52.8	52.8	97%	1e-06	71%	gi|533127499|XP_005378914.1
☐	PREDICTED: complement component 1, r subcomponent-like [	52.4	52.4	100%	2e-06	66%	gi|586991762|XP_006933531.1
☐	PREDICTED: complement C1r-A subcomponent-like [Microtus	52.8	96.7	100%	2e-06	71%	gi|532045173|XP_005365394.1
☐	PREDICTED: complement C1r subcomponent-like protein [Can	52.0	52.0	100%	2e-06	63%	gi|744596751|XP_010989121.1
☐	hypothetical protein PANDA_011233 [Ailuropoda melanoleuca]	52.0	52.0	100%	2e-06	69%	gi|281338369|EFB13953.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subc	52.0	52.0	100%	2e-06	69%	gi|524923662|XP_005066080.1
☐	PREDICTED: complement C1r subcomponent-like protein [Pero	51.6	51.6	100%	3e-06	69%	gi|589959162|XP_006992168.1
☐	PREDICTED: complement C1r subcomponent-like protein-like [	52.0	52.0	100%	3e-06	69%	gi|301773698|XP_002922303.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subc	51.6	51.6	100%	3e-06	66%	gi|511894085|XP_004766682.1
☐	PREDICTED: complement C1r subcomponent-like protein [Cav	51.6	51.6	100%	3e-06	66%	gi|348554938|XP_003463281.1
☐	PREDICTED: complement C1r subcomponent-like protein [Ory	51.2	51.2	100%	4e-06	63%	gi|634837986|XP_007935394.1
☐	Complement C1r subcomponent-like protein [Pteropus alecto]	51.2	51.2	100%	4e-06	69%	gi|431905373|ELK10418.1
☐	PREDICTED: complement C1r subcomponent-like protein [Pter	51.2	51.2	100%	5e-06	69%	gi|586563055|XP_006914777.1
☐	PREDICTED: complement C1r subcomponent-like protein [Equ	50.8	50.8	100%	6e-06	63%	gi|545219170|XP_005610954.1
☐	PREDICTED: complement component 1, r subcomponent-like i	49.7	49.7	100%	1e-05	63%	gi|545546513|XP_005637265.1
☐	PREDICTED: complement component 1, r subcomponent-like i	49.7	49.7	100%	1e-05	63%	gi|545546511|XP_005637264.1
☐	PREDICTED: complement component 1, r subcomponent-like i	49.7	49.7	100%	1e-05	63%	gi|545546509|XP_005637263.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subc	49.7	49.7	100%	1e-05	63%	gi|591327382|XP_007089640.1
☐	PREDICTED: complement component 1, r subcomponent-like i	49.7	49.7	100%	1e-05	63%	gi|545546507|XP_005637262.1
☐	PREDICTED: complement C1r subcomponent-like protein [Erin	49.7	49.7	100%	1e-05	63%	gi|617656833|XP_007535922.1
☐	PREDICTED: complement component 1, r subcomponent-like i	49.7	49.7	100%	1e-05	63%	gi|345792069|XP_543840.3
☐	PREDICTED: complement C1r subcomponent-like protein isofc	48.9	48.9	100%	2e-05	66%	gi|488554131|XP_004468199.1

☐	PREDICTED: complement C1r subcomponent-like protein isofc	48.9	48.9	100%	3e-05	66%	gi|488554125|XP_004468197.1
☐	PREDICTED: complement C1r subcomponent-like protein [Fuk	48.5	48.5	100%	3e-05	60%	gi|731282854|XP_010610027.1
☐	PREDICTED: complement C1r subcomponent-like protein [Cap	48.5	48.5	100%	3e-05	60%	gi|548468413|XP_005681065.1
☐	PREDICTED: complement C1r subcomponent-like protein [Turs	48.5	48.5	100%	4e-05	60%	gi|470606249|XP_004314129.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subc	48.5	48.5	100%	4e-05	60%	gi|556724329|XP_005957969.1
☐	Complement C1r subcomponent [Fukomys damarensis]	48.5	89.3	100%	5e-05	60%	gi|676263566|KFO20277.1
☐	PREDICTED: complement C1r subcomponent-like protein [Lipc	48.1	48.1	100%	5e-05	60%	gi|602718526|XP_007469443.1
☐	PREDICTED: complement C1r subcomponent-like protein [Orci	48.1	48.1	100%	5e-05	60%	gi|466055133|XP_004279184.1
☐	PREDICTED: complement C1r subcomponent-like protein [Het	47.8	47.8	100%	7e-05	58%	gi|512941192|XP_004909584.1
☐	PREDICTED: complement C1r subcomponent-like protein [Myc	47.8	47.8	100%	7e-05	60%	gi|584074754|XP_006757609.1
☐	PREDICTED: complement C1r subcomponent-like protein [Myc	47.8	47.8	100%	7e-05	60%	gi|558104592|XP_006084250.1
☐	Complement C1r subcomponent-like protein [Bos mutus]	47.4	47.4	100%	9e-05	60%	gi|440891813|ELR45306.1
☐	PREDICTED: complement C1r subcomponent-like protein [Myc	47.4	47.4	100%	9e-05	60%	gi|554558619|XP_005873711.1
☐	PREDICTED: complement C1r subcomponent [Heterocephalus	47.8	92.0	100%	9e-05	58%	gi|513016514|XP_004869588.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subc	47.4	47.4	100%	9e-05	60%	gi|555998080|XP_005910755.1
☐	PREDICTED: complement C1r subcomponent-like protein [Bala	47.4	47.4	100%	1e-04	60%	gi|594633415|XP_007170182.1
☐	PREDICTED: complement C1r subcomponent-like protein [Lox	47.4	47.4	100%	1e-04	60%	gi|731515679|XP_010600946.1
☐	PREDICTED: complement C1r subcomponent-like protein [Chr	47.0	47.0	100%	1e-04	63%	gi|586464372|XP_006862815.1
☐	PREDICTED: complement component 1, r subcomponent-like [	46.6	46.6	100%	2e-04	60%	gi|545890542|XP_005658603.1
☐	PREDICTED: complement C1r subcomponent-like [Nomascus	43.1	43.1	100%	3e-04	46%	gi|332267693|XP_003282816.1
☐	PREDICTED: complement C1r subcomponent-like protein [Sair	45.4	45.4	65%	3e-04	87%	gi|725609801|XP_010331194.1
☐	PREDICTED: complement C1r subcomponent-like protein isofc	45.8	45.8	100%	3e-04	57%	gi|741927976|XP_010803881.1
☐	TPA: complement component 1, r subcomponent-like [Bos taur	45.8	45.8	100%	3e-04	57%	gi|296487145|DAA29258.1
☐	PREDICTED: complement C1r subcomponent-like protein isofc	45.8	45.8	100%	3e-04	57%	gi|741927974|XP_010803880.1
☐	complement C1r subcomponent-like protein [Bos taurus]	45.8	45.8	100%	3e-04	57%	gi|300798717|NP_001179084.1

Alignments

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complement C1r subcomponent-like protein isoform 2 precursor [Homo sapiens]

Sequence ID: gi|663071006|ref|NP_001284569.1| **Length:** 445 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 175 to 209 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.9 bits(180)	3e-14	34/35(97%)	35/35(100%)	0/35(0%)

```
Query  1    KDRQDGEEVLQCMPVCGRPVTPIAQDQTTLGSSRA  35
            KDRQDGEEVLQCMPVCGRPVTPIAQ+QTTLGSSRA
Sbjct  175  KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  209
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: complement C1r subcomponent-like protein isoform 3 [Nomascus leucogenys]

Sequence ID: gi|441670266|ref|XP_004092185.1| **Length:** 445 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 175 to 209 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.9 bits(180)	3e-14	34/35(97%)	35/35(100%)	0/35(0%)

```
Query  1    KDRQDGEEVLQCMPVCGRPVTPIAQDQTTLGSSRA  35
            KDRQDGEEVLQCMPVCGRPVTPIAQ+QTTLGSSRA
Sbjct  175  KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  209
```

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PREDICTED: complement C1r subcomponent-like protein isoform 1 [Nomascus leucogenys]

Sequence ID: gi|332249352|ref|XP_003273827.1| **Length:** 487 **Number of Matches:** 1

Range 1: 217 to 251 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.9 bits(180)	4e-14	34/35(97%)	35/35(100%)	0/35(0%)

```
Query  1    KDRQDGEEVLQCMPVCGRPVTPIAQDQTTLGSSRA  35
            KDRQDGEEVLQCMPVCGRPVTPIAQ+QTTLGSSRA
Sbjct  217  KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  251
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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complement C1r subcomponent-like protein isoform 1 precursor [Homo sapiens]

Sequence ID: gi|289547636|ref|NP_057630.2| **Length:** 487 **Number of Matches:** 1

▷ See 2 more title(s)

Range 1: 217 to 251 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.9 bits(180)	4e-14	34/35(97%)	35/35(100%)	0/35(0%)

```
Query  1    KDRQDGEEVLQCMPVCGRPVTPIAQDQTTLGSSRA  35
            KDRQDGEEVLQCMPVCGRPVTPIAQ+QTTLGSSRA
Sbjct  217  KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  251
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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PREDICTED: complement C1r subcomponent-like protein isoform X1 [Pan troglodytes]

Sequence ID: gi|114643162|ref|XP_001163902.1| **Length:** 487 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 217 to 251 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.9 bits(180)	4e-14	34/35(97%)	35/35(100%)	0/35(0%)

```
Query  1    KDRQDGEEVLQCMPVCGRPVTPIAQDQTTLGSSRA  35
            KDRQDGEEVLQCMPVCGRPVTPIAQ+QTTLGSSRA
Sbjct  217  KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  251
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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C1RL_KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA_NonMod

RID B92A40H101R (Expires on 01-14 09:56 am)

Query ID lcl|220454
Description None
Molecule type amino acid
Query Length 35

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

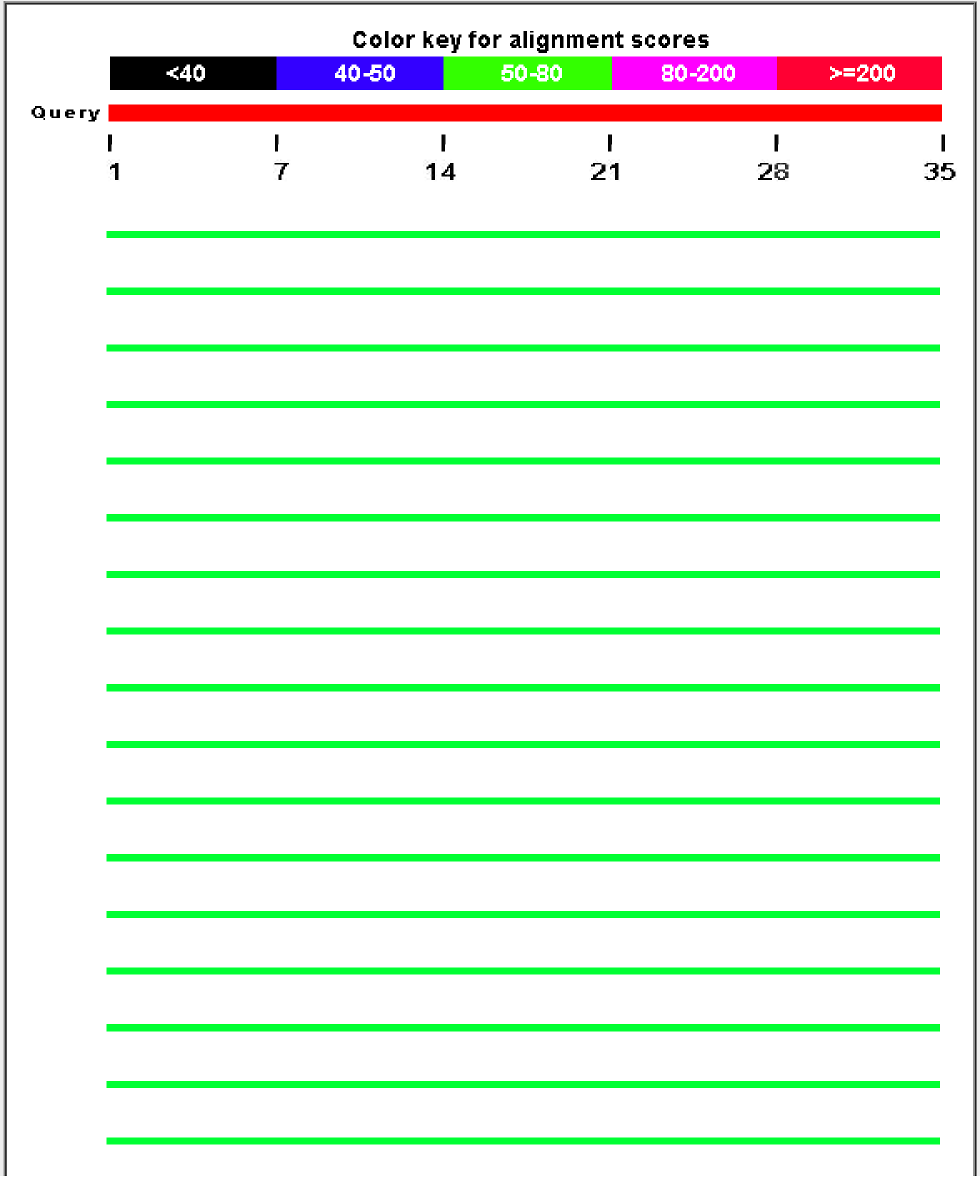
Graphic Summary

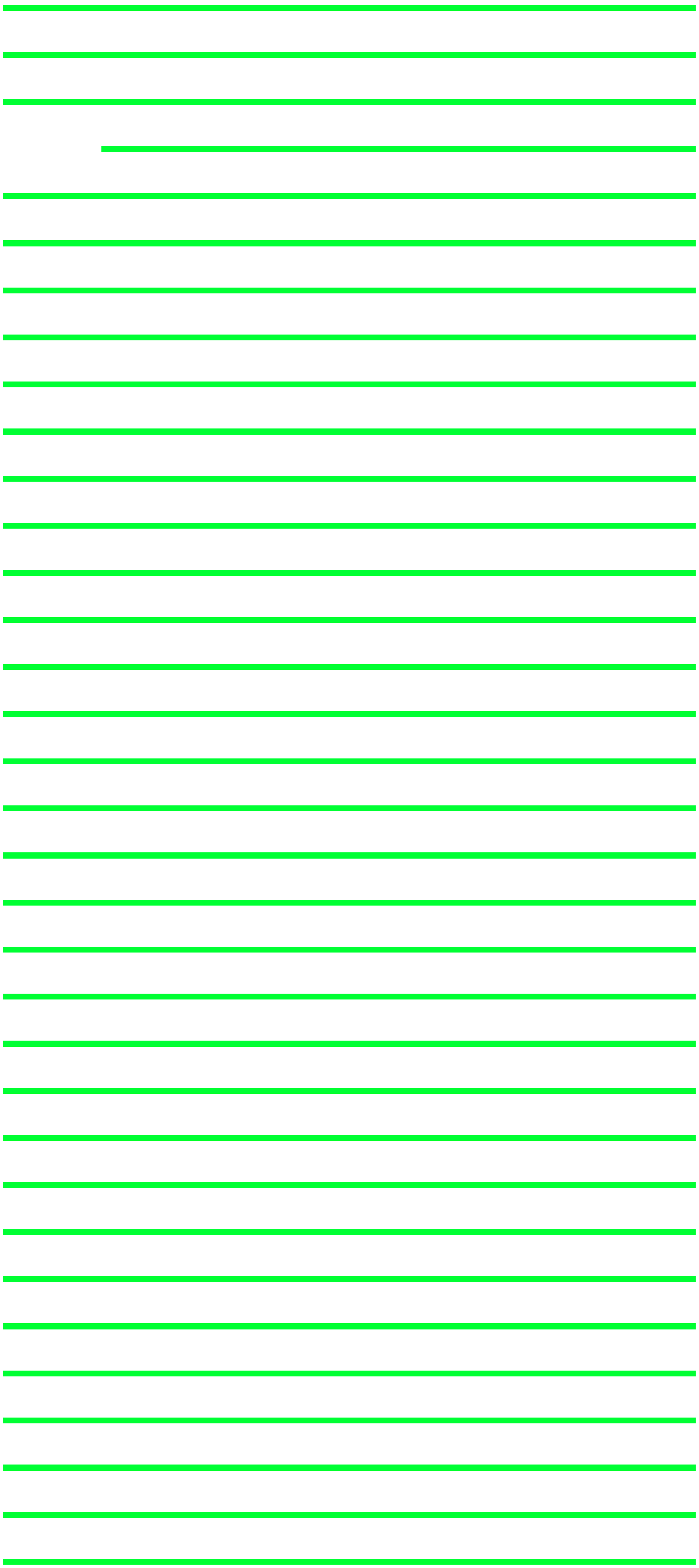
Show Conserved Domains

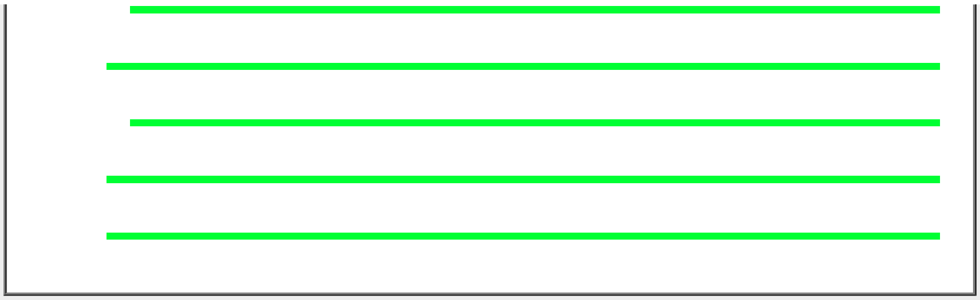
No putative conserved domains have been detected

Distribution of 104 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	complement C1r subcomponent-like protein isoform 2 precursor [H	75.9	75.9	100%	7e-15	100%	gi|663071006|NP_001284569.1
☐	PREDICTED: complement C1r subcomponent-like protein isoform	75.9	75.9	100%	7e-15	100%	gi|441670266|XP_004092185.1
☐	PREDICTED: complement C1r subcomponent-like protein isoform	75.9	75.9	100%	8e-15	100%	gi|332249352|XP_003273827.1
☐	complement C1r subcomponent-like protein isoform 1 precursor [H	75.9	75.9	100%	8e-15	100%	gi|289547636|NP_057630.2
☐	PREDICTED: complement C1r subcomponent-like protein isoform	75.9	75.9	100%	8e-15	100%	gi|114643162|XP_001163902.1
☐	complement component 1, r subcomponent-like precursor variant [H	75.9	75.9	100%	8e-15	100%	gi|62897163|BAD96522.1
☐	complement C1r-like proteinase precursor [Homo sapiens]	75.9	75.9	100%	8e-15	100%	gi|7271475|AAF44349.1
☐	PREDICTED: complement C1r subcomponent-like protein isoform	75.9	75.9	100%	8e-15	100%	gi|441670263|XP_004092184.1
☐	PREDICTED: complement C1r subcomponent-like protein isoform	75.9	75.9	100%	8e-15	100%	gi|675757427|XP_008971903.1
☐	PREDICTED: complement C1r subcomponent-like protein [Gorilla	73.6	73.6	100%	5e-14	97%	gi|426371473|XP_004052671.1
☐	unnamed protein product [Homo sapiens]	72.8	72.8	100%	8e-14	97%	gi|10436374|BAB14819.1
☐	PREDICTED: complement C1r subcomponent-like protein [Macaca	72.8	72.8	100%	9e-14	97%	gi|544469176|XP_005570609.1
☐	PREDICTED: complement C1r subcomponent-like protein isoform	72.8	72.8	100%	1e-13	97%	gi|402884997|XP_003905955.1
☐	Complement C1r subcomponent-like protein [Macaca fascicularis]	72.8	72.8	100%	1e-13	97%	gi|355785846|EHH66029.1
☐	PREDICTED: complement C1r subcomponent-like protein isoform	72.8	72.8	100%	1e-13	97%	gi|685570876|XP_009178379.1
☐	Complement C1r subcomponent-like protein [Macaca mulatta]	71.2	71.2	100%	3e-13	94%	gi|355563948|EHH20448.1
☐	PREDICTED: complement C1r subcomponent-like protein [Chloroc	70.5	70.5	100%	6e-13	94%	gi|635063155|XP_007965642.1
☐	PREDICTED: complement C1r subcomponent-like protein [Callithri	65.9	65.9	100%	3e-11	86%	gi|675677706|XP_009001758.1
☐	PREDICTED: complement C1r subcomponent-like protein [Galeopt	64.7	64.7	100%	7e-11	83%	gi|667290276|XP_008577472.1
☐	PREDICTED: complement C1r subcomponent-like protein [Otolemu	63.5	63.5	100%	2e-10	80%	gi|395847725|XP_003796517.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subcom	60.5	60.5	85%	1e-09	93%	gi|686739538|XP_009245669.1
☐	PREDICTED: complement C1r subcomponent-like protein isoform	59.3	59.3	100%	5e-09	77%	gi|671039595|XP_008681740.1
☐	PREDICTED: complement C1r subcomponent-like protein isoform	59.3	59.3	100%	6e-09	77%	gi|671039593|XP_008681739.1
☐	C1r-like protein [Mus musculus]	58.2	58.2	100%	8e-09	71%	gi|30842778|AAP41416.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subcom	58.9	58.9	100%	8e-09	74%	gi|532105686|XP_005338428.1
☐	complement C1r subcomponent-like protein precursor [Rattus norve	58.5	58.5	100%	1e-08	74%	gi|50657416|NP_001002804.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subcom	58.5	58.5	100%	1e-08	74%	gi|674104757|XP_008823575.1
☐	complement component 1, r subcomponent-like [Rattus norvegicus	58.5	58.5	100%	1e-08	74%	gi|149049502|EDM01956.1
☐	C1r-like protein [Mus musculus]	58.2	58.2	100%	1e-08	71%	gi|30842780|AAP41417.1
☐							

	complement component 1, r subcomponent-like [Mus musculus]	58.2	58.2	100%	1e-08	71%	gi|148667322|EDK99738.1
☐	unnamed protein product [Mus musculus]	58.2	58.2	100%	1e-08	71%	gi|74225714|BAE21686.1
☐	complement C1r subcomponent-like protein precursor [Mus muscul	58.2	58.2	100%	1e-08	71%	gi|269973899|NP_851989.3
☐	PREDICTED: complement C1r subcomponent-like protein [Ochotor	57.4	57.4	100%	3e-08	74%	gi|504173912|XP_004596521.1
☐	PREDICTED: complement C1r subcomponent-like protein [Leptony	57.4	57.4	100%	3e-08	74%	gi|585171947|XP_006737937.1
☐	PREDICTED: complement C1r subcomponent-like protein [Odoben	57.4	57.4	100%	3e-08	74%	gi|472376494|XP_004407682.1
☐	Complement C1r subcomponent-like protein [Tupaia chinensis]	57.0	57.0	100%	4e-08	74%	gi|444510890|ELV09737.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subcomp	57.0	57.0	100%	5e-08	74%	gi|562886979|XP_006170901.1
☐	PREDICTED: complement C1r subcomponent-like protein [Elephan	55.8	55.8	100%	9e-08	71%	gi|585679250|XP_006891411.1
☐	Complement C1r subcomponent-like protein [Cricetulus griseus]	55.5	55.5	100%	1e-07	74%	gi|344242458|EGV98561.1
☐	PREDICTED: complement C1r subcomponent-like protein isoform X	55.5	55.5	100%	1e-07	74%	gi|354467327|XP_003496121.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subcomp	55.5	55.5	100%	1e-07	71%	gi|507697361|XP_004643633.1
☐	PREDICTED: complement C1r subcomponent-like protein [Trichech	55.5	55.5	100%	2e-07	71%	gi|471411548|XP_004387327.1
☐	complement C1r-A subcomponent [Cricetulus griseus]	55.5	98.6	100%	2e-07	74%	gi|537136510|ERE66562.1
☐	PREDICTED: complement component 1, r subcomponent-like [Felis	54.3	54.3	100%	3e-07	69%	gi|586991762|XP_006933531.1
☐	PREDICTED: complement C1r-A subcomponent-like [Microtus ochr	54.7	99.0	100%	4e-07	74%	gi|532045173|XP_005365394.1
☐	hypothetical protein PANDA_011233 [Ailuropoda melanoleuca]	53.9	53.9	100%	4e-07	71%	gi|281338369|EFB13953.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subcomp	53.9	53.9	100%	4e-07	71%	gi|524923662|XP_005066080.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subcomp	53.9	53.9	100%	5e-07	66%	gi|560893125|XP_006173072.1
☐	complement C1r subcomponent-like protein [Camelus ferus]	53.9	53.9	100%	5e-07	66%	gi|528770117|EPY89776.1
☐	PREDICTED: complement C1r subcomponent-like protein [Peromys	53.5	53.5	100%	5e-07	71%	gi|589959162|XP_006992168.1
☐	PREDICTED: complement C1r subcomponent-like protein-like [Ailu	53.9	53.9	100%	5e-07	71%	gi|301773698|XP_002922303.1
☐	PREDICTED: complement C1r subcomponent-like protein isoform X	53.5	53.5	97%	5e-07	71%	gi|533127501|XP_005378915.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subcomp	53.5	53.5	100%	6e-07	69%	gi|511894085|XP_004766682.1
☐	PREDICTED: complement C1r subcomponent-like protein isoform X	53.5	53.5	97%	6e-07	71%	gi|533127499|XP_005378914.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subcomp	53.5	53.5	100%	6e-07	66%	gi|560977345|XP_006210952.1
☐	PREDICTED: complement C1r subcomponent-like protein isoform X	53.1	53.1	100%	8e-07	69%	gi|291392803|XP_002712893.1
☐	PREDICTED: complement C1r subcomponent-like protein isoform X	53.1	53.1	100%	8e-07	69%	gi|655831423|XP_008257993.1
☐	PREDICTED: complement C1r subcomponent-like protein [Oryctero	53.1	53.1	100%	9e-07	66%	gi|634837986|XP_007935394.1
☐	Complement C1r subcomponent-like protein [Pteropus alecto]	53.1	53.1	100%	9e-07	71%	gi|431905373|ELK10418.1
☐	PREDICTED: complement C1r subcomponent-like protein [Pteropu	53.1	53.1	100%	9e-07	71%	gi|586563055|XP_006914777.1
☐	PREDICTED: complement C1r subcomponent-like protein [Equus p	52.8	52.8	100%	1e-06	66%	gi|664759598|XP_008537368.1
☐	PREDICTED: complement C1r subcomponent-like protein [Equus c	52.8	52.8	100%	1e-06	66%	gi|545219170|XP_005610954.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement C1r subcomp	51.6	51.6	100%	3e-06	66%	gi|591327382|XP_007089640.1
☐	PREDICTED: complement C1r subcomponent-like protein [Ceratoth	51.6	51.6	100%	3e-06	66%	gi|478529432|XP_004438886.1
☐	PREDICTED: complement C1r subcomponent-like protein [Tursiops	50.4	50.4	100%	7e-06	63%	gi|470606249|XP_004314129.1
☐	PREDICTED: complement component 1, r subcomponent-like isofo	50.1	50.1	100%	9e-06	63%	gi|545546513|XP_005637265.1
☐	PREDICTED: complement component 1, r subcomponent-like isofo	50.1	50.1	100%	9e-06	63%	gi|545546511|XP_005637264.1
☐	PREDICTED: complement component 1, r subcomponent-like isofo	50.1	50.1	100%	1e-05	63%	gi|545546509|XP_005637263.1
☐	PREDICTED: complement component 1, r subcomponent-like isofo	50.1	50.1	100%	1e-05	63%	gi|545546507|XP_005637262.1
☐	PREDICTED: complement component 1, r subcomponent-like isofo	50.1	50.1	100%	1e-05	63%	gi|345792069|XP_543840.3
☐	PREDICTED: complement C1r subcomponent-like protein [Lipotes	50.1	50.1	100%	1e-05	63%	gi|602718526|XP_007469443.1
☐	PREDICTED: complement C1r subcomponent-like protein [Orcinus	50.1	50.1	100%	1e-05	63%	gi|466055133|XP_004279184.1
☐	PREDICTED: complement C1r subcomponent-like protein isoform 3	49.3	49.3	100%	1e-05	66%	gi|488554131|XP_004468199.1
☐	PREDICTED: complement C1r subcomponent-like protein [Myotis d	49.7	49.7	100%	1e-05	63%	gi|584074754|XP_006757609.1

☐ PREDICTED: complement C1r subcomponent-like protein [Cavia p	49.7	49.7	100%	1e-05	63%	gi|348554938|XP_003463281.1
☐ PREDICTED: complement C1r subcomponent-like protein [Myotis l	49.7	49.7	100%	1e-05	63%	gi|558104592|XP_006084250.1
☐ PREDICTED: complement C1r subcomponent-like protein [Erinaceu	49.7	49.7	100%	1e-05	63%	gi|617656833|XP_007535922.1
☐ PREDICTED: complement C1r subcomponent-like protein [Fukomy	49.3	49.3	100%	1e-05	60%	gi|731282854|XP_010610027.1
☐ PREDICTED: complement C1r subcomponent-like protein isoform 1	49.3	49.3	100%	2e-05	66%	gi|488554125|XP_004468197.1
☐ PREDICTED: complement C1r subcomponent-like protein [Myotis b	49.3	49.3	100%	2e-05	63%	gi|554558619|XP_005873711.1
☐ PREDICTED: complement C1r subcomponent-like protein [Balaeno	49.3	49.3	100%	2e-05	63%	gi|594633415|XP_007170182.1
☐ PREDICTED: complement C1r subcomponent-like protein [Loxodor	49.3	49.3	100%	2e-05	63%	gi|731515679|XP_010600946.1
☐ PREDICTED: complement C1r subcomponent-like protein [Capra h	48.9	48.9	100%	2e-05	60%	gi|548468413|XP_005681065.1
☐ Complement C1r subcomponent [Fukomys damarensis]	49.3	90.5	100%	2e-05	60%	gi|676263566|KFO20277.1
☐ PREDICTED: LOW QUALITY PROTEIN: complement C1r subcomp	48.9	48.9	100%	3e-05	60%	gi|556724329|XP_005957969.1
☐ PREDICTED: complement C1r subcomponent-like protein [Chrysoc	48.9	48.9	100%	3e-05	66%	gi|586464372|XP_006862815.1
☐ PREDICTED: complement component 1, r subcomponent-like [Sus	48.5	48.5	100%	4e-05	63%	gi|545890542|XP_005658603.1
☐ PREDICTED: complement C1r subcomponent-like protein [Saimiri b	47.4	47.4	65%	5e-05	91%	gi|725609801|XP_010331194.1
☐ Complement C1r subcomponent-like protein [Bos mutus]	47.8	47.8	100%	6e-05	60%	gi|440891813|ELR45306.1
☐ PREDICTED: complement C1r subcomponent-like protein [Heteroc	47.8	47.8	100%	6e-05	58%	gi|512941192|XP_004909584.1
☐ PREDICTED: LOW QUALITY PROTEIN: complement C1r subcomp	47.8	47.8	100%	7e-05	60%	gi|555998080|XP_005910755.1
☐ PREDICTED: complement C1r subcomponent [Heterocephalus glal	47.8	92.4	100%	9e-05	58%	gi|513016514|XP_004869588.1
☐ PREDICTED: complement C1r subcomponent-like protein [Physete	47.4	47.4	91%	9e-05	66%	gi|593724491|XP_007108376.1
☐ PREDICTED: complement C1r subcomponent-like [Nomascus leuc	43.9	43.9	100%	1e-04	46%	gi|332267693|XP_003282816.1
☐ PREDICTED: complement C1r subcomponent-like protein [Rhinopit	46.6	46.6	65%	2e-04	91%	gi|724942380|XP_010386350.1
☐ TPA: complement component 1, r subcomponent-like [Bos taurus]	46.2	46.2	100%	2e-04	57%	gi|296487145|DAA29258.1
☐ complement C1r subcomponent-like protein [Bos taurus]	46.2	46.2	100%	2e-04	57%	gi|300798717|NP_001179084.1
☐ PREDICTED: complement component 1, r subcomponent-like isofo	46.2	46.2	100%	3e-04	57%	gi|528950936|XP_005207183.1
☐ PREDICTED: complement C1r subcomponent [Trichechus manatus	46.2	46.2	100%	3e-04	49%	gi|471411492|XP_004387299.1
☐ PREDICTED: complement C1r subcomponent [Chinchilla lanigera]	46.2	46.2	100%	3e-04	49%	gi|533127497|XP_005378913.1

⊟ Alignments

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complement C1r subcomponent-like protein isoform 2 precursor [Homo sapiens]

Sequence ID: gi|663071006|ref|NP_001284569.1| **Length:** 445 **Number of Matches:** 1

Range 1: 175 to 209 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.9 bits(185)	7e-15	35/35(100%)	35/35(100%)	0/35(0%)

```
Query  1    KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  35
            KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA
Sbjct  175  KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  209
```

Related Information

Gene - associated gene details

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PREDICTED: complement C1r subcomponent-like protein isoform 3 [Nomascus leucogenys]

Sequence ID: gi|441670266|ref|XP_004092185.1| **Length:** 445 **Number of Matches:** 1

Range 1: 175 to 209 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.9 bits(185)	7e-15	35/35(100%)	35/35(100%)	0/35(0%)

```
Query  1    KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  35
            KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA
Sbjct  175  KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  209
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: complement C1r subcomponent-like protein isoform 1 [Nomascus leucogenys]

Sequence ID: gi|332249352|ref|XP_003273827.1| **Length:** 487 **Number of Matches:** 1

Range 1: 217 to 251 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.9 bits(185)	8e-15	35/35(100%)	35/35(100%)	0/35(0%)

```
Query  1    KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  35
            KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA
Sbjct  217  KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  251
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

complement C1r subcomponent-like protein isoform 1 precursor [Homo sapiens]

Sequence ID: gi|289547636|ref|NP_057630.2| **Length:** 487 **Number of Matches:** 1

▷ See 2 more title(s)

Range 1: 217 to 251 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.9 bits(185)	8e-15	35/35(100%)	35/35(100%)	0/35(0%)

```
Query  1    KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  35
            KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA
Sbjct  217  KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  251
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: complement C1r subcomponent-like protein isoform X1 [Pan troglodytes]

Sequence ID: gi|114643162|ref|XP_001163902.1| **Length:** 487 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 217 to 251 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.9 bits(185)	8e-15	35/35(100%)	35/35(100%)	0/35(0%)

```
Query  1    KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  35
            KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA
Sbjct  217  KDRQDGEEVLQCMPVCGRPVTPIAQNQTTLGSSRA  251
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   Formatting options   Download   How to read this page   Blast report description

C4BPB_KEWDDTTTECRL_ModMod

RID BTF85YDR013 (Expires on 01-20 15:15 pm)

Query ID	lcl|15197	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	12		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

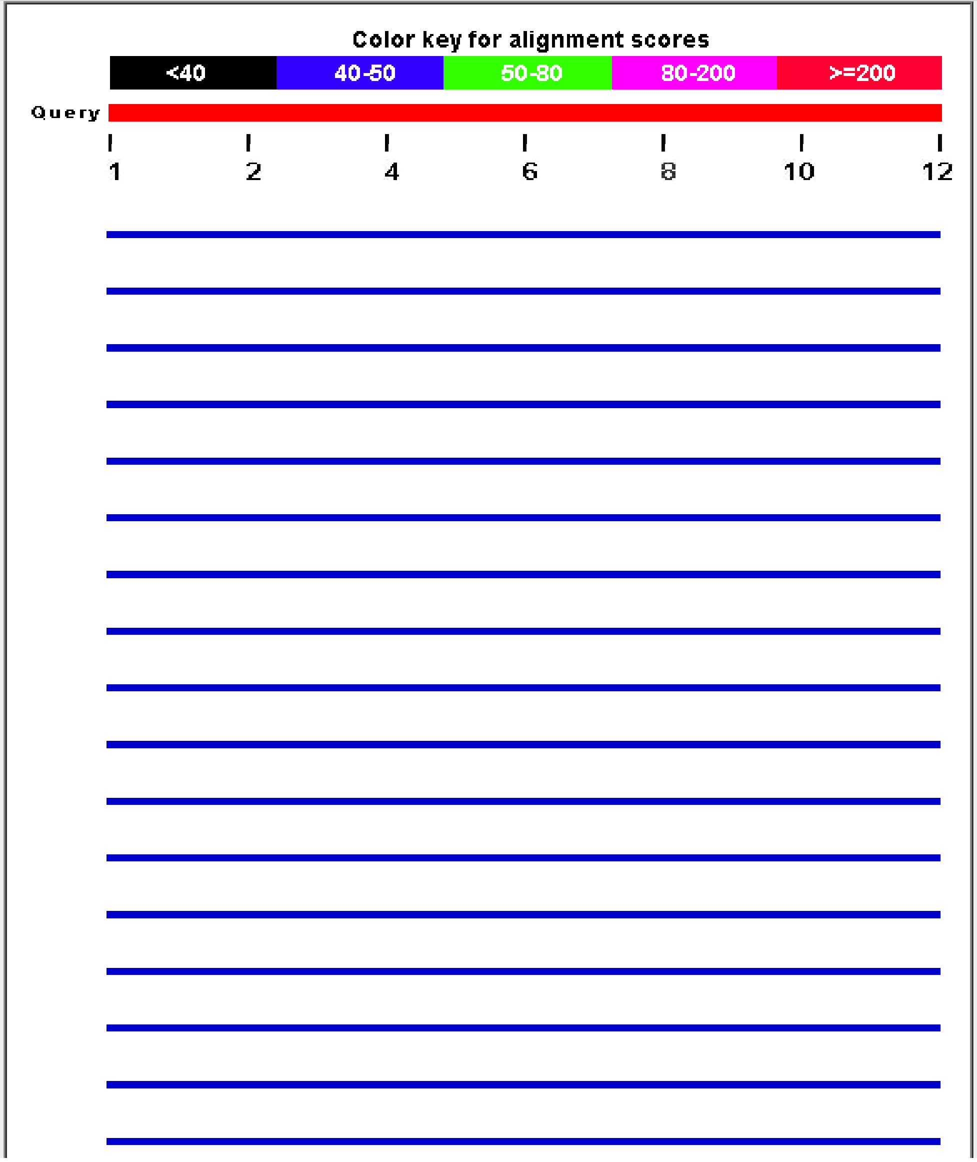
Graphic Summary

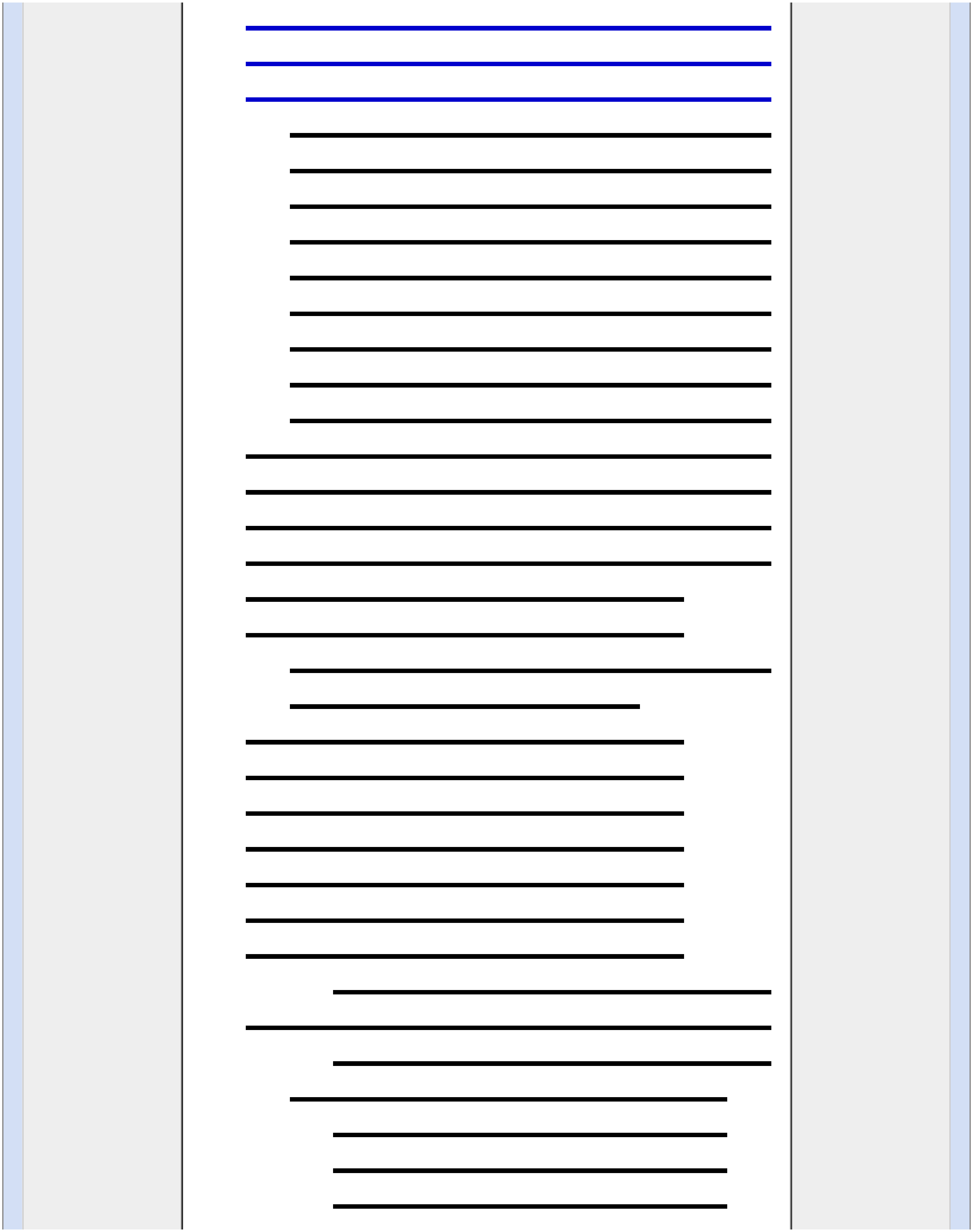
Show Conserved Domains

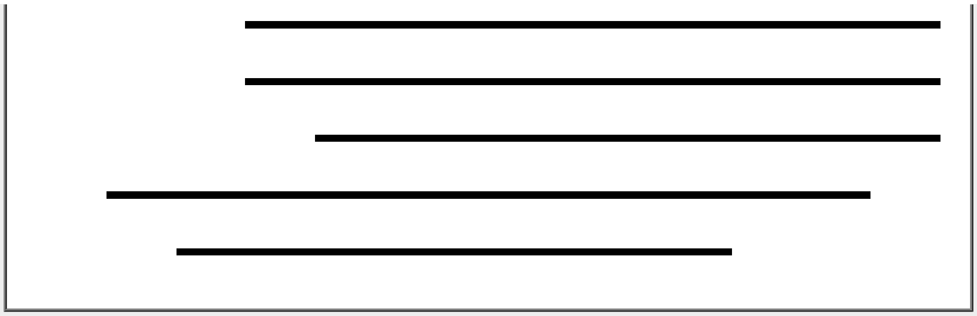
No putative conserved domains have been detected

Distribution of 105 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	42.2	42.2	100%	0.002	92%	gi|194373591|BAG56891.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan t	42.2	42.2	100%	0.002	92%	gi|694891540|XP_009439669.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan p	42.2	42.2	100%	0.002	92%	gi|675771724|XP_008974762.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Hom	42.2	42.2	100%	0.002	92%	gi|530366462|XP_005273312.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Rhin	42.2	42.2	100%	0.002	92%	gi|724836382|XP_010363947.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan t	42.2	42.2	100%	0.002	92%	gi|694891534|XP_009439665.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Papi	42.2	42.2	100%	0.002	92%	gi|685519789|XP_009186662.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan p	42.2	42.2	100%	0.002	92%	gi|675771715|XP_008974759.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Maca	42.2	42.2	100%	0.002	92%	gi|544399939|XP_005540733.1
☐	C4b-binding protein beta chain isoform 2 precursor [Homo sapi	42.2	42.2	100%	0.002	92%	gi|62912462|NP_001017364.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Rhin	42.2	42.2	100%	0.002	92%	gi|724836379|XP_010363946.1
☐	C4b-binding protein beta chain isoform 1 precursor [Homo sapi	42.2	42.2	100%	0.002	92%	gi|4502505|NP_000707.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Maca	42.2	42.2	100%	0.002	92%	gi|544399931|XP_005540729.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Papi	42.2	42.2	100%	0.002	92%	gi|685519785|XP_009186656.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan p	42.2	42.2	100%	0.002	92%	gi|397504761|XP_003822949.1
☐	hypothetical protein EGM_01442 [Macaca fascicularis]	42.2	42.2	100%	0.002	92%	gi|355745961|EHH50586.1
☐	hypothetical protein EGK_01712 [Macaca mulatta]	42.2	42.2	100%	0.002	92%	gi|355558818|EHH15598.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan t	42.2	42.2	100%	0.002	92%	gi|114572288|XP_001166306.1
☐	PREDICTED: c4b-binding protein beta chain isoform 3 [Macac	42.2	42.2	100%	0.002	92%	gi|109018561|XP_001083216.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Maca	42.2	42.2	100%	0.002	92%	gi|544399929|XP_005540728.1
☐	PREDICTED: C4b-binding protein beta chain isoform X9 [Chlor	39.2	39.2	91%	0.023	91%	gi|635130917|XP_007986833.1
☐	PREDICTED: C4b-binding protein beta chain isoform X8 [Chlor	39.2	39.2	91%	0.024	91%	gi|635130915|XP_007986832.1
☐	PREDICTED: C4b-binding protein beta chain isoform X7 [Chlor	39.2	39.2	91%	0.024	91%	gi|635130913|XP_007986831.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Chlor	39.2	39.2	91%	0.024	91%	gi|635130911|XP_007986830.1
☐	PREDICTED: C4b-binding protein beta chain isoform X5 [Chlor	39.2	39.2	91%	0.024	91%	gi|635130907|XP_007986828.1
☐	PREDICTED: C4b-binding protein beta chain isoform X4 [Chlor	39.2	39.2	91%	0.025	91%	gi|635130905|XP_007986827.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Chlor	39.2	39.2	91%	0.025	91%	gi|635130903|XP_007986826.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Chlor	39.2	39.2	91%	0.025	91%	gi|635130901|XP_007986825.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Chlor	39.2	39.2	91%	0.025	91%	gi|635130899|XP_007986823.1

☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pong	38.8	38.8	100%	0.032	83%	gi|686700216|XP_009236698.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pong	38.8	38.8	100%	0.033	83%	gi|686700213|XP_009236694.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pong	38.8	38.8	100%	0.033	83%	gi|297662141|XP_002809574.1
☐	PREDICTED: C4b-binding protein beta chain isoform 1 [Nomas	38.0	38.0	100%	0.064	83%	gi|332266848|XP_003282407.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Callitl	35.8	35.8	83%	0.32	90%	gi|675749407|XP_008983835.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Callitl	35.8	35.8	83%	0.32	90%	gi|296230632|XP_002760794.1
☐	PREDICTED: C4b-binding protein beta chain [Cavia porcellus]	31.2	31.2	91%	11	73%	gi|348577871|XP_003474707.1
☐	hypothetical protein [Clostridium sp. CAG:62]	31.2	31.2	66%	11	100%	gi|548057742|WP_022376409.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Saimi	30.8	30.8	83%	15	80%	gi|725574024|XP_010339305.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Saimi	30.8	30.8	83%	15	80%	gi|403277664|XP_003930472.1
☐	hypothetical protein [Vibrio nigripulchritudo]	30.3	30.3	83%	18	70%	gi|740359636|WP_038195698.1
☐	hypothetical protein [Vibrio nigripulchritudo]	30.3	30.3	83%	19	70%	gi|740309755|WP_038147115.1
☐	putative Fimh-like protein [Vibrio nigripulchritudo]	30.3	30.3	83%	19	70%	gi|550352361|WP_022612127.1
☐	putative Fimh-like protein [Vibrio nigripulchritudo]	30.3	30.3	83%	19	70%	gi|550281458|WP_022607838.1
☐	hypothetical protein VINI7043_08940 [Vibrio nigripulchritudo AT	30.3	30.3	83%	19	70%	gi|342820393|EGU55216.1
☐	PREDICTED: fibroin heavy chain-like [Callithrix jacchus]	29.9	93.8	83%	28	83%	gi|675768476|XP_008987859.1
☐	PREDICTED: C4b-binding protein beta chain [Nannospalax gal	29.5	29.5	100%	38	75%	gi|674096417|XP_008821570.1
☐	PREDICTED: C4b-binding protein beta chain [Ictidomys tridece	29.1	29.1	83%	52	80%	gi|532087633|XP_005329528.1
☐	hypothetical protein TRIUR3_31016 [Triticum urartu]	29.1	29.1	83%	54	70%	gi|473936676|EMS50150.1
☐	glyoxalase/bleomycin resistance protein/dioxygenase [Enterocc	28.6	28.6	75%	61	78%	gi|488246961|WP_002318169.1
☐	glyoxalase [Enterococcus faecium]	28.6	28.6	75%	65	78%	gi|488218002|WP_002289210.1
☐	glyoxalase [Enterococcus avium]	28.6	28.6	75%	65	78%	gi|510805076|WP_016179839.1
☐	hypothetical protein Csa_5G017790 [Cucumis sativus]	28.6	28.6	83%	66	82%	gi|700194418|KGN49595.1
☐	PREDICTED: uncharacterized protein LOC101232668 [Cucumi	28.6	28.6	83%	67	82%	gi|449526640|XP_004170321.1
☐	Receptor-type tyrosine-protein phosphatase alpha [Crassostrea	28.6	28.6	75%	72	89%	gi|405963146|EKC28746.1
☐	serine/threonine kinase [Naegleria gruberi strain NEG-M]	28.6	28.6	91%	75	64%	gi|290996855|XP_002680997.1
☐	non-ribosomal peptide synthetase [Myxococcus xanthus]	28.6	67.2	66%	76	88%	gi|499872920|WP_011553654.1
☐	hypothetical protein [Rhizobium leguminosarum]	28.2	28.2	91%	96	75%	gi|653792155|WP_027686102.1
☐	hypothetical protein [Rhizobium leguminosarum]	28.2	28.2	91%	96	75%	gi|502299986|WP_012755944.1
☐	hypothetical protein [Rhizobium leguminosarum]	28.2	28.2	91%	96	75%	gi|501551999|WP_012556512.1
☐	hypothetical protein RLEG3_10980 [Rhizobium leguminosarum	28.2	28.2	91%	96	67%	gi|573465435|AHF82317.1
☐	hypothetical protein SCHCODRAFT_104079 [Schizophyllum cc	28.2	28.2	83%	99	80%	gi|302698025|XP_003038691.1
☐	xylulokinase [Treponema maltophilum]	28.2	28.2	83%	100	67%	gi|513870852|WP_016524615.1
☐	xylulokinase [Treponema lecithinolyticum]	28.2	28.2	83%	100	67%	gi|545449279|WP_021686299.1
☐	hypothetical protein PFICI_04849 [Pestalotiopsis fici W106-1]	28.2	28.2	83%	100	80%	gi|630015271|XP_007831621.1
☐	pleckstrin domain-containing protein [Polysphondylium pallidum	28.2	28.2	75%	101	73%	gi|281205479|EFA79670.1
☐	cotH protein [Clostridium sp. CAG:230]	28.2	28.2	100%	101	43%	gi|547728152|WP_022142301.1
☐	hypothetical protein [Mycobacterium smegmatis]	27.8	27.8	58%	124	100%	gi|505111008|WP_015298110.1
☐	ECF subfamily RNA polymerase sigma-24 factor [Rhodococcus	27.8	27.8	58%	129	100%	gi|490034641|WP_003937064.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	27.8	27.8	91%	131	64%	gi|533120065|XP_005375468.1
☐	PREDICTED: uncharacterized protein LOC104565074 [Tinamu	27.8	27.8	58%	132	100%	gi|719742278|XP_010210028.1
☐	hypothetical protein [Halococcus thailandensis]	27.8	27.8	58%	134	100%	gi|495011748|WP_007737760.1
☐	hypothetical protein [Escherichia coli]	27.8	27.8	58%	134	100%	gi|545278327|WP_021565543.1
☐	hypothetical protein [Clostridium botulinum]	27.8	27.8	58%	134	100%	gi|502039998|WP_012704248.1
☐	hypothetical protein [Clostridium botulinum]	27.8	27.8	58%	134	100%	gi|544673624|WP_021106489.1

☐	hypothetical protein G647_02930 [Cladophialophora carrionii C	27.8	27.8	58%	135	100%	gi|671170064|XP_008725498.1
☐	S-layer-related protein [Bacteroidales bacterium CF50]	27.8	27.8	58%	135	100%	gi|553027585|AGY53002.1
☐	usher protein [Enterobacteriaceae bacterium LSJC7]	27.8	27.8	91%	137	73%	gi|648277699|WP_026058848.1
☐	von Willebrand factor A [Chryseobacterium vrystaatense]	27.8	27.8	66%	138	88%	gi|736746476|WP_034750228.1
☐	hypothetical protein LOTGIDRAFT_158683 [Lottia gigantea]	27.8	27.8	83%	138	67%	gi|676444278|XP_009050377.1
☐	alpha-amylase [Rhizobium sp. 2MFCol3.1]	27.8	27.8	58%	138	100%	gi|648591778|WP_026283529.1
☐	benzoate transporter [Saccharophagus degradans]	27.8	27.8	58%	139	100%	gi|499788666|WP_011469400.1
☐	hypothetical protein [Fischerella sp. PCC 9339]	27.8	27.8	66%	139	88%	gi|648362402|WP_026081876.1
☐	PREDICTED: C4b-binding protein beta chain [Jaculus jaculus]	27.4	27.4	91%	179	73%	gi|507559572|XP_004663509.1
☐	hypothetical protein [Verrucomicrobia bacterium SCGC AAA16	27.4	27.4	83%	181	80%	gi|740295650|WP_038133801.1
☐	phosphoserine aminotransferase [Alistipes sp. CAG:435]	27.4	27.4	91%	182	73%	gi|547921208|WP_022323484.1
☐	phosphoserine aminotransferase [Alistipes sp. CAG:514]	27.4	27.4	91%	182	73%	gi|546330868|WP_021838129.1
☐	Xylulokinase [Bacillus licheniformis]	27.4	27.4	83%	184	75%	gi|1546887|CAB02315.1
☐	xylulose kinase [Bacillus licheniformis]	27.4	27.4	83%	185	75%	gi|737355726|WP_035337931.1
☐	xylulose kinase [Bacillus sp. SB47]	27.4	27.4	83%	185	75%	gi|651585103|WP_026580281.1
☐	xylulose kinase [Bacillus licheniformis]	27.4	27.4	83%	185	75%	gi|647500858|WP_025810601.1
☐	D-xylulose kinase [Bacillus licheniformis]	27.4	27.4	83%	185	75%	gi|499511774|WP_011198414.1
☐	xylulose kinase [Bacillus licheniformis S 16]	27.4	27.4	83%	185	75%	gi|584582009|EWH21359.1
☐	D-xylulose kinase [Bacillus sp. CPSM8]	27.4	27.4	83%	185	75%	gi|564753737|WP_023856989.1
☐	MULTISPECIES: D-xylulose kinase [Anoxybacillus]	27.4	27.4	83%	185	75%	gi|518246519|WP_019416727.1
☐	hypothetical protein [Salsuginibacillus kocurii]	27.4	27.4	83%	185	75%	gi|517752777|WP_018922985.1
☐	xylulose kinase XylB [Bacillus licheniformis]	27.4	27.4	83%	185	75%	gi|521289100|WP_020453368.1
☐	MULTISPECIES: D-xylulose kinase [Bacillus]	27.4	27.4	83%	185	75%	gi|489278555|WP_003186220.1
☐	Protein F54D5.15, isoform b [Haemonchus contortus]	27.4	27.4	66%	185	88%	gi|560120563|CDJ94804.1
☐	hypothetical protein [Nocardiopsis halotolerans]	27.4	27.4	66%	186	88%	gi|516140786|WP_017571366.1
☐	hypothetical protein [Nocardiopsis dassonvillei]	27.4	27.4	66%	186	88%	gi|502917959|WP_013152935.1

⊟ Alignments

Error loading alignment ...Try again

NCBI/ BLAST/ blastp suite/ Formatting Results - B92AJCNC01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download
How to read this page Blast report description

C4BPB_KEWDNTTTECRL_NonMod

RID B92AJCNC01R (Expires on 01-14 09:56 am)

Query ID	lcl|225053	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	12	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

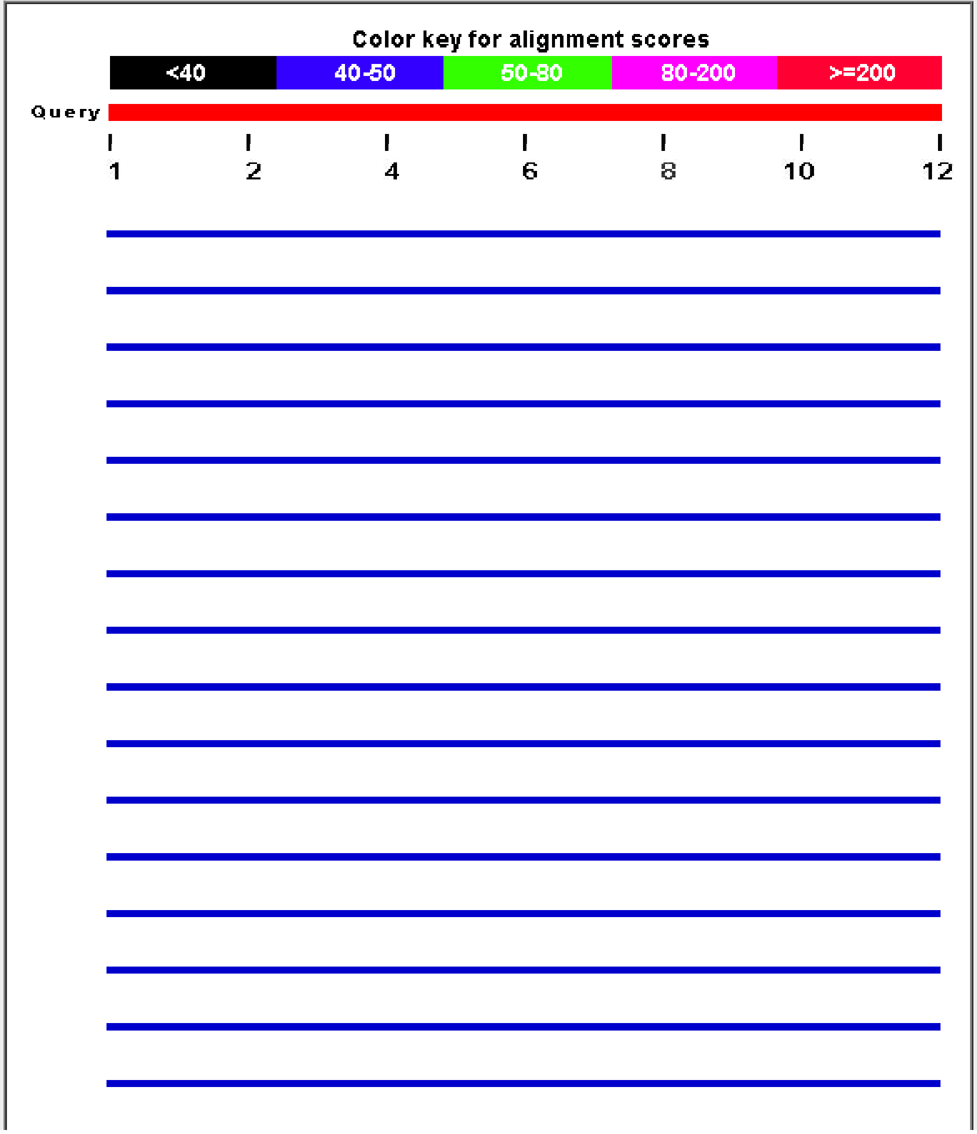
Graphic Summary

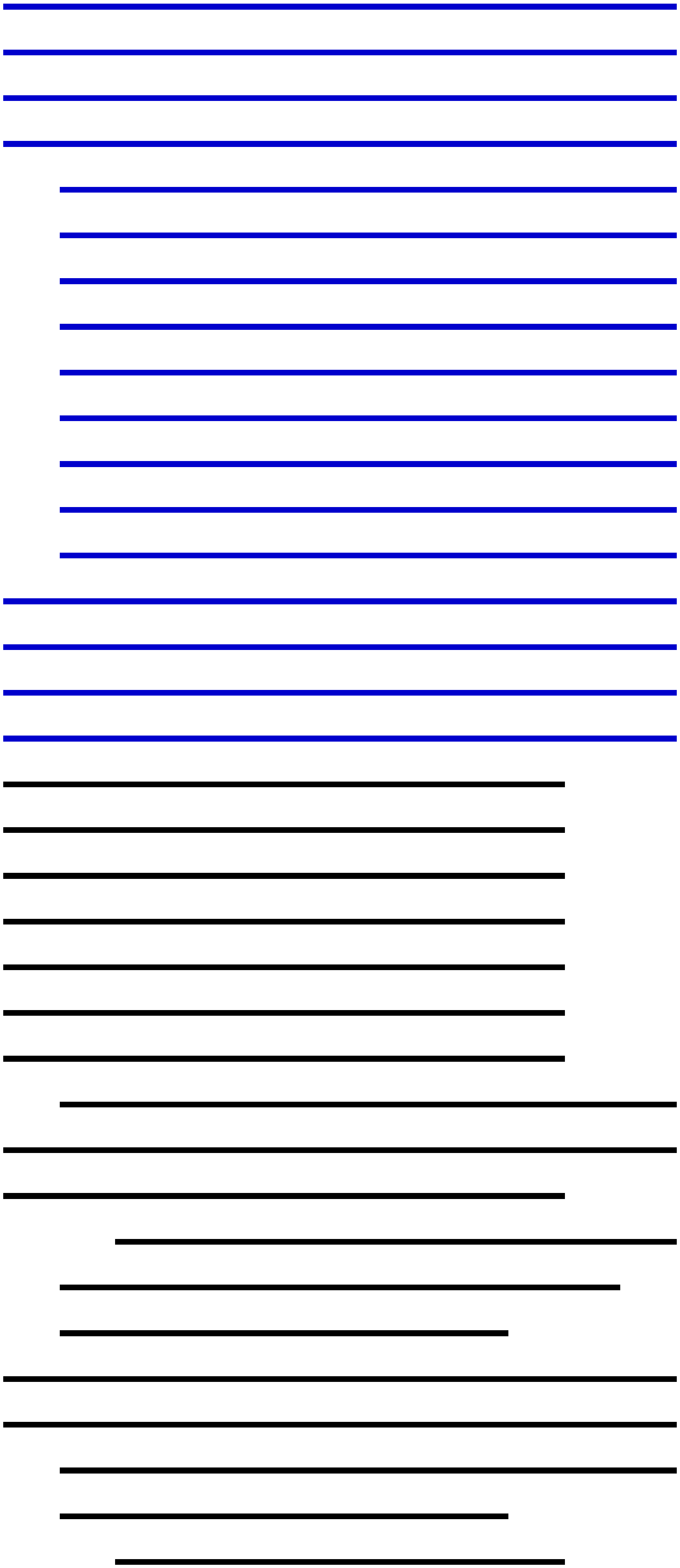
Show Conserved Domains

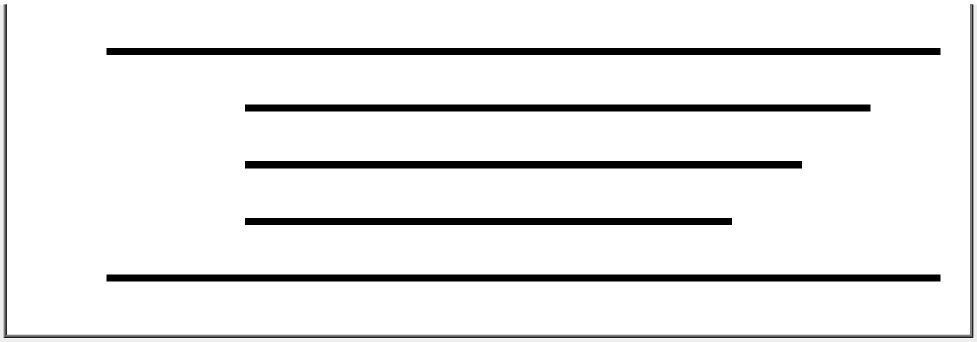
No putative conserved domains have been detected

Distribution of 103 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	44.8	44.8	100%	3e-04	100%	gi|194373591|BAG56891.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan troglo	44.8	44.8	100%	3e-04	100%	gi|694891540|XP_009439669.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan panis	44.8	44.8	100%	3e-04	100%	gi|675771724|XP_008974762.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sap	44.8	44.8	100%	3e-04	100%	gi|530366462|XP_005273312.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinopith	44.8	44.8	100%	3e-04	100%	gi|724836382|XP_010363947.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan troglo	44.8	44.8	100%	3e-04	100%	gi|694891534|XP_009439665.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Papio anu	44.8	44.8	100%	3e-04	100%	gi|685519789|XP_009186662.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan panis	44.8	44.8	100%	3e-04	100%	gi|675771715|XP_008974759.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Macaca fa	44.8	44.8	100%	3e-04	100%	gi|544399939|XP_005540733.1
☐	C4b-binding protein beta chain isoform 2 precursor [Homo sapiens]	44.8	44.8	100%	3e-04	100%	gi|62912462|NP_001017364.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Rhinopith	44.8	44.8	100%	3e-04	100%	gi|724836379|XP_010363946.1
☐	C4b-binding protein beta chain isoform 1 precursor [Homo sapiens]	44.8	44.8	100%	3e-04	100%	gi|4502505|NP_000707.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Macaca fa	44.8	44.8	100%	3e-04	100%	gi|544399931|XP_005540729.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Papio anu	44.8	44.8	100%	3e-04	100%	gi|685519785|XP_009186656.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan panis	44.8	44.8	100%	3e-04	100%	gi|397504761|XP_003822949.1
☐	hypothetical protein EGM_01442 [Macaca fascicularis]	44.8	44.8	100%	3e-04	100%	gi|355745961|EHH50586.1
☐	hypothetical protein EGK_01712 [Macaca mulatta]	44.8	44.8	100%	3e-04	100%	gi|355558818|EHH15598.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan troglo	44.8	44.8	100%	3e-04	100%	gi|114572288|XP_001166306.1
☐	PREDICTED: c4b-binding protein beta chain isoform 3 [Macaca mu	44.8	44.8	100%	3e-04	100%	gi|109018561|XP_001083216.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Macaca fa	44.8	44.8	100%	3e-04	100%	gi|544399929|XP_005540728.1
☐	PREDICTED: C4b-binding protein beta chain isoform X9 [Chlorocel	41.8	41.8	91%	0.003	100%	gi|635130917|XP_007986833.1
☐	PREDICTED: C4b-binding protein beta chain isoform X8 [Chlorocel	41.8	41.8	91%	0.003	100%	gi|635130915|XP_007986832.1
☐	PREDICTED: C4b-binding protein beta chain isoform X7 [Chlorocel	41.8	41.8	91%	0.003	100%	gi|635130913|XP_007986831.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Chlorocel	41.8	41.8	91%	0.003	100%	gi|635130911|XP_007986830.1
☐	PREDICTED: C4b-binding protein beta chain isoform X5 [Chlorocel	41.8	41.8	91%	0.003	100%	gi|635130907|XP_007986828.1
☐	PREDICTED: C4b-binding protein beta chain isoform X4 [Chlorocel	41.8	41.8	91%	0.003	100%	gi|635130905|XP_007986827.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Chlorocel	41.8	41.8	91%	0.003	100%	gi|635130903|XP_007986826.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Chlorocel	41.8	41.8	91%	0.003	100%	gi|635130901|XP_007986825.1
☐							

PREDICTED: C4b-binding protein beta chain isoform X1 [Chlorocel	41.8	41.8	91%	0.003	100%	gi|635130899|XP_007986823.1
☐ PREDICTED: C4b-binding protein beta chain isoform X3 [Pongo ab	41.4	41.4	100%	0.004	92%	gi|686700216|XP_009236698.1
☐ PREDICTED: C4b-binding protein beta chain isoform X2 [Pongo ab	41.4	41.4	100%	0.004	92%	gi|686700213|XP_009236694.1
☐ PREDICTED: C4b-binding protein beta chain isoform X1 [Pongo ab	41.4	41.4	100%	0.004	92%	gi|297662141|XP_002809574.1
☐ PREDICTED: C4b-binding protein beta chain isoform 1 [Nomascus	40.5	40.5	100%	0.009	92%	gi|332266848|XP_003282407.1
☐ PREDICTED: C4b-binding protein beta chain isoform X2 [Callithrix j	38.4	38.4	83%	0.044	100%	gi|675749407|XP_008983835.1
☐ PREDICTED: C4b-binding protein beta chain isoform X1 [Callithrix j	38.4	38.4	83%	0.044	100%	gi|296230632|XP_002760794.1
☐ PREDICTED: C4b-binding protein beta chain isoform X2 [Saimiri bo	33.3	33.3	83%	2.1	90%	gi|725574024|XP_010339305.1
☐ PREDICTED: C4b-binding protein beta chain isoform X1 [Saimiri bo	33.3	33.3	83%	2.1	90%	gi|403277664|XP_003930472.1
☐ putative Fimh-like protein [Vibrio nigripulchritudo]	32.9	32.9	83%	2.7	80%	gi|550352361|WP_022612127.1
☐ putative Fimh-like protein [Vibrio nigripulchritudo]	32.9	32.9	83%	2.7	80%	gi|550281458|WP_022607838.1
☐ hypothetical protein [Vibrio nigripulchritudo]	32.9	32.9	83%	2.7	80%	gi|490542018|WP_004407142.1
☐ PREDICTED: C4b-binding protein beta chain [Cavia porcellus]	30.8	30.8	91%	14	73%	gi|348577871|XP_003474707.1
☐ PREDICTED: C4b-binding protein beta chain [Nannospalax galili]	30.8	30.8	100%	14	75%	gi|674096417|XP_008821570.1
☐ putative Fimh-like protein [Vibrio nigripulchritudo]	29.5	29.5	83%	35	70%	gi|549773927|WP_022549773.1
☐ PREDICTED: fibroin heavy chain-like [Callithrix jacchus]	29.1	87.8	83%	49	75%	gi|675768476|XP_008987859.1
☐ hypothetical protein TRIUR3_31016 [Triticum urartu]	28.6	28.6	83%	70	70%	gi|473936676|EMS50150.1
☐ hypothetical protein [Clostridium sp. CAG:62]	28.6	28.6	66%	70	88%	gi|548057742|WP_022376409.1
☐ PREDICTED: C4b-binding protein beta chain isoform X2 [Galeopter	28.2	28.2	100%	90	58%	gi|667314769|XP_008585888.1
☐ PREDICTED: C4b-binding protein beta chain isoform X1 [Galeopter	28.2	28.2	100%	91	58%	gi|667314766|XP_008585886.1
☐ hypothetical protein HMPREF1541_04550 [Cyphellophora europaea	28.2	28.2	91%	91	73%	gi|671157189|XP_008717117.1
☐ ATP-dependent protease ATP-binding subunit HslU [Psychromonas	28.2	28.2	66%	94	88%	gi|655482811|WP_028864616.1
☐ predicted protein [Capsaspora owczarzaki ATCC 30864]	28.2	28.2	66%	96	88%	gi|470297261|XP_004345571.1
☐ cotH protein [Clostridium sp. CAG:230]	28.2	28.2	100%	96	43%	gi|547728152|WP_022142301.1
☐ hypothetical protein VOLCADRAFT_95860 [Volvox carteri f. nagarie	28.2	28.2	75%	96	78%	gi|302846827|XP_002954949.1
☐ predicted protein [Capsaspora owczarzaki ATCC 30864]	28.2	28.2	66%	96	88%	gi|470297265|XP_004345572.1
☐ MULTISPECIES: hypothetical protein [Mycobacterium]	27.8	27.8	58%	118	100%	gi|499882067|WP_011562801.1
☐ hypothetical protein C922_01705 [Plasmodium inui San Antonio 1]	27.8	27.8	100%	122	67%	gi|672191245|XP_008815530.1
☐ putative daunorubicin C-13 ketoreductase [Colletotrichum sublineol	27.8	27.8	58%	127	100%	gi|640919754|KDN64268.1
☐ daunorubicin C-13 ketoreductase [Colletotrichum graminicola M1.00	27.8	27.8	58%	127	100%	gi|310798716|EFQ33609.1
☐ hypothetical protein IX49_03610 [Cellulophaga lytica]	27.8	27.8	66%	128	88%	gi|682032523|AIM59647.1
☐ LVIVD repeat-containing protein [Cellulophaga geojensis KL-A]	27.8	27.8	66%	128	88%	gi|584428234|EWH12917.1
☐ hypothetical protein SCHCODRAFT_104079 [Schizophyllum comm	27.8	27.8	83%	128	80%	gi|302698025|XP_003038691.1
☐ hypothetical protein [Enterococcus faecalis]	27.8	27.8	58%	130	100%	gi|488311279|WP_002380664.1
☐ predicted protein [Postia placenta Mad-698-R]	27.8	27.8	100%	130	75%	gi|242211098|XP_002471389.1
☐ envelope glycoprotein [Human immunodeficiency virus 1]	27.8	27.8	58%	131	100%	gi|328550401|AEB22053.1
☐ hypothetical protein KGM_12763 [Danaus plexippus]	27.8	27.8	75%	132	78%	gi|357601730|EHJ63136.1
☐ PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta c	27.4	27.4	91%	170	64%	gi|533120065|XP_005375468.1
☐ PREDICTED: C4b-binding protein beta chain [Jaculus jaculus]	27.4	27.4	91%	170	73%	gi|507559572|XP_004663509.1
☐ PREDICTED: peroxisome biogenesis factor 10 [Echinops telfairi]	27.4	27.4	91%	174	73%	gi|507657324|XP_004705535.1
☐ PREDICTED: uncharacterized protein LOC103849553 [Brassica rap	27.4	27.4	75%	176	80%	gi|685385017|XP_009124564.1
☐ PREDICTED: aminopeptidase Q [Callithrix jacchus]	27.4	27.4	75%	178	56%	gi|296193920|XP_002744734.1
☐ dynein heavy chain axonemal [Clonorchis sinensis]	27.4	27.4	66%	180	88%	gi|358339229|GAA47333.1
☐ hypothetical protein T265_13739 [Opisthorchis viverrini]	27.4	27.4	66%	180	88%	gi|684386665|XP_009168537.1
☐ hypothetical protein DFA_06522 [Dictyostelium fasciculatum]	26.9	26.9	83%	189	62%	gi|470268001|XP_004362223.1

☐	HNH endonuclease [Deinococcus gobiensis]	26.9	26.9	75%	223	78%	gi|504499146|WP_014686248.1
☐	HNH endonuclease [Deinococcus aquatilis]	26.9	26.9	75%	226	78%	gi|648607162|WP_026298913.1
☐	HNH endonuclease [Deinococcus sp. RL]	26.9	26.9	75%	227	78%	gi|656341992|KEF34954.1
☐	HNH endonuclease [Deinococcus murrayi]	26.9	26.9	75%	227	78%	gi|653254237|WP_027459639.1
☐	hypothetical protein [Ruminobacter sp. RM87]	26.9	26.9	66%	227	88%	gi|671608437|WP_031580001.1
☐	CG32297-PA [Cryptosporidium hominis TU502]	26.9	26.9	83%	235	53%	gi|67624775|XP_668670.1
☐	phosphoserine aminotransferase [Alistipes sp. CAG:435]	26.9	26.9	91%	235	73%	gi|547921208|WP_022323484.1
☐	phosphoserine aminotransferase [Alistipes sp. CAG:514]	26.9	26.9	91%	235	73%	gi|546330868|WP_021838129.1
☐	hypothetical protein [Cryptosporidium parvum Iowa II]	26.9	26.9	83%	238	53%	gi|66359168|XP_626762.1
☐	hypothetical protein DX03_09100 [Stenotrophomonas rhizophila]	26.9	26.9	75%	238	78%	gi|627789612|AHY58828.1
☐	dolichyl-phosphate-mannose--protein mannosyltransferase [Kibdel	26.9	26.9	66%	239	88%	gi|703217979|WP_033383461.1
☐	acyl-CoA synthetase [Nitrosomonas cryotolerans]	26.9	26.9	75%	240	64%	gi|655011745|WP_028460811.1
☐	PREDICTED: bile salt-activated lipase-like [Latimeria chalumnae]	26.9	26.9	75%	241	78%	gi|557007729|XP_006005124.1
☐	PREDICTED: LOW QUALITY PROTEIN: NLR family, pyrin domain	26.9	26.9	83%	242	70%	gi|512938701|XP_004921487.1
☐	single-stranded DNA-binding protein [Hawaiian green turtle herpesv	26.9	26.9	83%	242	70%	gi|53759079|AAU93328.1
☐	NACHT, LRR and PYD domains-containing protein 3 [Heterocephal	26.9	26.9	83%	242	70%	gi|351715200|EHB18119.1
☐	PREDICTED: LOW QUALITY PROTEIN: NLR family, pyrin domain	26.9	26.9	83%	242	70%	gi|513027226|XP_004921286.1
☐	F-UL29 protein [Chelonid herpesvirus 5]	26.9	26.9	83%	242	70%	gi|558852253|AHA93358.1
☐	UL29 [Fibropapilloma-associated turtle herpesvirus]	26.9	26.9	83%	242	70%	gi|52551097|AAU84533.1
☐	single-stranded DNA binding protein [Green turtle herpesvirus]	26.9	26.9	83%	242	70%	gi|34419905|AAQ67362.1
☐	serine/threonine kinase [Naegleria gruberi strain NEG-M]	26.9	26.9	91%	243	64%	gi|290996855|XP_002680997.1
☐	hypothetical protein YQE_11666 [Dendroctonus ponderosae]	26.9	26.9	91%	243	73%	gi|478251089|ENN71565.1
☐	hypothetical protein D910_10359 [Dendroctonus ponderosae]	26.9	26.9	91%	243	73%	gi|546683217|ERL93057.1
☐	PREDICTED: 1-phosphatidylinositol 4,5-bisphosphate phosphodies	26.9	26.9	75%	244	78%	gi|700428978|XP_009953149.1
☐	PREDICTED: 1-phosphatidylinositol 4,5-bisphosphate phosphodies	26.9	26.9	75%	244	78%	gi|700428976|XP_009953148.1
☐	DNA repair protein RadA [Aeromonas media]	26.5	26.5	100%	299	75%	gi|375813447|AFA84952.1
☐	DNA repair protein RadA [Aeromonas salmonicida]	26.5	26.5	100%	299	75%	gi|375813439|AFA84948.1

Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194373591|dbj|BAG56891.1| **Length:** 218 **Number of Matches:** 1

Range 1: 57 to 68 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.8 bits(98)	3e-04	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    KEWDNTTTECRL  12
            KEWDNTTTECRL
Sbjct  57   KEWDNTTTECRL  68
```

Related Information

Gene - associated gene details

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan troglodytes]

Sequence ID: gi|694891540|ref|XP_009439669.1| **Length:** 227 **Number of Matches:** 1

Range 1: 66 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.8 bits(98)	3e-04	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    KEWDNTTTECRL  12
```

Related Information

Gene - associated gene details

```
                 KEWDNTTTECRL
Sbjct  66   KEWDNTTTECRL  77
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan paniscus]

Sequence ID: gi|675771724|ref|XP_008974762.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 66 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.8 bits(98)	3e-04	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    KEWDNTTTECRL  12
            KEWDNTTTECRL
Sbjct  66   KEWDNTTTECRL  77
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sapiens]

Sequence ID: gi|530366462|ref|XP_005273312.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 66 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.8 bits(98)	3e-04	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    KEWDNTTTECRL  12
            KEWDNTTTECRL
Sbjct  66   KEWDNTTTECRL  77
```

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PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinopithecus roxellana]

Sequence ID: gi|724836382|ref|XP_010363947.1| **Length:** 251 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 66 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.8 bits(98)	3e-04	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    KEWDNTTTECRL  12
            KEWDNTTTECRL
Sbjct  66   KEWDNTTTECRL  77
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BTF8S851016

Your search parameters were adjusted to search for a short input sequence.

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C4BPB_KKTLFCDASKE_Mod

RID BTF8S851016 (Expires on 01-20 15:15 pm)

Query ID	lcl|92315	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	11		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

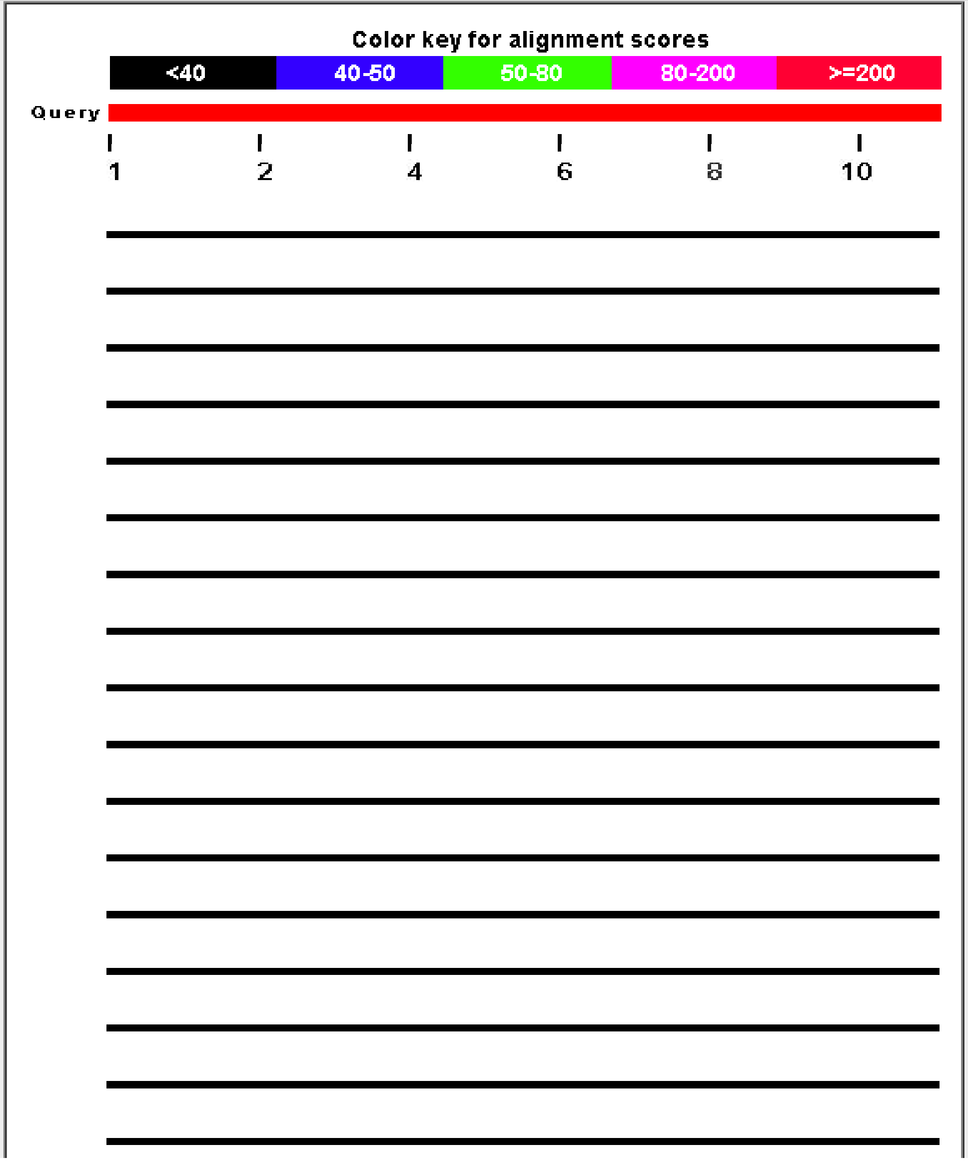
Graphic Summary

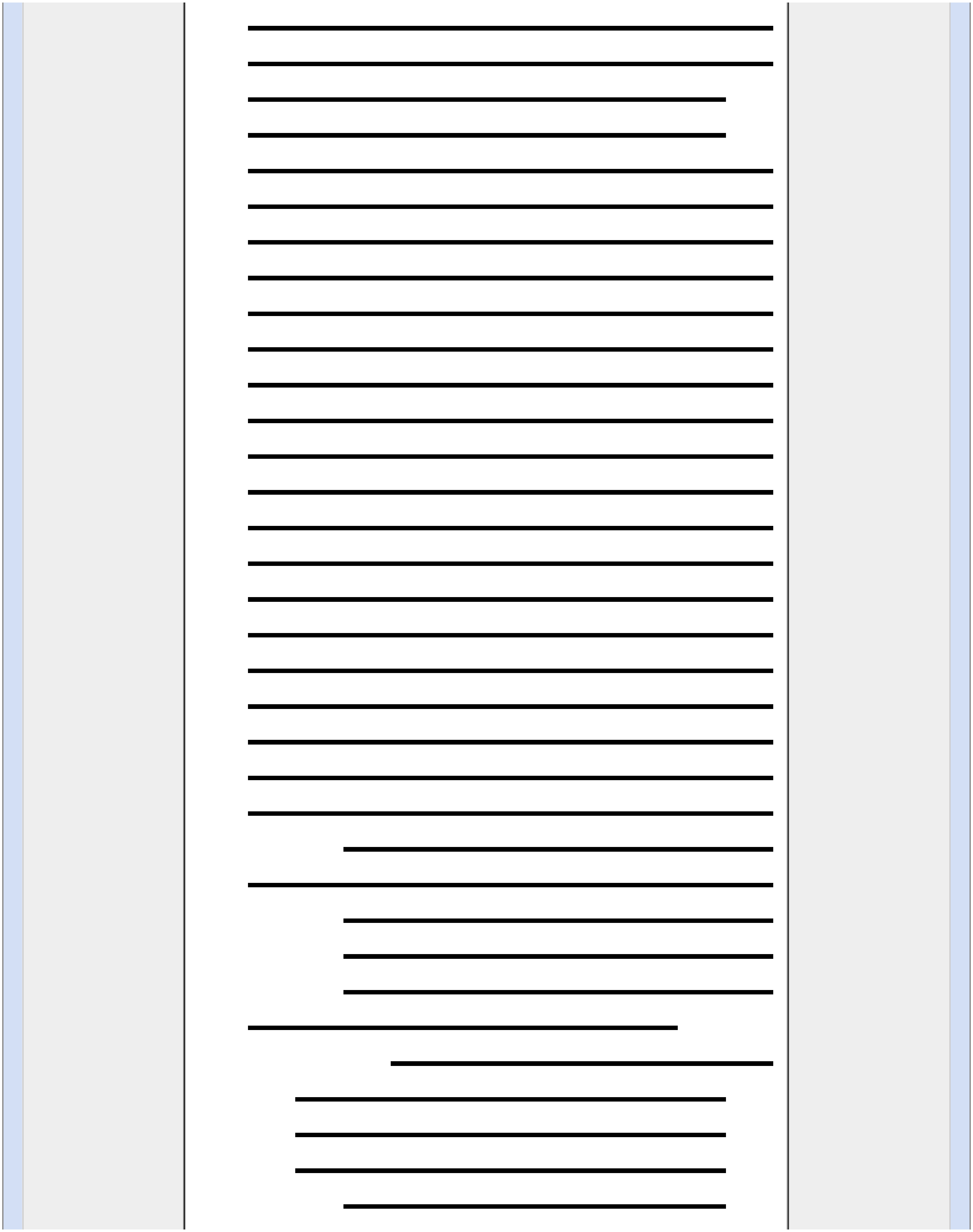
Show Conserved Domains

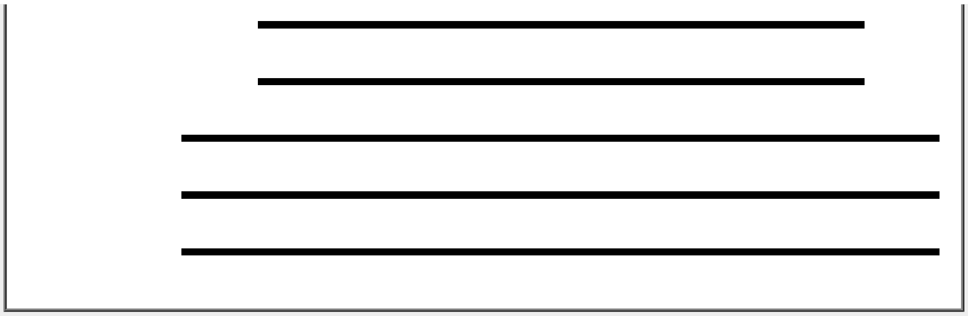
No putative conserved domains have been detected

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pong	35.4	35.4	100%	0.39	91%	gi|686700216|XP_009236698.1
☐	unnamed protein product [Homo sapiens]	35.4	35.4	100%	0.39	91%	gi|194373591|BAG56891.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan t	35.4	35.4	100%	0.39	91%	gi|694891540|XP_009439669.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan p	35.4	35.4	100%	0.39	91%	gi|675771724|XP_008974762.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Homo	35.4	35.4	100%	0.39	91%	gi|530366462|XP_005273312.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Rhino	35.4	35.4	100%	0.40	91%	gi|724836382|XP_010363947.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan t	35.4	35.4	100%	0.40	91%	gi|694891534|XP_009439665.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pong	35.4	35.4	100%	0.40	91%	gi|686700213|XP_009236694.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan p	35.4	35.4	100%	0.40	91%	gi|675771715|XP_008974759.1
☐	C4b-binding protein beta chain isoform 2 precursor [Homo sapi	35.4	35.4	100%	0.40	91%	gi|62912462|NP_001017364.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Rhino	35.4	35.4	100%	0.40	91%	gi|724836379|XP_010363946.1
☐	C4b-binding protein beta chain isoform 1 precursor [Homo sapi	35.4	35.4	100%	0.40	91%	gi|4502505|NP_000707.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan p	35.4	35.4	100%	0.40	91%	gi|397504761|XP_003822949.1
☐	PREDICTED: C4b-binding protein beta chain isoform 1 [Nomas	35.4	35.4	100%	0.40	91%	gi|332266848|XP_003282407.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pong	35.4	35.4	100%	0.40	91%	gi|297662141|XP_002809574.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan t	35.4	35.4	100%	0.40	91%	gi|114572288|XP_001166306.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Callitl	35.4	35.4	100%	0.40	91%	gi|675749407|XP_008983835.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Callitl	35.4	35.4	100%	0.40	91%	gi|296230632|XP_002760794.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	35.4	35.4	100%	0.40	91%	gi|471369765|XP_004375397.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Saimi	32.0	32.0	90%	5.2	90%	gi|725574024|XP_010339305.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Saimi	32.0	32.0	90%	5.2	90%	gi|403277664|XP_003930472.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Papio	31.6	31.6	100%	7.1	82%	gi|685519789|XP_009186662.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Maca	31.6	31.6	100%	7.1	82%	gi|544399939|XP_005540733.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Maca	31.6	31.6	100%	7.1	82%	gi|544399931|XP_005540729.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Papio	31.6	31.6	100%	7.1	82%	gi|685519785|XP_009186656.1
☐	hypothetical protein EGM_01442 [Macaca fascicularis]	31.6	31.6	100%	7.1	82%	gi|355745961|EHH50586.1
☐	hypothetical protein EGK_01712 [Macaca mulatta]	31.6	31.6	100%	7.1	82%	gi|355558818|EHH15598.1
☐	PREDICTED: c4b-binding protein beta chain isoform 3 [Macaca	31.6	31.6	100%	7.1	82%	gi|109018561|XP_001083216.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Maca	31.6	31.6	100%	7.2	82%	gi|544399929|XP_005540728.1

☐	PREDICTED: C4b-binding protein beta chain isoform X9 [Chlor	30.8	30.8	100%	13	82%	gi|635130917|XP_007986833.1
☐	PREDICTED: C4b-binding protein beta chain isoform X8 [Chlor	30.8	30.8	100%	13	82%	gi|635130915|XP_007986832.1
☐	PREDICTED: C4b-binding protein beta chain isoform X7 [Chlor	30.8	30.8	100%	13	82%	gi|635130913|XP_007986831.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Chlor	30.8	30.8	100%	14	82%	gi|635130911|XP_007986830.1
☐	PREDICTED: C4b-binding protein beta chain isoform X5 [Chlor	30.8	30.8	100%	14	82%	gi|635130907|XP_007986828.1
☐	PREDICTED: C4b-binding protein beta chain isoform X4 [Chlor	30.8	30.8	100%	14	82%	gi|635130905|XP_007986827.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Chlor	30.8	30.8	100%	14	82%	gi|635130903|XP_007986826.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Chlor	30.8	30.8	100%	14	82%	gi|635130901|XP_007986825.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Chlor	30.8	30.8	100%	14	82%	gi|635130899|XP_007986823.1
☐	PREDICTED: C4b-binding protein beta chain [Chrysochloris as	30.8	30.8	100%	14	82%	gi|586450676|XP_006834269.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Gale	29.5	29.5	100%	34	73%	gi|667314769|XP_008585888.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis davidii]	29.5	29.5	81%	34	89%	gi|584068188|XP_006754475.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Gale	29.5	29.5	100%	35	73%	gi|667314766|XP_008585886.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Myoti	29.5	29.5	81%	35	89%	gi|554587742|XP_005885272.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis lucifugus]	29.5	29.5	81%	35	89%	gi|558152655|XP_006094937.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Myoti	29.5	29.5	81%	35	89%	gi|554587740|XP_005885271.1
☐	PREDICTED: C4b-binding protein beta chain [Ornithorhynchus	29.1	29.1	81%	40	89%	gi|620984032|XP_007659774.1
☐	hypothetical protein DDB_G0277599 [Dictyostelium discoideum	29.1	29.1	72%	46	100%	gi|66817412|XP_642559.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	29.1	29.1	81%	47	89%	gi|470641603|XP_004325529.1
☐	PREDICTED: C4b-binding protein beta chain [Orcinus orca]	29.1	29.1	81%	48	89%	gi|466071254|XP_004282462.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	29.1	29.1	81%	48	89%	gi|594636425|XP_007171607.1
☐	hypothetical protein GLOINDRAFT_344233 [Rhizophagus irreg	28.6	28.6	72%	62	100%	gi|552935896|ESA19211.1
☐	hypothetical protein RirG_017690 [Rhizophagus irregularis DA	28.6	28.6	72%	67	100%	gi|595497640|EXX78132.1
☐	hypothetical protein [Pelagibaca bermudensis]	28.6	28.6	72%	68	100%	gi|495078167|WP_007802992.1
☐	type I restriction-modification system [Nonlabens ulvanivorans]	28.2	28.2	90%	81	90%	gi|674968931|GAK74476.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Tarsi	28.2	28.2	90%	89	80%	gi|640811969|XP_008062626.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Tarsi	28.2	28.2	90%	89	80%	gi|640811967|XP_008062625.1
☐	type I restriction endonuclease EcoprrI subunit M [Streptococcu	28.2	28.2	90%	90	90%	gi|493309607|WP_006267109.1
☐	type I restriction-modification system, M subunit [Clostridium ce	28.2	28.2	90%	92	90%	gi|491353670|WP_005211592.1
☐	type I restriction endonuclease [Methanococcus vannielii]	28.2	28.2	90%	92	90%	gi|500677016|WP_011971897.1
☐	restriction endonuclease EcoR124II subunit M [Streptococcus s	28.2	28.2	90%	92	90%	gi|726978673|WP_033583435.1
☐	type I restriction-modification system, M subunit [Streptococcus	28.2	28.2	90%	92	90%	gi|565833921|WP_023917515.1
☐	type I restriction-modification system DNA methylase [Streptoc	28.2	28.2	90%	92	90%	gi|490381372|WP_004260888.1
☐	restriction endonuclease EcoR124II subunit M [Streptococcus r	28.2	28.2	90%	92	90%	gi|727224511|WP_033685435.1
☐	type I restriction-modification system, M subunit [Streptococcus	28.2	28.2	90%	92	90%	gi|662336358|KEQ35031.1
☐	type I restriction endonuclease EcoR124II subunit M [Streptoco	28.2	28.2	90%	92	90%	gi|446069119|WP_000146974.1
☐	type I restriction endonuclease EcoR124II subunit M [Streptoco	28.2	28.2	90%	92	90%	gi|565866706|WP_023948474.1
☐	type I restriction endonuclease EcoR124II subunit M [Streptoco	28.2	28.2	90%	92	90%	gi|527094332|WP_020900754.1
☐	type I restriction-modification system, M subunit [Streptococcus	28.2	28.2	90%	92	90%	gi|497415663|WP_009729861.1
☐	type I restriction endonuclease EcoR124II subunit M [Streptoco	28.2	28.2	90%	92	90%	gi|446069118|WP_000146973.1
☐	type I restriction endonuclease EcoR124II subunit M [Streptoco	28.2	28.2	90%	92	90%	gi|490330481|WP_004219903.1
☐	type I restriction-modification system, M subunit [Leptotrichia sp	28.2	28.2	90%	92	90%	gi|545620192|WP_021743778.1
☐	Type I restriction-modification system DNA methylase [Streptoc	28.2	28.2	90%	92	90%	gi|566220061|ETI85613.1
☐	type I restriction enzyme M protein [Streptococcus constellatus]	28.2	28.2	90%	92	90%	gi|538448218|WP_020997674.1
☐	type I restriction-modification system, M subunit [Clostridium sp	28.2	28.2	90%	92	90%	gi|490136279|WP_004036639.1

☐	type I restriction endonuclease EcoR124II subunit M [Gemella l	28.2	28.2	90%	92	90%	gi|490383956|WP_004263464.1
☐	type I restriction-modification system methyltransferase subunit	28.2	28.2	90%	92	90%	gi|540781673|GAD44102.1
☐	hypothetical protein VITISV_026155 [Vitis vinifera]	27.8	27.8	81%	124	90%	gi|147841644|CAN75317.1
☐	hypothetical protein VITISV_006848 [Vitis vinifera]	27.8	27.8	81%	127	90%	gi|147840420|CAN66134.1
☐	hypothetical protein VITISV_026962 [Vitis vinifera]	27.8	27.8	81%	127	90%	gi|147853844|CAN83807.1
☐	hypothetical protein VITISV_040550 [Vitis vinifera]	27.8	47.1	81%	128	90%	gi|147844291|CAN80038.1
☐	AGE-1 [Caenorhabditis elegans]	27.8	27.8	100%	128	75%	gi|1850329|AAC47459.1
☐	Protein AGE-1 [Caenorhabditis elegans]	27.8	27.8	100%	128	75%	gi|392891813|NP_496462.2
☐	hypothetical protein VITISV_031525 [Vitis vinifera]	27.8	27.8	81%	129	90%	gi|147791708|CAN64017.1
☐	hypothetical protein VITISV_004551 [Vitis vinifera]	27.8	27.8	81%	129	90%	gi|147772713|CAN76071.1
☐	protease [Alkaliflexus imshenetskii]	26.9	26.9	100%	228	82%	gi|651362089|WP_026474439.1
☐	transcriptional regulator, AraC family [[Clostridium hathewayi]	26.5	26.5	81%	310	89%	gi|493824527|WP_006771995.1
☐	PREDICTED: uncharacterized protein LOC102701146 [Oryza l	26.5	26.5	72%	316	88%	gi|573922176|XP_006648673.1
☐	xylulose kinase [Borrelia persica]	26.5	26.5	63%	316	100%	gi|639480741|WP_024653493.1
☐	hypothetical protein [Verrucomicrobia bacterium SCGC AAA02	26.5	26.5	63%	317	100%	gi|654808487|WP_028261818.1
☐	PREDICTED: dimethylaniline monooxygenase [N-oxide-formin	26.5	26.5	90%	318	70%	gi|533169627|XP_005398381.1
☐	hypothetical protein [Pseudoalteromonas sp. ECSMB14103]	26.1	26.1	90%	348	70%	gi|743520309|WP_039037640.1
☐	N-6 DNA Methylase [Helicobacter pylori]	26.1	26.1	100%	395	71%	gi|545301951|WP_021581577.1
☐	hypothetical protein M514_28437 [Trichuris suis]	26.1	26.1	63%	399	100%	gi|669318666|KFD59385.1
☐	type I restriction enzyme M protein [Helicobacter pylori NY40]	26.1	26.1	100%	399	71%	gi|647551735|BAO98539.1
☐	hypothetical protein [butyrate-producing bacterium SSC/2]	26.1	26.1	72%	399	88%	gi|505343629|WP_015530731.1
☐	aTP-dependent RNA helicase DDX50 [Firmicutes bacterium C	26.1	26.1	72%	399	88%	gi|548030350|WP_022374198.1
☐	uncharacterized protein [Lachnospiraceae bacterium CAG:25]	26.1	26.1	72%	399	88%	gi|547473484|WP_022091944.1
☐	RNA helicase [Lachnospiraceae bacterium 5_1_63FAA]	26.1	26.1	72%	399	88%	gi|496559170|WP_009265245.1
☐	MULTISPECIES: RNA helicase [Clostridiales]	26.1	26.1	72%	402	88%	gi|495669709|WP_008394288.1
☐	damage-inducible protein CinA [Chryseobacterium gregarium]	26.1	26.1	63%	406	100%	gi|736757959|WP_034761535.1

Alignments

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pongo abelii]

Sequence ID: gi|686700216|ref|XP_009236698.1| **Length:** 202 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 48 to 58 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
35.4 bits(76)	0.39	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1   KKTLFCDASKE  11
           KKTLFC+ASKE
Sbjct  48  KKTLFCNASKE  58
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194373591|dbj|BAG56891.1| **Length:** 218 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 48 to 58 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
35.4 bits(76)	0.39	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1   KKTLFCDASKE  11
           KKTLFC+ASKE
Sbjct  48  KKTLFCNASKE  58
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan troglodytes]

Sequence ID: gi|694891540|ref|XP_009439669.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 57 to 67 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
35.4 bits(76)	0.39	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1   KKTLFCDASKE  11
           KKTLFC+ASKE
Sbjct  57  KKTLFCNASKE  67
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan paniscus]

Sequence ID: gi|675771724|ref|XP_008974762.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 57 to 67 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
35.4 bits(76)	0.39	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1   KKTLFCDASKE  11
           KKTLFC+ASKE
Sbjct  57  KKTLFCNASKE  67
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sapiens]

Sequence ID: gi|530366462|ref|XP_005273312.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 57 to 67 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
35.4 bits(76)	0.39	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1   KKTLFCDASKE  11
           KKTLFC+ASKE
Sbjct  57  KKTLFCNASKE  67
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BTFP757B013

Your search parameters were adjusted to search for a short input sequence.

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C4BPB_KKTLFCDASKEWDDTTTECRL_Mod

RID	BTFP757B013 (Expires on 01-20 15:22 pm)		
Query ID	lcl|73178	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	21	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

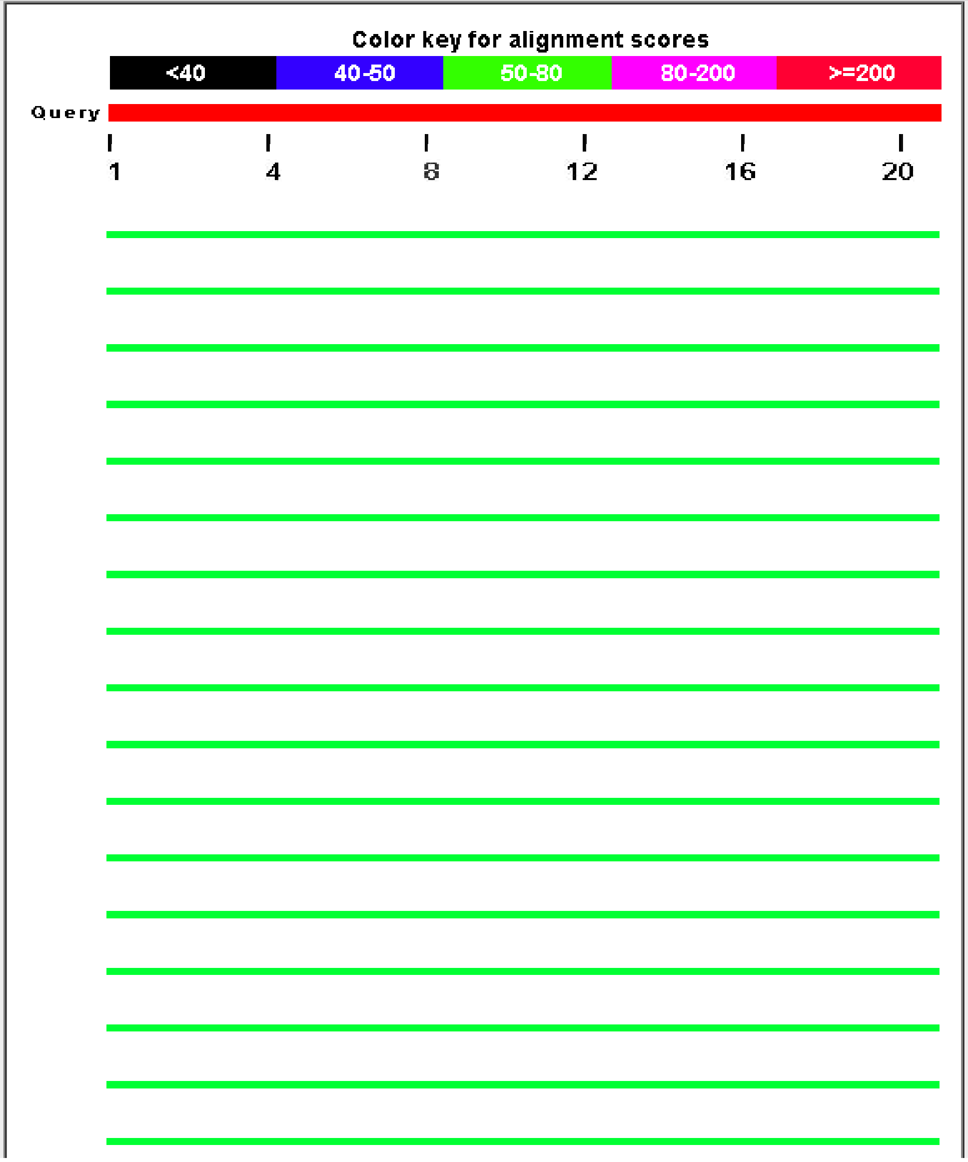
Graphic Summary

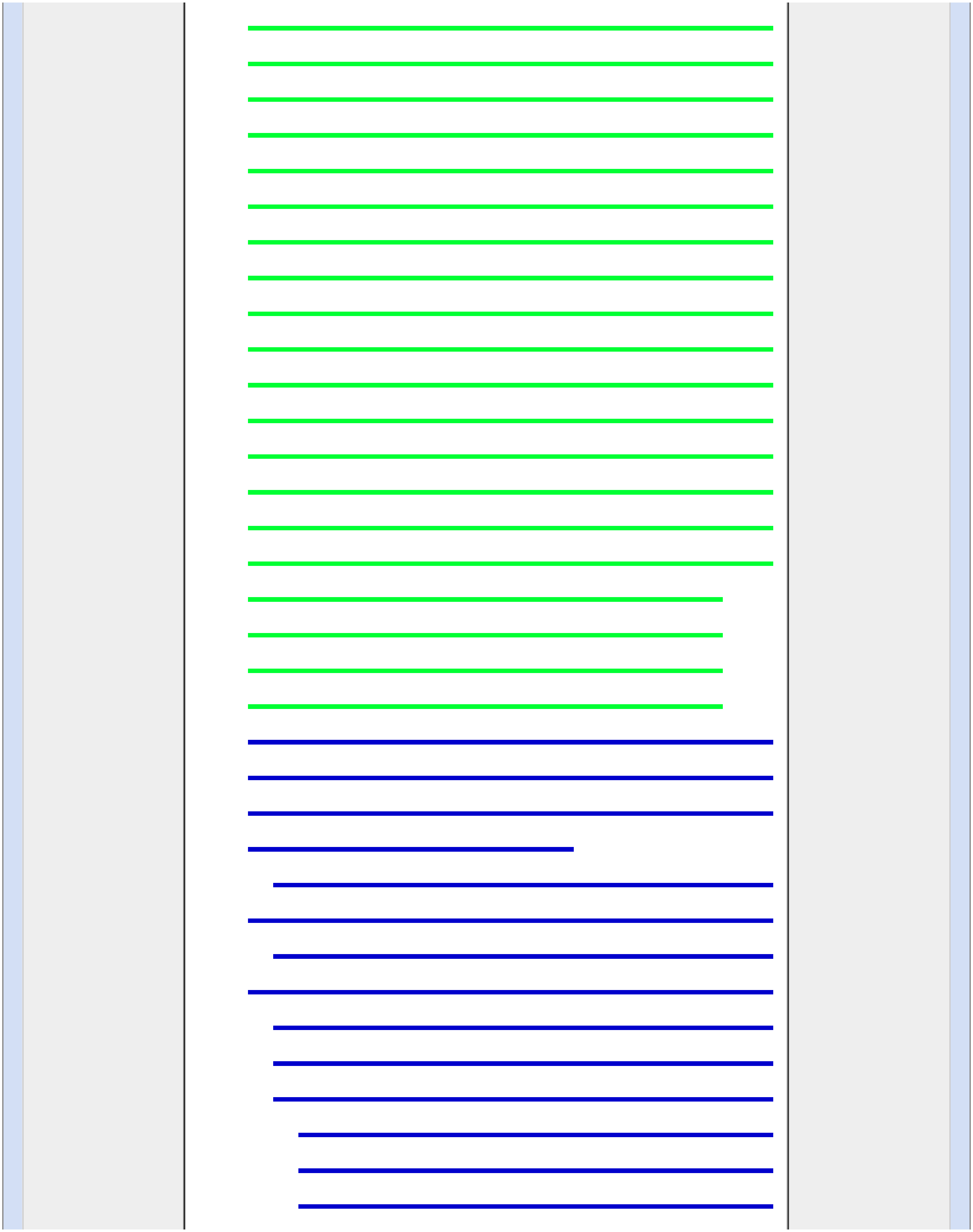
Show Conserved Domains

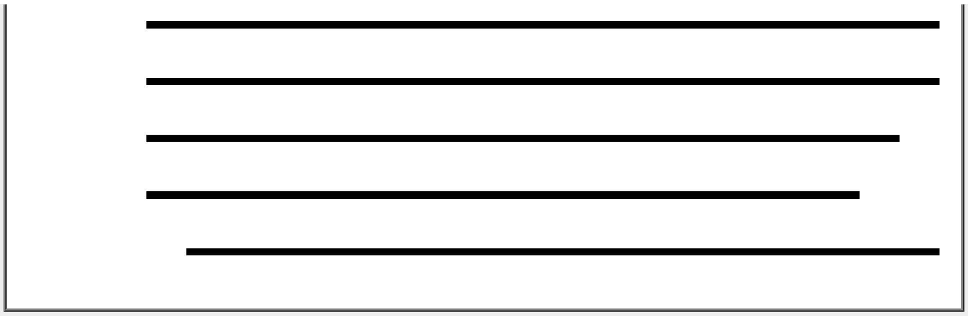
No putative conserved domains have been detected

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	68.1	68.1	100%	1e-11	90%	gi|194373591|BAG56891.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan t	68.1	68.1	100%	1e-11	90%	gi|694891540|XP_009439669.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan p	68.1	68.1	100%	1e-11	90%	gi|675771724|XP_008974762.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Homo	68.1	68.1	100%	1e-11	90%	gi|530366462|XP_005273312.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Rhino	68.1	68.1	100%	1e-11	90%	gi|724836382|XP_010363947.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan t	68.1	68.1	100%	1e-11	90%	gi|694891534|XP_009439665.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan p	68.1	68.1	100%	1e-11	90%	gi|675771715|XP_008974759.1
☐	C4b-binding protein beta chain isoform 2 precursor [Homo sapi	68.1	68.1	100%	1e-11	90%	gi|62912462|NP_001017364.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Rhino	68.1	68.1	100%	1e-11	90%	gi|724836379|XP_010363946.1
☐	C4b-binding protein beta chain isoform 1 precursor [Homo sapi	68.1	68.1	100%	1e-11	90%	gi|4502505|NP_000707.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan p	68.1	68.1	100%	1e-11	90%	gi|397504761|XP_003822949.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan t	68.1	68.1	100%	1e-11	90%	gi|114572288|XP_001166306.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pong	64.7	64.7	100%	2e-10	86%	gi|686700216|XP_009236698.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pong	64.7	64.7	100%	2e-10	86%	gi|686700213|XP_009236694.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pong	64.7	64.7	100%	2e-10	86%	gi|297662141|XP_002809574.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Papio	64.3	64.3	100%	3e-10	86%	gi|685519789|XP_009186662.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Maca	64.3	64.3	100%	3e-10	86%	gi|544399939|XP_005540733.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Maca	64.3	64.3	100%	3e-10	86%	gi|544399931|XP_005540729.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Papio	64.3	64.3	100%	3e-10	86%	gi|685519785|XP_009186656.1
☐	hypothetical protein EGM_01442 [Macaca fascicularis]	64.3	64.3	100%	3e-10	86%	gi|355745961|EHH50586.1
☐	hypothetical protein EGK_01712 [Macaca mulatta]	64.3	64.3	100%	3e-10	86%	gi|355558818|EHH15598.1
☐	PREDICTED: c4b-binding protein beta chain isoform 3 [Macaca	64.3	64.3	100%	3e-10	86%	gi|109018561|XP_001083216.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Maca	64.3	64.3	100%	3e-10	86%	gi|544399929|XP_005540728.1
☐	PREDICTED: C4b-binding protein beta chain isoform 1 [Nomas	63.8	63.8	100%	4e-10	86%	gi|332266848|XP_003282407.1
☐	PREDICTED: C4b-binding protein beta chain isoform X9 [Chlor	63.4	63.4	100%	5e-10	86%	gi|635130917|XP_007986833.1
☐	PREDICTED: C4b-binding protein beta chain isoform X8 [Chlor	63.4	63.4	100%	5e-10	86%	gi|635130915|XP_007986832.1
☐	PREDICTED: C4b-binding protein beta chain isoform X7 [Chlor	63.4	63.4	100%	5e-10	86%	gi|635130913|XP_007986831.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Chlor	63.4	63.4	100%	5e-10	86%	gi|635130911|XP_007986830.1
☐	PREDICTED: C4b-binding protein beta chain isoform X5 [Chlor	63.4	63.4	100%	5e-10	86%	gi|635130907|XP_007986828.1

☐	PREDICTED: C4b-binding protein beta chain isoform X4 [Chlor	63.4	63.4	100%	5e-10	86%	gi|635130905|XP_007986827.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Chlor	63.4	63.4	100%	5e-10	86%	gi|635130903|XP_007986826.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Chlor	63.4	63.4	100%	5e-10	86%	gi|635130901|XP_007986825.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Chlor	63.4	63.4	100%	5e-10	86%	gi|635130899|XP_007986823.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Callitl	61.7	61.7	90%	2e-09	89%	gi|675749407|XP_008983835.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Callitl	61.7	61.7	90%	2e-09	89%	gi|296230632|XP_002760794.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Saim	56.6	56.6	90%	1e-07	84%	gi|725574024|XP_010339305.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Saim	56.6	56.6	90%	1e-07	84%	gi|403277664|XP_003930472.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Galec	49.0	49.0	100%	3e-05	67%	gi|667314769|XP_008585888.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Galec	49.0	49.0	100%	4e-05	67%	gi|667314766|XP_008585886.1
☐	PREDICTED: C4b-binding protein beta chain [Chrysochloris as	46.0	46.0	100%	4e-04	71%	gi|586450676|XP_006834269.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	44.3	44.3	61%	0.001	92%	gi|471369765|XP_004375397.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	42.6	42.6	95%	0.004	65%	gi|594636425|XP_007171607.1
☐	PREDICTED: C4b-binding protein beta chain [Ictidomys tridece	42.2	42.2	100%	0.006	67%	gi|532087633|XP_005329528.1
☐	PREDICTED: C4b-binding protein beta chain [Nannospalax gal	42.2	42.2	95%	0.006	71%	gi|674096417|XP_008821570.1
☐	PREDICTED: C4b-binding protein beta chain [Cavia porcellus]	41.4	41.4	100%	0.011	62%	gi|348577871|XP_003474707.1
☐	PREDICTED: C4b-binding protein beta chain [Sus scrofa]	40.9	40.9	95%	0.016	60%	gi|311265148|XP_003130503.1
☐	PREDICTED: C4b-binding protein beta chain [Otolemur garnett	40.5	40.5	95%	0.021	65%	gi|395838946|XP_003792365.1
☐	PREDICTED: C4b-binding protein beta chain [Orcinus orca]	40.1	40.1	95%	0.029	60%	gi|466071254|XP_004282462.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Myoti	40.1	40.1	90%	0.029	68%	gi|554587742|XP_005885272.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis lucifugus]	40.1	40.1	90%	0.029	68%	gi|558152655|XP_006094937.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Myoti	40.1	40.1	90%	0.029	68%	gi|554587740|XP_005885271.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Tarsi	39.2	39.2	95%	0.055	60%	gi|640811969|XP_008062626.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Tarsi	39.2	39.2	95%	0.055	60%	gi|640811967|XP_008062625.1
☐	PREDICTED: C4b-binding protein beta chain [Ceratotherium si	38.8	38.8	90%	0.075	63%	gi|478501878|XP_004425250.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	38.0	38.0	85%	0.14	61%	gi|470641603|XP_004325529.1
☐	PREDICTED: C4b-binding protein beta chain [Eptesicus fuscus	36.3	36.3	90%	0.48	63%	gi|641725104|XP_008152491.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis davidii]	35.8	35.8	52%	0.65	82%	gi|584068188|XP_006754475.1
☐	PREDICTED: C4b-binding protein beta chain [Jaculus jaculus]	35.8	35.8	76%	0.66	69%	gi|507559572|XP_004663509.1
☐	PREDICTED: C4b-binding protein beta chain [Elephantulus edw	35.4	35.4	85%	0.90	61%	gi|585666900|XP_006888062.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Came	35.0	35.0	85%	1.2	56%	gi|743734558|XP_010961541.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Came	35.0	35.0	85%	1.2	56%	gi|743734556|XP_010961540.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	35.0	35.0	85%	1.2	56%	gi|560935168|XP_006193413.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	34.6	34.6	71%	1.7	67%	gi|533120065|XP_005375468.1
☐	PREDICTED: C4b-binding protein beta chain [Mustela putorius	34.1	34.1	95%	2.3	60%	gi|511871202|XP_004756233.1
☐	PREDICTED: C4b-binding protein beta chain [Ornithorhynchus	33.7	33.7	61%	2.7	77%	gi|620984032|XP_007659774.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	32.5	32.5	85%	8.1	56%	gi|560986663|XP_006215518.1
☐	Piso0_002582 [Millerozyma farinosa CBS 7064]	32.0	32.0	71%	11	67%	gi|448103382|XP_004200022.1
☐	conserved putative membrane protein [Melbournevirus]	32.0	32.0	61%	11	69%	gi|701447374|YP_009094746.1
☐	membrane protein [Cannes 8 virus]	32.0	32.0	61%	11	69%	gi|539398800|AGV01635.1
☐	polyphosphate kinase [Burkholderia sp. MP-1]	31.6	31.6	61%	15	46%	gi|737535990|WP_035509712.1
☐	glycogen branching protein [Halothece sp. PCC 7418]	31.6	31.6	76%	16	55%	gi|505038850|WP_015225952.1
☐	PREDICTED: C4b-binding protein beta chain [Canis lupus fami	31.2	31.2	61%	21	69%	gi|73960685|XP_851611.1
☐	hypothetical protein [Clostridium sp. CAG:62]	31.2	31.2	38%	22	100%	gi|548057742|WP_022376409.1
☐	C4b-binding protein beta chain [Heterocephalus glaber]	30.8	30.8	100%	29	52%	gi|351708103|EHB11022.1

☐	PREDICTED: C4b-binding protein beta chain [Heterocephalus	30.8	30.8	100%	29	52%	gi|512892965|XP_004897416.1
☐	PREDICTED: synaptonemal complex protein 2 [Ochotona princ	30.8	30.8	85%	30	55%	gi|504147512|XP_004586169.1
☐	hypothetical protein [Vibrio nigripulchritudo]	30.3	30.3	47%	39	70%	gi|740359636|WP_038195698.1
☐	hypothetical protein [Vibrio nigripulchritudo]	30.3	30.3	47%	39	70%	gi|740309755|WP_038147115.1
☐	putative Fimh-like protein [Vibrio nigripulchritudo]	30.3	30.3	47%	40	70%	gi|550352361|WP_022612127.1
☐	putative Fimh-like protein [Vibrio nigripulchritudo]	30.3	30.3	47%	40	70%	gi|550281458|WP_022607838.1
☐	hypothetical protein VINI7043_08940 [Vibrio nigripulchritudo A	30.3	30.3	47%	40	70%	gi|342820393|EGU55216.1
☐	PREDICTED: C4b-binding protein beta chain [Leptonychotes w	30.3	30.3	57%	40	67%	gi|585156269|XP_006730462.1
☐	transaldolase [Oribacterium sp. P6A1]	29.9	29.9	66%	56	64%	gi|738716700|WP_036611113.1
☐	transaldolase [Lachnospiraceae bacterium JC7]	29.9	29.9	66%	56	64%	gi|571148921|ETP72518.1
☐	PREDICTED: fibroin heavy chain-like [Callithrix jacchus]	29.9	50.1	76%	56	83%	gi|675768476|XP_008987859.1
☐	C4b-binding protein beta chain precursor [Rattus norvegicus]	29.9	29.9	90%	56	60%	gi|62198215|NP_058691.2
☐	RIFIN [Plasmodium falciparum]	29.9	29.9	52%	56	73%	gi|82394380|ABB72313.1
☐	RIFIN [Plasmodium falciparum]	29.9	29.9	52%	56	73%	gi|82394444|ABB72335.1
☐	hypothetical protein PFBG_00014 [Plasmodium falciparum 7G	29.9	29.9	52%	56	73%	gi|579134248|EUR82669.1
☐	hypothetical protein PFNF135_02825 [Plasmodium falciparum	29.9	29.9	57%	56	67%	gi|574981166|ETW42931.1
☐	protoporphyrin IX magnesium-chelatase [Stanieria cyanosphae	29.9	29.9	61%	57	67%	gi|505006979|WP_015194081.1
☐	hypothetical protein [Fimbriimonas ginsengisoli]	29.9	29.9	42%	57	89%	gi|740689768|WP_038475057.1
☐	glutamate synthase large subunit [Lentisphaera araneosa]	29.9	29.9	52%	58	64%	gi|494487169|WP_007276642.1
☐	hypothetical protein DFA_06522 [Dictyostelium fasciculatum]	29.5	29.5	80%	70	50%	gi|470268001|XP_004362223.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	29.5	29.5	71%	77	63%	gi|338224254|AEI88022.1
☐	hypothetical protein [Plasmodium knowlesi strain H]	29.5	29.5	61%	77	69%	gi|221054814|XP_002258546.1
☐	probable subtilisin-like serine protease [Claviceps purpurea 20.	29.5	29.5	71%	77	59%	gi|399164244|CCE34824.1
☐	RecName: Full=C4b-binding protein beta chain; Flags: Precurs	29.5	29.5	90%	78	60%	gi|2493794|Q63515.1
☐	arginyl-tRNA synthetase [Helicobacter apodemus]	29.5	29.5	66%	78	64%	gi|736540679|WP_034555246.1
☐	elongation factor Ts [Helicobacter pylori]	29.5	29.5	71%	78	67%	gi|445936521|WP_000014376.1

Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194373591|dbj|BAG56891.1| **Length:** 218 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 48 to 68 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	1e-11	19/21(90%)	21/21(100%)	0/21(0%)

```
Query  1   KKTLFCDASKEWDDTTTECRL  21
           KKTLFC+ASKEWD+TTTECRL
Sbjct  48  KKTLFCNASKEWDNTTTECRL  68
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan troglodytes]

Sequence ID: gi|694891540|ref|XP_009439669.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 57 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	1e-11	19/21(90%)	21/21(100%)	0/21(0%)

```
Query  1    KKTLFCDASKEWDDTTTECRL  21
            KKTLFC+ASKEWD+TTTECRL
Sbjct  57   KKTLFCNASKEWDNTTTECRL  77
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan paniscus]

Sequence ID: gi|675771724|ref|XP_008974762.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 57 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	1e-11	19/21(90%)	21/21(100%)	0/21(0%)

```
Query  1    KKTLFCDASKEWDDTTTECRL  21
            KKTLFC+ASKEWD+TTTECRL
Sbjct  57   KKTLFCNASKEWDNTTTECRL  77
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sapiens]

Sequence ID: gi|530366462|ref|XP_005273312.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 57 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	1e-11	19/21(90%)	21/21(100%)	0/21(0%)

```
Query  1    KKTLFCDASKEWDDTTTECRL  21
            KKTLFC+ASKEWD+TTTECRL
Sbjct  57   KKTLFCNASKEWDNTTTECRL  77
```

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PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinopithecus roxellana]

Sequence ID: gi|724836382|ref|XP_010363947.1| **Length:** 251 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 57 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	1e-11	19/21(90%)	21/21(100%)	0/21(0%)

```
Query  1    KKTLFCDASKEWDDTTTECRL  21
            KKTLFC+ASKEWD+TTTECRL
Sbjct  57   KKTLFCNASKEWDNTTTECRL  77
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - B92AVCHP01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

C4BPB_KKTLFCNASKE_NonMod

RID B92AVCHP01R (Expires on 01-14 09:56 am)

Query ID lcl|229493
Description None
Molecule type amino acid
Query Length 11

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

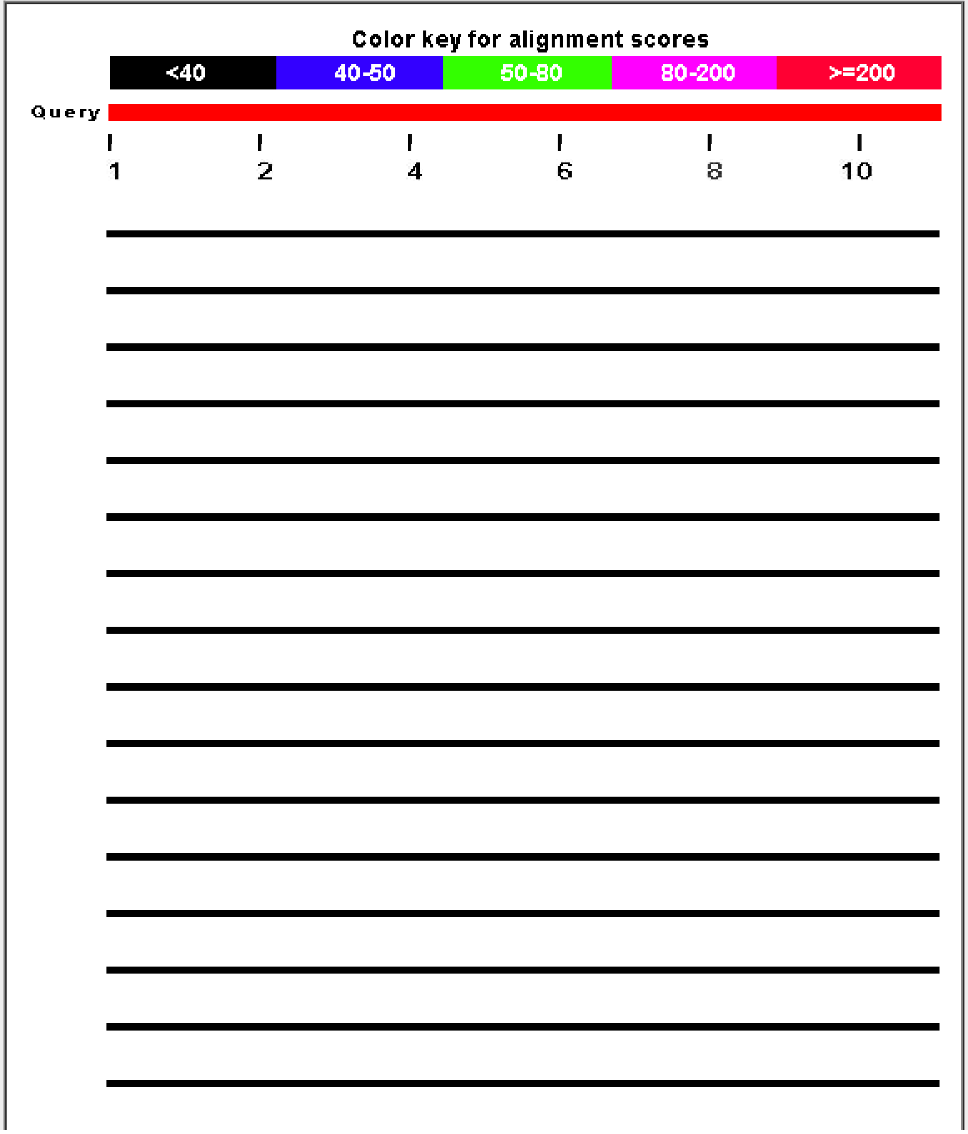
Graphic Summary

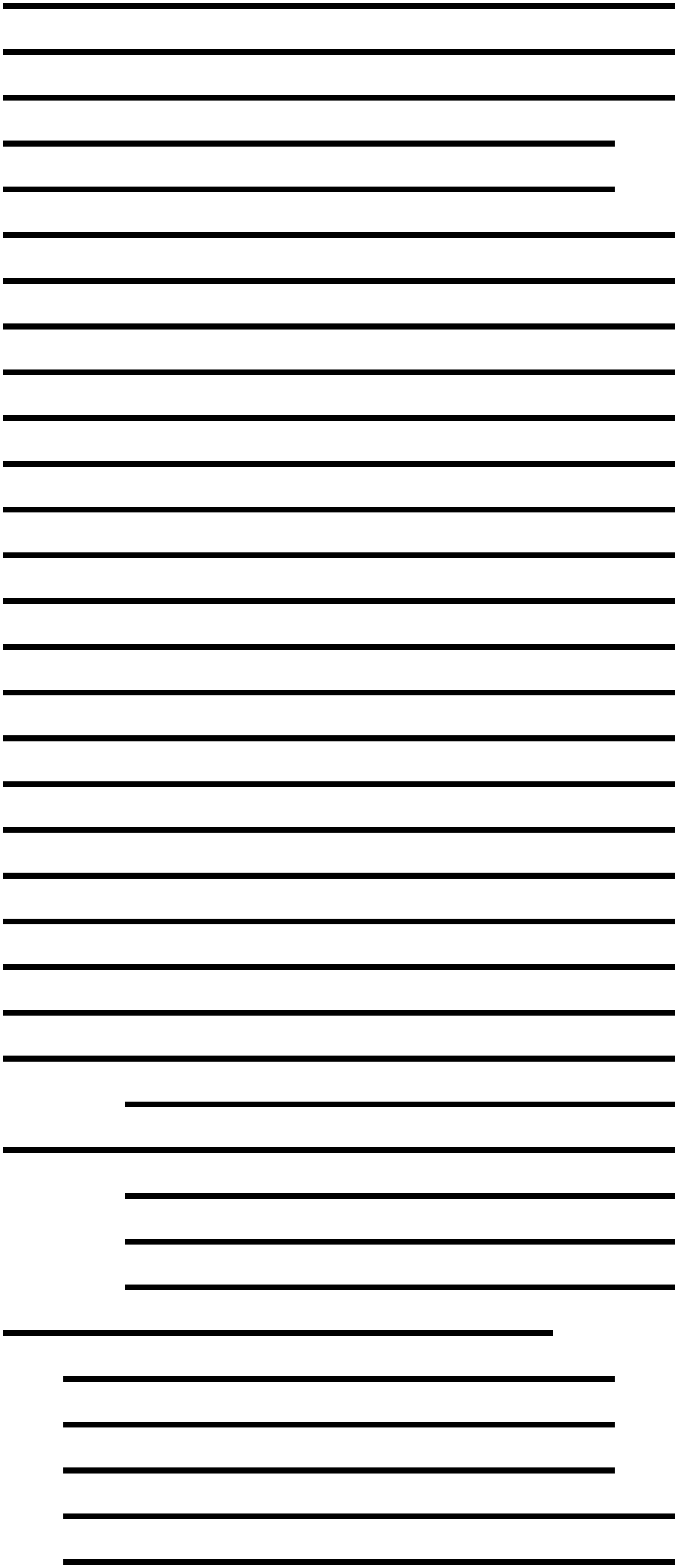
Show Conserved Domains

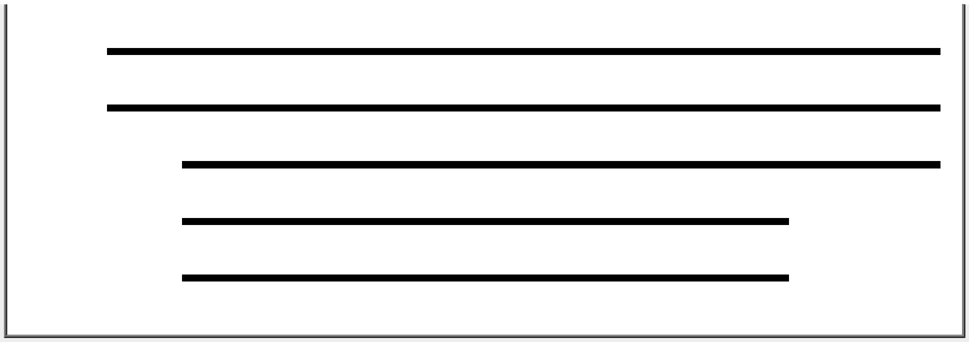
No putative conserved domains have been detected

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pongo ab	38.0	38.0	100%	0.052	100%	gi|686700216|XP_009236698.1
☐	unnamed protein product [Homo sapiens]	38.0	38.0	100%	0.052	100%	gi|194373591|BAG56891.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan trogl	38.0	38.0	100%	0.053	100%	gi|694891540|XP_009439669.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan panis	38.0	38.0	100%	0.053	100%	gi|675771724|XP_008974762.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sa	38.0	38.0	100%	0.053	100%	gi|530366462|XP_005273312.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinopith	38.0	38.0	100%	0.054	100%	gi|724836382|XP_010363947.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan trogl	38.0	38.0	100%	0.054	100%	gi|694891534|XP_009439665.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pongo ab	38.0	38.0	100%	0.054	100%	gi|686700213|XP_009236694.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan panis	38.0	38.0	100%	0.054	100%	gi|675771715|XP_008974759.1
☐	C4b-binding protein beta chain isoform 2 precursor [Homo sapiens]	38.0	38.0	100%	0.054	100%	gi|62912462|NP_001017364.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Rhinopith	38.0	38.0	100%	0.054	100%	gi|724836379|XP_010363946.1
☐	C4b-binding protein beta chain isoform 1 precursor [Homo sapiens]	38.0	38.0	100%	0.054	100%	gi|4502505|NP_000707.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan panis	38.0	38.0	100%	0.054	100%	gi|397504761|XP_003822949.1
☐	PREDICTED: C4b-binding protein beta chain isoform 1 [Nomascus	38.0	38.0	100%	0.054	100%	gi|332266848|XP_003282407.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pongo ab	38.0	38.0	100%	0.054	100%	gi|297662141|XP_002809574.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan trogl	38.0	38.0	100%	0.054	100%	gi|114572288|XP_001166306.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Callithrix	38.0	38.0	100%	0.054	100%	gi|675749407|XP_008983835.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Callithrix	38.0	38.0	100%	0.054	100%	gi|296230632|XP_002760794.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	38.0	38.0	100%	0.054	100%	gi|471369765|XP_004375397.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Saimiri b	34.6	34.6	90%	0.72	100%	gi|725574024|XP_010339305.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Saimiri b	34.6	34.6	90%	0.72	100%	gi|403277664|XP_003930472.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Papio an	34.1	34.1	100%	0.99	91%	gi|685519789|XP_009186662.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Macaca f	34.1	34.1	100%	0.99	91%	gi|544399939|XP_005540733.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Macaca f	34.1	34.1	100%	1.00	91%	gi|544399931|XP_005540729.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Papio an	34.1	34.1	100%	1.00	91%	gi|685519785|XP_009186656.1
☐	hypothetical protein EGM_01442 [Macaca fascicularis]	34.1	34.1	100%	1.00	91%	gi|355745961|EHH50586.1
☐	hypothetical protein EGK_01712 [Macaca mulatta]	34.1	34.1	100%	1.00	91%	gi|355558818|EHH15598.1
☐	PREDICTED: c4b-binding protein beta chain isoform 3 [Macaca mu	34.1	34.1	100%	1.00	91%	gi|109018561|XP_001083216.1
☐							

	PREDICTED: C4b-binding protein beta chain isoform X1 [Macaca fa	34.1	34.1	100%	1.0	91%	gi|544399929|XP_005540728.1
☐	PREDICTED: C4b-binding protein beta chain isoform X9 [Chlorocel	33.3	33.3	100%	1.8	91%	gi|635130917|XP_007986833.1
☐	PREDICTED: C4b-binding protein beta chain isoform X8 [Chlorocel	33.3	33.3	100%	1.9	91%	gi|635130915|XP_007986832.1
☐	PREDICTED: C4b-binding protein beta chain isoform X7 [Chlorocel	33.3	33.3	100%	1.9	91%	gi|635130913|XP_007986831.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Chlorocel	33.3	33.3	100%	1.9	91%	gi|635130911|XP_007986830.1
☐	PREDICTED: C4b-binding protein beta chain isoform X5 [Chlorocel	33.3	33.3	100%	1.9	91%	gi|635130907|XP_007986828.1
☐	PREDICTED: C4b-binding protein beta chain isoform X4 [Chlorocel	33.3	33.3	100%	1.9	91%	gi|635130905|XP_007986827.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Chlorocel	33.3	33.3	100%	1.9	91%	gi|635130903|XP_007986826.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Chlorocel	33.3	33.3	100%	1.9	91%	gi|635130901|XP_007986825.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Chlorocel	33.3	33.3	100%	1.9	91%	gi|635130899|XP_007986823.1
☐	PREDICTED: C4b-binding protein beta chain [Chrysochloris asiatic	33.3	33.3	100%	1.9	91%	gi|586450676|XP_006834269.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Galeopter	32.0	32.0	100%	4.8	82%	gi|667314769|XP_008585888.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis davidii]	32.0	32.0	81%	4.8	100%	gi|584068188|XP_006754475.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Galeopter	32.0	32.0	100%	4.9	82%	gi|667314766|XP_008585886.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Myotis bra	32.0	32.0	81%	4.9	100%	gi|554587742|XP_005885272.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis lucifugus]	32.0	32.0	81%	4.9	100%	gi|558152655|XP_006094937.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Myotis bra	32.0	32.0	81%	4.9	100%	gi|554587740|XP_005885271.1
☐	PREDICTED: C4b-binding protein beta chain [Ornithorhynchus ana	31.6	31.6	81%	5.4	100%	gi|620984032|XP_007659774.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	31.6	31.6	81%	6.7	100%	gi|470641603|XP_004325529.1
☐	PREDICTED: C4b-binding protein beta chain [Orcinus orca]	31.6	31.6	81%	6.8	100%	gi|466071254|XP_004282462.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	31.6	31.6	81%	6.8	100%	gi|594636425|XP_007171607.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Tarsius sy	30.8	30.8	90%	13	90%	gi|640811969|XP_008062626.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Tarsius sy	30.8	30.8	90%	13	90%	gi|640811967|XP_008062625.1
☐	AGE-1 [Caenorhabditis elegans]	30.3	30.3	100%	19	83%	gi|1850329|AAC47459.1
☐	Protein AGE-1 [Caenorhabditis elegans]	30.3	30.3	100%	19	83%	gi|392891813|NP_496462.2
☐	PREDICTED: dimethylaniline monooxygenase [N-oxide-forming] 5-	29.1	29.1	90%	47	80%	gi|533169627|XP_005398381.1
☐	PREDICTED: C4b-binding protein beta chain [Mustela putorius furo	28.6	28.6	72%	62	100%	gi|511871202|XP_004756233.1
☐	PREDICTED: C4b-binding protein beta chain [Ceratotherium simum	28.6	28.6	72%	62	100%	gi|478501878|XP_004425250.1
☐	PREDICTED: C4b-binding protein beta chain [Sus scrofa]	28.2	28.2	90%	84	80%	gi|311265148|XP_003130503.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	28.2	28.2	81%	85	89%	gi|560935168|XP_006193413.1
☐	PREDICTED: ubiquitin carboxyl-terminal hydrolase 16-like [Ciona ir	28.2	28.2	100%	88	73%	gi|699248632|XP_002128614.3
☐	hypothetical protein [Lactobacillus sp. ASF360]	28.2	28.2	90%	89	90%	gi|490145848|WP_004046179.1
☐	PREDICTED: C4b-binding protein beta chain [Canis lupus familiaris	27.4	27.4	81%	157	89%	gi|73960685|XP_851611.1
☐	PREDICTED: C4b-binding protein beta chain [Eptesicus fuscus]	27.4	27.4	81%	157	89%	gi|641725104|XP_008152491.1
☐	PREDICTED: C4b-binding protein beta chain [Otolemur garnettii]	27.4	27.4	90%	157	80%	gi|395838946|XP_003792365.1
☐	PREDICTED: golgin subfamily A member 4-like [Merops nubicus]	27.4	27.4	100%	160	73%	gi|675629007|XP_008942969.1
☐	Inhibitor of growth protein 3 [Camponotus floridanus]	27.4	27.4	81%	161	89%	gi|307175393|EFN65410.1
☐	hypothetical protein DDB_G0277599 [Dictyostelium discoideum AX	26.5	26.5	72%	285	88%	gi|66817412|XP_642559.1
☐	PREDICTED: C4b-binding protein beta chain [Elephantulus edward	26.5	26.5	72%	291	88%	gi|585666900|XP_006888062.1
☐	PREDICTED: C4b-binding protein beta chain [Leptonychotes wedd	26.5	26.5	90%	292	80%	gi|585156269|XP_006730462.1
☐	tyrosyl-tRNA synthetase [Onion yellows phytoplasma]	26.5	46.7	90%	299	70%	gi|499474180|WP_011160820.1
☐	hypothetical protein JAAARDRAFT_162852 [Jaapia argillacea MUC	26.5	26.5	63%	304	100%	gi|646387489|KDQ52424.1
☐	translation initiation factor eIF-3b [Gloeophyllum trabeum ATCC 11	26.5	26.5	63%	304	100%	gi|630343543|XP_007861072.1
☐	leucine rich repeat family protein [Stylonychia lemnae]	26.5	26.5	72%	306	88%	gi|678318019|CDW85492.1
☐	hypothetical protein [Neisseria sicca]	26.1	26.1	63%	310	100%	gi|489858884|WP_003762538.1

☐	hypothetical protein [Neisseria sicca]	26.1	26.1	63%	310	100%	gi|489858305|WP_003761962.1
☐	hypothetical protein [Prevotella nigrescens]	25.7	25.7	63%	335	100%	gi|490496588|WP_004362758.1
☐	hypothetical protein GLOINDRAFT_344233 [Rhizophagus irregulari	26.1	26.1	72%	382	88%	gi|552935896|ESA19211.1
☐	hypothetical protein [Prevotella disiens]	25.7	25.7	63%	395	100%	gi|545429973|WP_021668265.1
☐	hypothetical protein RirG_017690 [Rhizophagus irregularis DAOM 1	26.1	26.1	72%	408	88%	gi|595497640|EXX78132.1
☐	hypothetical protein [Asaia astilbes]	26.1	26.1	72%	409	88%	gi|647534967|WP_025824557.1
☐	hypothetical protein [Pelagibaca bermudensis]	26.1	26.1	72%	409	88%	gi|495078167|WP_007802992.1
☐	CBN-NDG-4 protein [Caenorhabditis brenneri]	26.1	26.1	63%	412	100%	gi|341896364|EGT52299.1
☐	Protein NDG-4, isoform b [Caenorhabditis elegans]	26.1	26.1	63%	412	100%	gi|71987048|NP_001022619.1
☐	Protein NDG-4, isoform a [Caenorhabditis elegans]	26.1	26.1	63%	412	100%	gi|71987043|NP_001022618.1
☐	Piso0_005440 [Millerozyma farinosa CBS 7064]	26.1	26.1	72%	417	88%	gi|448081536|XP_004194913.1
☐	type I restriction-modification system [Nonlabens ulvanivorans]	25.7	25.7	90%	506	80%	gi|674968931|GAK74476.1
☐	Zn-dependent hydrolase [Helicobacter bilis]	25.7	25.7	90%	536	70%	gi|696176423|KGL20850.1
☐	DNA helicase [Microscilla marina]	25.7	25.7	72%	540	88%	gi|488785593|WP_002698000.1
☐	PREDICTED: uncharacterized protein LOC101261934 isoform X2 [!	25.7	25.7	72%	540	88%	gi|723716780|XP_010323989.1
☐	PREDICTED: uncharacterized protein LOC101261934 isoform X1 [!	25.7	25.7	72%	541	88%	gi|723716777|XP_010323988.1
☐	PREDICTED: uncharacterized protein LOC102585817 [Solanum tul	25.7	25.7	72%	541	88%	gi|565403988|XP_006367433.1
☐	type I restriction endonuclease EcoprrI subunit M [Streptococcus co	25.7	25.7	90%	548	80%	gi|493309607|WP_006267109.1
☐	Zn-dependent hydrolase [Helicobacter bilis]	25.7	25.7	90%	552	70%	gi|696181945|KGL25316.1
☐	hypothetical protein [Helicobacter bilis]	25.7	25.7	90%	552	70%	gi|490187295|WP_004085896.1
☐	Zn-dependent hydrolase [Helicobacter bilis]	25.7	25.7	90%	552	70%	gi|491359440|WP_005217358.1
☐	Zn-dependent hydrolase [Helicobacter trogontum]	25.7	25.7	90%	553	70%	gi|696191037|KGL33027.1
☐	Zn-dependent hydrolase [Helicobacter trogontum]	25.7	25.7	90%	553	70%	gi|696189091|KGL31686.1
☐	type I restriction-modification system, M subunit [Clostridium celatu	25.7	25.7	90%	557	80%	gi|491353670|WP_005211592.1
☐	type I restriction endonuclease [Methanococcus vannielii]	25.7	25.7	90%	557	80%	gi|500677016|WP_011971897.1
☐	restriction endonuclease EcoR124II subunit M [Streptococcus sp. S	25.7	25.7	90%	557	80%	gi|726978673|WP_033583435.1
☐	type I restriction-modification system, M subunit [Streptococcus par	25.7	25.7	90%	557	80%	gi|565833921|WP_023917515.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Pongo abelii]

Sequence ID: gi|686700216|ref|XP_009236698.1| **Length:** 202 **Number of Matches:** 1

Range 1: 48 to 58 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
38.0 bits(82)	0.052	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    KKTLFCNASKE  11
            KKTLFCNASKE
Sbjct  48   KKTLFCNASKE  58
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194373591|dbj|BAG56891.1| **Length:** 218 **Number of Matches:** 1

Range 1: 48 to 58 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
38.0 bits(82)	0.052	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    KKTLFCNASKE  11
```

Related Information

Gene - associated gene details

```
           KKTLFCNASKE
Sbjct  48  KKTLFCNASKE  58
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan troglodytes]

Sequence ID: gi|694891540|ref|XP_009439669.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 57 to 67 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
38.0 bits(82)	0.053	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1   KKTLFCNASKE  11
           KKTLFCNASKE
Sbjct  57  KKTLFCNASKE  67
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan paniscus]

Sequence ID: gi|675771724|ref|XP_008974762.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 57 to 67 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
38.0 bits(82)	0.053	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1   KKTLFCNASKE  11
           KKTLFCNASKE
Sbjct  57  KKTLFCNASKE  67
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sapiens]

Sequence ID: gi|530366462|ref|XP_005273312.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 57 to 67 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
38.0 bits(82)	0.053	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1   KKTLFCNASKE  11
           KKTLFCNASKE
Sbjct  57  KKTLFCNASKE  67
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

C4BPB_KKTLFCNASKEWDDTTTECRL_Mod

RID BTF9GKPT013 (Expires on 01-20 15:15 pm)

Query ID lcl|30152
Description None
Molecule type amino acid
Query Length 21

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

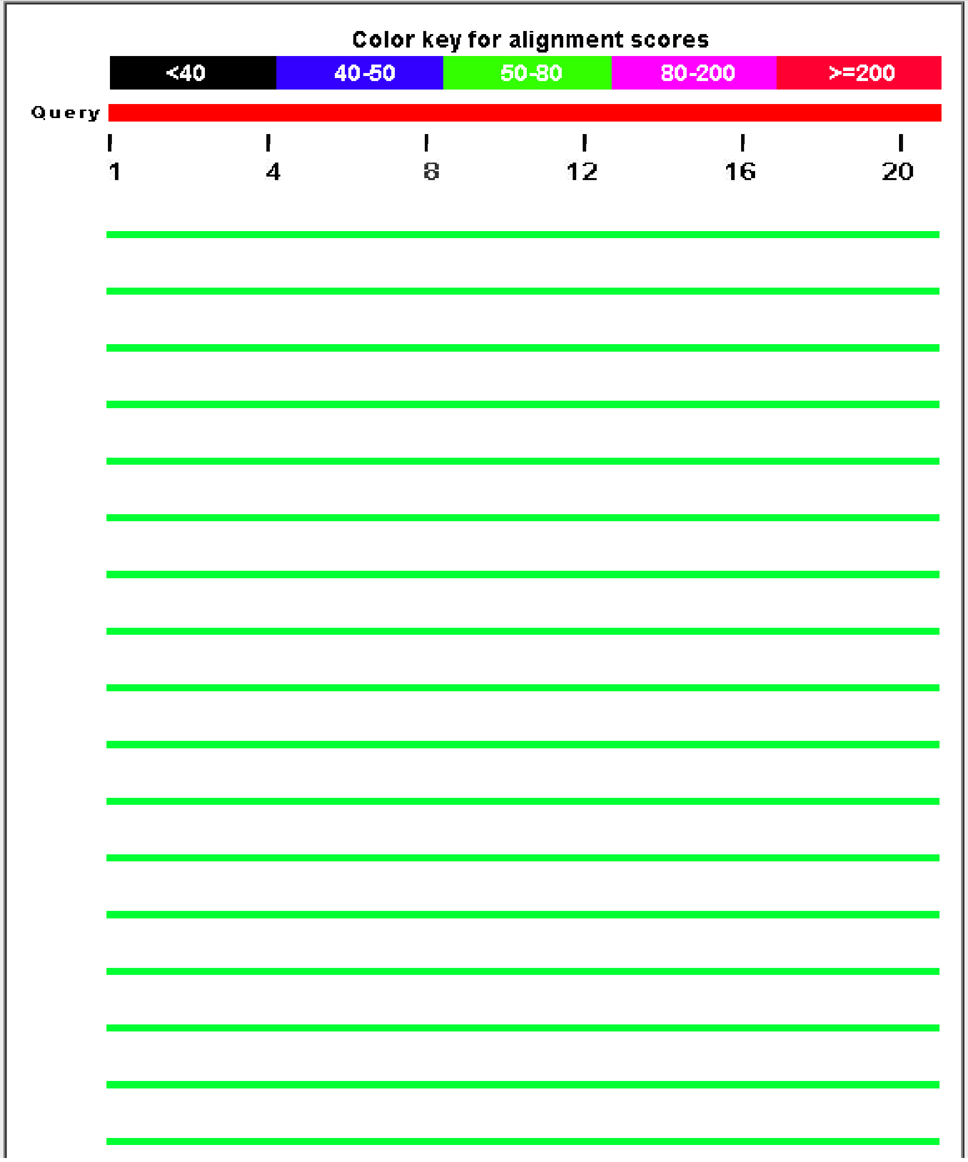
Graphic Summary

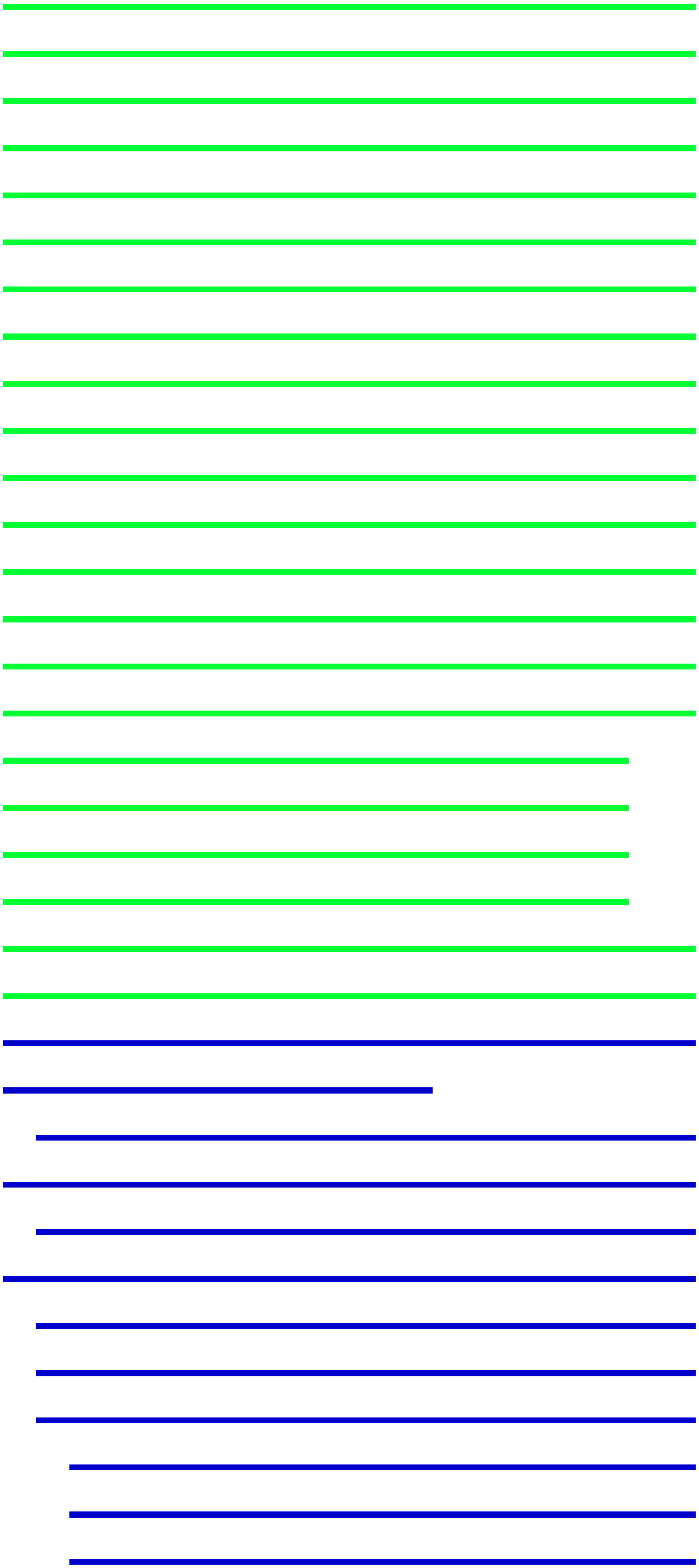
Show Conserved Domains

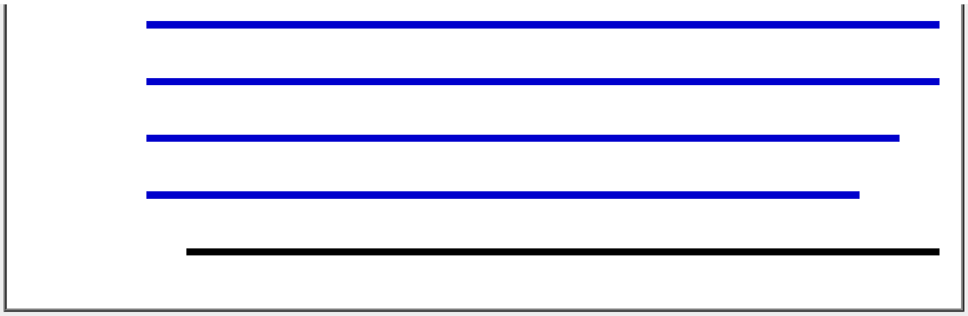
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	70.6	70.6	100%	2e-12	95%	gi|194373591|BAG56891.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan t	70.6	70.6	100%	2e-12	95%	gi|694891540|XP_009439669.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan p	70.6	70.6	100%	2e-12	95%	gi|675771724|XP_008974762.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Homo	70.6	70.6	100%	2e-12	95%	gi|530366462|XP_005273312.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Rhino	70.6	70.6	100%	2e-12	95%	gi|724836382|XP_010363947.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan t	70.6	70.6	100%	2e-12	95%	gi|694891534|XP_009439665.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan p	70.6	70.6	100%	2e-12	95%	gi|675771715|XP_008974759.1
☐	C4b-binding protein beta chain isoform 2 precursor [Homo sapi	70.6	70.6	100%	2e-12	95%	gi|62912462|NP_001017364.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Rhino	70.6	70.6	100%	2e-12	95%	gi|724836379|XP_010363946.1
☐	C4b-binding protein beta chain isoform 1 precursor [Homo sapi	70.6	70.6	100%	2e-12	95%	gi|4502505|NP_000707.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan p	70.6	70.6	100%	2e-12	95%	gi|397504761|XP_003822949.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan t	70.6	70.6	100%	2e-12	95%	gi|114572288|XP_001166306.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pong	67.2	67.2	100%	2e-11	90%	gi|686700216|XP_009236698.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pong	67.2	67.2	100%	2e-11	90%	gi|686700213|XP_009236694.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pong	67.2	67.2	100%	2e-11	90%	gi|297662141|XP_002809574.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Papio	66.8	66.8	100%	3e-11	90%	gi|685519789|XP_009186662.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Maca	66.8	66.8	100%	3e-11	90%	gi|544399939|XP_005540733.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Maca	66.8	66.8	100%	3e-11	90%	gi|544399931|XP_005540729.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Papio	66.8	66.8	100%	3e-11	90%	gi|685519785|XP_009186656.1
☐	hypothetical protein EGM_01442 [Macaca fascicularis]	66.8	66.8	100%	3e-11	90%	gi|355745961|EHH50586.1
☐	hypothetical protein EGK_01712 [Macaca mulatta]	66.8	66.8	100%	3e-11	90%	gi|355558818|EHH15598.1
☐	PREDICTED: c4b-binding protein beta chain isoform 3 [Macaca	66.8	66.8	100%	3e-11	90%	gi|109018561|XP_001083216.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Maca	66.8	66.8	100%	4e-11	90%	gi|544399929|XP_005540728.1
☐	PREDICTED: C4b-binding protein beta chain isoform 1 [Nomas	66.4	66.4	100%	5e-11	90%	gi|332266848|XP_003282407.1
☐	PREDICTED: C4b-binding protein beta chain isoform X9 [Chlor	66.0	66.0	100%	6e-11	90%	gi|635130917|XP_007986833.1
☐	PREDICTED: C4b-binding protein beta chain isoform X8 [Chlor	66.0	66.0	100%	7e-11	90%	gi|635130915|XP_007986832.1
☐	PREDICTED: C4b-binding protein beta chain isoform X7 [Chlor	66.0	66.0	100%	7e-11	90%	gi|635130913|XP_007986831.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Chlor	66.0	66.0	100%	7e-11	90%	gi|635130911|XP_007986830.1
☐	PREDICTED: C4b-binding protein beta chain isoform X5 [Chlor	66.0	66.0	100%	7e-11	90%	gi|635130907|XP_007986828.1

☐	PREDICTED: C4b-binding protein beta chain isoform X4 [Chlor	66.0	66.0	100%	7e-11	90%	gi|635130905|XP_007986827.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Chlor	66.0	66.0	100%	7e-11	90%	gi|635130903|XP_007986826.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Chlor	66.0	66.0	100%	7e-11	90%	gi|635130901|XP_007986825.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Chlor	66.0	66.0	100%	7e-11	90%	gi|635130899|XP_007986823.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Callit	64.3	64.3	90%	3e-10	95%	gi|675749407|XP_008983835.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Callit	64.3	64.3	90%	3e-10	95%	gi|296230632|XP_002760794.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Saim	59.2	59.2	90%	1e-08	89%	gi|725574024|XP_010339305.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Saim	59.2	59.2	90%	1e-08	89%	gi|403277664|XP_003930472.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Gale	51.5	51.5	100%	5e-06	71%	gi|667314769|XP_008585888.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Gale	51.5	51.5	100%	5e-06	71%	gi|667314766|XP_008585886.1
☐	PREDICTED: C4b-binding protein beta chain [Chrysochloris as	48.6	48.6	100%	5e-05	76%	gi|586450676|XP_006834269.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	46.9	46.9	61%	2e-04	100%	gi|471369765|XP_004375397.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	45.2	45.2	95%	7e-04	70%	gi|594636425|XP_007171607.1
☐	PREDICTED: C4b-binding protein beta chain [Ictidomys tridece	44.8	44.8	100%	0.001	71%	gi|532087633|XP_005329528.1
☐	PREDICTED: C4b-binding protein beta chain [Nannospalax gal	44.8	44.8	95%	0.001	76%	gi|674096417|XP_008821570.1
☐	PREDICTED: C4b-binding protein beta chain [Cavia porcellus]	43.9	43.9	100%	0.002	67%	gi|348577871|XP_003474707.1
☐	PREDICTED: C4b-binding protein beta chain [Sus scrofa]	43.5	43.5	95%	0.002	65%	gi|311265148|XP_003130503.1
☐	PREDICTED: C4b-binding protein beta chain [Otolemur garnett	43.1	43.1	95%	0.003	70%	gi|395838946|XP_003792365.1
☐	PREDICTED: C4b-binding protein beta chain [Orcinus orca]	42.6	42.6	95%	0.004	65%	gi|466071254|XP_004282462.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Myoti	42.6	42.6	90%	0.004	74%	gi|554587742|XP_005885272.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis lucifugus]	42.6	42.6	90%	0.004	74%	gi|558152655|XP_006094937.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Myoti	42.6	42.6	90%	0.004	74%	gi|554587740|XP_005885271.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Tarsi	41.8	41.8	95%	0.008	65%	gi|640811969|XP_008062626.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Tarsi	41.8	41.8	95%	0.008	65%	gi|640811967|XP_008062625.1
☐	PREDICTED: C4b-binding protein beta chain [Ceratotherium si	41.4	41.4	90%	0.011	68%	gi|478501878|XP_004425250.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	40.5	40.5	85%	0.021	67%	gi|470641603|XP_004325529.1
☐	PREDICTED: C4b-binding protein beta chain [Eptesicus fuscus	38.8	38.8	90%	0.075	68%	gi|641725104|XP_008152491.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis davidii]	38.4	38.4	52%	0.100	91%	gi|584068188|XP_006754475.1
☐	PREDICTED: C4b-binding protein beta chain [Jaculus jaculus]	38.4	38.4	76%	0.10	75%	gi|507559572|XP_004663509.1
☐	PREDICTED: C4b-binding protein beta chain [Elephantulus ed	38.0	38.0	85%	0.14	67%	gi|585666900|XP_006888062.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Came	37.5	37.5	85%	0.19	61%	gi|743734558|XP_010961541.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Came	37.5	37.5	85%	0.19	61%	gi|743734556|XP_010961540.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	37.5	37.5	85%	0.19	61%	gi|560935168|XP_006193413.1
☐	PREDICTED: C4b-binding protein beta chain [Mustela putorius	36.7	36.7	95%	0.35	65%	gi|511871202|XP_004756233.1
☐	PREDICTED: C4b-binding protein beta chain [Ornithorhynchus	36.3	36.3	61%	0.39	85%	gi|620984032|XP_007659774.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	34.1	34.1	85%	2.3	56%	gi|560986663|XP_006215518.1
☐	PREDICTED: C4b-binding protein beta chain [Canis lupus fami	33.7	33.7	61%	3.1	77%	gi|73960685|XP_851611.1
☐	C4b-binding protein beta chain [Heterocephalus glaber]	33.3	33.3	100%	4.3	57%	gi|351708103|EHB11022.1
☐	PREDICTED: C4b-binding protein beta chain [Heterocephalus	33.3	33.3	100%	4.3	57%	gi|512892965|XP_004897416.1
☐	PREDICTED: C4b-binding protein beta chain [Leptonychotes w	32.9	32.9	57%	5.9	75%	gi|585156269|XP_006730462.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	32.0	32.0	71%	11	69%	gi|338224254|AEI88022.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	32.0	32.0	71%	11	60%	gi|533120065|XP_005375468.1
☐	PREDICTED: C4b-binding protein beta chain [Pteropus alecto]	31.6	31.6	95%	15	55%	gi|586536223|XP_006922979.1
☐	C4b-binding protein beta chain [Pteropus alecto]	31.6	31.6	95%	15	55%	gi|431892854|ELK03282.1
☐	glycogen branching protein [Halothece sp. PCC 7418]	31.6	31.6	76%	16	55%	gi|505038850|WP_015225952.1

☐	envelope glycoprotein [Human immunodeficiency virus 1]	31.2	31.2	61%	20	61%	gi|345128523|AEN75212.1
☐	hypothetical protein PFNF135_02825 [Plasmodium falciparum I	31.2	31.2	57%	21	67%	gi|574981166|ETW42931.1
☐	hypothetical protein [Clostridium sp. CAG:62]	31.2	31.2	38%	22	100%	gi|548057742|WP_022376409.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.8	30.8	52%	29	75%	gi|30908538|AAP37305.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Felis	30.8	30.8	95%	29	55%	gi|587018341|XP_006942889.1
☐	hypothetical protein PANDA_018755 [Ailuropoda melanoleuca]	30.8	30.8	80%	29	59%	gi|281337925|EFB13509.1
☐	PREDICTED: C4b-binding protein beta chain [Ursus maritimus]	30.8	30.8	80%	29	59%	gi|670984389|XP_008683289.1
☐	PREDICTED: c4b-binding protein beta chain-like [Ailuropoda m	30.8	30.8	80%	29	59%	gi|301786617|XP_002928722.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Felis	30.8	30.8	95%	29	55%	gi|410986395|XP_003999496.1
☐	PREDICTED: complement C1r subcomponent [Stegastes partit	30.8	30.8	66%	30	63%	gi|657546451|XP_008278409.1
☐	hypothetical protein [Vibrio nigripulchritudo]	30.3	30.3	47%	39	70%	gi|740359636|WP_038195698.1
☐	hypothetical protein PFTANZ_02364 [Plasmodium falciparum T	30.3	30.3	52%	39	73%	gi|574974832|ETW36946.1
☐	hypothetical protein [Vibrio nigripulchritudo]	30.3	30.3	47%	39	70%	gi|740309755|WP_038147115.1
☐	putative Fimh-like protein [Vibrio nigripulchritudo]	30.3	30.3	47%	40	70%	gi|550352361|WP_022612127.1
☐	putative Fimh-like protein [Vibrio nigripulchritudo]	30.3	30.3	47%	40	70%	gi|550281458|WP_022607838.1
☐	hypothetical protein VINI7043_08940 [Vibrio nigripulchritudo AT	30.3	30.3	47%	40	70%	gi|342820393|EGU55216.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.3	30.3	57%	40	56%	gi|163637312|ABY27456.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.3	30.3	57%	40	56%	gi|163637310|ABY27455.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.3	30.3	57%	40	56%	gi|163637307|ABY27454.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.3	30.3	57%	40	56%	gi|163637305|ABY27453.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.3	30.3	57%	40	56%	gi|163637303|ABY27452.1
☐	hypothetical protein PFFCH_03778 [Plasmodium falciparum FC	30.3	30.3	52%	40	73%	gi|574965586|ETW28803.1
☐	hypothetical protein PFFVO_01913 [Plasmodium falciparum Vi	30.3	30.3	52%	40	73%	gi|574751318|ETW19338.1
☐	AGE-1 [Caenorhabditis elegans]	30.3	30.3	52%	41	83%	gi|1850329|AAC47459.1
☐	Protein AGE-1 [Caenorhabditis elegans]	30.3	30.3	52%	41	83%	gi|392891813|NP_496462.2
☐	hypothetical protein [Bacillus coagulans]	29.9	29.9	57%	54	75%	gi|737205332|WP_035190263.1

Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194373591|dbj|BAG56891.1| **Length:** 218 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 48 to 68 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.6 bits(159)	2e-12	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1   KKTLFCNASKEWDDTTTECRL  21
           KKTLFCNASKEWD+TTTECRL
Sbjct  48  KKTLFCNASKEWDNTTTECRL  68
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan troglodytes]

Sequence ID: gi|694891540|ref|XP_009439669.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 57 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.6 bits(159)	2e-12	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KKTLFCNASKEWDDTTTECRL  21
            KKTLFCNASKEWD+TTTECRL
Sbjct  57   KKTLFCNASKEWDNTTTECRL  77
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan paniscus]

Sequence ID: gi|675771724|ref|XP_008974762.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 57 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.6 bits(159)	2e-12	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KKTLFCNASKEWDDTTTECRL  21
            KKTLFCNASKEWD+TTTECRL
Sbjct  57   KKTLFCNASKEWDNTTTECRL  77
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sapiens]

Sequence ID: gi|530366462|ref|XP_005273312.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 57 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.6 bits(159)	2e-12	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KKTLFCNASKEWDDTTTECRL  21
            KKTLFCNASKEWD+TTTECRL
Sbjct  57   KKTLFCNASKEWDNTTTECRL  77
```

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PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinopithecus roxellana]

Sequence ID: gi|724836382|ref|XP_010363947.1| **Length:** 251 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 57 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.6 bits(159)	2e-12	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KKTLFCNASKEWDDTTTECRL  21
            KKTLFCNASKEWD+TTTECRL
Sbjct  57   KKTLFCNASKEWDNTTTECRL  77
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - B92B7UGG01R

Your search parameters were adjusted to search for a short input sequence.

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How to read this page | Blast report description

C4BPB_KKTLFCNASKEWDNTTTECRL_NonMod

RID	B92B7UGG01R (Expires on 01-14 09:56 am)		
Query ID	lcl|234110	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	21		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

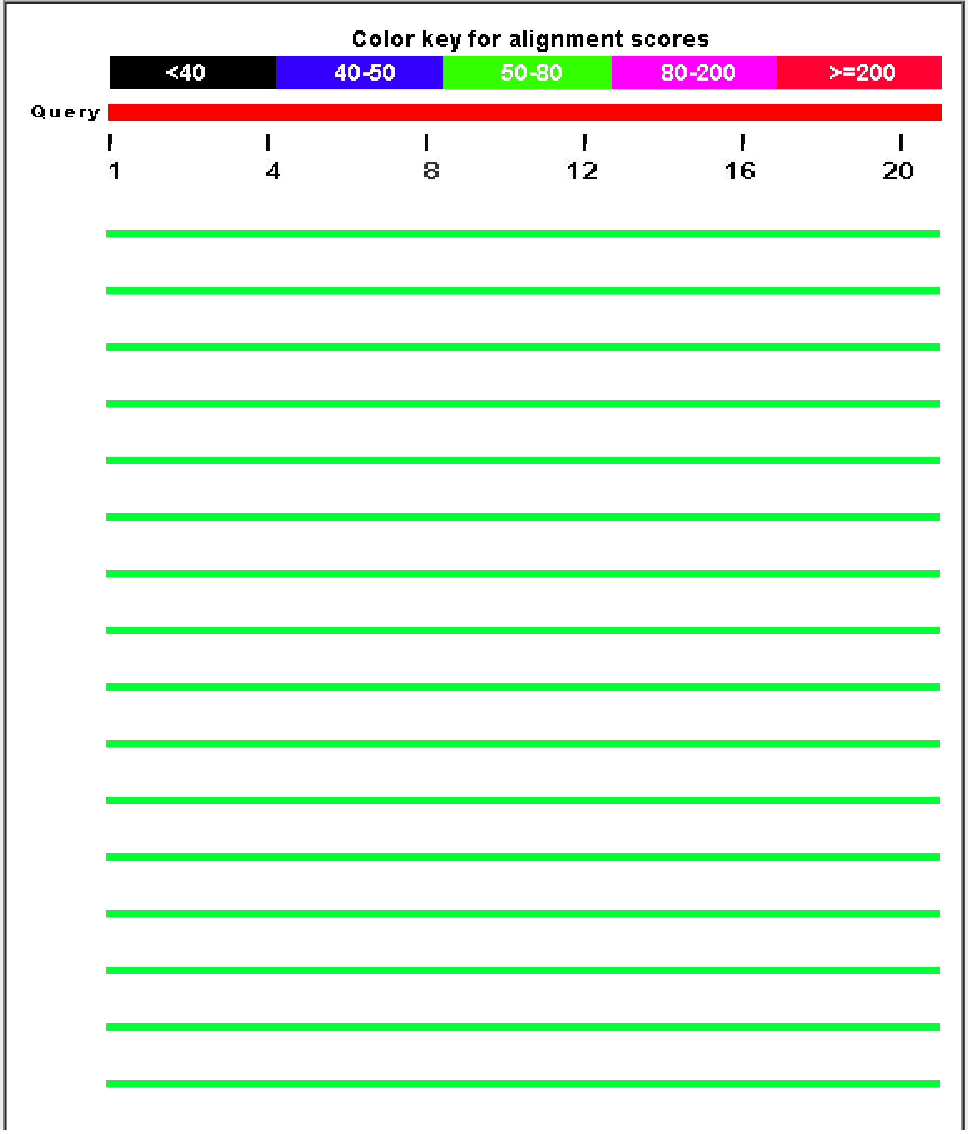
Graphic Summary

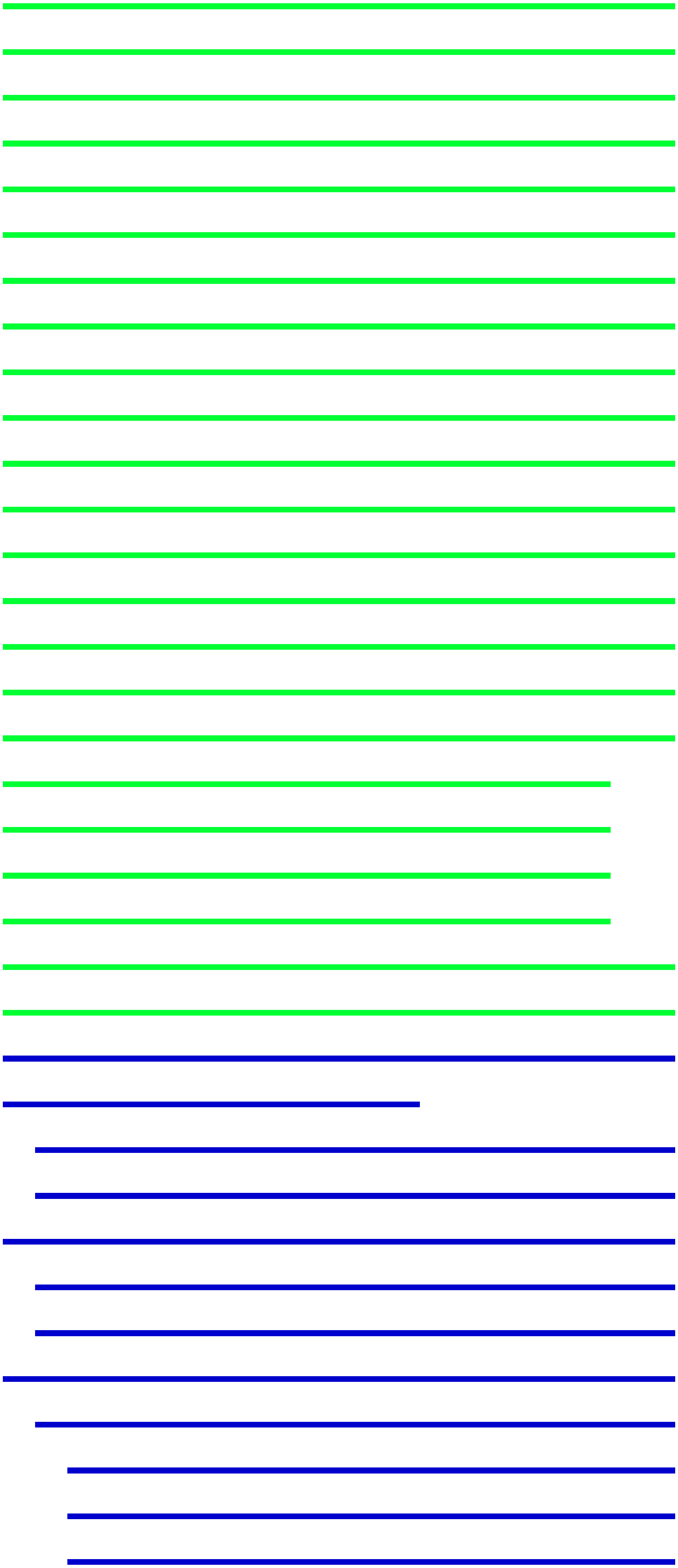
Show Conserved Domains

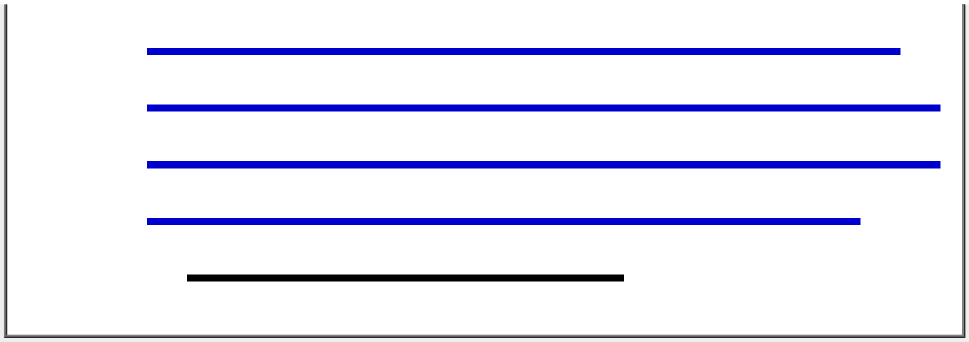
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	73.2	73.2	100%	2e-13	100%	gi|194373591|BAG56891.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan trogl	73.2	73.2	100%	2e-13	100%	gi|694891540|XP_009439669.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan panis	73.2	73.2	100%	2e-13	100%	gi|675771724|XP_008974762.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sa	73.2	73.2	100%	2e-13	100%	gi|530366462|XP_005273312.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinopith	73.2	73.2	100%	2e-13	100%	gi|724836382|XP_010363947.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan trogl	73.2	73.2	100%	2e-13	100%	gi|694891534|XP_009439665.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan panis	73.2	73.2	100%	2e-13	100%	gi|675771715|XP_008974759.1
☐	C4b-binding protein beta chain isoform 2 precursor [Homo sapiens]	73.2	73.2	100%	2e-13	100%	gi|62912462|NP_001017364.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Rhinopith	73.2	73.2	100%	2e-13	100%	gi|724836379|XP_010363946.1
☐	C4b-binding protein beta chain isoform 1 precursor [Homo sapiens]	73.2	73.2	100%	2e-13	100%	gi|4502505|NP_000707.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan panis	73.2	73.2	100%	2e-13	100%	gi|397504761|XP_003822949.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan trogl	73.2	73.2	100%	2e-13	100%	gi|114572288|XP_001166306.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pongo ab	69.8	69.8	100%	3e-12	95%	gi|686700216|XP_009236698.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pongo ab	69.8	69.8	100%	3e-12	95%	gi|686700213|XP_009236694.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pongo ab	69.8	69.8	100%	3e-12	95%	gi|297662141|XP_002809574.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Papio anu	69.4	69.4	100%	4e-12	95%	gi|685519789|XP_009186662.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Macaca fa	69.4	69.4	100%	4e-12	95%	gi|544399939|XP_005540733.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Macaca fa	69.4	69.4	100%	4e-12	95%	gi|544399931|XP_005540729.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Papio anu	69.4	69.4	100%	4e-12	95%	gi|685519785|XP_009186656.1
☐	hypothetical protein EGM_01442 [Macaca fascicularis]	69.4	69.4	100%	4e-12	95%	gi|355745961|EHH50586.1
☐	hypothetical protein EGK_01712 [Macaca mulatta]	69.4	69.4	100%	4e-12	95%	gi|355558818|EHH15598.1
☐	PREDICTED: c4b-binding protein beta chain isoform 3 [Macaca mu	69.4	69.4	100%	4e-12	95%	gi|109018561|XP_001083216.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Macaca fa	69.4	69.4	100%	5e-12	95%	gi|544399929|XP_005540728.1
☐	PREDICTED: C4b-binding protein beta chain isoform 1 [Nomascus	68.9	68.9	100%	6e-12	95%	gi|332266848|XP_003282407.1
☐	PREDICTED: C4b-binding protein beta chain isoform X9 [Chlorocel	68.5	68.5	100%	8e-12	95%	gi|635130917|XP_007986833.1
☐	PREDICTED: C4b-binding protein beta chain isoform X8 [Chlorocel	68.5	68.5	100%	9e-12	95%	gi|635130915|XP_007986832.1
☐	PREDICTED: C4b-binding protein beta chain isoform X7 [Chlorocel	68.5	68.5	100%	9e-12	95%	gi|635130913|XP_007986831.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Chlorocel	68.5	68.5	100%	9e-12	95%	gi|635130911|XP_007986830.1
☐							

	PREDICTED: C4b-binding protein beta chain isoform X5 [Chloroceb	68.5	68.5	100%	9e-12	95%	gi|635130907|XP_007986828.1
☐	PREDICTED: C4b-binding protein beta chain isoform X4 [Chloroceb	68.5	68.5	100%	9e-12	95%	gi|635130905|XP_007986827.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Chloroceb	68.5	68.5	100%	9e-12	95%	gi|635130903|XP_007986826.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Chloroceb	68.5	68.5	100%	9e-12	95%	gi|635130901|XP_007986825.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Chloroceb	68.5	68.5	100%	9e-12	95%	gi|635130899|XP_007986823.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Callithrix	66.8	66.8	90%	3e-11	100%	gi|675749407|XP_008983835.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Callithrix	66.8	66.8	90%	3e-11	100%	gi|296230632|XP_002760794.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Saimiri b	61.7	61.7	90%	2e-09	95%	gi|725574024|XP_010339305.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Saimiri b	61.7	61.7	90%	2e-09	95%	gi|403277664|XP_003930472.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Galeopte	53.2	53.2	100%	1e-06	71%	gi|667314769|XP_008585888.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Galeopte	53.2	53.2	100%	1e-06	71%	gi|667314766|XP_008585886.1
☐	PREDICTED: C4b-binding protein beta chain [Chrysochloris asiatic	48.1	48.1	100%	7e-05	76%	gi|586450676|XP_006834269.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	46.9	46.9	61%	2e-04	100%	gi|471369765|XP_004375397.1
☐	PREDICTED: C4b-binding protein beta chain [Nannospalax galili]	45.6	45.6	95%	5e-04	75%	gi|674096417|XP_008821570.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	44.8	44.8	95%	9e-04	70%	gi|594636425|XP_007171607.1
☐	PREDICTED: C4b-binding protein beta chain [Cavia porcellus]	43.5	43.5	100%	0.002	67%	gi|348577871|XP_003474707.1
☐	PREDICTED: C4b-binding protein beta chain [Sus scrofa]	43.1	43.1	95%	0.003	65%	gi|311265148|XP_003130503.1
☐	PREDICTED: C4b-binding protein beta chain [Otolemur garnettii]	42.6	42.6	95%	0.004	70%	gi|395838946|XP_003792365.1
☐	PREDICTED: C4b-binding protein beta chain [Ictidomys tridecemlin	42.2	42.2	100%	0.006	67%	gi|532087633|XP_005329528.1
☐	PREDICTED: C4b-binding protein beta chain [Orcinus orca]	42.2	42.2	95%	0.006	65%	gi|466071254|XP_004282462.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Myotis br	42.2	42.2	90%	0.006	74%	gi|554587742|XP_005885272.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis lucifugus]	42.2	42.2	90%	0.006	74%	gi|558152655|XP_006094937.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Myotis br	42.2	42.2	90%	0.006	74%	gi|554587740|XP_005885271.1
☐	PREDICTED: C4b-binding protein beta chain [Ceratotherium simu	41.4	41.4	90%	0.011	68%	gi|478501878|XP_004425250.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Tarsius s	41.4	41.4	95%	0.011	65%	gi|640811969|XP_008062626.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Tarsius s	41.4	41.4	95%	0.011	65%	gi|640811967|XP_008062625.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	40.1	40.1	85%	0.027	67%	gi|470641603|XP_004325529.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis davidii]	38.4	38.4	52%	0.095	91%	gi|584068188|XP_006754475.1
☐	PREDICTED: C4b-binding protein beta chain [Eptesicus fuscus]	38.4	38.4	90%	0.097	68%	gi|641725104|XP_008152491.1
☐	PREDICTED: C4b-binding protein beta chain [Jaculus jaculus]	38.4	38.4	76%	0.097	75%	gi|507559572|XP_004663509.1
☐	PREDICTED: C4b-binding protein beta chain [Elephantulus edward	37.5	37.5	85%	0.18	67%	gi|585666900|XP_006888062.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	37.1	37.1	85%	0.25	61%	gi|560935168|XP_006193413.1
☐	PREDICTED: C4b-binding protein beta chain [Ornithorhynchus ana	36.3	36.3	61%	0.37	85%	gi|620984032|XP_007659774.1
☐	PREDICTED: C4b-binding protein beta chain [Mustela putorius furo	36.3	36.3	95%	0.46	65%	gi|511871202|XP_004756233.1
☐	PREDICTED: C4b-binding protein beta chain [Canis lupus familiari	33.7	33.7	61%	3.0	77%	gi|73960685|XP_851611.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	33.7	33.7	85%	3.0	56%	gi|560986663|XP_006215518.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Felis catu	33.3	33.3	95%	4.1	60%	gi|587018341|XP_006942889.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Felis catu	33.3	33.3	95%	4.1	60%	gi|410986395|XP_003999496.1
☐	putative Fimh-like protein [Vibrio nigripulchritudo]	32.9	32.9	47%	5.4	80%	gi|550352361|WP_022612127.1
☐	putative Fimh-like protein [Vibrio nigripulchritudo]	32.9	32.9	47%	5.4	80%	gi|550281458|WP_022607838.1
☐	hypothetical protein [Vibrio nigripulchritudo]	32.9	32.9	47%	5.4	80%	gi|490542018|WP_004407142.1
☐	C4b-binding protein beta chain [Heterocephalus glaber]	32.9	32.9	100%	5.6	57%	gi|351708103|EHB11022.1
☐	PREDICTED: C4b-binding protein beta chain [Leptonychotes wedd	32.9	32.9	57%	5.6	75%	gi|585156269|XP_006730462.1
☐	PREDICTED: C4b-binding protein beta chain [Heterocephalus glab	32.9	32.9	100%	5.6	57%	gi|512892965|XP_004897416.1
☐	PREDICTED: C4b-binding protein beta chain [Pteropus alecto]	32.9	32.9	95%	5.6	55%	gi|586536223|XP_006922979.1

☐	C4b-binding protein beta chain [Pteropus alecto]	32.9	32.9	95%	5.6	55%	gi|431892854|ELK03282.1
☐	hypothetical protein [Plasmodium knowlesi strain H]	32.0	32.0	61%	10	75%	gi|221054814|XP_002258546.1
☐	hypothetical protein PFNF135_02825 [Plasmodium falciparum NF1	32.0	32.0	66%	11	63%	gi|574981166|ETW42931.1
☐	arginyl-tRNA synthetase [Helicobacter apodemus]	32.0	32.0	66%	11	71%	gi|696169675|KGL15468.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	31.6	31.6	71%	14	60%	gi|533120065|XP_005375468.1
☐	DNA repair protein RadA [Osedax symbiont Rs2]	31.6	31.6	76%	15	69%	gi|520769936|WP_020286673.1
☐	DNA repair protein RadA [Osedax symbiont Rs1]	31.6	31.6	76%	15	69%	gi|518641042|WP_019811142.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	31.2	31.2	52%	19	75%	gi|84873457|ABC67785.1
☐	PREDICTED: C4b-binding protein beta chain [Loxodonta africana]	31.2	31.2	100%	20	57%	gi|731475974|XP_010588717.1
☐	conserved putative membrane protein [Melbournevirus]	31.2	31.2	61%	20	62%	gi|701447374|YP_009094746.1
☐	membrane protein [Cannes 8 virus]	31.2	31.2	61%	20	62%	gi|539398800|AGV01635.1
☐	hypothetical protein [Treponema bryantii]	31.2	31.2	71%	20	60%	gi|551312583|WP_022932465.1
☐	envelope protein [Human immunodeficiency virus 1]	30.8	30.8	52%	26	75%	gi|515020035|AGO65073.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.8	30.8	47%	26	82%	gi|24079811|AAN46022.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.8	30.8	47%	28	82%	gi|42494103|AAS17398.1
☐	PREDICTED: complement C1r subcomponent [Stegastes partitus]	30.8	30.8	66%	29	63%	gi|657546451|XP_008278409.1
☐	von Willebrand factor D and EGF domain-containing protein [Crass	30.8	30.8	66%	29	71%	gi|405969928|EKC34871.1
☐	hypothetical protein PFTANZ_02364 [Plasmodium falciparum Tanza	30.3	30.3	52%	37	73%	gi|574974832|ETW36946.1
☐	hypothetical protein C922_01705 [Plasmodium inui San Antonio 1]	30.3	30.3	61%	38	69%	gi|672191245|XP_008815530.1
☐	hypothetical protein PANDA_018755 [Ailuropoda melanoleuca]	30.3	30.3	80%	38	59%	gi|281337925|EFB13509.1
☐	PREDICTED: C4b-binding protein beta chain [Ursus maritimus]	30.3	30.3	80%	38	59%	gi|670984389|XP_008683289.1
☐	hypothetical protein PFFCH_03778 [Plasmodium falciparum FCH/4	30.3	30.3	52%	38	73%	gi|574965586|ETW28803.1
☐	PREDICTED: c4b-binding protein beta chain-like [Ailuropoda melan	30.3	30.3	80%	38	59%	gi|301786617|XP_002928722.1
☐	hypothetical protein PFFVO_01913 [Plasmodium falciparum Vietna	30.3	30.3	52%	38	73%	gi|574751318|ETW19338.1
☐	proteinase inhibitor [Bacillus vallismortis]	30.3	30.3	66%	39	60%	gi|498017254|WP_010331410.1
☐	DNA repair protein RadA [Avibacterium paragallinarum]	30.3	30.3	76%	39	69%	gi|516416332|WP_017805730.1
☐	AGE-1 [Caenorhabditis elegans]	30.3	30.3	52%	39	83%	gi|1850329|AAC47459.1

⊟ Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194373591|dbj|BAG56891.1| **Length:** 218 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 48 to 68 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.2 bits(165)	2e-13	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KKTLFCNASKEWDNTTTECRL  21
            KKTLFCNASKEWDNTTTECRL
Sbjct  48   KKTLFCNASKEWDNTTTECRL  68
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Pan troglodytes]

Sequence ID: gi|694891540|ref|XP_009439669.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 57 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.2 bits(165)	2e-13	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KKTLFCNASKEWDNTTTECRL  21
```

```
                KKTLFCNASKEWDNTTTECRL
Sbjct  57   KKTLFCNASKEWDNTTTECRL  77
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan paniscus]

Sequence ID: gi|675771724|ref|XP_008974762.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 57 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.2 bits(165)	2e-13	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KKTLFCNASKEWDNTTTECRL  21
            KKTLFCNASKEWDNTTTECRL
Sbjct  57   KKTLFCNASKEWDNTTTECRL  77
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sapiens]

Sequence ID: gi|530366462|ref|XP_005273312.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 57 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.2 bits(165)	2e-13	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KKTLFCNASKEWDNTTTECRL  21
            KKTLFCNASKEWDNTTTECRL
Sbjct  57   KKTLFCNASKEWDNTTTECRL  77
```

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PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinopithecus roxellana]

Sequence ID: gi|724836382|ref|XP_010363947.1| **Length:** 251 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 57 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.2 bits(165)	2e-13	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KKTLFCNASKEWDNTTTECRL  21
            KKTLFCNASKEWDNTTTECRL
Sbjct  57   KKTLFCNASKEWDNTTTECRL  77
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

C4BPB_KTLFCDASKEWDDTTTECRL_Mod

RID BTFTXDBG016 (Expires on 01-20 15:24 pm)

Query ID	lcl|30962	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	20		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

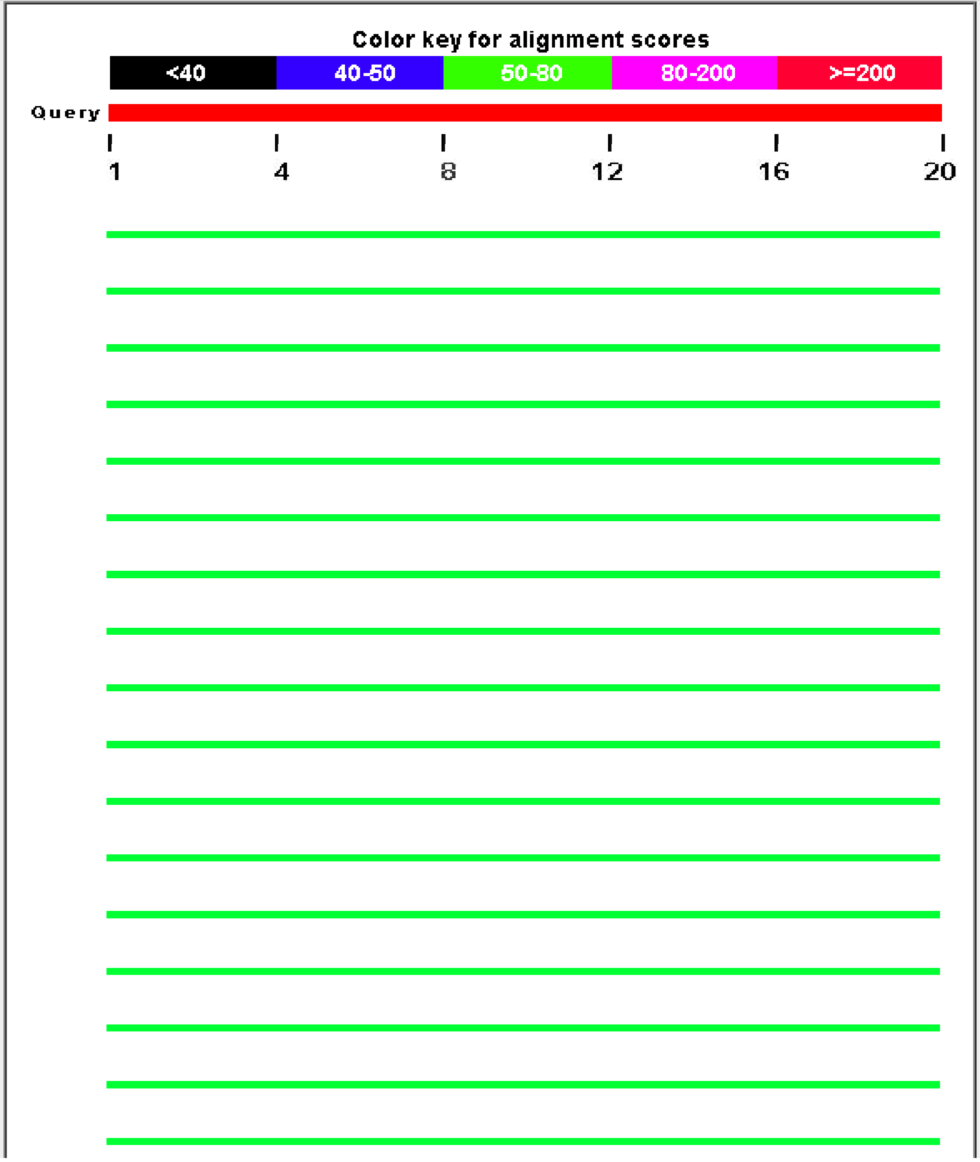
Graphic Summary

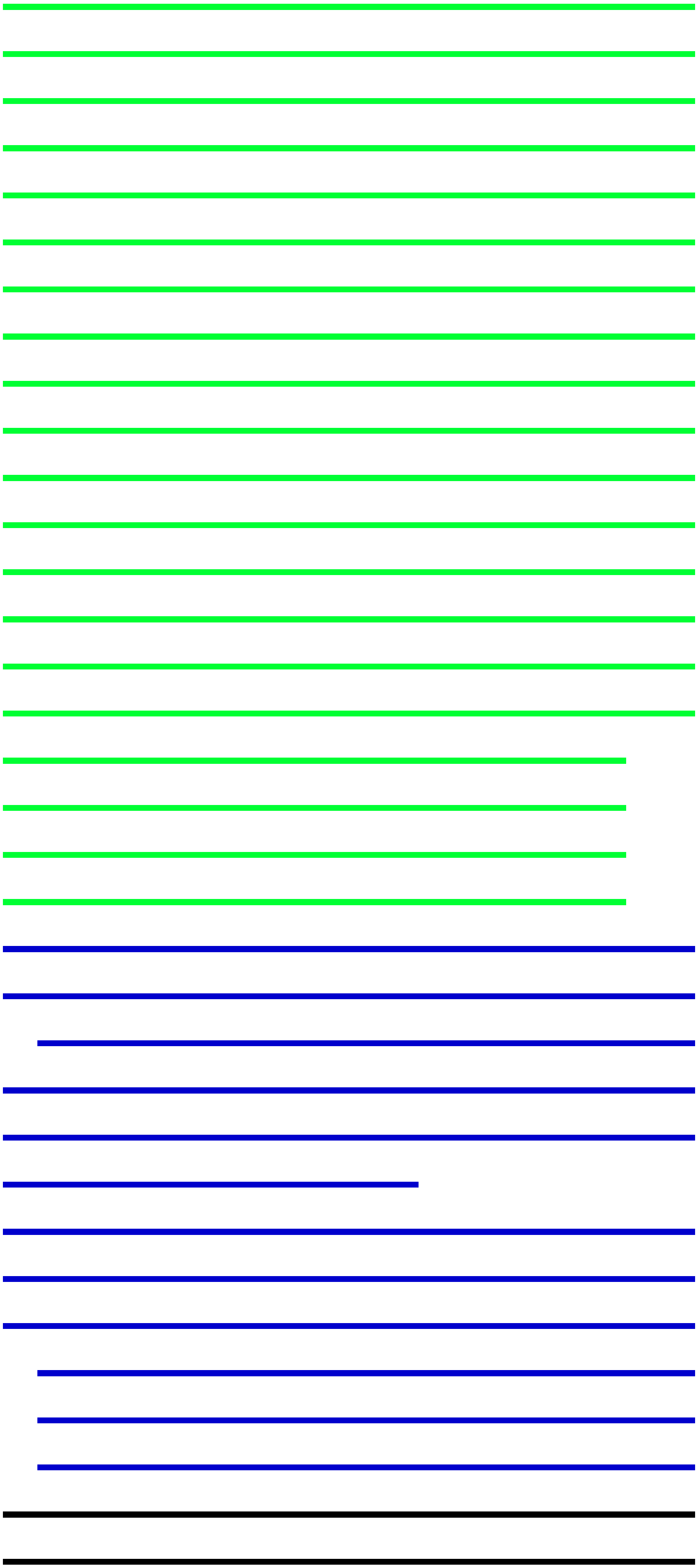
Show Conserved Domains

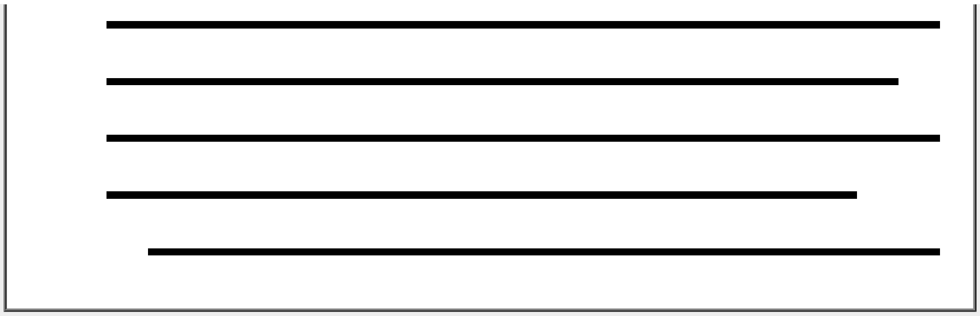
No putative conserved domains have been detected

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	65.1	65.1	100%	1e-10	90%	gi|194373591|BAG56891.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan t	65.1	65.1	100%	1e-10	90%	gi|694891540|XP_009439669.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan p	65.1	65.1	100%	1e-10	90%	gi|675771724|XP_008974762.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Homo	65.1	65.1	100%	1e-10	90%	gi|530366462|XP_005273312.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Rhino	65.1	65.1	100%	1e-10	90%	gi|724836382|XP_010363947.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan t	65.1	65.1	100%	1e-10	90%	gi|694891534|XP_009439665.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan p	65.1	65.1	100%	1e-10	90%	gi|675771715|XP_008974759.1
☐	C4b-binding protein beta chain isoform 2 precursor [Homo sapi	65.1	65.1	100%	1e-10	90%	gi|62912462|NP_001017364.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Rhino	65.1	65.1	100%	1e-10	90%	gi|724836379|XP_010363946.1
☐	C4b-binding protein beta chain isoform 1 precursor [Homo sapi	65.1	65.1	100%	1e-10	90%	gi|4502505|NP_000707.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan p	65.1	65.1	100%	1e-10	90%	gi|397504761|XP_003822949.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan t	65.1	65.1	100%	1e-10	90%	gi|114572288|XP_001166306.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pong	61.7	61.7	100%	2e-09	85%	gi|686700216|XP_009236698.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pong	61.7	61.7	100%	2e-09	85%	gi|686700213|XP_009236694.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pong	61.7	61.7	100%	2e-09	85%	gi|297662141|XP_002809574.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Papio	61.3	61.3	100%	2e-09	85%	gi|685519789|XP_009186662.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Maca	61.3	61.3	100%	2e-09	85%	gi|544399939|XP_005540733.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Maca	61.3	61.3	100%	2e-09	85%	gi|544399931|XP_005540729.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Papio	61.3	61.3	100%	2e-09	85%	gi|685519785|XP_009186656.1
☐	hypothetical protein EGM_01442 [Macaca fascicularis]	61.3	61.3	100%	2e-09	85%	gi|355745961|EHH50586.1
☐	hypothetical protein EGK_01712 [Macaca mulatta]	61.3	61.3	100%	2e-09	85%	gi|355558818|EHH15598.1
☐	PREDICTED: c4b-binding protein beta chain isoform 3 [Macaca	61.3	61.3	100%	2e-09	85%	gi|109018561|XP_001083216.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Maca	61.3	61.3	100%	2e-09	85%	gi|544399929|XP_005540728.1
☐	PREDICTED: C4b-binding protein beta chain isoform 1 [Nomas	60.9	60.9	100%	3e-09	85%	gi|332266848|XP_003282407.1
☐	PREDICTED: C4b-binding protein beta chain isoform X9 [Chlor	60.4	60.4	100%	4e-09	85%	gi|635130917|XP_007986833.1
☐	PREDICTED: C4b-binding protein beta chain isoform X8 [Chlor	60.4	60.4	100%	5e-09	85%	gi|635130915|XP_007986832.1
☐	PREDICTED: C4b-binding protein beta chain isoform X7 [Chlor	60.4	60.4	100%	5e-09	85%	gi|635130913|XP_007986831.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Chlor	60.4	60.4	100%	5e-09	85%	gi|635130911|XP_007986830.1
☐	PREDICTED: C4b-binding protein beta chain isoform X5 [Chlor	60.4	60.4	100%	5e-09	85%	gi|635130907|XP_007986828.1

☐	PREDICTED: C4b-binding protein beta chain isoform X4 [Chlor	60.4	60.4	100%	5e-09	85%	gi|635130905|XP_007986827.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Chlor	60.4	60.4	100%	5e-09	85%	gi|635130903|XP_007986826.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Chlor	60.4	60.4	100%	5e-09	85%	gi|635130901|XP_007986825.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Chlor	60.4	60.4	100%	5e-09	85%	gi|635130899|XP_007986823.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Callitl	58.7	58.7	90%	2e-08	89%	gi|675749407|XP_008983835.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Callitl	58.7	58.7	90%	2e-08	89%	gi|296230632|XP_002760794.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Saim	53.7	53.7	90%	9e-07	83%	gi|725574024|XP_010339305.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Saim	53.7	53.7	90%	9e-07	83%	gi|403277664|XP_003930472.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Galeo	46.0	46.0	100%	3e-04	65%	gi|667314769|XP_008585888.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Galeo	46.0	46.0	100%	3e-04	65%	gi|667314766|XP_008585886.1
☐	PREDICTED: C4b-binding protein beta chain [Chrysochloris as	44.8	44.8	95%	9e-04	74%	gi|586450676|XP_006834269.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	42.6	42.6	100%	0.004	65%	gi|594636425|XP_007171607.1
☐	PREDICTED: C4b-binding protein beta chain [Nannospalax gal	42.2	42.2	100%	0.006	71%	gi|674096417|XP_008821570.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	41.4	41.4	60%	0.011	92%	gi|471369765|XP_004375397.1
☐	PREDICTED: C4b-binding protein beta chain [Sus scrofa]	40.9	40.9	100%	0.015	60%	gi|311265148|XP_003130503.1
☐	PREDICTED: C4b-binding protein beta chain [Otolemur garnett	40.5	40.5	100%	0.020	65%	gi|395838946|XP_003792365.1
☐	PREDICTED: C4b-binding protein beta chain [Orcinus orca]	40.1	40.1	100%	0.027	60%	gi|466071254|XP_004282462.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Myoti	40.1	40.1	95%	0.027	68%	gi|554587742|XP_005885272.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis lucifugus]	40.1	40.1	95%	0.027	68%	gi|558152655|XP_006094937.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Myoti	40.1	40.1	95%	0.027	68%	gi|554587740|XP_005885271.1
☐	PREDICTED: C4b-binding protein beta chain [Ictidomys tridece	39.2	39.2	100%	0.051	65%	gi|532087633|XP_005329528.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Tarsiu	39.2	39.2	100%	0.051	60%	gi|640811969|XP_008062626.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Tarsiu	39.2	39.2	100%	0.051	60%	gi|640811967|XP_008062625.1
☐	PREDICTED: C4b-binding protein beta chain [Ceratotherium si	38.8	38.8	95%	0.070	63%	gi|478501878|XP_004425250.1
☐	PREDICTED: C4b-binding protein beta chain [Cavia porcellus]	38.4	38.4	100%	0.095	60%	gi|348577871|XP_003474707.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	38.0	38.0	90%	0.13	61%	gi|470641603|XP_004325529.1
☐	PREDICTED: C4b-binding protein beta chain [Eptesicus fuscus	36.3	36.3	95%	0.46	63%	gi|641725104|XP_008152491.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis davidii]	35.8	35.8	55%	0.61	82%	gi|584068188|XP_006754475.1
☐	PREDICTED: C4b-binding protein beta chain [Jaculus jaculus]	35.8	35.8	80%	0.62	69%	gi|507559572|XP_004663509.1
☐	PREDICTED: C4b-binding protein beta chain [Elephantulus edw	35.4	35.4	90%	0.84	61%	gi|585666900|XP_006888062.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Came	35.0	35.0	90%	1.2	56%	gi|743734558|XP_010961541.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Came	35.0	35.0	90%	1.2	56%	gi|743734556|XP_010961540.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	35.0	35.0	90%	1.2	56%	gi|560935168|XP_006193413.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	34.6	34.6	75%	1.6	67%	gi|533120065|XP_005375468.1
☐	PREDICTED: C4b-binding protein beta chain [Mustela putorius	34.1	34.1	100%	2.2	60%	gi|511871202|XP_004756233.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	32.5	32.5	90%	7.5	56%	gi|560986663|XP_006215518.1
☐	Piso0_002582 [Millerozyma farinosa CBS 7064]	32.0	32.0	75%	10	67%	gi|448103382|XP_004200022.1
☐	conserved putative membrane protein [Melbournevirus]	32.0	32.0	65%	11	69%	gi|701447374|YP_009094746.1
☐	membrane protein [Cannes 8 virus]	32.0	32.0	65%	11	69%	gi|539398800|AGV01635.1
☐	polyphosphate kinase [Burkholderia sp. MP-1]	31.6	31.6	65%	14	46%	gi|737535990|WP_035509712.1
☐	hypothetical protein [Clostridium sp. CAG:62]	31.2	31.2	40%	20	100%	gi|548057742|WP_022376409.1
☐	PREDICTED: C4b-binding protein beta chain [Ornithorhynchus	30.8	30.8	60%	24	75%	gi|620984032|XP_007659774.1
☐	hypothetical protein [Vibrio nigripulchritudo]	30.3	30.3	50%	35	70%	gi|740359636|WP_038195698.1
☐	hypothetical protein [Vibrio nigripulchritudo]	30.3	30.3	50%	35	70%	gi|740309755|WP_038147115.1
☐	putative Fimh-like protein [Vibrio nigripulchritudo]	30.3	30.3	50%	36	70%	gi|550352361|WP_022612127.1

☐	putative Fimh-like protein [Vibrio nigripulchritudo]	30.3	30.3	50%	36	70%	gi|550281458|WP_022607838.1
☐	hypothetical protein VINI7043_08940 [Vibrio nigripulchritudo AT	30.3	30.3	50%	36	70%	gi|342820393|EGU55216.1
☐	PREDICTED: C4b-binding protein beta chain [Leptonychotes w	30.3	30.3	60%	37	67%	gi|585156269|XP_006730462.1
☐	transaldolase [Oribacterium sp. P6A1]	29.9	29.9	70%	50	64%	gi|738716700|WP_036611113.1
☐	transaldolase [Lachnospiraceae bacterium JC7]	29.9	29.9	70%	50	64%	gi|571148921|ETP72518.1
☐	PREDICTED: fibroin heavy chain-like [Callithrix jacchus]	29.9	50.1	80%	51	83%	gi|675768476|XP_008987859.1
☐	RIFIN [Plasmodium falciparum]	29.9	29.9	55%	51	73%	gi|82394380|ABB72313.1
☐	RIFIN [Plasmodium falciparum]	29.9	29.9	55%	51	73%	gi|82394444|ABB72335.1
☐	hypothetical protein PFBG_00014 [Plasmodium falciparum 7G8	29.9	29.9	55%	51	73%	gi|579134248|EUR82669.1
☐	hypothetical protein PFNF135_02825 [Plasmodium falciparum I	29.9	29.9	60%	51	67%	gi|574981166|ETW42931.1
☐	protoporphyrin IX magnesium-chelatase [Stanieria cyanosphae	29.9	29.9	65%	52	67%	gi|505006979|WP_015194081.1
☐	hypothetical protein [Fimbriimonas ginsengisoli]	29.9	29.9	45%	52	89%	gi|740689768|WP_038475057.1
☐	glutamate synthase large subunit [Lentisphaera araneosa]	29.9	29.9	55%	53	64%	gi|494487169|WP_007276642.1
☐	hypothetical protein DFA_06522 [Dictyostelium fasciculatum]	29.5	29.5	85%	62	50%	gi|470268001|XP_004362223.1
☐	hypothetical protein [Plasmodium knowlesi strain H]	29.5	29.5	65%	69	69%	gi|221054814|XP_002258546.1
☐	probable subtilisin-like serine protease [Claviceps purpurea 20.	29.5	29.5	75%	70	59%	gi|399164244|CCE34824.1
☐	C4b-binding protein beta chain [Heterocephalus glaber]	29.5	29.5	80%	70	56%	gi|351708103|EHB11022.1
☐	PREDICTED: C4b-binding protein beta chain [Heterocephalus g	29.5	29.5	80%	70	56%	gi|512892965|XP_004897416.1
☐	arginyl-tRNA synthetase [Helicobacter apodemus]	29.5	29.5	70%	71	64%	gi|736540679|WP_034555246.1
☐	elongation factor Ts [Helicobacter pylori]	29.5	29.5	75%	71	67%	gi|445936521|WP_000014376.1
☐	hypothetical protein [Streptomyces scabrisporus]	29.5	29.5	60%	71	58%	gi|522040969|WP_020552178.1
☐	ABC transporter substrate-binding protein [Blautia hydrogenotro	29.5	29.5	70%	71	48%	gi|492755713|WP_005951864.1
☐	putative uncharacterized protein [Blautia hydrogenotrophica CA	29.5	29.5	70%	71	48%	gi|546358788|WP_021845827.1
☐	probable subtilisin-like serine protease [Claviceps purpurea 20.	29.5	29.5	75%	72	59%	gi|399166615|CCE32598.1
☐	hypothetical protein PFTANZ_02364 [Plasmodium falciparum T	29.1	29.1	55%	94	73%	gi|574974832|ETW36946.1
☐	hypothetical protein DDB_G0277599 [Dictyostelium discoideum	29.1	29.1	40%	96	100%	gi|66817412|XP_642559.1

Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194373591|dbj|BAG56891.1| **Length:** 218 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 49 to 68 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.1 bits(146)	1e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1   KTLFCDASKEWDDTTTECRL  20
           KTLFC+ASKEWD+TTTECRL
Sbjct  49  KTLFCNASKEWDNTTTECRL  68
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Pan troglodytes]

Sequence ID: gi|694891540|ref|XP_009439669.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 58 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.1 bits(146)	1e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KTLFCDASKEWDDTTTECRL  20
            KTLFC+ASKEWD+TTTECRL
Sbjct  58   KTLFCNASKEWDNTTTECRL  77
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Pan paniscus]

Sequence ID: gi|675771724|ref|XP_008974762.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 58 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.1 bits(146)	1e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KTLFCDASKEWDDTTTECRL  20
            KTLFC+ASKEWD+TTTECRL
Sbjct  58   KTLFCNASKEWDNTTTECRL  77
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sapiens]

Sequence ID: gi|530366462|ref|XP_005273312.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 58 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.1 bits(146)	1e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KTLFCDASKEWDDTTTECRL  20
            KTLFC+ASKEWD+TTTECRL
Sbjct  58   KTLFCNASKEWDNTTTECRL  77
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinopithecus roxellana]

Sequence ID: gi|724836382|ref|XP_010363947.1| **Length:** 251 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 58 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.1 bits(146)	1e-10	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KTLFCDASKEWDDTTTECRL  20
            KTLFC+ASKEWD+TTTECRL
Sbjct  58   KTLFCNASKEWDNTTTECRL  77
```

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C4BPB_KTLFCNASKEWDDTTTECRL_Mod

RID BTFREM8E013 (Expires on 01-20 15:23 pm)

Query ID	lcl|30044	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	20	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

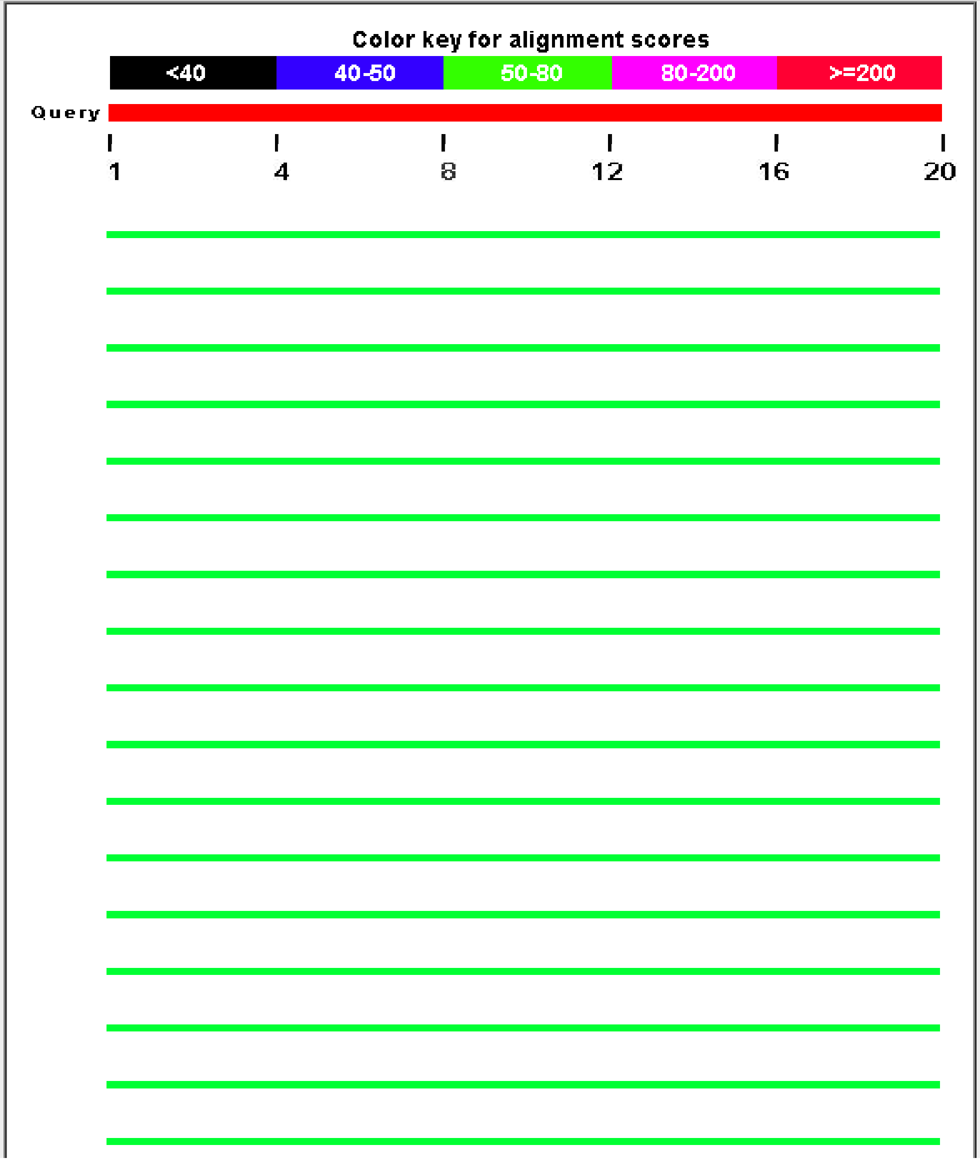
Graphic Summary

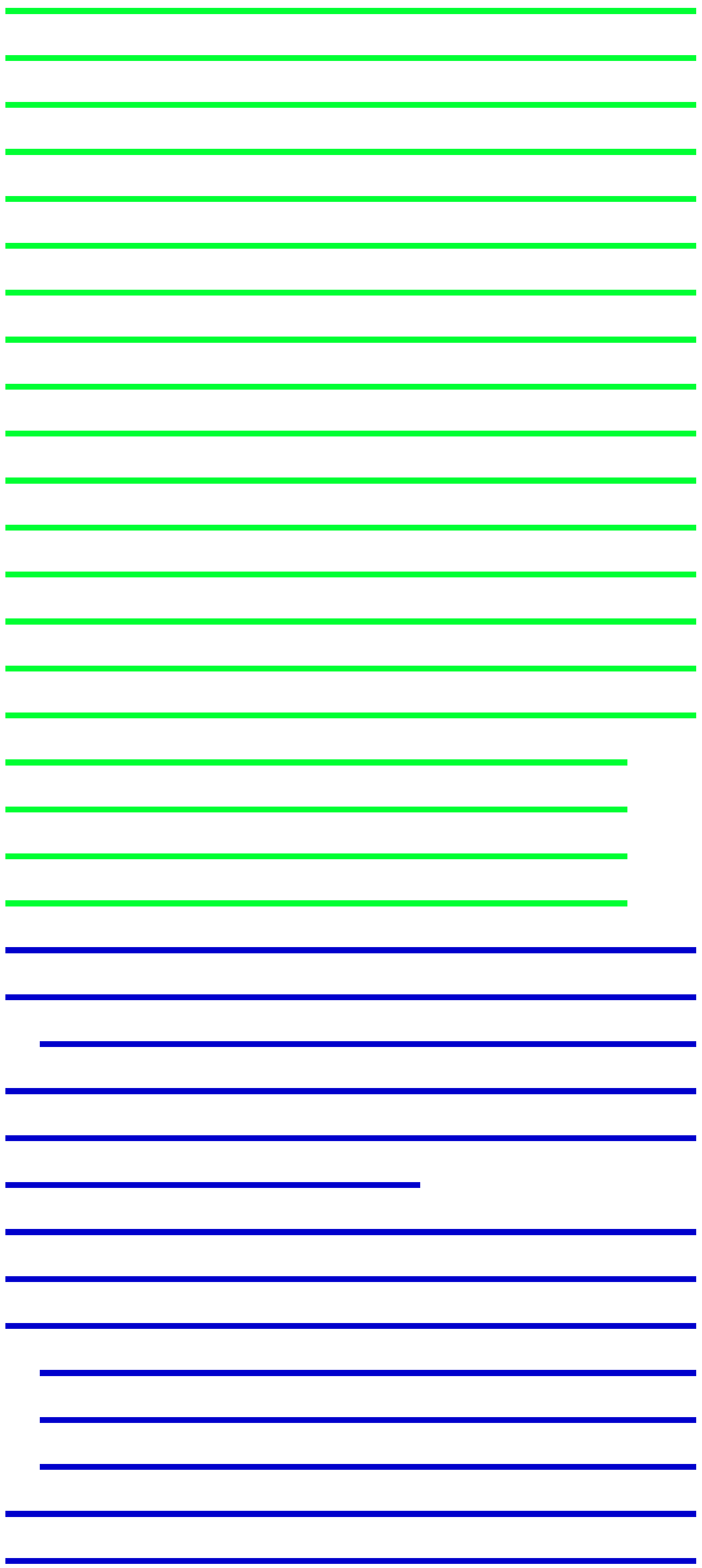
Show Conserved Domains

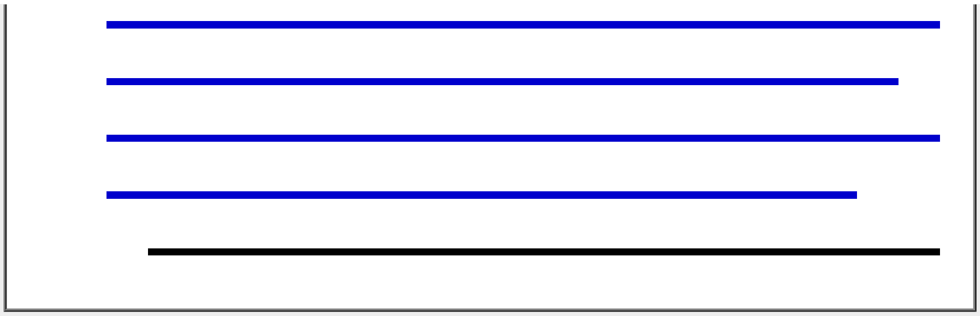
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	67.7	67.7	100%	1e-11	95%	gi|194373591|BAG56891.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan t	67.7	67.7	100%	1e-11	95%	gi|694891540|XP_009439669.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan p	67.7	67.7	100%	1e-11	95%	gi|675771724|XP_008974762.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Homo	67.7	67.7	100%	1e-11	95%	gi|530366462|XP_005273312.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinc	67.7	67.7	100%	2e-11	95%	gi|724836382|XP_010363947.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan t	67.7	67.7	100%	2e-11	95%	gi|694891534|XP_009439665.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan p	67.7	67.7	100%	2e-11	95%	gi|675771715|XP_008974759.1
☐	C4b-binding protein beta chain isoform 2 precursor [Homo sapi	67.7	67.7	100%	2e-11	95%	gi|62912462|NP_001017364.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Rhinc	67.7	67.7	100%	2e-11	95%	gi|724836379|XP_010363946.1
☐	C4b-binding protein beta chain isoform 1 precursor [Homo sapi	67.7	67.7	100%	2e-11	95%	gi|4502505|NP_000707.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan p	67.7	67.7	100%	2e-11	95%	gi|397504761|XP_003822949.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan t	67.7	67.7	100%	2e-11	95%	gi|114572288|XP_001166306.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pong	64.3	64.3	100%	2e-10	90%	gi|686700216|XP_009236698.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pong	64.3	64.3	100%	2e-10	90%	gi|686700213|XP_009236694.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pong	64.3	64.3	100%	2e-10	90%	gi|297662141|XP_002809574.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Papic	63.8	63.8	100%	3e-10	90%	gi|685519789|XP_009186662.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Maca	63.8	63.8	100%	3e-10	90%	gi|544399939|XP_005540733.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Maca	63.8	63.8	100%	3e-10	90%	gi|544399931|XP_005540729.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Papic	63.8	63.8	100%	3e-10	90%	gi|685519785|XP_009186656.1
☐	hypothetical protein EGM_01442 [Macaca fascicularis]	63.8	63.8	100%	3e-10	90%	gi|355745961|EHH50586.1
☐	hypothetical protein EGK_01712 [Macaca mulatta]	63.8	63.8	100%	3e-10	90%	gi|355558818|EHH15598.1
☐	PREDICTED: c4b-binding protein beta chain isoform 3 [Macaca	63.8	63.8	100%	3e-10	90%	gi|109018561|XP_001083216.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Maca	63.8	63.8	100%	3e-10	90%	gi|544399929|XP_005540728.1
☐	PREDICTED: C4b-binding protein beta chain isoform 1 [Nomas	63.4	63.4	100%	4e-10	90%	gi|332266848|XP_003282407.1
☐	PREDICTED: C4b-binding protein beta chain isoform X9 [Chlor	63.0	63.0	100%	6e-10	90%	gi|635130917|XP_007986833.1
☐	PREDICTED: C4b-binding protein beta chain isoform X8 [Chlor	63.0	63.0	100%	6e-10	90%	gi|635130915|XP_007986832.1
☐	PREDICTED: C4b-binding protein beta chain isoform X7 [Chlor	63.0	63.0	100%	6e-10	90%	gi|635130913|XP_007986831.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Chlor	63.0	63.0	100%	6e-10	90%	gi|635130911|XP_007986830.1
☐	PREDICTED: C4b-binding protein beta chain isoform X5 [Chlor	63.0	63.0	100%	6e-10	90%	gi|635130907|XP_007986828.1

☐	PREDICTED: C4b-binding protein beta chain isoform X4 [Chlor	63.0	63.0	100%	6e-10	90%	gi|635130905|XP_007986827.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Chlor	63.0	63.0	100%	7e-10	90%	gi|635130903|XP_007986826.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Chlor	63.0	63.0	100%	7e-10	90%	gi|635130901|XP_007986825.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Chlor	63.0	63.0	100%	7e-10	90%	gi|635130899|XP_007986823.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Callitl	61.3	61.3	90%	2e-09	94%	gi|675749407|XP_008983835.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Callitl	61.3	61.3	90%	2e-09	94%	gi|296230632|XP_002760794.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Saim	56.2	56.2	90%	1e-07	89%	gi|725574024|XP_010339305.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Saim	56.2	56.2	90%	1e-07	89%	gi|403277664|XP_003930472.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Galeo	48.6	48.6	100%	4e-05	70%	gi|667314769|XP_008585888.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Galeo	48.6	48.6	100%	5e-05	70%	gi|667314766|XP_008585886.1
☐	PREDICTED: C4b-binding protein beta chain [Chrysochloris as	47.3	47.3	95%	1e-04	79%	gi|586450676|XP_006834269.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	45.2	45.2	100%	6e-04	70%	gi|594636425|XP_007171607.1
☐	PREDICTED: C4b-binding protein beta chain [Nannospalax gal	44.8	44.8	100%	8e-04	76%	gi|674096417|XP_008821570.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	43.9	43.9	60%	0.002	100%	gi|471369765|XP_004375397.1
☐	PREDICTED: C4b-binding protein beta chain [Sus scrofa]	43.5	43.5	100%	0.002	65%	gi|311265148|XP_003130503.1
☐	PREDICTED: C4b-binding protein beta chain [Otolemur garnett	43.1	43.1	100%	0.003	70%	gi|395838946|XP_003792365.1
☐	PREDICTED: C4b-binding protein beta chain [Orcinus orca]	42.6	42.6	100%	0.004	65%	gi|466071254|XP_004282462.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Myoti	42.6	42.6	95%	0.004	74%	gi|554587742|XP_005885272.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis lucifugus]	42.6	42.6	95%	0.004	74%	gi|558152655|XP_006094937.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Myoti	42.6	42.6	95%	0.004	74%	gi|554587740|XP_005885271.1
☐	PREDICTED: C4b-binding protein beta chain [Ictidomys tridece	41.8	41.8	100%	0.008	70%	gi|532087633|XP_005329528.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Tarsi	41.8	41.8	100%	0.008	65%	gi|640811969|XP_008062626.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Tarsi	41.8	41.8	100%	0.008	65%	gi|640811967|XP_008062625.1
☐	PREDICTED: C4b-binding protein beta chain [Ceratotherium si	41.4	41.4	95%	0.011	68%	gi|478501878|XP_004425250.1
☐	PREDICTED: C4b-binding protein beta chain [Cavia porcellus]	40.9	40.9	100%	0.014	65%	gi|348577871|XP_003474707.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	40.5	40.5	90%	0.020	67%	gi|470641603|XP_004325529.1
☐	PREDICTED: C4b-binding protein beta chain [Eptesicus fuscus	38.8	38.8	95%	0.070	68%	gi|641725104|XP_008152491.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis davidii]	38.4	38.4	55%	0.094	91%	gi|584068188|XP_006754475.1
☐	PREDICTED: C4b-binding protein beta chain [Jaculus jaculus]	38.4	38.4	80%	0.096	75%	gi|507559572|XP_004663509.1
☐	PREDICTED: C4b-binding protein beta chain [Elephantulus edv	38.0	38.0	90%	0.13	67%	gi|585666900|XP_006888062.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Came	37.5	37.5	90%	0.18	61%	gi|743734558|XP_010961541.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Came	37.5	37.5	90%	0.18	61%	gi|743734556|XP_010961540.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	37.5	37.5	90%	0.18	61%	gi|560935168|XP_006193413.1
☐	PREDICTED: C4b-binding protein beta chain [Mustela putorius	36.7	36.7	100%	0.33	65%	gi|511871202|XP_004756233.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	34.1	34.1	90%	2.2	56%	gi|560986663|XP_006215518.1
☐	PREDICTED: C4b-binding protein beta chain [Ornithorhynchus	33.3	33.3	60%	3.5	83%	gi|620984032|XP_007659774.1
☐	PREDICTED: C4b-binding protein beta chain [Leptonychotes w	32.9	32.9	60%	5.5	75%	gi|585156269|XP_006730462.1
☐	C4b-binding protein beta chain [Heterocephalus glaber]	32.0	32.0	80%	10	63%	gi|351708103|EHB11022.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	32.0	32.0	75%	10	60%	gi|533120065|XP_005375468.1
☐	PREDICTED: C4b-binding protein beta chain [Heterocephalus g	32.0	32.0	80%	10	63%	gi|512892965|XP_004897416.1
☐	PREDICTED: C4b-binding protein beta chain [Pteropus alecto]	31.6	31.6	100%	14	55%	gi|586536223|XP_006922979.1
☐	C4b-binding protein beta chain [Pteropus alecto]	31.6	31.6	100%	14	55%	gi|431892854|ELK03282.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	31.2	31.2	65%	18	61%	gi|345128523|AEN75212.1
☐	hypothetical protein PFNF135_02825 [Plasmodium falciparum I	31.2	31.2	60%	20	67%	gi|574981166|ETW42931.1
☐	hypothetical protein [Clostridium sp. CAG:62]	31.2	31.2	40%	20	100%	gi|548057742|WP_022376409.1

☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.8	30.8	55%	26	75%	gi|338224254|AEI88022.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.8	30.8	55%	26	75%	gi|30908538|AAP37305.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Felis	30.8	30.8	100%	27	55%	gi|587018341|XP_006942889.1
☐	hypothetical protein PANDA_018755 [Ailuropoda melanoleuca]	30.8	30.8	85%	27	59%	gi|281337925|EFB13509.1
☐	PREDICTED: C4b-binding protein beta chain [Canis lupus fami	30.8	30.8	60%	27	75%	gi|73960685|XP_851611.1
☐	PREDICTED: C4b-binding protein beta chain [Ursus maritimus]	30.8	30.8	85%	27	59%	gi|670984389|XP_008683289.1
☐	PREDICTED: c4b-binding protein beta chain-like [Ailuropoda m	30.8	30.8	85%	27	59%	gi|301786617|XP_002928722.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Felis	30.8	30.8	100%	27	55%	gi|410986395|XP_003999496.1
☐	PREDICTED: complement C1r subcomponent [Stegastes partit	30.8	30.8	70%	28	63%	gi|657546451|XP_008278409.1
☐	hypothetical protein [Vibrio nigripulchritudo]	30.3	30.3	50%	35	70%	gi|740359636|WP_038195698.1
☐	hypothetical protein PFTANZ_02364 [Plasmodium falciparum T	30.3	30.3	55%	35	73%	gi|574974832|ETW36946.1
☐	hypothetical protein [Vibrio nigripulchritudo]	30.3	30.3	50%	35	70%	gi|740309755|WP_038147115.1
☐	putative Fimh-like protein [Vibrio nigripulchritudo]	30.3	30.3	50%	36	70%	gi|550352361|WP_022612127.1
☐	putative Fimh-like protein [Vibrio nigripulchritudo]	30.3	30.3	50%	36	70%	gi|550281458|WP_022607838.1
☐	hypothetical protein VINI7043_08940 [Vibrio nigripulchritudo AT	30.3	30.3	50%	36	70%	gi|342820393|EGU55216.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.3	30.3	60%	36	56%	gi|163637312|ABY27456.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.3	30.3	60%	36	56%	gi|163637310|ABY27455.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.3	30.3	60%	36	56%	gi|163637307|ABY27454.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.3	30.3	60%	36	56%	gi|163637305|ABY27453.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.3	30.3	60%	36	56%	gi|163637303|ABY27452.1
☐	hypothetical protein PFFCH_03778 [Plasmodium falciparum FC	30.3	30.3	55%	37	73%	gi|574965586|ETW28803.1
☐	hypothetical protein PFFVO_01913 [Plasmodium falciparum Vi	30.3	30.3	55%	37	73%	gi|574751318|ETW19338.1
☐	hypothetical protein [Bacillus coagulans]	29.9	29.9	60%	48	75%	gi|737205332|WP_035190263.1
☐	hypothetical protein [Bacillus coagulans]	29.9	29.9	60%	49	75%	gi|651961719|WP_026684018.1
☐	hypothetical protein [Bacillus coagulans]	29.9	29.9	60%	49	75%	gi|503862578|WP_014096572.1
☐	PREDICTED: fibroin heavy chain-like [Callithrix jacchus]	29.9	29.9	50%	51	83%	gi|675768476|XP_008987859.1

Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194373591|dbj|BAG56891.1| **Length:** 218 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 49 to 68 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.7 bits(152)	1e-11	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1   KTLFCNASKEWDDTTTECRL  20
           KTLFCNASKEWD+TTTECRL
Sbjct  49  KTLFCNASKEWDNTTTECRL  68
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Pan troglodytes]

Sequence ID: gi|694891540|ref|XP_009439669.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 58 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.7 bits(152)	1e-11	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1   KTLFCNASKEWDDTTTECRL  20
           KTLFCNASKEWD+TTTECRL
Sbjct  58  KTLFCNASKEWDNTTTECRL  77
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Pan paniscus]

Sequence ID: gi|675771724|ref|XP_008974762.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 58 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.7 bits(152)	1e-11	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1   KTLFCNASKEWDDTTTECRL  20
           KTLFCNASKEWD+TTTECRL
Sbjct  58  KTLFCNASKEWDNTTTECRL  77
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sapiens]

Sequence ID: gi|530366462|ref|XP_005273312.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 58 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.7 bits(152)	1e-11	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1   KTLFCNASKEWDDTTTECRL  20
           KTLFCNASKEWD+TTTECRL
Sbjct  58  KTLFCNASKEWDNTTTECRL  77
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinopithecus roxellana]

Sequence ID: gi|724836382|ref|XP_010363947.1| **Length:** 251 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 58 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.7 bits(152)	2e-11	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1   KTLFCNASKEWDDTTTECRL  20
           KTLFCNASKEWD+TTTECRL
Sbjct  58  KTLFCNASKEWDNTTTECRL  77
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - B92HDF4V01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download

How to read this page Blast report description

C4BPB_KTLFCNASKEWDNTTTECRL_NonMod

RID B92HDF4V01R (Expires on 01-14 09:59 am)

Query ID	lcl|304229	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ ▷Citation
Query Length	20		

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

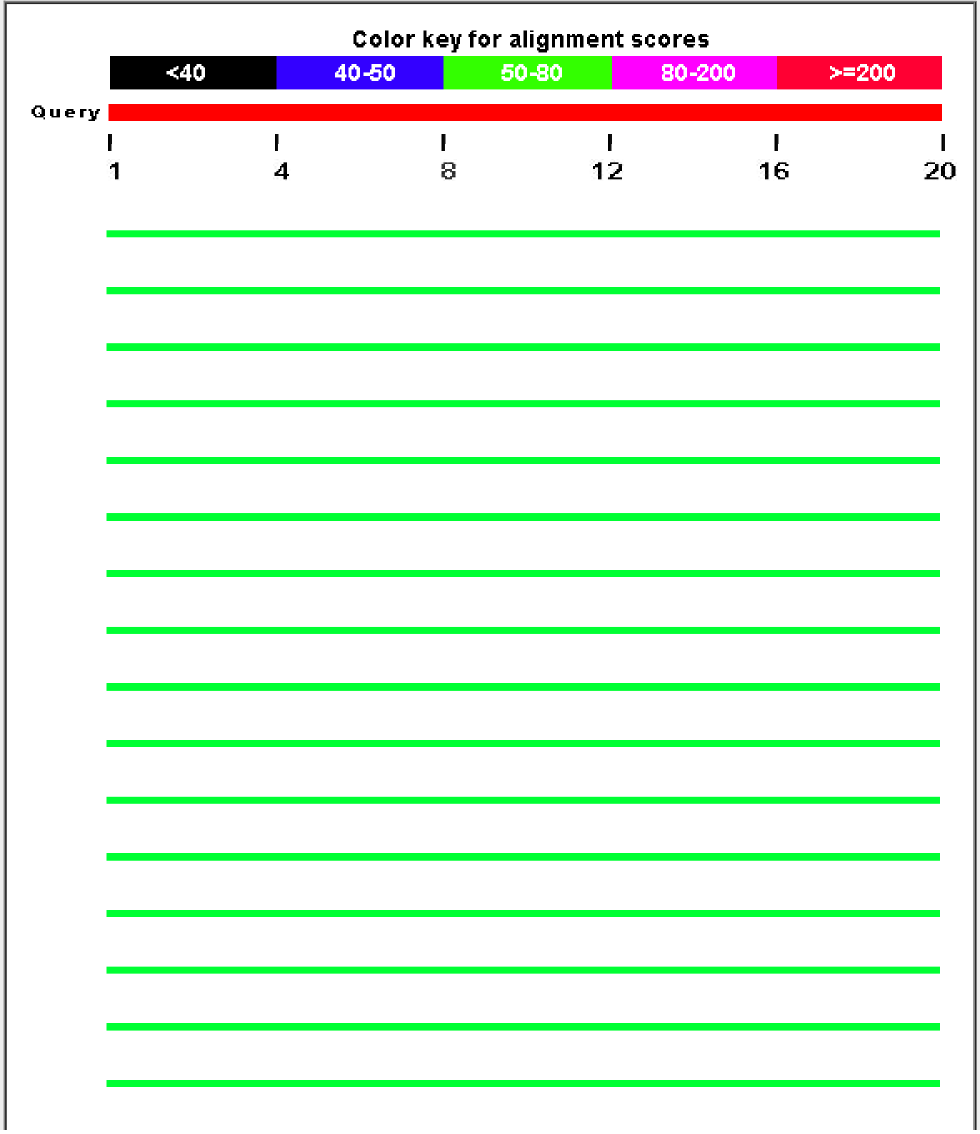
⊟Graphic Summary

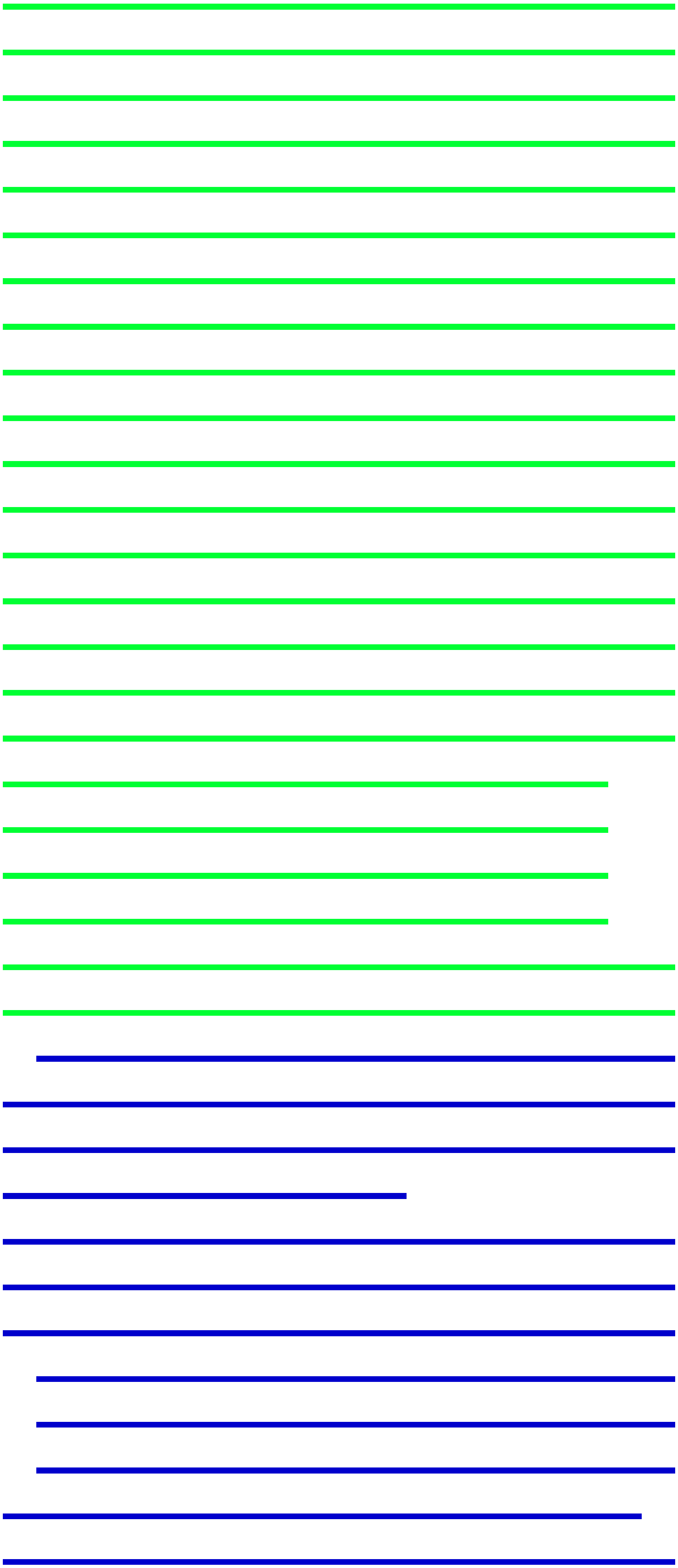
⊟Show Conserved Domains

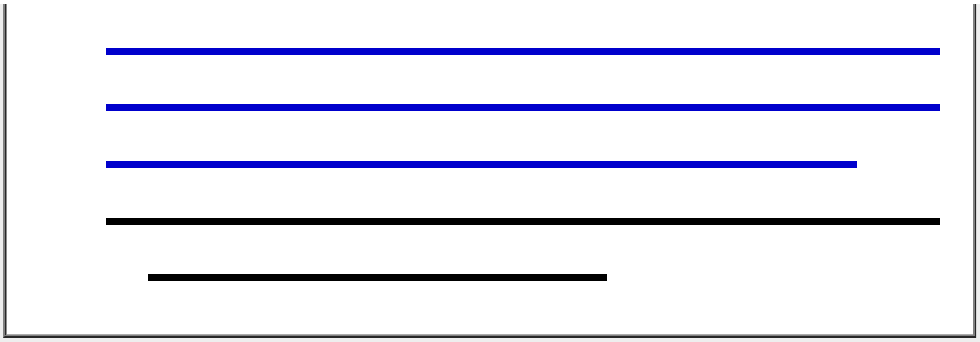
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	70.2	70.2	100%	2e-12	100%	gi|194373591|BAG56891.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan trogl	70.2	70.2	100%	2e-12	100%	gi|694891540|XP_009439669.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan panis	70.2	70.2	100%	2e-12	100%	gi|675771724|XP_008974762.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sa	70.2	70.2	100%	2e-12	100%	gi|530366462|XP_005273312.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinopith	70.2	70.2	100%	2e-12	100%	gi|724836382|XP_010363947.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan trogl	70.2	70.2	100%	2e-12	100%	gi|694891534|XP_009439665.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan panis	70.2	70.2	100%	2e-12	100%	gi|675771715|XP_008974759.1
☐	C4b-binding protein beta chain isoform 2 precursor [Homo sapiens]	70.2	70.2	100%	2e-12	100%	gi|62912462|NP_001017364.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Rhinopith	70.2	70.2	100%	2e-12	100%	gi|724836379|XP_010363946.1
☐	C4b-binding protein beta chain isoform 1 precursor [Homo sapiens]	70.2	70.2	100%	2e-12	100%	gi|4502505|NP_000707.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan panis	70.2	70.2	100%	2e-12	100%	gi|397504761|XP_003822949.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan trogl	70.2	70.2	100%	2e-12	100%	gi|114572288|XP_001166306.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pongo ab	66.8	66.8	100%	3e-11	95%	gi|686700216|XP_009236698.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pongo ab	66.8	66.8	100%	3e-11	95%	gi|686700213|XP_009236694.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pongo ab	66.8	66.8	100%	3e-11	95%	gi|297662141|XP_002809574.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Papio anu	66.4	66.4	100%	4e-11	95%	gi|685519789|XP_009186662.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Macaca f	66.4	66.4	100%	4e-11	95%	gi|544399939|XP_005540733.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Macaca f	66.4	66.4	100%	4e-11	95%	gi|544399931|XP_005540729.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Papio anu	66.4	66.4	100%	4e-11	95%	gi|685519785|XP_009186656.1
☐	hypothetical protein EGM_01442 [Macaca fascicularis]	66.4	66.4	100%	4e-11	95%	gi|355745961|EHH50586.1
☐	hypothetical protein EGK_01712 [Macaca mulatta]	66.4	66.4	100%	4e-11	95%	gi|355558818|EHH15598.1
☐	PREDICTED: c4b-binding protein beta chain isoform 3 [Macaca mu	66.4	66.4	100%	4e-11	95%	gi|109018561|XP_001083216.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Macaca f	66.4	66.4	100%	4e-11	95%	gi|544399929|XP_005540728.1
☐	PREDICTED: C4b-binding protein beta chain isoform 1 [Nomascus	66.0	66.0	100%	6e-11	95%	gi|332266848|XP_003282407.1
☐	PREDICTED: C4b-binding protein beta chain isoform X9 [Chloroce	65.5	65.5	100%	7e-11	95%	gi|635130917|XP_007986833.1
☐	PREDICTED: C4b-binding protein beta chain isoform X8 [Chloroce	65.5	65.5	100%	8e-11	95%	gi|635130915|XP_007986832.1
☐	PREDICTED: C4b-binding protein beta chain isoform X7 [Chloroce	65.5	65.5	100%	8e-11	95%	gi|635130913|XP_007986831.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Chloroce	65.5	65.5	100%	8e-11	95%	gi|635130911|XP_007986830.1
☐							

	PREDICTED: C4b-binding protein beta chain isoform X5 [Chloroce	65.5	65.5	100%	8e-11	95%	gi|635130907|XP_007986828.1
☐	PREDICTED: C4b-binding protein beta chain isoform X4 [Chloroce	65.5	65.5	100%	8e-11	95%	gi|635130905|XP_007986827.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Chloroce	65.5	65.5	100%	8e-11	95%	gi|635130903|XP_007986826.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Chloroce	65.5	65.5	100%	8e-11	95%	gi|635130901|XP_007986825.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Chloroce	65.5	65.5	100%	8e-11	95%	gi|635130899|XP_007986823.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Callithrix	63.8	63.8	90%	3e-10	100%	gi|675749407|XP_008983835.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Callithrix	63.8	63.8	90%	3e-10	100%	gi|296230632|XP_002760794.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Saimiri b	58.7	58.7	90%	2e-08	94%	gi|725574024|XP_010339305.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Saimiri b	58.7	58.7	90%	2e-08	94%	gi|403277664|XP_003930472.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Galeopte	50.3	50.3	100%	1e-05	70%	gi|667314769|XP_008585888.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Galeopte	50.3	50.3	100%	1e-05	70%	gi|667314766|XP_008585886.1
☐	PREDICTED: C4b-binding protein beta chain [Chrysochloris asiatic	46.9	46.9	95%	2e-04	79%	gi|586450676|XP_006834269.1
☐	PREDICTED: C4b-binding protein beta chain [Nannospalax galili]	45.6	45.6	100%	4e-04	75%	gi|674096417|XP_008821570.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	44.8	44.8	100%	8e-04	70%	gi|594636425|XP_007171607.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	43.9	43.9	60%	0.002	100%	gi|471369765|XP_004375397.1
☐	PREDICTED: C4b-binding protein beta chain [Sus scrofa]	43.1	43.1	100%	0.003	65%	gi|311265148|XP_003130503.1
☐	PREDICTED: C4b-binding protein beta chain [Otolemur garnettii]	42.6	42.6	100%	0.004	70%	gi|395838946|XP_003792365.1
☐	PREDICTED: C4b-binding protein beta chain [Orcinus orca]	42.2	42.2	100%	0.005	65%	gi|466071254|XP_004282462.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Myotis br	42.2	42.2	95%	0.005	74%	gi|554587742|XP_005885272.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis lucifugus]	42.2	42.2	95%	0.005	74%	gi|558152655|XP_006094937.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Myotis br	42.2	42.2	95%	0.005	74%	gi|554587740|XP_005885271.1
☐	PREDICTED: C4b-binding protein beta chain [Ceratotherium simu	41.4	41.4	95%	0.010	68%	gi|478501878|XP_004425250.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Tarsius s	41.4	41.4	100%	0.010	65%	gi|640811969|XP_008062626.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Tarsius s	41.4	41.4	100%	0.010	65%	gi|640811967|XP_008062625.1
☐	PREDICTED: C4b-binding protein beta chain [Cavia porcellus]	40.5	40.5	100%	0.019	65%	gi|348577871|XP_003474707.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	40.1	40.1	90%	0.026	67%	gi|470641603|XP_004325529.1
☐	PREDICTED: C4b-binding protein beta chain [Ictidomys tridecemlin	39.2	39.2	100%	0.048	65%	gi|532087633|XP_005329528.1
☐	PREDICTED: C4b-binding protein beta chain [Myotis davidii]	38.4	38.4	55%	0.089	91%	gi|584068188|XP_006754475.1
☐	PREDICTED: C4b-binding protein beta chain [Eptesicus fuscus]	38.4	38.4	95%	0.091	68%	gi|641725104|XP_008152491.1
☐	PREDICTED: C4b-binding protein beta chain [Jaculus jaculus]	38.4	38.4	80%	0.091	75%	gi|507559572|XP_004663509.1
☐	PREDICTED: C4b-binding protein beta chain [Elephantulus edward	37.5	37.5	90%	0.17	67%	gi|585666900|XP_006888062.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	37.1	37.1	90%	0.23	61%	gi|560935168|XP_006193413.1
☐	PREDICTED: C4b-binding protein beta chain [Mustela putorius furo	36.3	36.3	100%	0.43	65%	gi|511871202|XP_004756233.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	33.7	33.7	90%	2.8	56%	gi|560986663|XP_006215518.1
☐	PREDICTED: C4b-binding protein beta chain [Ornithorhynchus ana	33.3	33.3	60%	3.3	83%	gi|620984032|XP_007659774.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Felis catu	33.3	33.3	100%	3.8	60%	gi|587018341|XP_006942889.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Felis catu	33.3	33.3	100%	3.8	60%	gi|410986395|XP_003999496.1
☐	putative Fimh-like protein [Vibrio nigripulchritudo]	32.9	32.9	50%	5.0	80%	gi|550352361|WP_022612127.1
☐	putative Fimh-like protein [Vibrio nigripulchritudo]	32.9	32.9	50%	5.0	80%	gi|550281458|WP_022607838.1
☐	hypothetical protein [Vibrio nigripulchritudo]	32.9	32.9	50%	5.0	80%	gi|490542018|WP_004407142.1
☐	PREDICTED: C4b-binding protein beta chain [Leptonychotes wedd	32.9	32.9	60%	5.2	75%	gi|585156269|XP_006730462.1
☐	PREDICTED: C4b-binding protein beta chain [Pteropus alecto]	32.9	32.9	100%	5.2	55%	gi|586536223|XP_006922979.1
☐	C4b-binding protein beta chain [Pteropus alecto]	32.9	32.9	100%	5.2	55%	gi|431892854|ELK03282.1
☐	hypothetical protein [Plasmodium knowlesi strain H]	32.0	32.0	65%	9.6	75%	gi|221054814|XP_002258546.1
☐	hypothetical protein PFNF135_02825 [Plasmodium falciparum NF1	32.0	32.0	70%	9.9	63%	gi|574981166|ETW42931.1

☐	arginyl-tRNA synthetase [Helicobacter apodemus]	32.0	32.0	70%	9.9	71%	gi|696169675|KGL15468.1
☐	C4b-binding protein beta chain [Heterocephalus glaber]	31.6	31.6	80%	13	63%	gi|351708103|EHB11022.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	31.6	31.6	75%	13	60%	gi|533120065|XP_005375468.1
☐	PREDICTED: C4b-binding protein beta chain [Heterocephalus glab	31.6	31.6	80%	13	63%	gi|512892965|XP_004897416.1
☐	DNA repair protein RadA [Osedax symbiont Rs2]	31.6	31.6	80%	14	69%	gi|520769936|WP_020286673.1
☐	DNA repair protein RadA [Osedax symbiont Rs1]	31.6	31.6	80%	14	69%	gi|518641042|WP_019811142.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	31.2	31.2	55%	17	75%	gi|84873457|ABC67785.1
☐	conserved putative membrane protein [Melbournevirus]	31.2	31.2	65%	19	62%	gi|701447374|YP_009094746.1
☐	membrane protein [Cannes 8 virus]	31.2	31.2	65%	19	62%	gi|539398800|AGV01635.1
☐	hypothetical protein [Treponema bryantii]	31.2	31.2	75%	19	60%	gi|551312583|WP_022932465.1
☐	envelope protein [Human immunodeficiency virus 1]	30.8	30.8	55%	24	75%	gi|515020035|AGO65073.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.8	30.8	50%	24	82%	gi|24079811|AAN46022.1
☐	PREDICTED: C4b-binding protein beta chain [Canis lupus familiaris	30.8	30.8	60%	25	75%	gi|73960685|XP_851611.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.8	30.8	50%	25	82%	gi|42494103|AAS17398.1
☐	PREDICTED: complement C1r subcomponent [Stegastes partitus]	30.8	30.8	70%	26	63%	gi|657546451|XP_008278409.1
☐	von Willebrand factor D and EGF domain-containing protein [Crass	30.8	30.8	70%	26	71%	gi|405969928|EKC34871.1
☐	hypothetical protein PFTANZ_02364 [Plasmodium falciparum Tanz	30.3	30.3	55%	33	73%	gi|574974832|ETW36946.1
☐	hypothetical protein C922_01705 [Plasmodium inui San Antonio 1]	30.3	30.3	65%	34	69%	gi|672191245|XP_008815530.1
☐	hypothetical protein PANDA_018755 [Ailuropoda melanoleuca]	30.3	30.3	85%	35	59%	gi|281337925|EFB13509.1
☐	PREDICTED: C4b-binding protein beta chain [Ursus maritimus]	30.3	30.3	85%	35	59%	gi|670984389|XP_008683289.1
☐	hypothetical protein PFFCH_03778 [Plasmodium falciparum FCH/4	30.3	30.3	55%	35	73%	gi|574965586|ETW28803.1
☐	PREDICTED: c4b-binding protein beta chain-like [Ailuropoda melan	30.3	30.3	85%	35	59%	gi|301786617|XP_002928722.1
☐	hypothetical protein PFFVO_01913 [Plasmodium falciparum Vietna	30.3	30.3	55%	35	73%	gi|574751318|ETW19338.1
☐	DNA repair protein RadA [Avibacterium paragallinarum]	30.3	30.3	80%	35	69%	gi|516416332|WP_017805730.1
☐	hypothetical protein [Bacillus coagulans]	29.9	29.9	60%	47	75%	gi|651961719|WP_026684018.1
☐	hypothetical protein [Bacillus coagulans]	29.9	29.9	60%	47	75%	gi|503862578|WP_014096572.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	29.9	29.9	50%	47	82%	gi|323406966|ADX63958.1

Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194373591|dbj|BAG56891.1| **Length:** 218 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 49 to 68 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.2 bits(158)	2e-12	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KTLFCNASKEWDNTTTECRL  20
            KTLFCNASKEWDNTTTECRL
Sbjct  49   KTLFCNASKEWDNTTTECRL  68
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Pan troglodytes]

Sequence ID: gi|694891540|ref|XP_009439669.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 58 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.2 bits(158)	2e-12	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KTLFCNASKEWDNTTTECRL  20
```

```
               KTLFCNASKEWDNTTTECRL
Sbjct  58   KTLFCNASKEWDNTTTECRL  77
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan paniscus]

Sequence ID: gi|675771724|ref|XP_008974762.1| **Length:** 227 **Number of Matches:** 1

Range 1: 58 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.2 bits(158)	2e-12	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KTLFCNASKEWDNTTTECRL  20
            KTLFCNASKEWDNTTTECRL
Sbjct  58   KTLFCNASKEWDNTTTECRL  77
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sapiens]

Sequence ID: gi|530366462|ref|XP_005273312.1| **Length:** 227 **Number of Matches:** 1

Range 1: 58 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.2 bits(158)	2e-12	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KTLFCNASKEWDNTTTECRL  20
            KTLFCNASKEWDNTTTECRL
Sbjct  58   KTLFCNASKEWDNTTTECRL  77
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinopithecus roxellana]

Sequence ID: gi|724836382|ref|XP_010363947.1| **Length:** 251 **Number of Matches:** 1

Range 1: 58 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.2 bits(158)	2e-12	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KTLFCNASKEWDNTTTECRL  20
            KTLFCNASKEWDNTTTECRL
Sbjct  58   KTLFCNASKEWDNTTTECRL  77
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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NCBI/ BLAST/ blastp suite/ Formatting Results - BTFUBAAD013

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

C4BPB_RLGHCPDPVLVDGEFSSSGPVDVSDKI_Mod

RID BTFUBAAD013 (Expires on 01-20 15:24 pm)

Query ID lcl|91775
Description None
Molecule type amino acid
Query Length 27

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

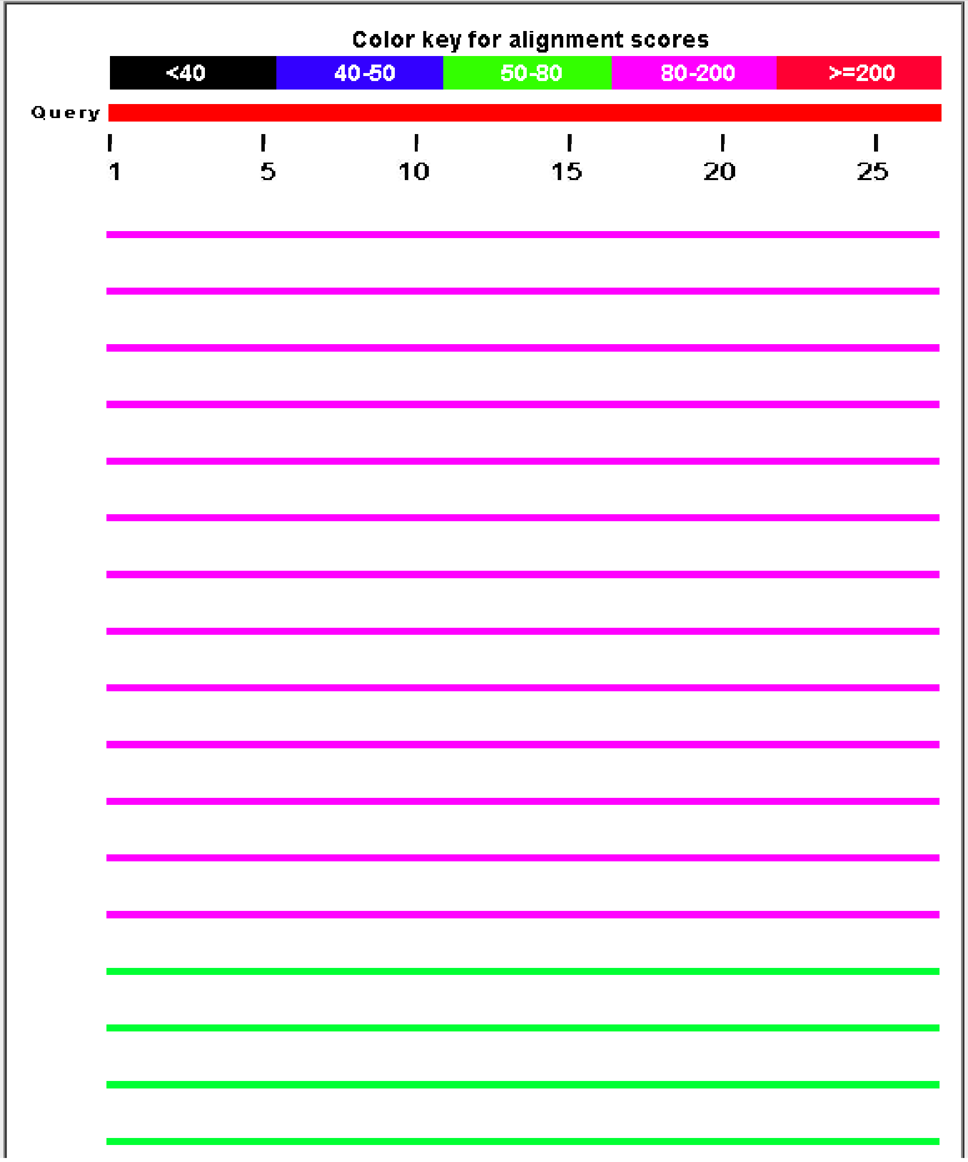
Graphic Summary

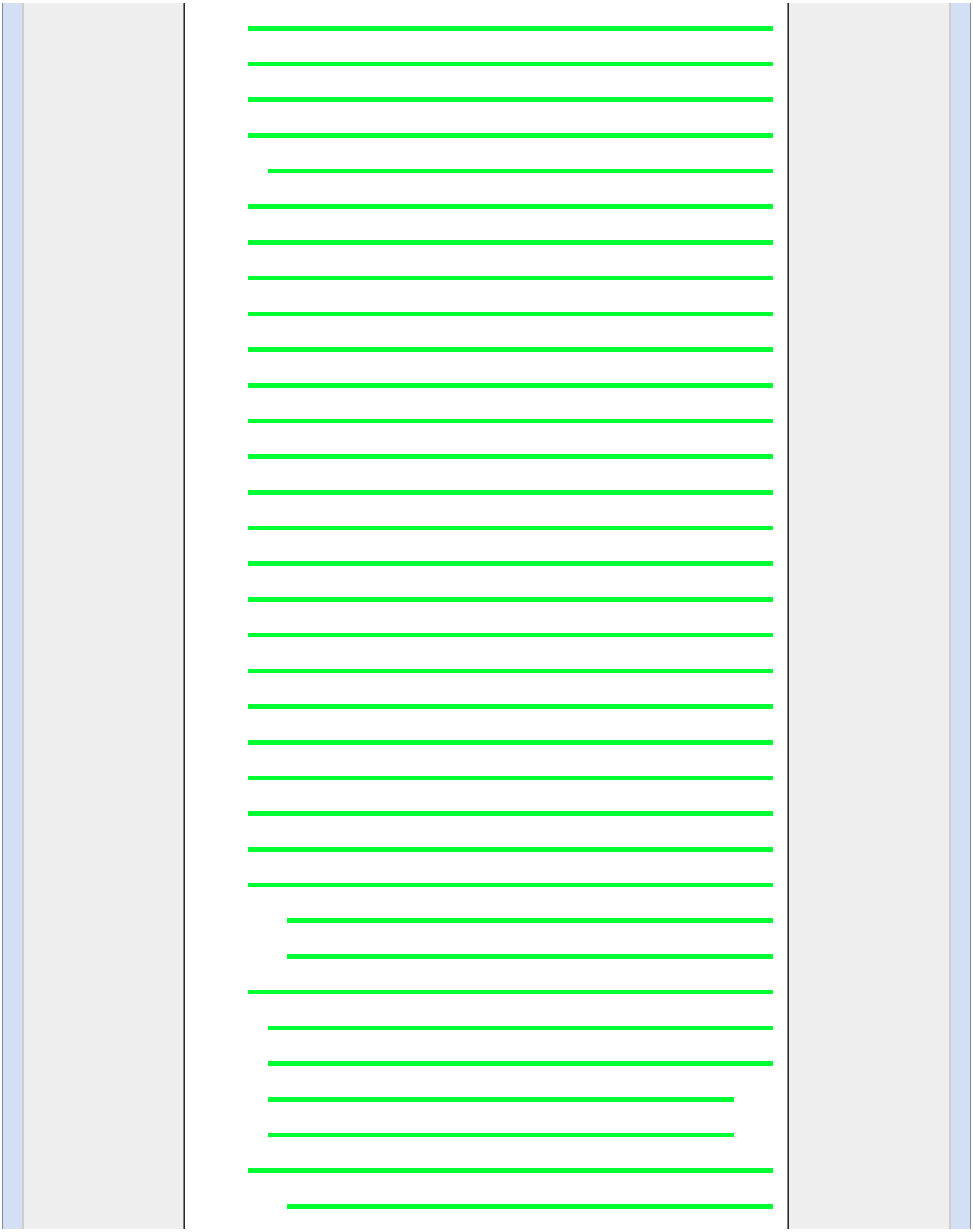
Show Conserved Domains

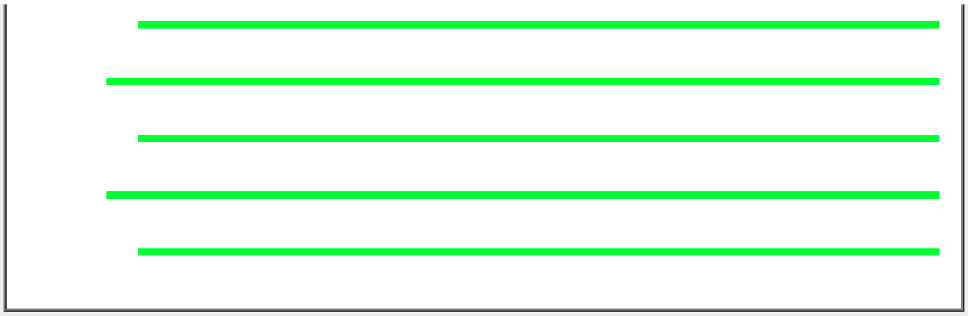
No putative conserved domains have been detected

Distribution of 108 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pong	82.5	82.5	100%	3e-16	93%	gi|686700216|XP_009236698.1
☐	unnamed protein product [Homo sapiens]	82.5	82.5	100%	3e-16	93%	gi|194373591|BAG56891.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan t	82.5	82.5	100%	3e-16	93%	gi|694891540|XP_009439669.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan p	82.5	82.5	100%	3e-16	93%	gi|675771724|XP_008974762.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Homo	82.5	82.5	100%	3e-16	93%	gi|530366462|XP_005273312.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan t	82.5	103	100%	3e-16	93%	gi|694891534|XP_009439665.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pong	82.5	82.5	100%	3e-16	93%	gi|686700213|XP_009236694.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan p	82.5	103	100%	3e-16	93%	gi|675771715|XP_008974759.1
☐	C4b-binding protein beta chain isoform 2 precursor [Homo sapi	82.5	103	100%	3e-16	93%	gi|62912462|NP_001017364.1
☐	C4b-binding protein beta chain isoform 1 precursor [Homo sapi	82.5	103	100%	3e-16	93%	gi|4502505|NP_000707.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan p	82.5	103	100%	3e-16	93%	gi|397504761|XP_003822949.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pong	82.5	82.5	100%	3e-16	93%	gi|297662141|XP_002809574.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan t	82.5	103	100%	3e-16	93%	gi|114572288|XP_001166306.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Papic	80.0	80.0	100%	2e-15	89%	gi|685519789|XP_009186662.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Papic	80.0	80.0	100%	2e-15	89%	gi|685519785|XP_009186656.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Tarsi	77.8	77.8	100%	1e-14	85%	gi|640811969|XP_008062626.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Tarsi	77.8	77.8	100%	1e-14	85%	gi|640811967|XP_008062625.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Maca	76.1	76.1	100%	5e-14	85%	gi|544399939|XP_005540733.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Maca	76.1	76.1	100%	5e-14	85%	gi|544399931|XP_005540729.1
☐	hypothetical protein EGM_01442 [Macaca fascicularis]	76.1	76.1	100%	5e-14	85%	gi|355745961|EHH50586.1
☐	hypothetical protein EGK_01712 [Macaca mulatta]	76.1	76.1	100%	5e-14	85%	gi|355558818|EHH15598.1
☐	PREDICTED: C4b-binding protein beta chain isoform 1 [Nomas	76.1	76.1	96%	5e-14	88%	gi|332266848|XP_003282407.1
☐	PREDICTED: c4b-binding protein beta chain isoform 3 [Macaca	76.1	76.1	100%	5e-14	85%	gi|109018561|XP_001083216.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Maca	76.1	76.1	100%	5e-14	85%	gi|544399929|XP_005540728.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinc	72.3	72.3	100%	1e-12	81%	gi|724836382|XP_010363947.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Rhinc	72.3	72.3	100%	1e-12	81%	gi|724836379|XP_010363946.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Galec	71.5	71.5	100%	2e-12	81%	gi|667314769|XP_008585888.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Galec	71.5	71.5	100%	2e-12	81%	gi|667314766|XP_008585886.1
☐	PREDICTED: C4b-binding protein beta chain isoform X9 [Chlor	71.0	71.0	100%	2e-12	81%	gi|635130917|XP_007986833.1

☐	PREDICTED: C4b-binding protein beta chain isoform X8 [Chlor	71.0	71.0	100%	3e-12	81%	gi|635130915|XP_007986832.1
☐	PREDICTED: C4b-binding protein beta chain isoform X7 [Chlor	71.0	71.0	100%	3e-12	81%	gi|635130913|XP_007986831.1
☐	PREDICTED: C4b-binding protein beta chain [Nannospalax gal	71.0	71.0	100%	3e-12	81%	gi|674096417|XP_008821570.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Chlor	71.0	71.0	100%	3e-12	81%	gi|635130911|XP_007986830.1
☐	PREDICTED: C4b-binding protein beta chain isoform X5 [Chlor	71.0	71.0	100%	3e-12	81%	gi|635130907|XP_007986828.1
☐	PREDICTED: C4b-binding protein beta chain isoform X4 [Chlor	71.0	71.0	100%	3e-12	81%	gi|635130905|XP_007986827.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Chlor	71.0	71.0	100%	3e-12	81%	gi|635130903|XP_007986826.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Chlor	71.0	71.0	100%	3e-12	81%	gi|635130901|XP_007986825.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Chlor	71.0	71.0	100%	3e-12	81%	gi|635130899|XP_007986823.1
☐	C4b-binding protein beta chain [Heterocephalus glaber]	68.9	68.9	100%	1e-11	81%	gi|351708103|EHB11022.1
☐	PREDICTED: C4b-binding protein beta chain [Cavia porcellus]	68.9	68.9	100%	1e-11	81%	gi|348577871|XP_003474707.1
☐	PREDICTED: C4b-binding protein beta chain [Heterocephalus	68.9	68.9	100%	1e-11	81%	gi|512892965|XP_004897416.1
☐	PREDICTED: C4b-binding protein beta chain [Ursus maritimus]	68.5	68.5	100%	2e-11	85%	gi|670984389|XP_008683289.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Equu	67.7	67.7	92%	3e-11	84%	gi|664745777|XP_008530230.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Equu	67.7	67.7	92%	3e-11	84%	gi|664745775|XP_008530229.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	66.4	66.4	100%	1e-10	78%	gi|533120065|XP_005375468.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Callit	66.4	66.4	96%	1e-10	85%	gi|675749407|XP_008983835.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Callit	66.4	66.4	96%	1e-10	85%	gi|296230632|XP_002760794.1
☐	C4b-binding protein beta chain [Fukomys damarensis]	66.4	66.4	88%	1e-10	88%	gi|676262835|KFO19654.1
☐	PREDICTED: C4b-binding protein beta chain [Fukomys damare	66.4	66.4	88%	1e-10	88%	gi|731286435|XP_010611521.1
☐	PREDICTED: C4b-binding protein beta chain [Mustela putorius	66.0	66.0	100%	1e-10	81%	gi|511871202|XP_004756233.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement compone	65.1	65.1	92%	2e-10	84%	gi|545215409|XP_005615108.1
☐	PREDICTED: C4b-binding protein beta chain [Loxodonta africa	65.1	65.1	96%	3e-10	77%	gi|731475974|XP_010588717.1
☐	hypothetical protein PANDA_018755 [Ailuropoda melanoleuca]	63.4	63.4	100%	1e-09	81%	gi|281337925|EFB13509.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Panth	63.4	63.4	96%	1e-09	81%	gi|591341473|XP_007096179.1
☐	PREDICTED: c4b-binding protein beta chain-like [Ailuropoda m	63.4	63.4	100%	1e-09	81%	gi|301786617|XP_002928722.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Panth	63.4	63.4	96%	1e-09	81%	gi|591341471|XP_007096178.1
☐	PREDICTED: C4b-binding protein beta chain [Pteropus alecto]	63.4	63.4	96%	1e-09	79%	gi|586536223|XP_006922979.1
☐	C4b-binding protein beta chain [Pteropus alecto]	63.4	63.4	96%	1e-09	79%	gi|431892854|ELK03282.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Saimi	63.0	63.0	96%	1e-09	81%	gi|725574024|XP_010339305.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Saimi	63.0	63.0	96%	1e-09	81%	gi|403277664|XP_003930472.1
☐	PREDICTED: C4b-binding protein beta chain [Otolemur garnett	63.0	63.0	100%	1e-09	70%	gi|395838946|XP_003792365.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	61.7	61.7	100%	4e-09	74%	gi|594636425|XP_007171607.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Felis	60.9	81.9	96%	7e-09	77%	gi|587018341|XP_006942889.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Felis	60.9	81.9	96%	7e-09	77%	gi|410986395|XP_003999496.1
☐	PREDICTED: C4b-binding protein beta chain [Orycteropus afer	60.0	60.0	92%	1e-08	80%	gi|634826787|XP_007951309.1
☐	PREDICTED: C4b-binding protein beta chain [Leptonychotes w	60.0	60.0	100%	1e-08	81%	gi|585156269|XP_006730462.1
☐	PREDICTED: C4b-binding protein beta chain [Orcinus orca]	59.6	59.6	92%	2e-08	76%	gi|466071254|XP_004282462.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	59.2	59.2	96%	3e-08	81%	gi|471369765|XP_004375397.1
☐	PREDICTED: C4b-binding protein beta chain [Ictidomys tridece	58.7	58.7	100%	4e-08	67%	gi|532087633|XP_005329528.1
☐	PREDICTED: C4b-binding protein beta chain [Ceratotherium si	57.5	57.5	100%	1e-07	70%	gi|478501878|XP_004425250.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	56.2	56.2	88%	3e-07	75%	gi|470641603|XP_004325529.1
☐	PREDICTED: C4b-binding protein beta chain [Odobenus rosma	56.2	56.2	100%	3e-07	78%	gi|472392625|XP_004415587.1
☐	PREDICTED: C4b-binding protein beta chain [Echinops telfairi]	55.4	55.4	96%	5e-07	73%	gi|507635442|XP_004700185.1
☐	PREDICTED: C4b-binding protein beta chain [Erinaceus europ	54.9	54.9	85%	7e-07	74%	gi|617638324|XP_007531172.1

☐	PREDICTED: C4b-binding protein beta chain [Chrysochloris as	54.9	54.9	100%	7e-07	70%	gi|586450676|XP_006834269.1
☐	C4b-binding protein beta chain precursor [Rattus norvegicus]	54.5	54.5	96%	1e-06	69%	gi|62198215|NP_058691.2
☐	RecName: Full=C4b-binding protein beta chain; Flags: Precurs	54.5	54.5	96%	1e-06	69%	gi|2493794|Q63515.1
☐	PREDICTED: C4b-binding protein beta chain [Jaculus jaculus]	54.5	54.5	100%	1e-06	70%	gi|507559572|XP_004663509.1
☐	PREDICTED: C4b-binding protein beta chain [Lipotes vexillifer]	53.2	53.2	85%	2e-06	74%	gi|602721258|XP_007470782.1
☐	PREDICTED: C4b-binding protein beta chain [Physeter catodo	53.2	53.2	85%	2e-06	74%	gi|593718317|XP_007105536.1
☐	PREDICTED: C4b-binding protein beta chain [Octodon degus]	52.8	52.8	96%	3e-06	73%	gi|507688352|XP_004641253.1
☐	PREDICTED: C4b-binding protein beta chain [Sus scrofa]	50.3	50.3	100%	2e-05	67%	gi|311265148|XP_003130503.1
☐	PREDICTED: C4b-binding protein beta chain [Canis lupus fami	49.8	49.8	96%	3e-05	68%	gi|73960685|XP_851611.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Micro	49.8	49.8	100%	3e-05	67%	gi|532009098|XP_005348366.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Micro	49.8	49.8	100%	3e-05	67%	gi|532009096|XP_005348365.1
☐	PREDICTED: C4b-binding protein beta chain [Peromyscus mar	47.3	47.3	100%	2e-04	63%	gi|589966374|XP_006995716.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Capr	46.4	46.4	85%	4e-04	70%	gi|548497748|XP_005690484.1
☐	C4b-binding protein beta chain precursor [Bos taurus]	46.4	46.4	85%	4e-04	70%	gi|99028955|NP_776678.2
☐	RecName: Full=C4b-binding protein beta chain; Flags: Precurs	46.4	46.4	85%	4e-04	70%	gi|2493793|Q28066.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Bos t	46.4	46.4	85%	4e-04	70%	gi|528979094|XP_005216707.1
☐	PREDICTED: C4b-binding protein beta chain [Pantholops hodg	46.4	46.4	85%	4e-04	70%	gi|556742954|XP_005966995.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Capr	46.4	46.4	85%	4e-04	70%	gi|548497744|XP_005690482.1
☐	complement component 4 binding protein, beta [Ovis aries]	46.4	46.4	85%	4e-04	70%	gi|444733674|CCQ71779.1
☐	PREDICTED: C4b-binding protein beta chain [Cricetulus griseu	45.6	45.6	96%	7e-04	62%	gi|625186859|XP_007614708.1
☐	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 [Cricetu	45.6	45.6	96%	8e-04	62%	gi|344244855|EGW00959.1
☐	6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 2 isofor	45.6	45.6	96%	8e-04	62%	gi|537167880|ERE73717.1
☐	6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 2 isofor	45.6	45.6	96%	8e-04	62%	gi|537167879|ERE73716.1
☐	PREDICTED: C4b-binding protein beta chain [Tupaia chinensis	43.9	43.9	96%	0.003	65%	gi|562862067|XP_006159349.1
☐	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 [Tupai	43.9	43.9	96%	0.003	65%	gi|444706417|ELW47759.1
☐	PREDICTED: C4b-binding protein beta chain [Mesocricetus au	43.5	43.5	92%	0.003	64%	gi|524960013|XP_005079950.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Pongo abelii]

Sequence ID: gi|686700216|ref|XP_009236698.1| **Length:** 202 **Number of Matches:** 1

Range 1: 67 to 93 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.5 bits(187)	3e-16	25/27(93%)	27/27(100%)	0/27(0%)

```
Query  1   RLGHCPDPVLVDGEFSSSGPVDVSDKI  27
           RLGHCPDPVLV+GEFSSSGPV+VSDKI
Sbjct  67  RLGHCPDPVLVNGEFSSSGPVNVSDKI  93
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: gi|194373591|dbj|BAG56891.1| **Length:** 218 **Number of Matches:** 1

Range 1: 67 to 93 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.5 bits(187)	3e-16	25/27(93%)	27/27(100%)	0/27(0%)

Related Information

Gene - associated gene details

```
Query  1   RLGHCPDPVLVDGEFSSSGPVDVSDKI  27
           RLGHCPDPVLV+GEFSSSGPV+VSDKI
Sbjct  67  RLGHCPDPVLVNGEFSSSGPVNVSDKI  93
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Pan troglodytes]

Sequence ID: gi|694891540|ref|XP_009439669.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 76 to 102 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.5 bits(187)	3e-16	25/27(93%)	27/27(100%)	0/27(0%)

```
Query  1    RLGHCPDPVLVDGEFSSSGPVDVSDKI  27
            RLGHCPDPVLV+GEFSSSGPV+VSDKI
Sbjct  76   RLGHCPDPVLVNGEFSSSGPVNVSDKI  102
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan paniscus]

Sequence ID: gi|675771724|ref|XP_008974762.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 76 to 102 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.5 bits(187)	3e-16	25/27(93%)	27/27(100%)	0/27(0%)

```
Query  1    RLGHCPDPVLVDGEFSSSGPVDVSDKI  27
            RLGHCPDPVLV+GEFSSSGPV+VSDKI
Sbjct  76   RLGHCPDPVLVNGEFSSSGPVNVSDKI  102
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sapiens]

Sequence ID: gi|530366462|ref|XP_005273312.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 76 to 102 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.5 bits(187)	3e-16	25/27(93%)	27/27(100%)	0/27(0%)

```
Query  1    RLGHCPDPVLVDGEFSSSGPVDVSDKI  27
            RLGHCPDPVLV+GEFSSSGPV+VSDKI
Sbjct  76   RLGHCPDPVLVNGEFSSSGPVNVSDKI  102
```

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Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

C4BPB_RLGHCPDPVLVNGEFSSSGPVDVSDKI_Mod

RID BTFUYYBP013 (Expires on 01-20 15:25 pm)

Query ID	lcl|91292	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	27		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

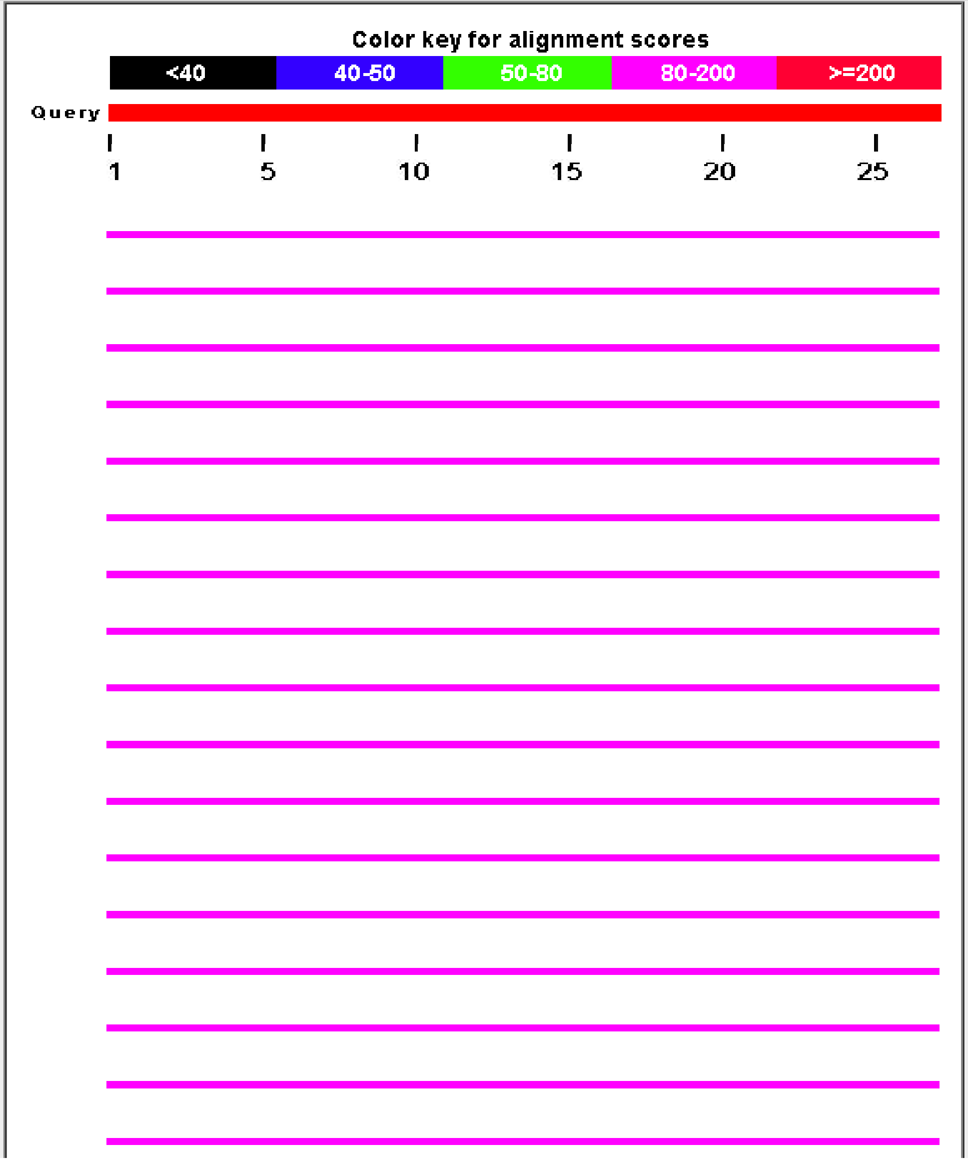
Graphic Summary

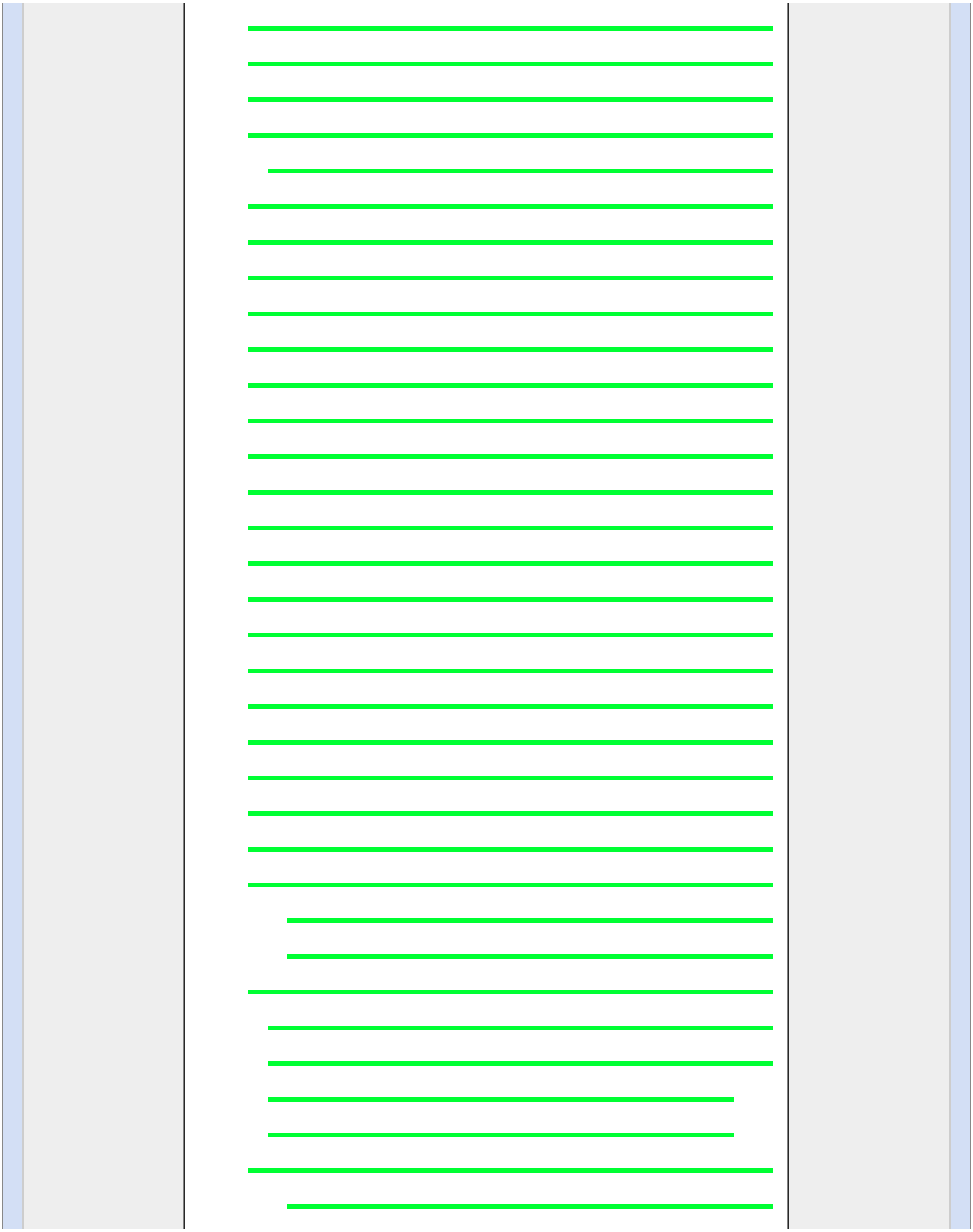
Show Conserved Domains

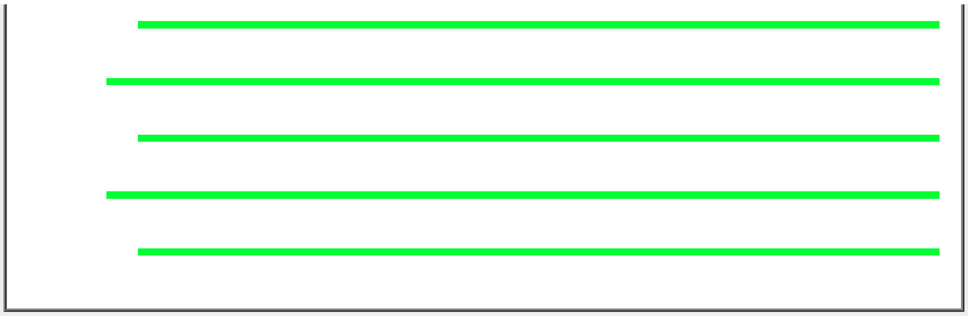
No putative conserved domains have been detected

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pong	85.0	85.0	100%	4e-17	96%	gi|686700216|XP_009236698.1
☐	unnamed protein product [Homo sapiens]	85.0	85.0	100%	4e-17	96%	gi|194373591|BAG56891.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan t	85.0	85.0	100%	4e-17	96%	gi|694891540|XP_009439669.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan p	85.0	85.0	100%	4e-17	96%	gi|675771724|XP_008974762.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Homo	85.0	85.0	100%	4e-17	96%	gi|530366462|XP_005273312.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan t	85.0	85.0	100%	4e-17	96%	gi|694891534|XP_009439665.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pong	85.0	85.0	100%	4e-17	96%	gi|686700213|XP_009236694.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan p	85.0	85.0	100%	4e-17	96%	gi|675771715|XP_008974759.1
☐	C4b-binding protein beta chain isoform 2 precursor [Homo sapi	85.0	85.0	100%	4e-17	96%	gi|62912462|NP_001017364.1
☐	C4b-binding protein beta chain isoform 1 precursor [Homo sapi	85.0	85.0	100%	4e-17	96%	gi|4502505|NP_000707.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan p	85.0	85.0	100%	4e-17	96%	gi|397504761|XP_003822949.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pong	85.0	85.0	100%	4e-17	96%	gi|297662141|XP_002809574.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan t	85.0	85.0	100%	4e-17	96%	gi|114572288|XP_001166306.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Papic	82.5	82.5	100%	3e-16	93%	gi|685519789|XP_009186662.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Papic	82.5	82.5	100%	3e-16	93%	gi|685519785|XP_009186656.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Tarsi	80.4	80.4	100%	2e-15	89%	gi|640811969|XP_008062626.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Tarsi	80.4	80.4	100%	2e-15	89%	gi|640811967|XP_008062625.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Maca	78.7	78.7	100%	7e-15	89%	gi|544399939|XP_005540733.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Maca	78.7	78.7	100%	7e-15	89%	gi|544399931|XP_005540729.1
☐	hypothetical protein EGM_01442 [Macaca fascicularis]	78.7	78.7	100%	7e-15	89%	gi|355745961|EHH50586.1
☐	hypothetical protein EGK_01712 [Macaca mulatta]	78.7	78.7	100%	7e-15	89%	gi|355558818|EHH15598.1
☐	PREDICTED: C4b-binding protein beta chain isoform 1 [Nomas	78.7	78.7	96%	7e-15	92%	gi|332266848|XP_003282407.1
☐	PREDICTED: c4b-binding protein beta chain isoform 3 [Macaca	78.7	78.7	100%	7e-15	89%	gi|109018561|XP_001083216.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Maca	78.7	78.7	100%	7e-15	89%	gi|544399929|XP_005540728.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinc	74.9	74.9	100%	1e-13	85%	gi|724836382|XP_010363947.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Rhinc	74.9	74.9	100%	1e-13	85%	gi|724836379|XP_010363946.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Galec	74.0	74.0	100%	2e-13	85%	gi|667314769|XP_008585888.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Galec	74.0	74.0	100%	3e-13	85%	gi|667314766|XP_008585886.1
☐	PREDICTED: C4b-binding protein beta chain isoform X9 [Chlor	73.6	73.6	100%	3e-13	85%	gi|635130917|XP_007986833.1

☐	PREDICTED: C4b-binding protein beta chain isoform X8 [Chlor	73.6	73.6	100%	4e-13	85%	gi|635130915|XP_007986832.1
☐	PREDICTED: C4b-binding protein beta chain isoform X7 [Chlor	73.6	73.6	100%	4e-13	85%	gi|635130913|XP_007986831.1
☐	PREDICTED: C4b-binding protein beta chain [Nannospalax gal	73.6	73.6	100%	4e-13	85%	gi|674096417|XP_008821570.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Chlor	73.6	73.6	100%	4e-13	85%	gi|635130911|XP_007986830.1
☐	PREDICTED: C4b-binding protein beta chain isoform X5 [Chlor	73.6	73.6	100%	4e-13	85%	gi|635130907|XP_007986828.1
☐	PREDICTED: C4b-binding protein beta chain isoform X4 [Chlor	73.6	73.6	100%	4e-13	85%	gi|635130905|XP_007986827.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Chlor	73.6	73.6	100%	4e-13	85%	gi|635130903|XP_007986826.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Chlor	73.6	73.6	100%	4e-13	85%	gi|635130901|XP_007986825.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Chlor	73.6	73.6	100%	4e-13	85%	gi|635130899|XP_007986823.1
☐	C4b-binding protein beta chain [Heterocephalus glaber]	71.5	71.5	100%	2e-12	85%	gi|351708103|EHB11022.1
☐	PREDICTED: C4b-binding protein beta chain [Cavia porcellus]	71.5	71.5	100%	2e-12	85%	gi|348577871|XP_003474707.1
☐	PREDICTED: C4b-binding protein beta chain [Heterocephalus	71.5	71.5	100%	2e-12	85%	gi|512892965|XP_004897416.1
☐	PREDICTED: C4b-binding protein beta chain [Ursus maritimus]	71.0	71.0	100%	3e-12	89%	gi|670984389|XP_008683289.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Equu	70.2	70.2	92%	5e-12	88%	gi|664745777|XP_008530230.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Equu	70.2	70.2	92%	5e-12	88%	gi|664745775|XP_008530229.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	68.9	68.9	100%	1e-11	81%	gi|533120065|XP_005375468.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Callitl	68.9	68.9	96%	1e-11	88%	gi|675749407|XP_008983835.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Callitl	68.9	68.9	96%	1e-11	88%	gi|296230632|XP_002760794.1
☐	C4b-binding protein beta chain [Fukomys damarensis]	68.9	68.9	88%	1e-11	92%	gi|676262835|KFO19654.1
☐	PREDICTED: C4b-binding protein beta chain [Fukomys damare	68.9	68.9	88%	1e-11	92%	gi|731286435|XP_010611521.1
☐	PREDICTED: C4b-binding protein beta chain [Mustela putorius	68.5	68.5	100%	2e-11	85%	gi|511871202|XP_004756233.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement compone	67.7	67.7	92%	3e-11	88%	gi|545215409|XP_005615108.1
☐	PREDICTED: C4b-binding protein beta chain [Loxodonta africa	67.7	88.7	96%	4e-11	81%	gi|731475974|XP_010588717.1
☐	hypothetical protein PANDA_018755 [Ailuropoda melanoleuca]	66.0	66.0	100%	1e-10	85%	gi|281337925|EFB13509.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Panth	66.0	66.0	96%	1e-10	85%	gi|591341473|XP_007096179.1
☐	PREDICTED: c4b-binding protein beta chain-like [Ailuropoda m	66.0	66.0	100%	1e-10	85%	gi|301786617|XP_002928722.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Panth	66.0	66.0	96%	1e-10	85%	gi|591341471|XP_007096178.1
☐	PREDICTED: C4b-binding protein beta chain [Pteropus alecto]	66.0	66.0	96%	1e-10	82%	gi|586536223|XP_006922979.1
☐	C4b-binding protein beta chain [Pteropus alecto]	66.0	66.0	96%	1e-10	82%	gi|431892854|ELK03282.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Saimi	65.5	65.5	96%	2e-10	85%	gi|725574024|XP_010339305.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Saimi	65.5	65.5	96%	2e-10	85%	gi|403277664|XP_003930472.1
☐	PREDICTED: C4b-binding protein beta chain [Otolemur garnett	65.5	65.5	100%	2e-10	74%	gi|395838946|XP_003792365.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	64.3	64.3	100%	5e-10	78%	gi|594636425|XP_007171607.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Felis	63.4	63.4	96%	1e-09	81%	gi|587018341|XP_006942889.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Felis	63.4	63.4	96%	1e-09	81%	gi|410986395|XP_003999496.1
☐	PREDICTED: C4b-binding protein beta chain [Orycteropus afer	62.6	62.6	92%	2e-09	84%	gi|634826787|XP_007951309.1
☐	PREDICTED: C4b-binding protein beta chain [Leptonychotes w	62.6	62.6	100%	2e-09	85%	gi|585156269|XP_006730462.1
☐	PREDICTED: C4b-binding protein beta chain [Orcinus orca]	62.1	62.1	92%	3e-09	80%	gi|466071254|XP_004282462.1
☐	PREDICTED: C4b-binding protein beta chain [Ictidomys tridece	61.3	61.3	100%	5e-09	70%	gi|532087633|XP_005329528.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	60.9	60.9	96%	7e-09	81%	gi|471369765|XP_004375397.1
☐	PREDICTED: C4b-binding protein beta chain [Ceratotherium si	60.0	60.0	100%	1e-08	74%	gi|478501878|XP_004425250.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein b	58.7	58.7	88%	4e-08	79%	gi|470641603|XP_004325529.1
☐	PREDICTED: C4b-binding protein beta chain [Odobenus rosma	58.7	58.7	100%	4e-08	81%	gi|472392625|XP_004415587.1
☐	PREDICTED: C4b-binding protein beta chain [Echinops telfairi]	57.9	57.9	96%	7e-08	77%	gi|507635442|XP_004700185.1
☐	PREDICTED: C4b-binding protein beta chain [Erinaceus europa	57.5	57.5	85%	1e-07	78%	gi|617638324|XP_007531172.1

☐	PREDICTED: C4b-binding protein beta chain [Chrysochloris as	57.5	57.5	100%	1e-07	74%	gi|586450676|XP_006834269.1
☐	C4b-binding protein beta chain precursor [Rattus norvegicus]	57.1	57.1	96%	1e-07	73%	gi|62198215|NP_058691.2
☐	RecName: Full=C4b-binding protein beta chain; Flags: Precurs	57.1	57.1	96%	1e-07	73%	gi|2493794|Q63515.1
☐	PREDICTED: C4b-binding protein beta chain [Jaculus jaculus]	57.1	57.1	100%	1e-07	74%	gi|507559572|XP_004663509.1
☐	PREDICTED: C4b-binding protein beta chain [Lipotes vexillifer]	55.8	55.8	85%	3e-07	78%	gi|602721258|XP_007470782.1
☐	PREDICTED: C4b-binding protein beta chain [Physeter catodo	55.8	55.8	85%	3e-07	78%	gi|593718317|XP_007105536.1
☐	PREDICTED: C4b-binding protein beta chain [Octodon degus]	55.4	55.4	96%	5e-07	77%	gi|507688352|XP_004641253.1
☐	PREDICTED: C4b-binding protein beta chain [Sus scrofa]	52.8	52.8	100%	3e-06	70%	gi|311265148|XP_003130503.1
☐	PREDICTED: C4b-binding protein beta chain [Canis lupus fami	52.4	52.4	96%	5e-06	71%	gi|73960685|XP_851611.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Micro	52.4	52.4	100%	5e-06	70%	gi|532009098|XP_005348366.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Micro	52.4	52.4	100%	5e-06	70%	gi|532009096|XP_005348365.1
☐	PREDICTED: C4b-binding protein beta chain [Peromyscus mar	49.8	49.8	100%	3e-05	67%	gi|589966374|XP_006995716.1
☐	PREDICTED: C4b-binding protein beta chain [Cricetulus griseu	48.1	48.1	96%	1e-04	65%	gi|625186859|XP_007614708.1
☐	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 [Cricetu	48.1	48.1	96%	1e-04	65%	gi|344244855|EGW00959.1
☐	6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 2 isofor	48.1	48.1	96%	1e-04	65%	gi|537167880|ERE73717.1
☐	6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 2 isofor	48.1	48.1	96%	1e-04	65%	gi|537167879|ERE73716.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Capra	47.7	47.7	85%	1e-04	70%	gi|548497748|XP_005690484.1
☐	C4b-binding protein beta chain precursor [Bos taurus]	47.7	47.7	85%	1e-04	70%	gi|99028955|NP_776678.2
☐	RecName: Full=C4b-binding protein beta chain; Flags: Precurs	47.7	47.7	85%	1e-04	70%	gi|2493793|Q28066.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Bos t	47.7	47.7	85%	1e-04	70%	gi|528979094|XP_005216707.1
☐	PREDICTED: C4b-binding protein beta chain [Pantholops hodg	47.7	47.7	85%	1e-04	70%	gi|556742954|XP_005966995.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Capra	47.7	47.7	85%	1e-04	70%	gi|548497744|XP_005690482.1
☐	complement component 4 binding protein, beta [Ovis aries]	47.7	47.7	85%	1e-04	70%	gi|444733674|CCQ71779.1
☐	PREDICTED: C4b-binding protein beta chain [Tupaia chinensis	46.4	46.4	96%	4e-04	69%	gi|562862067|XP_006159349.1
☐	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 [Tupaia	46.4	46.4	96%	4e-04	69%	gi|444706417|ELW47759.1
☐	PREDICTED: C4b-binding protein beta chain [Mesocricetus au	46.0	46.0	92%	5e-04	68%	gi|524960013|XP_005079950.1

⊟ Alignments

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pongo abelii]

Sequence ID: gi|686700216|ref|XP_009236698.1| **Length:** 202 **Number of Matches:** 1

Range 1: 67 to 93 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
85.0 bits(193)	4e-17	26/27(96%)	27/27(100%)	0/27(0%)

```
Query  1   RLGHCPDPVLVNGEFSSSGPVDVSDKI  27
           RLGHCPDPVLVNGEFSSSGPV+VSDKI
Sbjct  67  RLGHCPDPVLVNGEFSSSGPVNVSDKI  93
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: gi|194373591|dbj|BAG56891.1| **Length:** 218 **Number of Matches:** 1

Range 1: 67 to 93 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
85.0 bits(193)	4e-17	26/27(96%)	27/27(100%)	0/27(0%)

Related Information

Gene - associated gene details

```
Query  1   RLGHCPDPVLVNGEFSSSGPVDVSDKI  27
           RLGHCPDPVLVNGEFSSSGPV+VSDKI
Sbjct  67  RLGHCPDPVLVNGEFSSSGPVNVSDKI  93
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan troglodytes]

Sequence ID: gi|694891540|ref|XP_009439669.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 76 to 102 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
85.0 bits(193)	4e-17	26/27(96%)	27/27(100%)	0/27(0%)

```
Query  1    RLGHCPDPVLVNGEFSSSGPVDVSDKI  27
            RLGHCPDPVLVNGEFSSSGPV+VSDKI
Sbjct  76   RLGHCPDPVLVNGEFSSSGPVNVSDKI  102
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan paniscus]

Sequence ID: gi|675771724|ref|XP_008974762.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 76 to 102 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
85.0 bits(193)	4e-17	26/27(96%)	27/27(100%)	0/27(0%)

```
Query  1    RLGHCPDPVLVNGEFSSSGPVDVSDKI  27
            RLGHCPDPVLVNGEFSSSGPV+VSDKI
Sbjct  76   RLGHCPDPVLVNGEFSSSGPVNVSDKI  102
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sapiens]

Sequence ID: gi|530366462|ref|XP_005273312.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 76 to 102 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
85.0 bits(193)	4e-17	26/27(96%)	27/27(100%)	0/27(0%)

```
Query  1    RLGHCPDPVLVNGEFSSSGPVDVSDKI  27
            RLGHCPDPVLVNGEFSSSGPV+VSDKI
Sbjct  76   RLGHCPDPVLVNGEFSSSGPVNVSDKI  102
```

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - B92C29JM01R

Your search parameters were adjusted to search for a short input sequence.

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How to read this page   Blast report description

C4BPB_RLGHCPDPVLVNGEFSSSGPVNVSDKI_NonMod

RID B92C29JM01R (Expires on 01-14 09:57 am)

Query ID	lcl|242114	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	27		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

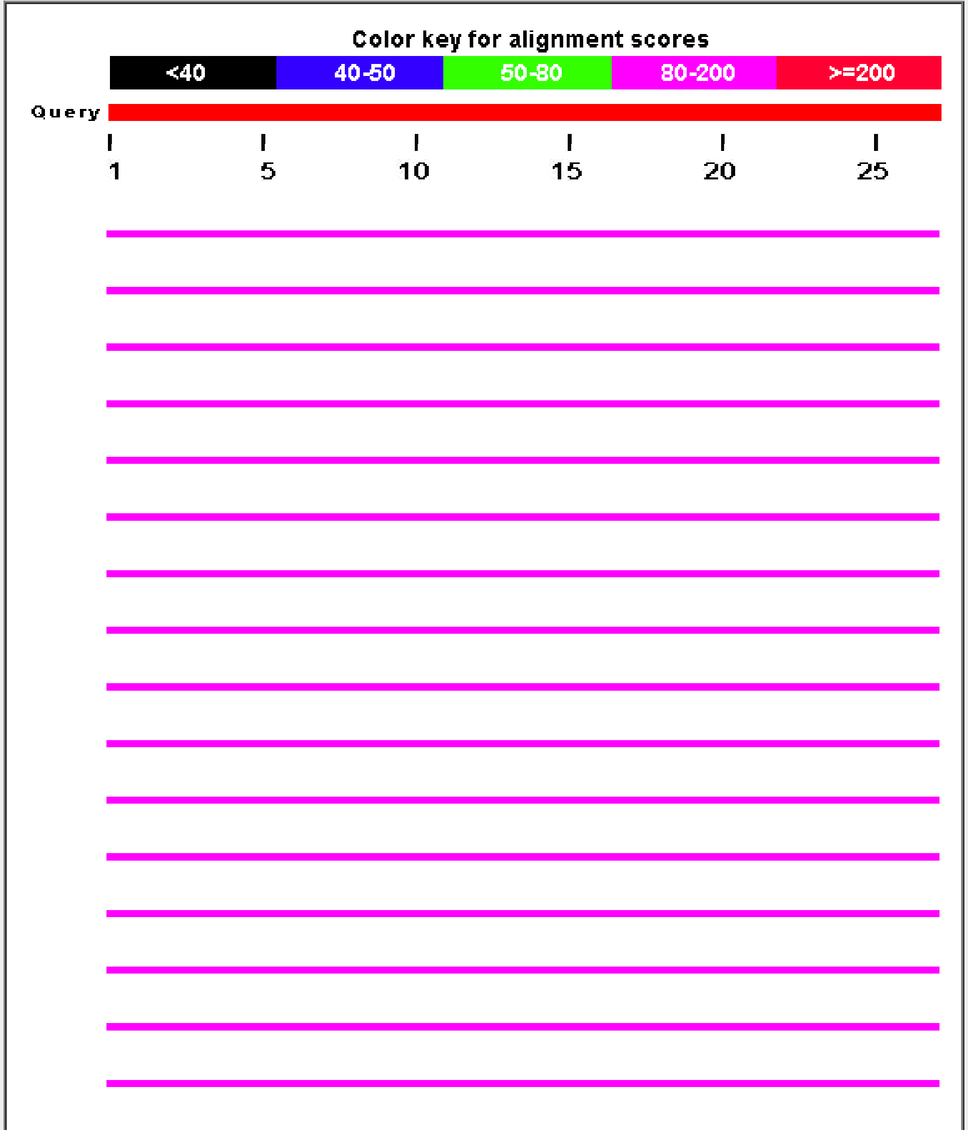
Graphic Summary

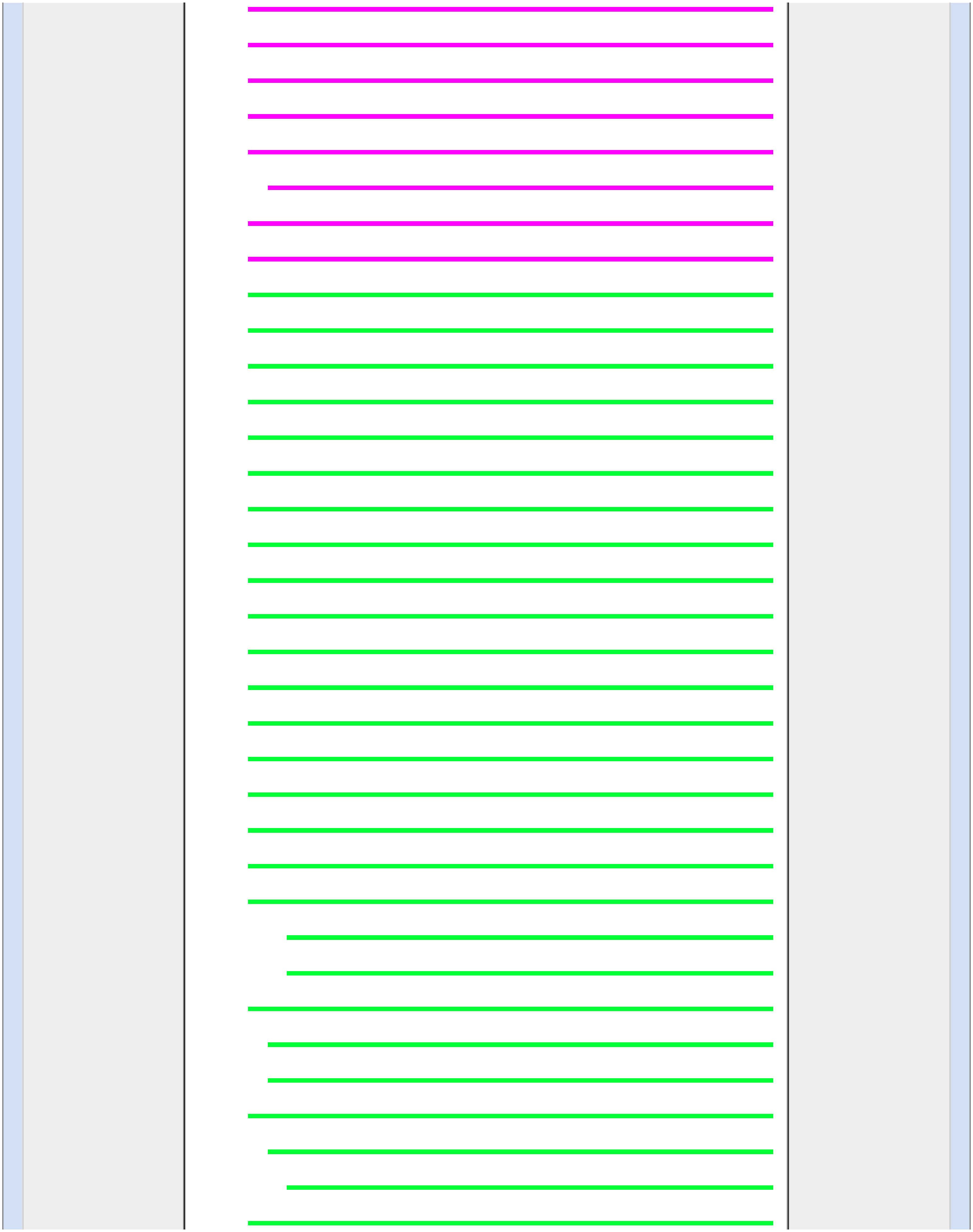
Show Conserved Domains

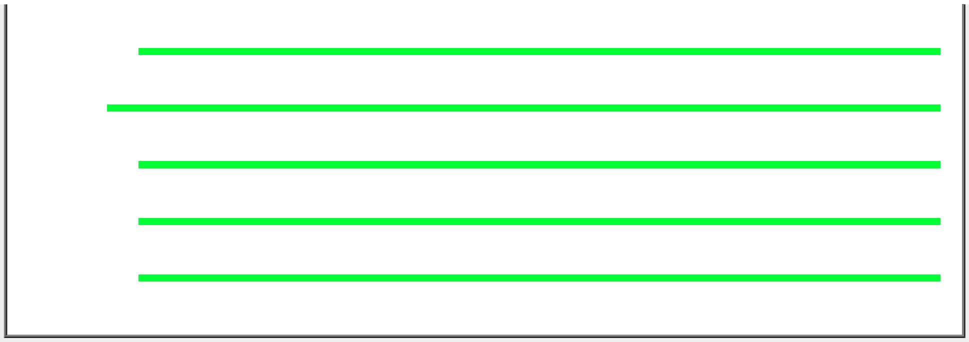
No putative conserved domains have been detected

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pongo ab	87.6	87.6	100%	5e-18	100%	gi|686700216|XP_009236698.1
☐	unnamed protein product [Homo sapiens]	87.6	87.6	100%	5e-18	100%	gi|194373591|BAG56891.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan troglo	87.6	87.6	100%	5e-18	100%	gi|694891540|XP_009439669.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Pan panis	87.6	87.6	100%	5e-18	100%	gi|675771724|XP_008974762.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sap	87.6	87.6	100%	5e-18	100%	gi|530366462|XP_005273312.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan troglo	87.6	87.6	100%	5e-18	100%	gi|694891534|XP_009439665.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pongo ab	87.6	87.6	100%	5e-18	100%	gi|686700213|XP_009236694.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Pan panis	87.6	87.6	100%	5e-18	100%	gi|675771715|XP_008974759.1
☐	C4b-binding protein beta chain isoform 2 precursor [Homo sapiens]	87.6	87.6	100%	5e-18	100%	gi|62912462|NP_001017364.1
☐	C4b-binding protein beta chain isoform 1 precursor [Homo sapiens]	87.6	87.6	100%	5e-18	100%	gi|4502505|NP_000707.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan panis	87.6	87.6	100%	5e-18	100%	gi|397504761|XP_003822949.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pongo ab	87.6	87.6	100%	5e-18	100%	gi|297662141|XP_002809574.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Pan troglo	87.6	87.6	100%	5e-18	100%	gi|114572288|XP_001166306.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Papio anu	85.0	85.0	100%	4e-17	96%	gi|685519789|XP_009186662.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Papio anu	85.0	85.0	100%	4e-17	96%	gi|685519785|XP_009186656.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Tarsius sy	82.9	82.9	100%	2e-16	93%	gi|640811969|XP_008062626.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Tarsius sy	82.9	82.9	100%	2e-16	93%	gi|640811967|XP_008062625.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Macaca fa	81.2	81.2	100%	8e-16	93%	gi|544399939|XP_005540733.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Macaca fa	81.2	81.2	100%	8e-16	93%	gi|544399931|XP_005540729.1
☐	hypothetical protein EGM_01442 [Macaca fascicularis]	81.2	81.2	100%	8e-16	93%	gi|355745961|EHH50586.1
☐	hypothetical protein EGK_01712 [Macaca mulatta]	81.2	81.2	100%	8e-16	93%	gi|355558818|EHH15598.1
☐	PREDICTED: C4b-binding protein beta chain isoform 1 [Nomascus	81.2	81.2	96%	8e-16	96%	gi|332266848|XP_003282407.1
☐	PREDICTED: c4b-binding protein beta chain isoform 3 [Macaca mu	81.2	81.2	100%	8e-16	93%	gi|109018561|XP_001083216.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Macaca fa	81.2	81.2	100%	9e-16	93%	gi|544399929|XP_005540728.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Rhinopith	77.4	77.4	100%	2e-14	89%	gi|724836382|XP_010363947.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Rhinopith	77.4	77.4	100%	2e-14	89%	gi|724836379|XP_010363946.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Galeopter	76.6	76.6	100%	3e-14	89%	gi|667314769|XP_008585888.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Galeopter	76.6	76.6	100%	3e-14	89%	gi|667314766|XP_008585886.1
☐							

	PREDICTED: C4b-binding protein beta chain isoform X9 [Chlorocel	76.1	76.1	100%	4e-14	89%	gi|635130917|XP_007986833.1
☐	PREDICTED: C4b-binding protein beta chain isoform X8 [Chlorocel	76.1	76.1	100%	5e-14	89%	gi|635130915|XP_007986832.1
☐	PREDICTED: C4b-binding protein beta chain isoform X7 [Chlorocel	76.1	76.1	100%	5e-14	89%	gi|635130913|XP_007986831.1
☐	PREDICTED: C4b-binding protein beta chain [Nannospalax galili]	76.1	76.1	100%	5e-14	89%	gi|674096417|XP_008821570.1
☐	PREDICTED: C4b-binding protein beta chain isoform X6 [Chlorocel	76.1	76.1	100%	5e-14	89%	gi|635130911|XP_007986830.1
☐	PREDICTED: C4b-binding protein beta chain isoform X5 [Chlorocel	76.1	76.1	100%	5e-14	89%	gi|635130907|XP_007986828.1
☐	PREDICTED: C4b-binding protein beta chain isoform X4 [Chlorocel	76.1	76.1	100%	5e-14	89%	gi|635130905|XP_007986827.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Chlorocel	76.1	76.1	100%	5e-14	89%	gi|635130903|XP_007986826.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Chlorocel	76.1	76.1	100%	5e-14	89%	gi|635130901|XP_007986825.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Chlorocel	76.1	76.1	100%	5e-14	89%	gi|635130899|XP_007986823.1
☐	C4b-binding protein beta chain [Heterocephalus glaber]	74.0	74.0	100%	2e-13	89%	gi|351708103|EHB11022.1
☐	PREDICTED: C4b-binding protein beta chain [Cavia porcellus]	74.0	74.0	100%	2e-13	89%	gi|348577871|XP_003474707.1
☐	PREDICTED: C4b-binding protein beta chain [Heterocephalus glab	74.0	74.0	100%	2e-13	89%	gi|512892965|XP_004897416.1
☐	PREDICTED: C4b-binding protein beta chain [Ursus maritimus]	73.6	73.6	100%	3e-13	93%	gi|670984389|XP_008683289.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Equus pr	72.7	72.7	92%	6e-13	92%	gi|664745777|XP_008530230.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Equus pr	72.7	72.7	92%	6e-13	92%	gi|664745775|XP_008530229.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	71.5	71.5	100%	2e-12	85%	gi|533120065|XP_005375468.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Callithrix	71.5	71.5	96%	2e-12	92%	gi|675749407|XP_008983835.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Callithrix	71.5	71.5	96%	2e-12	92%	gi|296230632|XP_002760794.1
☐	PREDICTED: C4b-binding protein beta chain [Mustela putorius furo	71.0	71.0	100%	3e-12	89%	gi|511871202|XP_004756233.1
☐	PREDICTED: C4b-binding protein beta chain [Loxodonta africana]	70.2	91.2	96%	5e-12	85%	gi|731475974|XP_010588717.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement component 4	69.4	69.4	92%	9e-12	88%	gi|545215409|XP_005615108.1
☐	hypothetical protein PANDA_018755 [Ailuropoda melanoleuca]	68.5	68.5	100%	2e-11	89%	gi|281337925|EFB13509.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Panthera	68.5	68.5	96%	2e-11	88%	gi|591341473|XP_007096179.1
☐	PREDICTED: c4b-binding protein beta chain-like [Ailuropoda melan	68.5	68.5	100%	2e-11	89%	gi|301786617|XP_002928722.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Panthera	68.5	68.5	96%	2e-11	88%	gi|591341471|XP_007096178.1
☐	PREDICTED: C4b-binding protein beta chain [Pteropus alecto]	68.5	68.5	96%	2e-11	86%	gi|586536223|XP_006922979.1
☐	C4b-binding protein beta chain [Pteropus alecto]	68.5	68.5	96%	2e-11	86%	gi|431892854|ELK03282.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Saimiri bo	68.1	68.1	96%	3e-11	88%	gi|725574024|XP_010339305.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Saimiri bo	68.1	68.1	96%	3e-11	88%	gi|403277664|XP_003930472.1
☐	PREDICTED: C4b-binding protein beta chain [Otolemur garnettii]	68.1	68.1	100%	3e-11	78%	gi|395838946|XP_003792365.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	66.8	66.8	100%	7e-11	81%	gi|594636425|XP_007171607.1
☐	C4b-binding protein beta chain [Fukomys damarensis]	66.4	66.4	88%	1e-10	88%	gi|676262835|KFO19654.1
☐	PREDICTED: C4b-binding protein beta chain [Fukomys damarensis	66.4	66.4	88%	1e-10	88%	gi|731286435|XP_010611521.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Felis catu	66.0	66.0	96%	1e-10	85%	gi|587018341|XP_006942889.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Felis catu	66.0	66.0	96%	1e-10	85%	gi|410986395|XP_003999496.1
☐	PREDICTED: C4b-binding protein beta chain [Orcinus orca]	64.7	64.7	92%	4e-10	84%	gi|466071254|XP_004282462.1
☐	PREDICTED: C4b-binding protein beta chain [Orycteropus afer afer	64.3	64.3	92%	5e-10	84%	gi|634826787|XP_007951309.1
☐	PREDICTED: C4b-binding protein beta chain [Leptonychotes wedd	64.3	64.3	100%	5e-10	85%	gi|585156269|XP_006730462.1
☐	PREDICTED: C4b-binding protein beta chain [Ictidomys tridecemlin	63.8	63.8	100%	7e-10	73%	gi|532087633|XP_005329528.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	62.1	62.1	96%	3e-09	81%	gi|471369765|XP_004375397.1
☐	PREDICTED: C4b-binding protein beta chain [Ceratotherium simum	61.7	61.7	100%	4e-09	74%	gi|478501878|XP_004425250.1
☐	PREDICTED: LOW QUALITY PROTEIN: C4b-binding protein beta	61.3	61.3	88%	5e-09	83%	gi|470641603|XP_004325529.1
☐	PREDICTED: C4b-binding protein beta chain [Odobenus rosmarus	60.4	60.4	100%	1e-08	81%	gi|472392625|XP_004415587.1
☐	PREDICTED: C4b-binding protein beta chain [Chrysochloris asiatic	60.0	60.0	100%	1e-08	78%	gi|586450676|XP_006834269.1

☐	C4b-binding protein beta chain precursor [Rattus norvegicus]	59.6	59.6	96%	2e-08	77%	gi|62198215|NP_058691.2
☐	RecName: Full=C4b-binding protein beta chain; Flags: Precursor [F	59.6	59.6	96%	2e-08	77%	gi|2493794|Q63515.1
☐	PREDICTED: C4b-binding protein beta chain [Jaculus jaculus]	59.6	59.6	100%	2e-08	78%	gi|507559572|XP_004663509.1
☐	PREDICTED: C4b-binding protein beta chain [Echinops telfairi]	59.6	59.6	96%	2e-08	77%	gi|507635442|XP_004700185.1
☐	PREDICTED: C4b-binding protein beta chain [Erinaceus europaeus	59.2	59.2	85%	3e-08	78%	gi|617638324|XP_007531172.1
☐	PREDICTED: C4b-binding protein beta chain [Lipotes vexillifer]	58.3	58.3	85%	5e-08	83%	gi|602721258|XP_007470782.1
☐	PREDICTED: C4b-binding protein beta chain [Physeter catodon]	58.3	58.3	85%	5e-08	83%	gi|593718317|XP_007105536.1
☐	PREDICTED: C4b-binding protein beta chain [Octodon degus]	57.9	57.9	96%	7e-08	81%	gi|507688352|XP_004641253.1
☐	PREDICTED: C4b-binding protein beta chain [Sus scrofa]	55.4	55.4	100%	5e-07	74%	gi|311265148|XP_003130503.1
☐	PREDICTED: C4b-binding protein beta chain [Canis lupus familiaris	54.9	54.9	96%	7e-07	75%	gi|73960685|XP_851611.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Microtus (	54.9	54.9	100%	7e-07	74%	gi|532009098|XP_005348366.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Microtus (	54.9	54.9	100%	7e-07	74%	gi|532009096|XP_005348365.1
☐	PREDICTED: C4b-binding protein beta chain [Peromyscus manicul	52.4	52.4	100%	4e-06	70%	gi|589966374|XP_006995716.1
☐	PREDICTED: C4b-binding protein beta chain [Cricetulus griseus]	50.7	50.7	96%	2e-05	69%	gi|625186859|XP_007614708.1
☐	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 [Cricetulus	50.7	50.7	96%	2e-05	69%	gi|344244855|EGW00959.1
☐	6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 2 isoform 3 [	50.7	50.7	96%	2e-05	69%	gi|537167880|ERE73717.1
☐	6-phosphofructo-2-kinase/fructose-2, 6-biphosphatase 2 isoform 2 [	50.7	50.7	96%	2e-05	69%	gi|537167879|ERE73716.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Capra hir	50.3	50.3	85%	2e-05	74%	gi|548497748|XP_005690484.1
☐	C4b-binding protein beta chain precursor [Bos taurus]	50.3	50.3	85%	2e-05	74%	gi|99028955|NP_776678.2
☐	RecName: Full=C4b-binding protein beta chain; Flags: Precursor [E	50.3	50.3	85%	2e-05	74%	gi|2493793|Q28066.1
☐	PREDICTED: C4b-binding protein beta chain isoform X3 [Bos tauru	50.3	50.3	85%	2e-05	74%	gi|528979094|XP_005216707.1
☐	PREDICTED: C4b-binding protein beta chain isoform X2 [Bos tauru	50.3	50.3	85%	2e-05	74%	gi|528979092|XP_005216706.1
☐	PREDICTED: C4b-binding protein beta chain [Pantholops hodgsoni	50.3	50.3	85%	2e-05	74%	gi|556742954|XP_005966995.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Capra hir	50.3	50.3	85%	2e-05	74%	gi|548497744|XP_005690482.1
☐	complement component 4 binding protein, beta [Ovis aries]	50.3	50.3	85%	2e-05	74%	gi|444733674|CCQ71779.1
☐	PREDICTED: C4b-binding protein beta chain isoform X1 [Bos tauru	50.3	50.3	85%	2e-05	74%	gi|528979090|XP_005216705.1
☐	PREDICTED: C4b-binding protein beta chain [Mesocricetus auratus	48.6	48.6	92%	7e-05	72%	gi|524960013|XP_005079950.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Pongo abelii]

Sequence ID: gi|686700216|ref|XP_009236698.1| **Length:** 202 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 67 to 93 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
87.6 bits(199)	5e-18	27/27(100%)	27/27(100%)	0/27(0%)

```
Query  1    RLGHCPDPVLVNGEFSSSGPVNVSDKI  27
            RLGHCPDPVLVNGEFSSSGPVNVSDKI
Sbjct  67   RLGHCPDPVLVNGEFSSSGPVNVSDKI  93
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: gi|194373591|dbj|BAG56891.1| **Length:** 218 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 67 to 93 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
87.6 bits(199)	5e-18	27/27(100%)	27/27(100%)	0/27(0%)

```
Query  1    RLGHCPDPVLVNGEFSSSGPVNVSDKI  27
```

```
             RLGHCPDPVLVNGEFSSSGPVNVSDKI
Sbjct  67  RLGHCPDPVLVNGEFSSSGPVNVSDKI  93
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan troglodytes]

Sequence ID: gi|694891540|ref|XP_009439669.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 76 to 102 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
87.6 bits(199)	5e-18	27/27(100%)	27/27(100%)	0/27(0%)

```
Query  1    RLGHCPDPVLVNGEFSSSGPVNVSDKI  27
            RLGHCPDPVLVNGEFSSSGPVNVSDKI
Sbjct  76   RLGHCPDPVLVNGEFSSSGPVNVSDKI  102
```

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PREDICTED: C4b-binding protein beta chain isoform X3 [Pan paniscus]

Sequence ID: gi|675771724|ref|XP_008974762.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 76 to 102 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
87.6 bits(199)	5e-18	27/27(100%)	27/27(100%)	0/27(0%)

```
Query  1    RLGHCPDPVLVNGEFSSSGPVNVSDKI  27
            RLGHCPDPVLVNGEFSSSGPVNVSDKI
Sbjct  76   RLGHCPDPVLVNGEFSSSGPVNVSDKI  102
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: C4b-binding protein beta chain isoform X3 [Homo sapiens]

Sequence ID: gi|530366462|ref|XP_005273312.1| **Length:** 227 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 76 to 102 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
87.6 bits(199)	5e-18	27/27(100%)	27/27(100%)	0/27(0%)

```
Query  1    RLGHCPDPVLVNGEFSSSGPVNVSDKI  27
            RLGHCPDPVLVNGEFSSSGPVNVSDKI
Sbjct  76   RLGHCPDPVLVNGEFSSSGPVNVSDKI  102
```

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Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download   How to read this page   Blast report description

CD44_KAFDSTLPTMAQMEKA_Mod

RID BTFX2FSH016 (Expires on 01-20 15:26 pm)

Query ID lcl|86069
Description None
Molecule type amino acid
Query Length 16

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

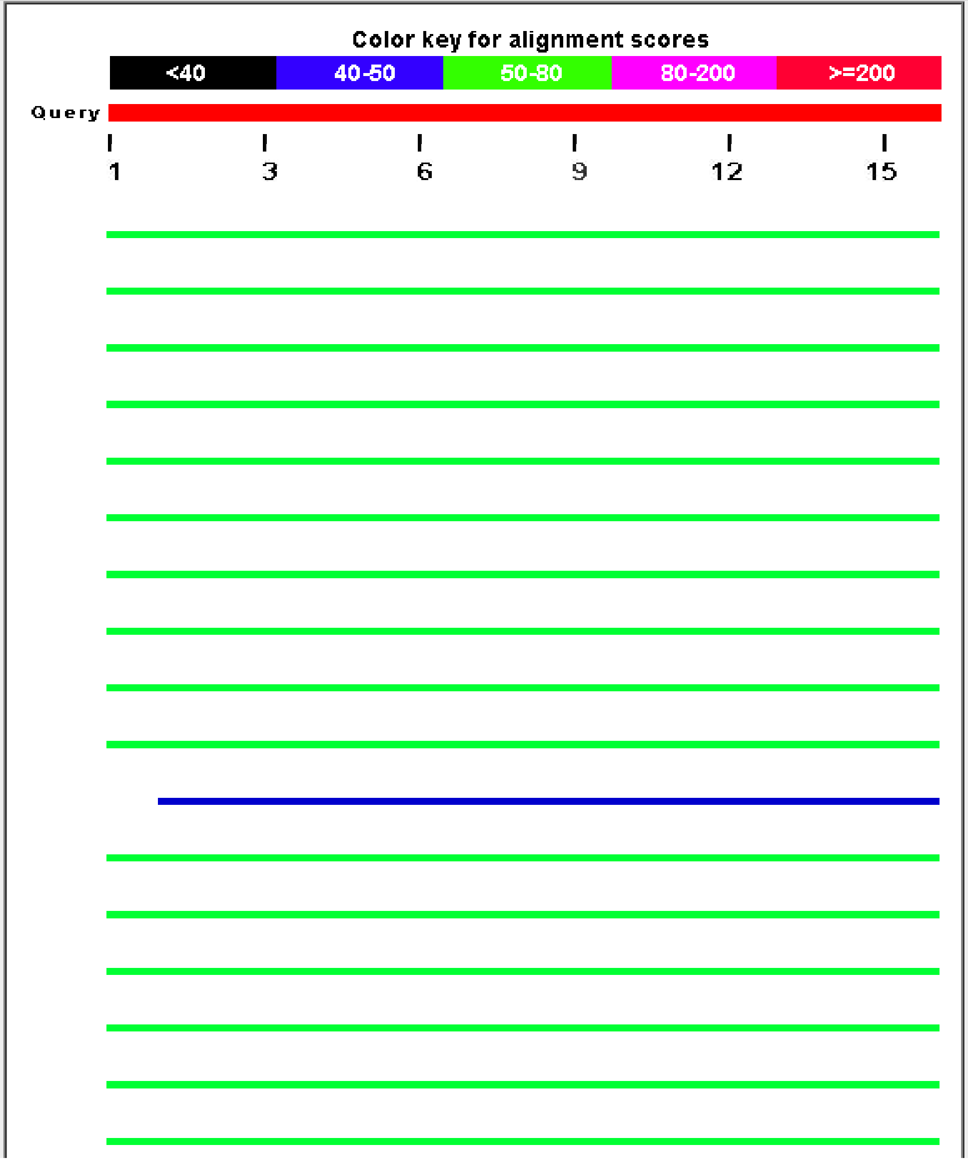
Graphic Summary

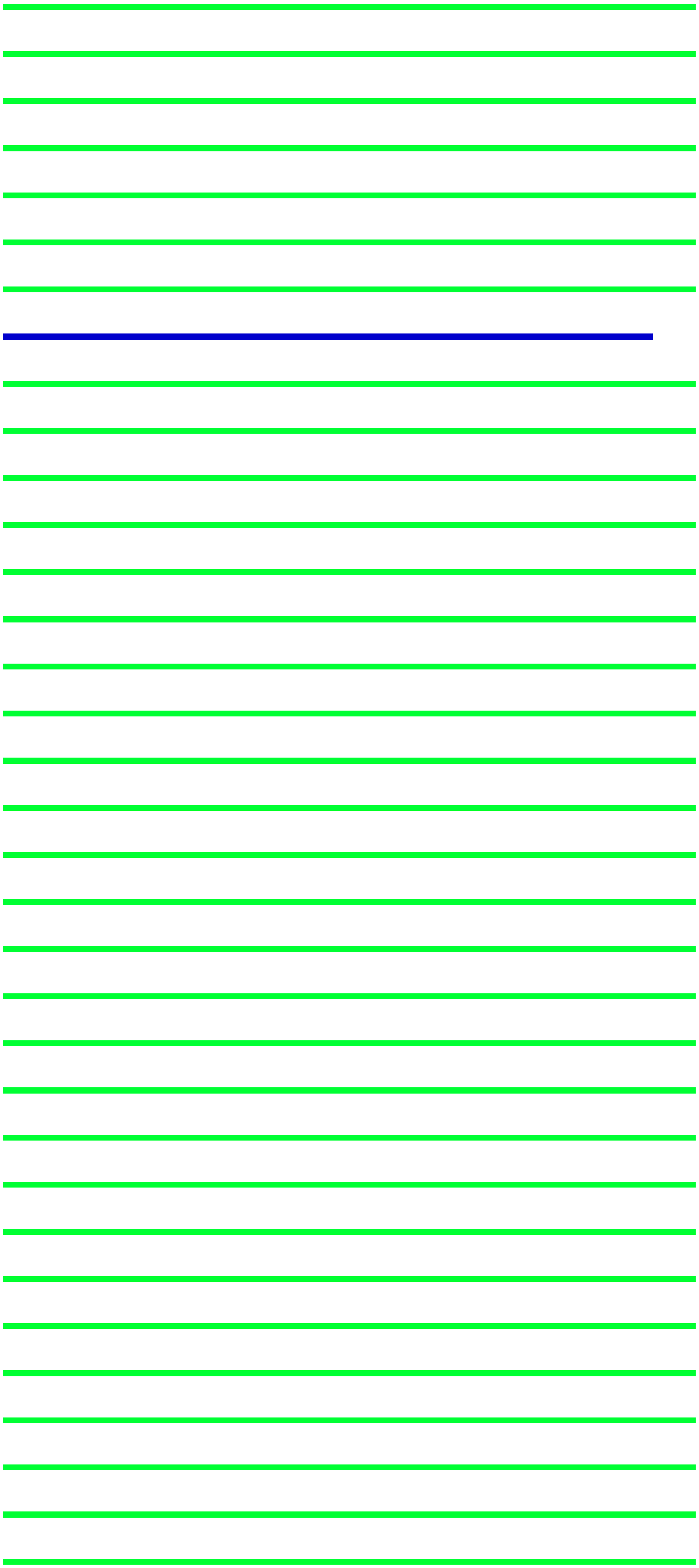
Show Conserved Domains

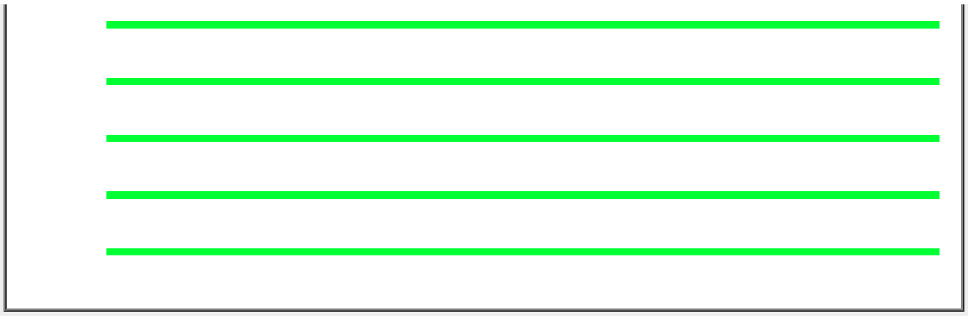
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	CD44 protein [Homo sapiens]	52.4	52.4	100%	7e-07	94%	gi|30353933|AAH52287.1
☐	PREDICTED: LOW QUALITY PROTEIN: CD44 antigen-like [Pc	52.4	52.4	100%	8e-07	94%	gi|686774195|XP_009235328.1
☐	unnamed protein product [Macaca fascicularis]	52.4	52.4	100%	1e-06	94%	gi|90076134|BAE87747.1
☐	PREDICTED: CD44 antigen-like [Gorilla gorilla gorilla]	52.4	52.4	100%	1e-06	94%	gi|426367956|XP_004050985.1
☐	PREDICTED: CD44 antigen isoform X7 [Orycteropus afer afer]	52.4	52.4	100%	1e-06	94%	gi|634854877|XP_007941453.1
☐	PREDICTED: CD44 antigen isoform X7 [Pan paniscus]	52.4	52.4	100%	1e-06	94%	gi|675794911|XP_008954098.1
☐	PREDICTED: CD44 antigen isoform X20 [Callithrix jacchus]	52.4	52.4	100%	1e-06	94%	gi|675699631|XP_009006179.1
☐	CD44 antigen isoform 5 precursor [Homo sapiens]	52.4	52.4	100%	1e-06	94%	gi|48255943|NP_001001392.1
☐	PREDICTED: CD44 antigen isoform X15 [Pan troglodytes]	52.4	52.4	100%	1e-06	94%	gi|332836157|XP_003313029.1
☐	PREDICTED: CD44 antigen isoform 8 [Nomascus leucogenys]	52.4	52.4	100%	1e-06	94%	gi|332210732|XP_003254465.1
☐	85 kda glioma membrane protein/CD44 homolog [Homo sapien	49.4	49.4	93%	1e-06	93%	gi|998625|AAB32708.1
☐	Chain A, High-resolution Crystal Structure Of The Human Cd44	52.4	52.4	100%	1e-06	94%	gi|685425709|4PZ3_A
☐	Chain A, High-resolution Crystal Structure Of The Human Cd44	52.4	52.4	100%	1e-06	94%	gi|685425712|4PZ4_A
☐	Chain A, Solution Structure Of The Hyaluronan Binding Domair	52.4	52.4	100%	1e-06	94%	gi|47168555|1POZ_A
☐	Chain A, Hyaluronan-Binding Domain Of Cd44 In Its Ligand-Bo	52.4	52.4	100%	1e-06	94%	gi|119390067|2I83_A
☐	Hermes antigen gp90 homing receptor precursor [Homo sapien	52.4	52.4	100%	2e-06	94%	gi|186661|AAA36138.1
☐	PREDICTED: CD44 antigen isoform X5 [Pan paniscus]	52.4	52.4	100%	2e-06	94%	gi|675794908|XP_008954097.1
☐	CD44 antigen isoform 8 precursor [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|321400142|NP_001189486.1
☐	unnamed protein product [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|194387514|BAG60121.1
☐	CD44 antigen isoform 7 precursor [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|321400140|NP_001189485.1
☐	PREDICTED: CD44 antigen isoform X18 [Macaca fascicularis]	52.4	52.4	100%	2e-06	94%	gi|544486523|XP_005578264.1
☐	PREDICTED: CD44 antigen isoform 6 [Nomascus leucogenys]	52.4	52.4	100%	2e-06	94%	gi|332210728|XP_003254463.1
☐	PREDICTED: CD44 antigen isoform X6 [Orycteropus afer afer]	52.4	52.4	100%	2e-06	94%	gi|634854874|XP_007941452.1
☐	unnamed protein product [Macaca fascicularis]	52.4	52.4	100%	2e-06	94%	gi|90077486|BAE88423.1
☐	CD44 molecule [Homo sapiens]	49.8	49.8	93%	2e-06	93%	gi|228008043|BAH57528.1
☐	PREDICTED: CD44 antigen isoform X14 [Rhinopithecus roxella	52.4	52.4	100%	2e-06	94%	gi|724966856|XP_010356691.1
☐	PREDICTED: CD44 antigen isoform X4 [Pan paniscus]	52.4	52.4	100%	2e-06	94%	gi|675794906|XP_008954096.1
☐	PREDICTED: CD44 antigen isoform X19 [Chlorocebus sabaeus	52.4	52.4	100%	2e-06	94%	gi|635014254|XP_008000349.1
☐	CDw44 antigen precursor [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|180197|AAA35674.1

☐	CD44 antigen [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|21429241|AAM50041.1
☐	CD44 antigen isoform 4 precursor [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|48255941|NP_001001391.1
☐	cell adhesion molecule [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|180130|AAA51950.1
☐	cell surface glycoprotein CD44 [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|1101786|AAA82949.1
☐	PREDICTED: CD44 antigen isoform X17 [Macaca fascicularis]	52.4	52.4	100%	2e-06	94%	gi|544486521|XP_005578263.1
☐	PREDICTED: CD44 antigen isoform X5 [Papio anubis]	52.4	52.4	100%	2e-06	94%	gi|402893830|XP_003910087.1
☐	PREDICTED: CD44 antigen isoform 2 [Nomascus leucogenys]	52.4	52.4	100%	2e-06	94%	gi|332210720|XP_003254459.1
☐	unnamed protein product [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|158261871|BAF83113.1
☐	PREDICTED: CD44 antigen isoform X14 [Pan troglodytes]	52.4	52.4	100%	2e-06	94%	gi|114637008|XP_001152726.1
☐	hypothetical protein [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|30268334|CAD89965.1
☐	PREDICTED: CD44 antigen isoform X8 [Saimiri boliviensis boli	52.4	52.4	100%	2e-06	94%	gi|725549291|XP_010331704.1
☐	PREDICTED: CD44 antigen isoform X16 [Callithrix jacchus]	52.4	52.4	100%	2e-06	94%	gi|675699620|XP_009006176.1
☐	CD44 antigen [synthetic construct]	52.4	52.4	100%	2e-06	94%	gi|60830199|AAX36916.1
☐	CD44 antigen [synthetic construct]	52.4	52.4	100%	2e-06	94%	gi|60654139|AAX29762.1
☐	RecName: Full=CD44 antigen; AltName: Full=Extracellular mat	52.4	52.4	100%	2e-06	94%	gi|116004|P14745.1
☐	CD44 protein [Callithrix jacchus]	52.4	52.4	100%	2e-06	94%	gi|148749357|ABR09546.1
☐	PREDICTED: CD44 antigen isoform X11 [Ursus maritimus]	52.4	52.4	100%	2e-06	94%	gi|670988033|XP_008685036.1
☐	PREDICTED: CD44 antigen isoform X5 [Orycteropus afer afer]	52.4	52.4	100%	2e-06	94%	gi|634854870|XP_007941451.1
☐	PREDICTED: CD44 antigen [Odobenus rosmarus divergens]	52.4	52.4	100%	2e-06	94%	gi|472373321|XP_004406132.1
☐	CD44R5 [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|435700|AAB27919.1
☐	CD44 antigen (Indian blood group), isoform CRA_i [Homo sapie	52.4	52.4	100%	2e-06	94%	gi|119588560|EAW68154.1
☐	PREDICTED: CD44 antigen isoform X13 [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|578820976|XP_006718453.1
☐	PREDICTED: CD44 antigen isoform X10 [Ursus maritimus]	52.4	52.4	100%	2e-06	94%	gi|670988031|XP_008685035.1
☐	PREDICTED: CD44 antigen isoform X13 [Pan troglodytes]	52.4	52.4	100%	2e-06	94%	gi|694944091|XP_009458500.1
☐	PREDICTED: CD44 antigen isoform X13 [Rhinopithecus roxella	52.4	52.4	100%	2e-06	94%	gi|724966854|XP_010356690.1
☐	CD44R4 [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|7705157|AAB27918.2
☐	CD44 antigen (Indian blood group), isoform CRA_b [Homo sapi	52.4	52.4	100%	2e-06	94%	gi|119588551|EAW68145.1
☐	PREDICTED: CD44 antigen isoform X15 [Callithrix jacchus]	52.4	52.4	100%	2e-06	94%	gi|675699617|XP_009006175.1
☐	PREDICTED: CD44 antigen isoform X18 [Chlorocebus sabaeus	52.4	52.4	100%	2e-06	94%	gi|635014252|XP_008000344.1
☐	PREDICTED: CD44 antigen isoform X16 [Macaca fascicularis]	52.4	52.4	100%	2e-06	94%	gi|544486519|XP_005578262.1
☐	PREDICTED: CD44 antigen isoform 5 [Nomascus leucogenys]	52.4	52.4	100%	2e-06	94%	gi|332210726|XP_003254462.1
☐	CD44 antigen isoform 6 precursor [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|321400138|NP_001189484.1
☐	PREDICTED: CD44 antigen isoform X12 [Pan troglodytes]	52.4	52.4	100%	2e-06	94%	gi|114637002|XP_001151845.1
☐	PREDICTED: CD44 antigen isoform X14 [Callithrix jacchus]	52.4	52.4	100%	2e-06	94%	gi|675699613|XP_009006174.1
☐	PREDICTED: CD44 antigen isoform X4 [Orycteropus afer afer]	52.4	52.4	100%	2e-06	94%	gi|634854867|XP_007941450.1
☐	PREDICTED: CD44 antigen isoform X3 [Papio anubis]	52.4	52.4	100%	2e-06	94%	gi|685586972|XP_009184576.1
☐	PREDICTED: CD44 antigen isoform X9 [Ursus maritimus]	52.4	52.4	100%	2e-06	94%	gi|670988029|XP_008685034.1
☐	PREDICTED: CD44 antigen isoform X12 [Rhinopithecus roxella	52.4	52.4	100%	2e-06	94%	gi|724966852|XP_010356689.1
☐	PREDICTED: CD44 antigen isoform X2 [Papio anubis]	52.4	52.4	100%	2e-06	94%	gi|685586970|XP_009184575.1
☐	PREDICTED: CD44 antigen isoform X3 [Pan paniscus]	52.4	52.4	100%	2e-06	94%	gi|675794904|XP_008954095.1
☐	PREDICTED: CD44 antigen isoform X11 [Rhinopithecus roxella	52.4	52.4	100%	2e-06	94%	gi|724966850|XP_010356688.1
☐	PREDICTED: CD44 antigen isoform X2 [Pan paniscus]	52.4	52.4	100%	2e-06	94%	gi|675794902|XP_008954093.1
☐	PREDICTED: CD44 antigen isoform X17 [Chlorocebus sabaeus	52.4	52.4	100%	2e-06	94%	gi|635014250|XP_008000338.1
☐	CD44 antigen precursor [Pongo abelii]	52.4	52.4	100%	2e-06	94%	gi|197101303|NP_001125856.1
☐	CD44E (epithelial form) [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|29801|CAA38951.1

☐	PREDICTED: CD44 antigen isoform X1 [Papio anubis]	52.4	52.4	100%	2e-06	94%	gi|402893828|XP_003910086.1
☐	PREDICTED: CD44 antigen isoform 1 [Nomascus leucogenys]	52.4	52.4	100%	2e-06	94%	gi|332210718|XP_003254458.1
☐	PREDICTED: CD44 antigen isoform X11 [Pan troglodytes]	52.4	52.4	100%	2e-06	94%	gi|114636992|XP_001152795.1
☐	PREDICTED: CD44 antigen isoform 10 [Macaca mulatta]	52.4	52.4	100%	2e-06	94%	gi|109106774|XP_001115390.1
☐	CD44 antigen isoform 3 precursor [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|48255939|NP_001001390.1
☐	PREDICTED: CD44 antigen isoform X13 [Callithrix jacchus]	52.4	52.4	100%	2e-06	94%	gi|675699609|XP_009006173.1
☐	PREDICTED: CD44 antigen isoform X7 [Saimiri boliviensis boli	52.4	52.4	100%	2e-06	94%	gi|725549289|XP_010331699.1
☐	PREDICTED: CD44 antigen isoform X3 [Orycteropus afer afer]	52.4	52.4	100%	2e-06	94%	gi|634854864|XP_007941449.1
☐	PREDICTED: CD44 antigen isoform X12 [Callithrix jacchus]	52.4	52.4	100%	2e-06	94%	gi|675699603|XP_009006172.1
☐	PREDICTED: CD44 antigen isoform X8 [Ursus maritimus]	52.4	52.4	100%	2e-06	94%	gi|670988027|XP_008685033.1
☐	PREDICTED: CD44 antigen isoform X11 [Callithrix jacchus]	52.4	52.4	100%	2e-06	94%	gi|675699599|XP_009006171.1
☐	PREDICTED: CD44 antigen isoform X10 [Pan troglodytes]	52.4	52.4	100%	2e-06	94%	gi|694944087|XP_009458498.1
☐	PREDICTED: CD44 antigen isoform X10 [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|530396022|XP_005253297.1
☐	PREDICTED: CD44 antigen isoform X1 [Pan paniscus]	52.4	52.4	100%	2e-06	94%	gi|675794900|XP_008954092.1
☐	PREDICTED: CD44 antigen isoform X10 [Callithrix jacchus]	52.4	52.4	100%	2e-06	94%	gi|675699596|XP_009006170.1
☐	PREDICTED: CD44 antigen isoform X14 [Macaca fascicularis]	52.4	52.4	100%	2e-06	94%	gi|544486515|XP_005578260.1
☐	PREDICTED: CD44 antigen isoform X6 [Saimiri boliviensis boli	52.4	52.4	100%	2e-06	94%	gi|725549287|XP_010331696.1
☐	PREDICTED: CD44 antigen isoform X10 [Rhinopithecus roxella	52.4	52.4	100%	2e-06	94%	gi|724966848|XP_010356687.1
☐	PREDICTED: CD44 antigen isoform X13 [Macaca fascicularis]	52.4	52.4	100%	2e-06	94%	gi|544486513|XP_005578259.1
☐	PREDICTED: CD44 antigen isoform X7 [Ursus maritimus]	52.4	52.4	100%	2e-06	94%	gi|670988025|XP_008685032.1
☐	PREDICTED: CD44 antigen isoform X6 [Ursus maritimus]	52.4	52.4	100%	2e-06	94%	gi|670988023|XP_008685031.1
☐	PREDICTED: CD44 antigen isoform X5 [Saimiri boliviensis boli	52.4	52.4	100%	2e-06	94%	gi|725549285|XP_010331692.1
☐	PREDICTED: CD44 antigen isoform X9 [Homo sapiens]	52.4	52.4	100%	2e-06	94%	gi|530396020|XP_005253296.1
☐	PREDICTED: CD44 antigen isoform X9 [Callithrix jacchus]	52.4	52.4	100%	2e-06	94%	gi|675699592|XP_009006169.1
☐	PREDICTED: CD44 antigen isoform X16 [Chlorocebus sabaeus	52.4	52.4	100%	2e-06	94%	gi|635014248|XP_008000329.1
☐	PREDICTED: CD44 antigen isoform X9 [Rhinopithecus roxellar	52.4	52.4	100%	2e-06	94%	gi|724966846|XP_010356686.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

CD44 protein [Homo sapiens]

Sequence ID: gi|30353933|gb|AAH52287.1| **Length:** 80 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 54 to 69 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	7e-07	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1   KAFDSTLPTMAQMEKA  16
           KAF+STLPTMAQMEKA
Sbjct  54  KAFNSTLPTMAQMEKA  69
```

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PREDICTED: LOW QUALITY PROTEIN: CD44 antigen-like, partial [Pongo abelii]

Sequence ID: gi|686774195|ref|XP_009235328.1| **Length:** 91 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 31 to 46 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	8e-07	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1   KAFDSTLPTMAQMEKA  16
           KAF+STLPTMAQMEKA
Sbjct  31  KAFNSTLPTMAQMEKA  46
```

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unnamed protein product [Macaca fascicularis]

Sequence ID: gi|90076134|dbj|BAE87747.1| **Length:** 114 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 54 to 69 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	1e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1   KAFDSTLPTMAQMEKA  16
           KAF+STLPTMAQMEKA
Sbjct  54  KAFNSTLPTMAQMEKA  69
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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PREDICTED: CD44 antigen-like [Gorilla gorilla gorilla]

Sequence ID: gi|426367956|ref|XP_004050985.1| **Length:** 132 **Number of Matches:** 1

Range 1: 54 to 69 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	1e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1   KAFDSTLPTMAQMEKA  16
           KAF+STLPTMAQMEKA
Sbjct  54  KAFNSTLPTMAQMEKA  69
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: CD44 antigen isoform X7 [Orycteropus afer afer]

Sequence ID: gi|634854877|ref|XP_007941453.1| **Length:** 138 **Number of Matches:** 1

Range 1: 54 to 69 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	1e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1   KAFDSTLPTMAQMEKA  16
           KAF+STLPTMAQMEKA
Sbjct  54  KAFNSTLPTMAQMEKA  69
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

CD44_KAFNSTLPTMAQMEKA_NonMod

RID B92JYCA501R (Expires on 01-14 10:00 am)

Query ID lcl|320990
Description None
Molecule type amino acid
Query Length 16

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

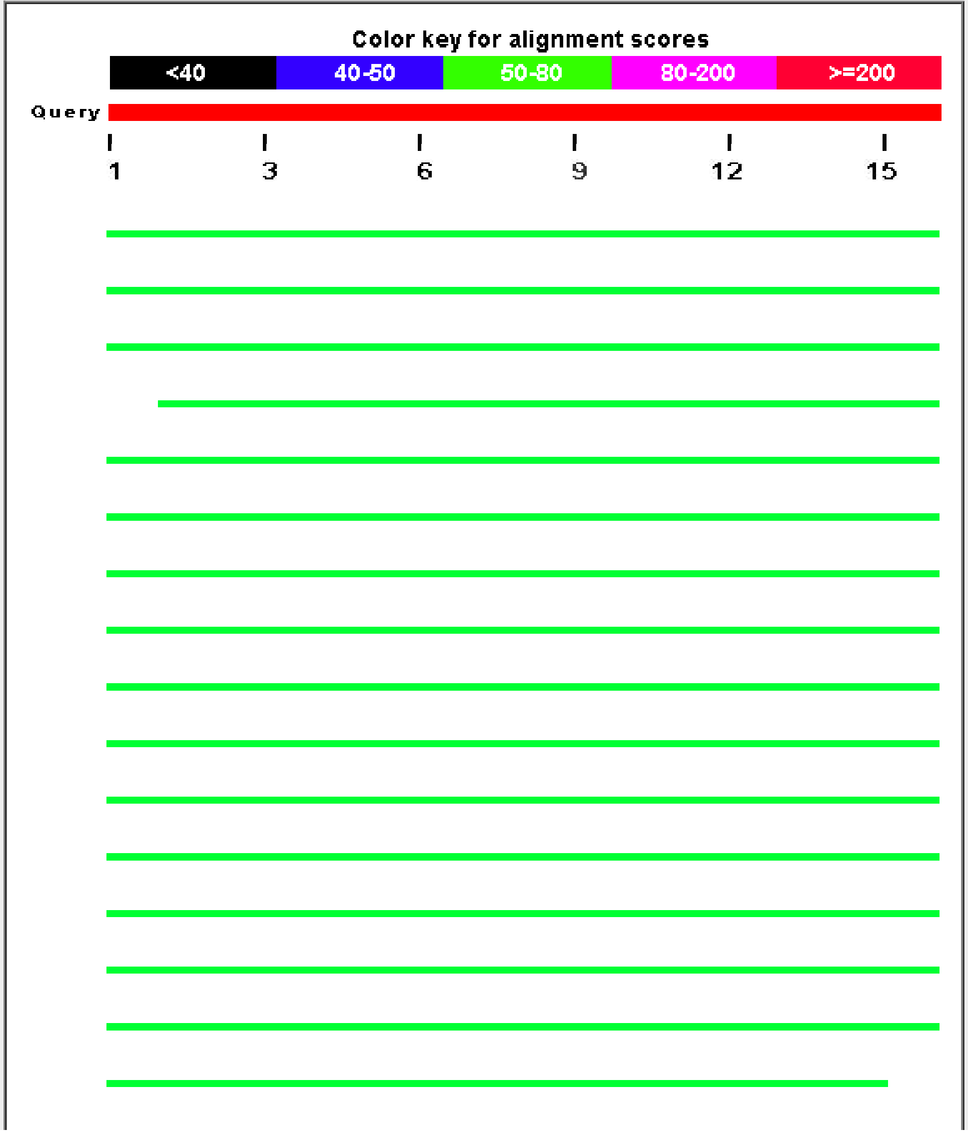
Graphic Summary

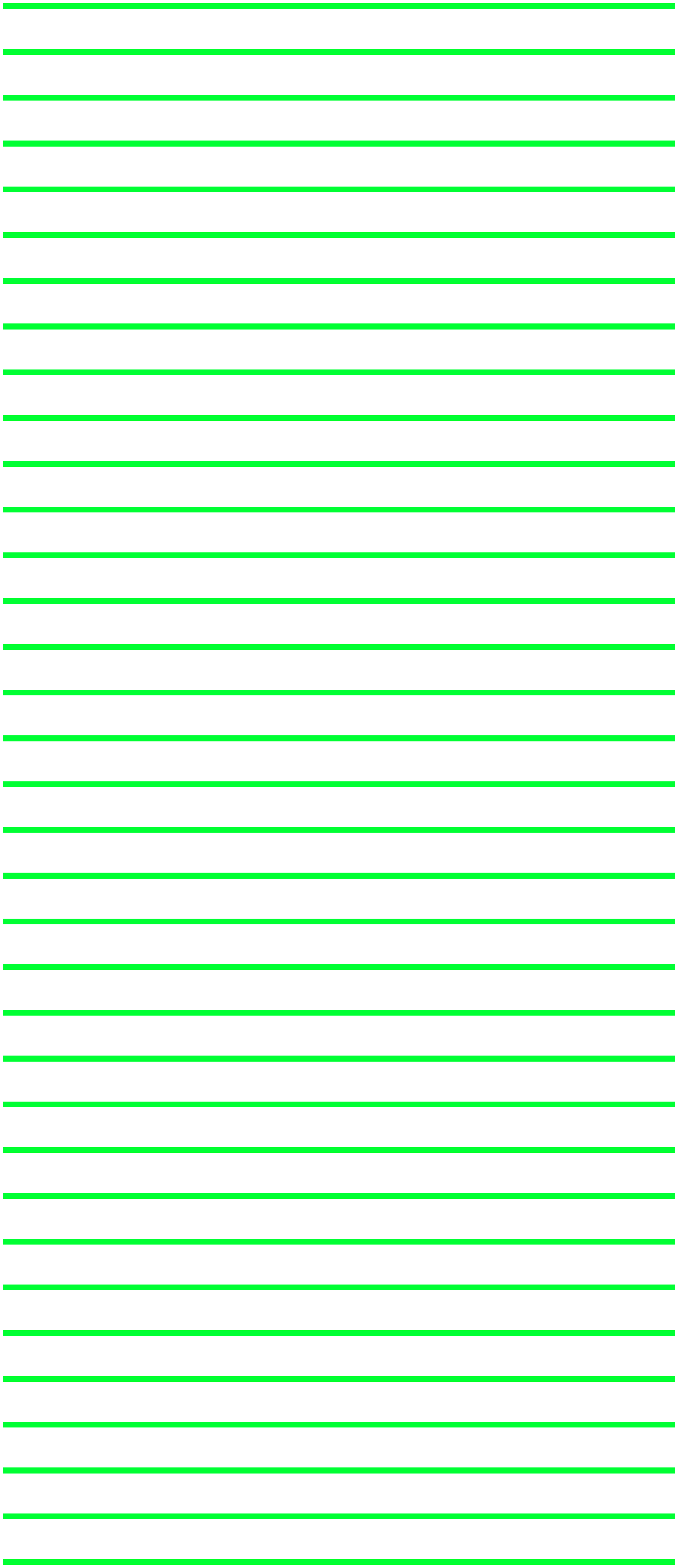
Show Conserved Domains

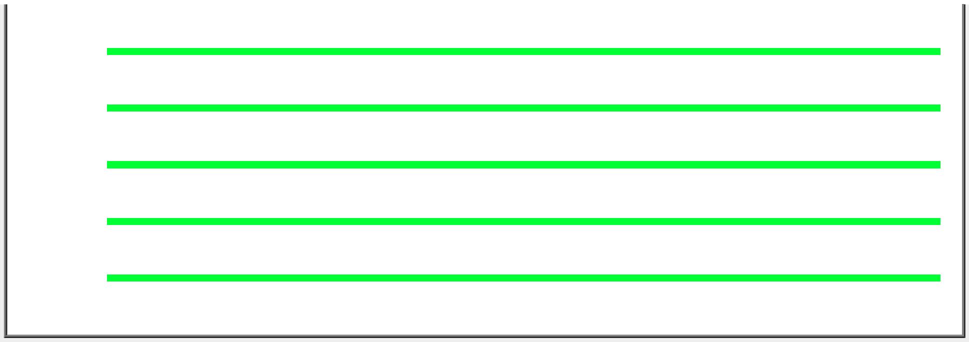
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	CD44 protein [Homo sapiens]	54.9	54.9	100%	9e-08	100%	gi|30353933|AAH52287.1
☐	PREDICTED: LOW QUALITY PROTEIN: CD44 antigen-like [Pongo	54.9	54.9	100%	1e-07	100%	gi|686774195|XP_009235328.1
☐	unnamed protein product [Macaca fascicularis]	54.9	54.9	100%	1e-07	100%	gi|90076134|BAE87747.1
☐	85 kda glioma membrane protein/CD44 homolog [Homo sapiens]	52.0	52.0	93%	1e-07	100%	gi|998625|AAB32708.1
☐	PREDICTED: CD44 antigen-like [Gorilla gorilla gorilla]	54.9	54.9	100%	1e-07	100%	gi|426367956|XP_004050985.1
☐	PREDICTED: CD44 antigen isoform X7 [Orycteropus afer afer]	54.9	54.9	100%	1e-07	100%	gi|634854877|XP_007941453.1
☐	PREDICTED: CD44 antigen isoform X7 [Pan paniscus]	54.9	54.9	100%	1e-07	100%	gi|675794911|XP_008954098.1
☐	PREDICTED: CD44 antigen isoform X20 [Callithrix jacchus]	54.9	54.9	100%	1e-07	100%	gi|675699631|XP_009006179.1
☐	CD44 antigen isoform 5 precursor [Homo sapiens]	54.9	54.9	100%	1e-07	100%	gi|48255943|NP_001001392.1
☐	PREDICTED: CD44 antigen isoform X15 [Pan troglodytes]	54.9	54.9	100%	1e-07	100%	gi|332836157|XP_003313029.1
☐	PREDICTED: CD44 antigen isoform 8 [Nomascus leucogenys]	54.9	54.9	100%	1e-07	100%	gi|332210732|XP_003254465.1
☐	Chain A, High-resolution Crystal Structure Of The Human Cd44 Hya	54.9	54.9	100%	2e-07	100%	gi|685425709|4PZ3_A
☐	Chain A, High-resolution Crystal Structure Of The Human Cd44 Hya	54.9	54.9	100%	2e-07	100%	gi|685425712|4PZ4_A
☐	Chain A, Solution Structure Of The Hyaluronan Binding Domain Of	54.9	54.9	100%	2e-07	100%	gi|47168555|1POZ_A
☐	Chain A, Hyaluronan-Binding Domain Of Cd44 In Its Ligand-Bound	54.9	54.9	100%	2e-07	100%	gi|119390067|2I83_A
☐	CD44 molecule [Homo sapiens]	52.4	52.4	93%	2e-07	100%	gi|228008043|BAH57528.1
☐	Hermes antigen gp90 homing receptor precursor [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|186661|AAA36138.1
☐	PREDICTED: CD44 antigen isoform X5 [Pan paniscus]	54.9	54.9	100%	2e-07	100%	gi|675794908|XP_008954097.1
☐	CD44 antigen isoform 8 precursor [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|321400142|NP_001189486.1
☐	unnamed protein product [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|194387514|BAG60121.1
☐	CD44 antigen isoform 7 precursor [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|321400140|NP_001189485.1
☐	PREDICTED: CD44 antigen isoform X18 [Macaca fascicularis]	54.9	54.9	100%	2e-07	100%	gi|544486523|XP_005578264.1
☐	PREDICTED: CD44 antigen isoform 6 [Nomascus leucogenys]	54.9	54.9	100%	2e-07	100%	gi|332210728|XP_003254463.1
☐	PREDICTED: CD44 antigen isoform X6 [Orycteropus afer afer]	54.9	54.9	100%	2e-07	100%	gi|634854874|XP_007941452.1
☐	unnamed protein product [Macaca fascicularis]	54.9	54.9	100%	2e-07	100%	gi|90077486|BAE88423.1
☐	PREDICTED: CD44 antigen isoform X14 [Rhinopithecus roxellana]	54.9	54.9	100%	2e-07	100%	gi|724966856|XP_010356691.1
☐	PREDICTED: CD44 antigen isoform X4 [Pan paniscus]	54.9	54.9	100%	2e-07	100%	gi|675794906|XP_008954096.1
☐	PREDICTED: CD44 antigen isoform X19 [Chlorocebus sabaeus]	54.9	54.9	100%	2e-07	100%	gi|635014254|XP_008000349.1
☐							

	CDw44 antigen precursor [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|180197|AAA35674.1
☐	CD44 antigen [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|21429241|AAM50041.1
☐	CD44 antigen isoform 4 precursor [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|48255941|NP_001001391.1
☐	cell adhesion molecule [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|180130|AAA51950.1
☐	cell surface glycoprotein CD44 [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|1101786|AAA82949.1
☐	PREDICTED: CD44 antigen isoform X17 [Macaca fascicularis]	54.9	54.9	100%	2e-07	100%	gi|544486521|XP_005578263.1
☐	PREDICTED: CD44 antigen isoform X5 [Papio anubis]	54.9	54.9	100%	2e-07	100%	gi|402893830|XP_003910087.1
☐	PREDICTED: CD44 antigen isoform 2 [Nomascus leucogenys]	54.9	54.9	100%	2e-07	100%	gi|332210720|XP_003254459.1
☐	unnamed protein product [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|158261871|BAF83113.1
☐	PREDICTED: CD44 antigen isoform X14 [Pan troglodytes]	54.9	54.9	100%	2e-07	100%	gi|114637008|XP_001152726.1
☐	hypothetical protein [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|30268334|CAD89965.1
☐	PREDICTED: CD44 antigen isoform X8 [Saimiri boliviensis bolivien	54.9	54.9	100%	2e-07	100%	gi|725549291|XP_010331704.1
☐	PREDICTED: CD44 antigen isoform X16 [Callithrix jacchus]	54.9	54.9	100%	2e-07	100%	gi|675699620|XP_009006176.1
☐	CD44 antigen [synthetic construct]	54.9	54.9	100%	2e-07	100%	gi|60830199|AAX36916.1
☐	CD44 antigen [synthetic construct]	54.9	54.9	100%	2e-07	100%	gi|60654139|AAX29762.1
☐	RecName: Full=CD44 antigen; AltName: Full=Extracellular matrix re	54.9	54.9	100%	2e-07	100%	gi|116004|P14745.1
☐	CD44 protein [Callithrix jacchus]	54.9	54.9	100%	2e-07	100%	gi|148749357|ABR09546.1
☐	PREDICTED: CD44 antigen isoform X11 [Ursus maritimus]	54.9	54.9	100%	2e-07	100%	gi|670988033|XP_008685036.1
☐	PREDICTED: CD44 antigen isoform X5 [Orycteropus afer afer]	54.9	54.9	100%	2e-07	100%	gi|634854870|XP_007941451.1
☐	PREDICTED: CD44 antigen [Odobenus rosmarus divergens]	54.9	54.9	100%	2e-07	100%	gi|472373321|XP_004406132.1
☐	CD44R5 [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|435700|AAB27919.1
☐	CD44 antigen (Indian blood group), isoform CRA_i [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|119588560|EAW68154.1
☐	PREDICTED: CD44 antigen isoform X13 [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|578820976|XP_006718453.1
☐	PREDICTED: CD44 antigen isoform X10 [Ursus maritimus]	54.9	54.9	100%	2e-07	100%	gi|670988031|XP_008685035.1
☐	PREDICTED: CD44 antigen isoform X13 [Pan troglodytes]	54.9	54.9	100%	2e-07	100%	gi|694944091|XP_009458500.1
☐	PREDICTED: CD44 antigen isoform X13 [Rhinopithecus roxellana]	54.9	54.9	100%	2e-07	100%	gi|724966854|XP_010356690.1
☐	CD44R4 [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|7705157|AAB27918.2
☐	CD44 antigen (Indian blood group), isoform CRA_b [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|119588551|EAW68145.1
☐	PREDICTED: CD44 antigen isoform X15 [Callithrix jacchus]	54.9	54.9	100%	2e-07	100%	gi|675699617|XP_009006175.1
☐	PREDICTED: CD44 antigen isoform X18 [Chlorocebus sabaeus]	54.9	54.9	100%	2e-07	100%	gi|635014252|XP_008000344.1
☐	PREDICTED: CD44 antigen isoform X16 [Macaca fascicularis]	54.9	54.9	100%	2e-07	100%	gi|544486519|XP_005578262.1
☐	PREDICTED: CD44 antigen isoform 5 [Nomascus leucogenys]	54.9	54.9	100%	2e-07	100%	gi|332210726|XP_003254462.1
☐	CD44 antigen isoform 6 precursor [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|321400138|NP_001189484.1
☐	PREDICTED: CD44 antigen isoform X12 [Pan troglodytes]	54.9	54.9	100%	2e-07	100%	gi|114637002|XP_001151845.1
☐	PREDICTED: CD44 antigen isoform X14 [Callithrix jacchus]	54.9	54.9	100%	2e-07	100%	gi|675699613|XP_009006174.1
☐	PREDICTED: CD44 antigen isoform X4 [Orycteropus afer afer]	54.9	54.9	100%	2e-07	100%	gi|634854867|XP_007941450.1
☐	PREDICTED: CD44 antigen isoform X3 [Papio anubis]	54.9	54.9	100%	2e-07	100%	gi|685586972|XP_009184576.1
☐	PREDICTED: CD44 antigen isoform X9 [Ursus maritimus]	54.9	54.9	100%	2e-07	100%	gi|670988029|XP_008685034.1
☐	PREDICTED: CD44 antigen isoform X12 [Rhinopithecus roxellana]	54.9	54.9	100%	2e-07	100%	gi|724966852|XP_010356689.1
☐	PREDICTED: CD44 antigen isoform X2 [Papio anubis]	54.9	54.9	100%	2e-07	100%	gi|685586970|XP_009184575.1
☐	PREDICTED: CD44 antigen isoform X3 [Pan paniscus]	54.9	54.9	100%	2e-07	100%	gi|675794904|XP_008954095.1
☐	PREDICTED: CD44 antigen isoform X11 [Rhinopithecus roxellana]	54.9	54.9	100%	2e-07	100%	gi|724966850|XP_010356688.1
☐	PREDICTED: CD44 antigen isoform X2 [Pan paniscus]	54.9	54.9	100%	2e-07	100%	gi|675794902|XP_008954093.1
☐	PREDICTED: CD44 antigen isoform X17 [Chlorocebus sabaeus]	54.9	54.9	100%	2e-07	100%	gi|635014250|XP_008000338.1
☐	CD44 antigen precursor [Pongo abelii]	54.9	54.9	100%	2e-07	100%	gi|197101303|NP_001125856.1

☐	CD44E (epithelial form) [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|29801|CAA38951.1
☐	PREDICTED: CD44 antigen isoform X1 [Papio anubis]	54.9	54.9	100%	2e-07	100%	gi|402893828|XP_003910086.1
☐	PREDICTED: CD44 antigen isoform 1 [Nomascus leucogenys]	54.9	54.9	100%	2e-07	100%	gi|332210718|XP_003254458.1
☐	PREDICTED: CD44 antigen isoform X11 [Pan troglodytes]	54.9	54.9	100%	2e-07	100%	gi|114636992|XP_001152795.1
☐	PREDICTED: CD44 antigen isoform 10 [Macaca mulatta]	54.9	54.9	100%	2e-07	100%	gi|109106774|XP_001115390.1
☐	CD44 antigen isoform 3 precursor [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|48255939|NP_001001390.1
☐	PREDICTED: CD44 antigen isoform X13 [Callithrix jacchus]	54.9	54.9	100%	2e-07	100%	gi|675699609|XP_009006173.1
☐	PREDICTED: CD44 antigen isoform X7 [Saimiri boliviensis bolivien	54.9	54.9	100%	2e-07	100%	gi|725549289|XP_010331699.1
☐	PREDICTED: CD44 antigen isoform X3 [Orycteropus afer afer]	54.9	54.9	100%	2e-07	100%	gi|634854864|XP_007941449.1
☐	PREDICTED: CD44 antigen isoform X12 [Callithrix jacchus]	54.9	54.9	100%	2e-07	100%	gi|675699603|XP_009006172.1
☐	PREDICTED: CD44 antigen isoform X8 [Ursus maritimus]	54.9	54.9	100%	2e-07	100%	gi|670988027|XP_008685033.1
☐	PREDICTED: CD44 antigen isoform X11 [Callithrix jacchus]	54.9	54.9	100%	2e-07	100%	gi|675699599|XP_009006171.1
☐	PREDICTED: CD44 antigen isoform X10 [Pan troglodytes]	54.9	54.9	100%	2e-07	100%	gi|694944087|XP_009458498.1
☐	PREDICTED: CD44 antigen isoform X10 [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|530396022|XP_005253297.1
☐	PREDICTED: CD44 antigen isoform X1 [Pan paniscus]	54.9	54.9	100%	2e-07	100%	gi|675794900|XP_008954092.1
☐	PREDICTED: CD44 antigen isoform X10 [Callithrix jacchus]	54.9	54.9	100%	2e-07	100%	gi|675699596|XP_009006170.1
☐	PREDICTED: CD44 antigen isoform X14 [Macaca fascicularis]	54.9	54.9	100%	2e-07	100%	gi|544486515|XP_005578260.1
☐	PREDICTED: CD44 antigen isoform X6 [Saimiri boliviensis bolivien	54.9	54.9	100%	2e-07	100%	gi|725549287|XP_010331696.1
☐	PREDICTED: CD44 antigen isoform X10 [Rhinopithecus roxellana]	54.9	54.9	100%	2e-07	100%	gi|724966848|XP_010356687.1
☐	PREDICTED: CD44 antigen isoform X13 [Macaca fascicularis]	54.9	54.9	100%	2e-07	100%	gi|544486513|XP_005578259.1
☐	PREDICTED: CD44 antigen isoform X7 [Ursus maritimus]	54.9	54.9	100%	2e-07	100%	gi|670988025|XP_008685032.1
☐	PREDICTED: CD44 antigen isoform X6 [Ursus maritimus]	54.9	54.9	100%	2e-07	100%	gi|670988023|XP_008685031.1
☐	PREDICTED: CD44 antigen isoform X5 [Saimiri boliviensis bolivien	54.9	54.9	100%	2e-07	100%	gi|725549285|XP_010331692.1
☐	PREDICTED: CD44 antigen isoform X9 [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|530396020|XP_005253296.1
☐	PREDICTED: CD44 antigen isoform X9 [Callithrix jacchus]	54.9	54.9	100%	2e-07	100%	gi|675699592|XP_009006169.1
☐	PREDICTED: CD44 antigen isoform X16 [Chlorocebus sabaeus]	54.9	54.9	100%	2e-07	100%	gi|635014248|XP_008000329.1
☐	PREDICTED: CD44 antigen isoform X9 [Rhinopithecus roxellana]	54.9	54.9	100%	2e-07	100%	gi|724966846|XP_010356686.1

Alignments

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CD44 protein [Homo sapiens]

Sequence ID: gi|30353933|gb|AAH52287.1| **Length:** 80 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 54 to 69 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.9 bits(122)	9e-08	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    KAFNSTLPTMAQMEKA  16
            KAFNSTLPTMAQMEKA
Sbjct  54   KAFNSTLPTMAQMEKA  69
```

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PREDICTED: LOW QUALITY PROTEIN: CD44 antigen-like, partial [Pongo abelii]

Sequence ID: gi|686774195|ref|XP_009235328.1| **Length:** 91 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 31 to 46 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.9 bits(122)	1e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    KAFNSTLPTMAQMEKA  16
```

```
              KAFNSTLPTMAQMEKA
Sbjct  31   KAFNSTLPTMAQMEKA  46
```

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unnamed protein product [Macaca fascicularis]

Sequence ID: gi|90076134|dbj|BAE87747.1| **Length:** 114 **Number of Matches:** 1

▶ See 1 more title(s)

Range 1: 54 to 69 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.9 bits(122)	1e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    KAFNSTLPTMAQMEKA  16
              KAFNSTLPTMAQMEKA
Sbjct  54   KAFNSTLPTMAQMEKA  69
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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85 kda glioma membrane protein/CD44 homolog [Homo sapiens]

Sequence ID: gi|998625|gb|AAB32708.1| **Length:** 25 **Number of Matches:** 1

Range 1: 1 to 15 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.0 bits(115)	1e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  2    AFNSTLPTMAQMEKA  16
              AFNSTLPTMAQMEKA
Sbjct  1    AFNSTLPTMAQMEKA  15
```

Related Information

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: CD44 antigen-like [Gorilla gorilla gorilla]

Sequence ID: gi|426367956|ref|XP_004050985.1| **Length:** 132 **Number of Matches:** 1

Range 1: 54 to 69 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.9 bits(122)	1e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    KAFNSTLPTMAQMEKA  16
              KAFNSTLPTMAQMEKA
Sbjct  54   KAFNSTLPTMAQMEKA  69
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - BTG0M0SN013

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CDH5_REVYPWYDLTVEAKE_Mod

RID	BTG0M0SN013 (Expires on 01-20 15:28 pm)		
Query ID	lcl|1316	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	15	**Program**	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

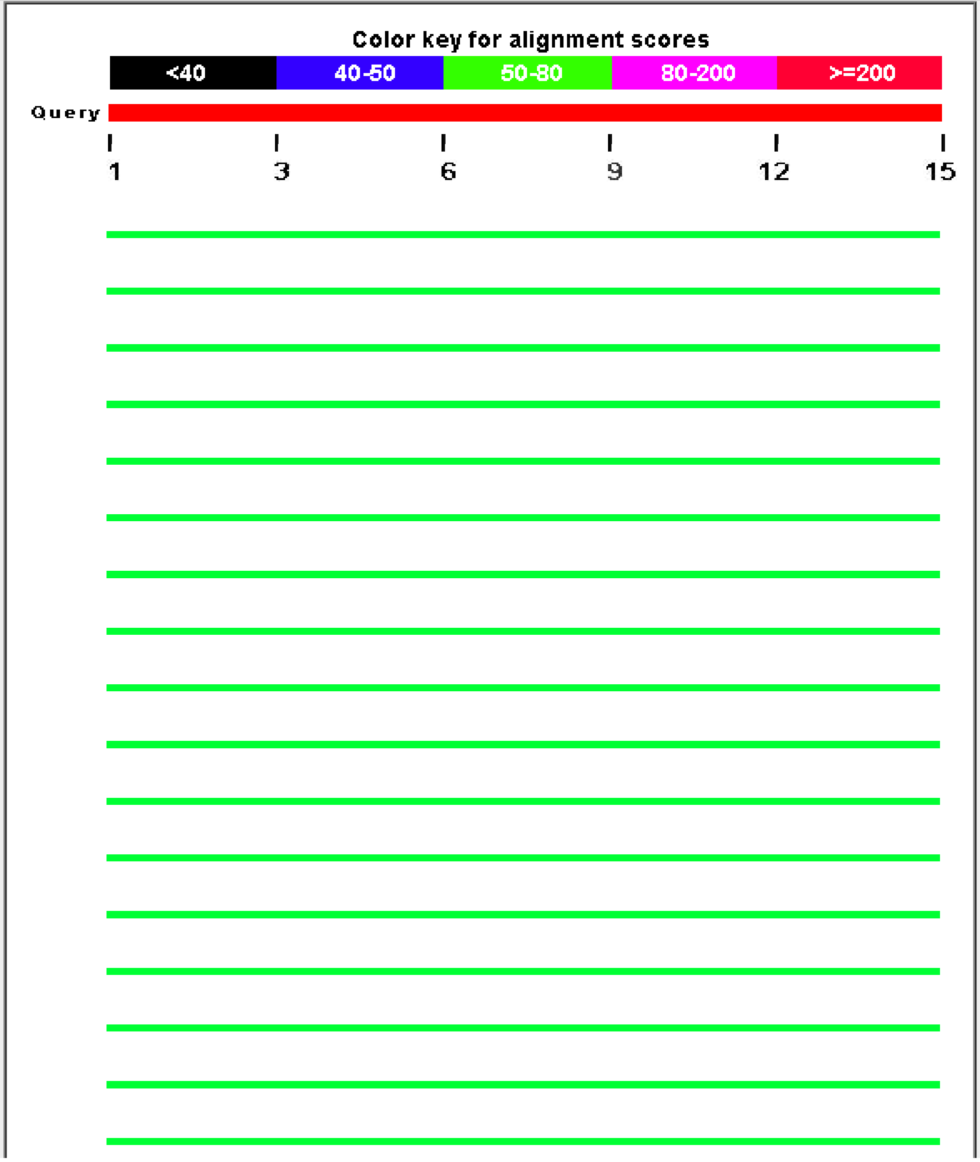
⊟ Graphic Summary

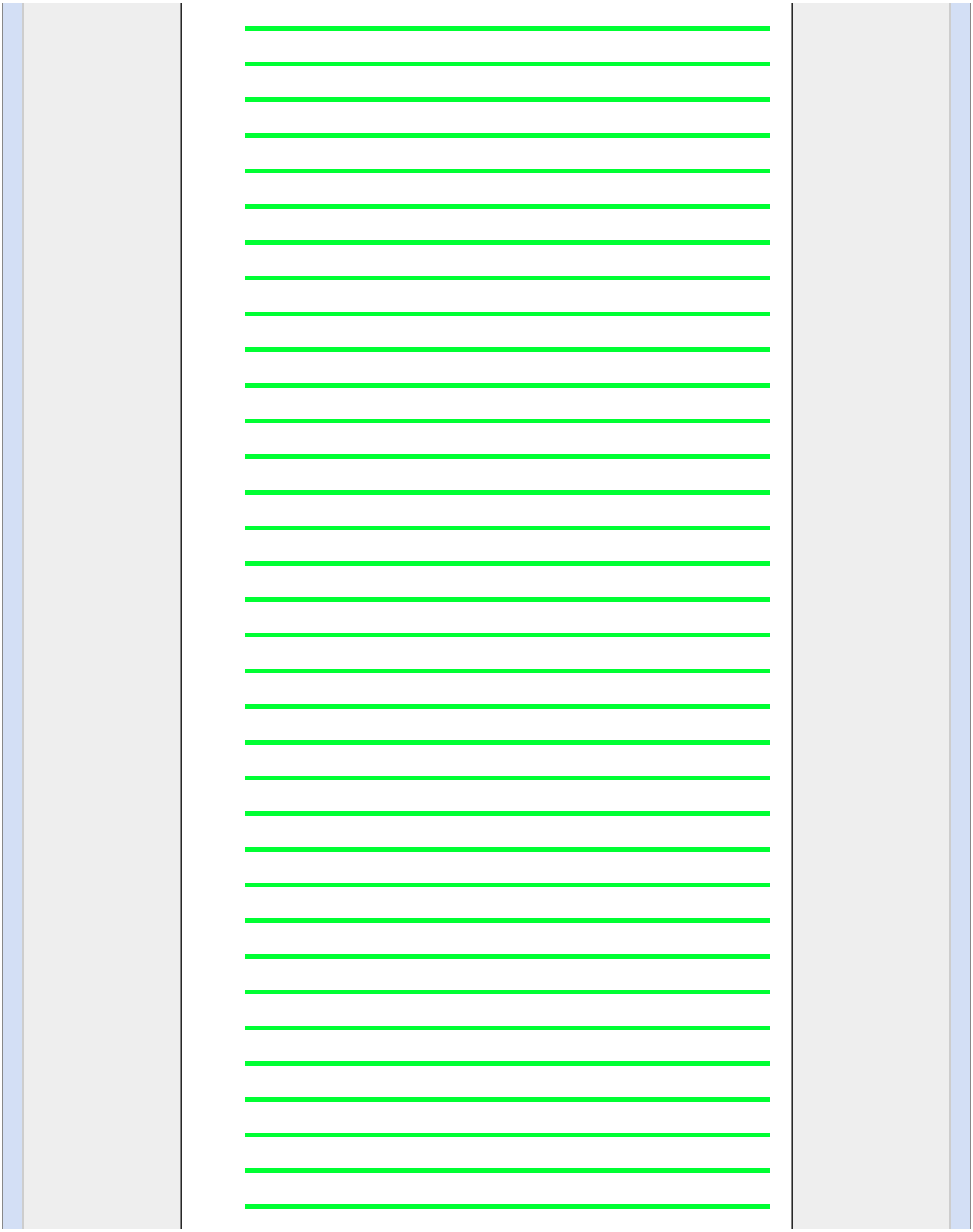
⊟ Show Conserved Domains

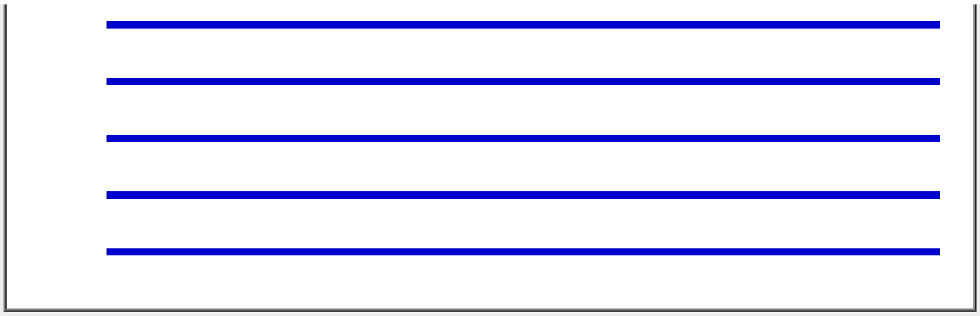
No putative conserved domains have been detected

Distribution of 102 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	52.4	52.4	100%	1e-06	93%	gi|194390586|BAG62052.1
☐	TPA: cadherin-5 precursor [Bos taurus]	52.4	52.4	100%	1e-06	93%	gi|296477907|DAA20022.1
☐	Cadherin-5 [Tupaia chinensis]	52.4	52.4	100%	1e-06	93%	gi|444715905|ELW56766.1
☐	PREDICTED: cadherin-5 isoform X1 [Pongo abelii]	52.4	52.4	100%	1e-06	93%	gi|686750801|XP_009249057.1
☐	PREDICTED: cadherin-5 [Tupaia chinensis]	52.4	52.4	100%	1e-06	93%	gi|562854134|XP_006155681.1
☐	unnamed protein product [Homo sapiens]	52.4	52.4	100%	1e-06	93%	gi|194390842|BAG62180.1
☐	PREDICTED: cadherin-5 [Macaca mulatta]	52.4	52.4	100%	1e-06	93%	gi|297284162|XP_002802558.1
☐	PREDICTED: cadherin-5 [Ovis aries]	52.4	52.4	100%	1e-06	93%	gi|426242469|XP_004015095.1
☐	PREDICTED: cadherin-5 [Camelus dromedarius]	52.4	52.4	100%	2e-06	93%	gi|744581321|XP_010983993.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-5 [Felis catu	52.4	52.4	100%	2e-06	93%	gi|587014936|XP_006941627.1
☐	cadherin-5 [Homo sapiens]	52.4	52.4	100%	2e-06	93%	gi|29593|CAA42468.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-5 [Vicugna p	52.4	52.4	100%	2e-06	93%	gi|560962576|XP_006203720.1
☐	PREDICTED: cadherin-5 [Camelus ferus]	52.4	52.4	100%	2e-06	93%	gi|560908802|XP_006180715.1
☐	VE cadherin [Sus scrofa]	52.4	52.4	100%	2e-06	93%	gi|18146997|BAB82983.1
☐	cadherin-5 precursor [Sus scrofa]	52.4	52.4	100%	2e-06	93%	gi|48976065|NP_001001649.2
☐	PREDICTED: cadherin-5 isoform X1 [Bubalus bubalis]	52.4	52.4	100%	2e-06	93%	gi|594098001|XP_006072178.1
☐	PREDICTED: cadherin-5 [Pantholops hodgsonii]	52.4	52.4	100%	2e-06	93%	gi|556727010|XP_005959261.1
☐	PREDICTED: cadherin-5 isoform X2 [Capra hircus]	52.4	52.4	100%	2e-06	93%	gi|548503374|XP_005692159.1
☐	PREDICTED: cadherin-5 [Bos mutus]	52.4	52.4	100%	2e-06	93%	gi|555969230|XP_005896642.1
☐	cadherin-5 precursor [Bos taurus]	52.4	52.4	100%	2e-06	93%	gi|48675381|NP_001001601.1
☐	PREDICTED: cadherin-5 [Rhinopithecus roxellana]	52.4	52.4	100%	2e-06	93%	gi|724956739|XP_010353493.1
☐	cadherin-5 preproprotein [Homo sapiens]	52.4	52.4	100%	2e-06	93%	gi|166362713|NP_001786.2
☐	PREDICTED: cadherin-5 isoform X1 [Capra hircus]	52.4	52.4	100%	2e-06	93%	gi|548503369|XP_005692158.1
☐	PREDICTED: cadherin-5 [Gorilla gorilla gorilla]	52.4	52.4	100%	2e-06	93%	gi|426382415|XP_004057800.1
☐	VE-cadherin [Homo sapiens]	52.4	52.4	100%	2e-06	93%	gi|599834|CAA56306.1
☐	PREDICTED: cadherin-5 [Pan troglodytes]	52.4	52.4	100%	2e-06	93%	gi|332846093|XP_523383.3
☐	PREDICTED: cadherin-5 isoform X2 [Pongo abelii]	52.4	52.4	100%	2e-06	93%	gi|686750804|XP_009249058.1
☐	PREDICTED: cadherin-5 [Saimiri boliviensis boliviensis]	52.4	52.4	100%	2e-06	93%	gi|725587922|XP_010345034.1
☐	PREDICTED: cadherin-5 [Callithrix jacchus]	52.4	52.4	100%	2e-06	93%	gi|675751676|XP_008984237.1

☐	PREDICTED: cadherin-5 [Chlorocebus sabaeus]	52.4	52.4	100%	2e-06	93%	gi|635032884|XP_007991751.1
☐	PREDICTED: cadherin-5 [Papio anubis]	52.4	52.4	100%	2e-06	93%	gi|402908616|XP_003917032.1
☐	PREDICTED: cadherin-5 isoform 3 [Macaca mulatta]	52.4	52.4	100%	2e-06	93%	gi|109128804|XP_001082641.1
☐	cadherin-5 precursor [Camelus ferus]	52.4	52.4	100%	2e-06	93%	gi|528764579|EPY84238.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-5 [Camelus	52.4	52.4	100%	2e-06	93%	gi|743733051|XP_010960727.1
☐	PREDICTED: cadherin-5 [Bison bison bison]	52.4	52.4	100%	2e-06	93%	gi|742168920|XP_010849432.1
☐	PREDICTED: cadherin-5 [Nomascus leucogenys]	52.4	52.4	100%	2e-06	93%	gi|441597734|XP_003263044.2
☐	cadherin 5, type 2 preproprotein variant [Homo sapiens]	52.4	52.4	100%	2e-06	93%	gi|62089402|BAD93145.1
☐	PREDICTED: cadherin-5 [Panthera tigris altaica]	52.4	52.4	100%	2e-06	93%	gi|591329126|XP_007090445.1
☐	cadherin-5 [Mustela putorius furo]	50.3	50.3	100%	7e-06	87%	gi|226875148|ACO88922.1
☐	PREDICTED: cadherin-5-like [Leptonychotes weddellii]	50.3	50.3	100%	8e-06	87%	gi|585197558|XP_006749826.1
☐	PREDICTED: cadherin-5 [Sarcophilus harrisii]	50.3	69.6	100%	8e-06	87%	gi|395508265|XP_003758433.1
☐	PREDICTED: cadherin-5 [Canis lupus familiaris]	50.3	50.3	100%	8e-06	87%	gi|73957557|XP_546894.2
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-5 [Ursus ma	50.3	50.3	100%	8e-06	87%	gi|671019829|XP_008700743.1
☐	PREDICTED: cadherin-5-like [Ailuropoda melanoleuca]	50.3	50.3	100%	8e-06	87%	gi|301766044|XP_002918443.1
☐	PREDICTED: cadherin-5 [Equus caballus]	50.3	50.3	100%	8e-06	87%	gi|194208672|XP_001495945.2
☐	PREDICTED: cadherin-5 [Mustela putorius furo]	50.3	50.3	100%	8e-06	87%	gi|511839697|XP_004744358.1
☐	PREDICTED: cadherin-5 [Erinaceus europaeus]	50.3	50.3	100%	8e-06	87%	gi|617578262|XP_007517858.1
☐	PREDICTED: cadherin-5 [Odobenus rosmarus divergens]	50.3	50.3	100%	8e-06	87%	gi|472347531|XP_004393487.1
☐	PREDICTED: cadherin-5 [Equus przewalskii]	50.3	50.3	100%	8e-06	87%	gi|664707002|XP_008507790.1
☐	PREDICTED: cadherin-5 [Trichechus manatus latirostris]	50.3	50.3	100%	8e-06	87%	gi|471362314|XP_004371717.1
☐	PREDICTED: cadherin-5 [Chrysochloris asiatica]	50.3	50.3	100%	8e-06	87%	gi|586466154|XP_006863694.1
☐	PREDICTED: cadherin-5 [Sorex araneus]	49.0	49.0	100%	2e-05	87%	gi|505770491|XP_004600986.1
☐	PREDICTED: cadherin-5 [Condylura cristata]	49.0	49.0	100%	2e-05	87%	gi|507970985|XP_004690559.1
☐	PREDICTED: cadherin-5 [Pteropus alecto]	48.6	48.6	100%	3e-05	87%	gi|586549436|XP_006909789.1
☐	PREDICTED: cadherin-5 [Orycteropus afer afer]	48.6	48.6	100%	3e-05	87%	gi|634846452|XP_007938408.1
☐	PREDICTED: cadherin-5 [Tarsius syrichta]	48.6	48.6	100%	3e-05	87%	gi|640786228|XP_008048850.1
☐	PREDICTED: cadherin-5 [Oryctolagus cuniculus]	48.1	48.1	100%	4e-05	87%	gi|655787380|XP_008255604.1
☐	PREDICTED: cadherin-5 [Ictidomys tridecemlineatus]	48.1	48.1	100%	4e-05	87%	gi|532064908|XP_005318316.1
☐	PREDICTED: cadherin-5 isoform X1 [Monodelphis domestica]	48.1	67.4	100%	4e-05	80%	gi|611983494|XP_007477155.1
☐	PREDICTED: cadherin-5 isoform X2 [Fukomys damarensis]	46.9	46.9	100%	1e-04	80%	gi|731283855|XP_010610445.1
☐	PREDICTED: cadherin-5 isoform X1 [Fukomys damarensis]	46.9	46.9	100%	1e-04	80%	gi|731283852|XP_010610444.1
☐	PREDICTED: cadherin-5 [Chinchilla lanigera]	46.9	46.9	100%	1e-04	80%	gi|533148306|XP_005388518.1
☐	PREDICTED: cadherin-5 [Ceratotherium simum simum]	46.9	46.9	100%	1e-04	80%	gi|478514976|XP_004431736.1
☐	PREDICTED: cadherin-5 [Jaculus jaculus]	46.9	46.9	100%	1e-04	80%	gi|507559632|XP_004663539.1
☐	Cadherin-5 [Fukomys damarensis]	46.9	46.9	100%	1e-04	80%	gi|676263212|KFO19951.1
☐	PREDICTED: cadherin-5 [Orcinus orca]	46.4	46.4	100%	2e-04	87%	gi|466063942|XP_004280947.1
☐	PREDICTED: cadherin-5 [Lipotes vexillifer]	46.4	46.4	100%	2e-04	87%	gi|602690374|XP_007457381.1
☐	PREDICTED: cadherin-5 isoform X1 [Balaenoptera acutorostra	46.4	46.4	100%	2e-04	87%	gi|594627004|XP_007198115.1
☐	PREDICTED: cadherin-5 [Physeter catodon]	46.4	46.4	100%	2e-04	87%	gi|593728968|XP_007110305.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-5 [Tursiops	46.4	46.4	100%	2e-04	87%	gi|470599892|XP_004312079.1
☐	PREDICTED: cadherin-5 [Dasypus novemcinctus]	46.0	46.0	100%	2e-04	80%	gi|488538668|XP_004460971.1
☐	PREDICTED: cadherin-5 [Otolemur garnettii]	46.0	46.0	100%	2e-04	80%	gi|395853972|XP_003799472.1
☐	PREDICTED: cadherin-5 [Eptesicus fuscus]	45.6	45.6	100%	3e-04	87%	gi|641699668|XP_008138341.1
☐	PREDICTED: cadherin-5-like [Myotis lucifugus]	45.6	45.6	100%	3e-04	87%	gi|558214330|XP_006108333.1

☐	PREDICTED: cadherin-5 [Echinops telfairi]	45.6	45.6	100%	3e-04	80%	gi|507654772|XP_004704918.1
☐	Cadherin-5 [Myotis davidii]	45.6	45.6	100%	3e-04	87%	gi|432093659|ELK25641.1
☐	PREDICTED: cadherin-5 [Myotis brandtii]	45.6	45.6	100%	3e-04	87%	gi|554564388|XP_005876511.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-5 [Myotis da	45.6	45.6	100%	3e-04	87%	gi|584050367|XP_006769887.1
☐	PREDICTED: cadherin-5 [Ochotona princeps]	42.6	42.6	100%	0.003	80%	gi|504143531|XP_004584199.1
☐	PREDICTED: cadherin-5 [Cavia porcellus]	41.4	41.4	100%	0.007	73%	gi|348572421|XP_003471991.1
☐	PREDICTED: cadherin-5 [Nannospalax galili]	41.4	41.4	100%	0.007	73%	gi|674058723|XP_008835942.1
☐	PREDICTED: cadherin-5 isoform X2 [Heterocephalus glaber]	41.4	41.4	100%	0.007	73%	gi|512961812|XP_004843169.1
☐	PREDICTED: cadherin-5 isoform X1 [Heterocephalus glaber]	41.4	41.4	100%	0.007	73%	gi|512961810|XP_004843168.1
☐	PREDICTED: cadherin-5 [Heterocephalus glaber]	41.4	41.4	100%	0.007	73%	gi|512867808|XP_004891539.1
☐	Cadherin-5 [Heterocephalus glaber]	41.4	41.4	100%	0.007	73%	gi|351704405|EHB07324.1
☐	cadherin:ISOTYPE=VE [Mus musculus]	40.5	40.5	100%	0.014	73%	gi|1588293|2208309A
☐	unnamed protein product [Mus musculus]	40.5	40.5	100%	0.014	73%	gi|74198375|BAE39672.1
☐	cadherin-5 precursor [Mus musculus]	40.5	40.5	100%	0.014	73%	gi|38490561|NP_033998.2
☐	PREDICTED: cadherin-5 [Octodon degus]	39.7	39.7	100%	0.027	73%	gi|507624164|XP_004626098.1
☐	PREDICTED: cadherin-5 [Peromyscus maniculatus bairdii]	39.2	39.2	100%	0.037	73%	gi|589931486|XP_006978546.1
☐	Cadherin-5 [Cricetulus griseus]	37.1	37.1	100%	0.18	67%	gi|344242493|EGV98596.1
☐	PREDICTED: cadherin-5 isoform X2 [Cricetulus griseus]	37.1	37.1	100%	0.18	67%	gi|625281830|XP_007632574.1
☐	PREDICTED: cadherin-5 isoform X1 [Cricetulus griseus]	37.1	37.1	100%	0.18	67%	gi|354475023|XP_003499729.1
☐	peptidase M24 [Halalkalicoccus jeotgali]	35.4	35.4	100%	0.62	73%	gi|495693044|WP_008417623.1
☐	cadherin-5 [Rattus norvegicus]	35.0	35.0	100%	0.88	67%	gi|157817743|NP_001100877.1
☐	PREDICTED: cadherin-5 [Microtus ochrogaster]	35.0	35.0	100%	0.88	67%	gi|532002685|XP_005345597.1
☐	PREDICTED: cadherin-5 [Mesocricetus auratus]	35.0	35.0	100%	0.88	67%	gi|524957484|XP_005078704.1
☐	hypothetical protein [Bifidobacterium biavatii]	33.7	33.7	80%	2.3	69%	gi|705395722|WP_033493886.1
☐	histidine kinase [Actinokineospora sp. EG49]	32.9	32.9	80%	4.0	77%	gi|737297371|WP_035280438.1
☐	ATP-binding region, ATPase-like protein [Actinokineospora sp.	32.9	32.9	80%	4.0	77%	gi|583003441|EWC62912.1

Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194390586|dbj|BAG62052.1| **Length:** 525 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 176 to 190 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	1e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    REVYPWYDLTVEAKE  15
            REVYPWY+LTVEAKE
Sbjct  176  REVYPWYNLTVEAKE  190
```

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TPA: cadherin-5 precursor [Bos taurus]

Sequence ID: gi|296477907|tpg|DAA20022.1| **Length:** 618 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 434 to 448 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	1e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    REVYPWYDLTVEAKE  15
            REVYPWY+LTVEAKE
Sbjct  434  REVYPWYNLTVEAKE  448
```

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Cadherin-5 [Tupaia chinensis]

Sequence ID: gi|444715905|gb|ELW56766.1| **Length:** 684 **Number of Matches:** 1

Related Information

Range 1: 489 to 503 GenPept Graphics

Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	1e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    REVYPWYDLTVEAKE  15
            REVYPWY+LTVEAKE
Sbjct  489  REVYPWYNLTVEAKE  503
```

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PREDICTED: cadherin-5 isoform X1 [Pongo abelii]

Sequence ID: gi|686750801|ref|XP_009249057.1| **Length:** 706 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 435 to 449 GenPept Graphics

Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	1e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    REVYPWYDLTVEAKE  15
            REVYPWY+LTVEAKE
Sbjct  435  REVYPWYNLTVEAKE  449
```

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PREDICTED: cadherin-5 [Tupaia chinensis]

Sequence ID: gi|562854134|ref|XP_006155681.1| **Length:** 715 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 432 to 446 GenPept Graphics

Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	1e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    REVYPWYDLTVEAKE  15
            REVYPWY+LTVEAKE
Sbjct  432  REVYPWYNLTVEAKE  446
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - B92K89GF01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download

How to read this page | Blast report description

CDH5_REVYPWYNLTVEAKE_NonMod

RID B92K89GF01R (Expires on 01-14 10:00 am)

Query ID lcl|324617
Description None
Molecule type amino acid
Query Length 15

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

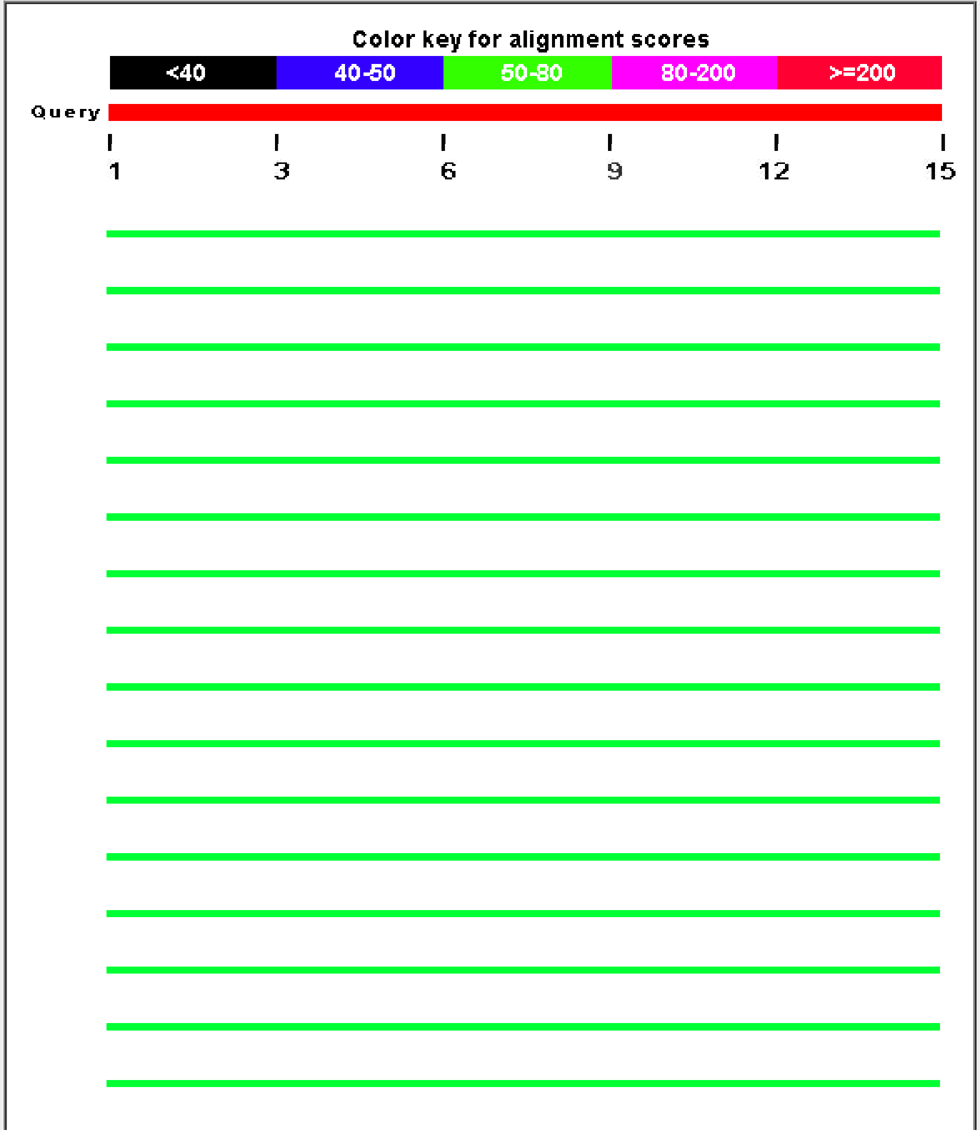
Graphic Summary

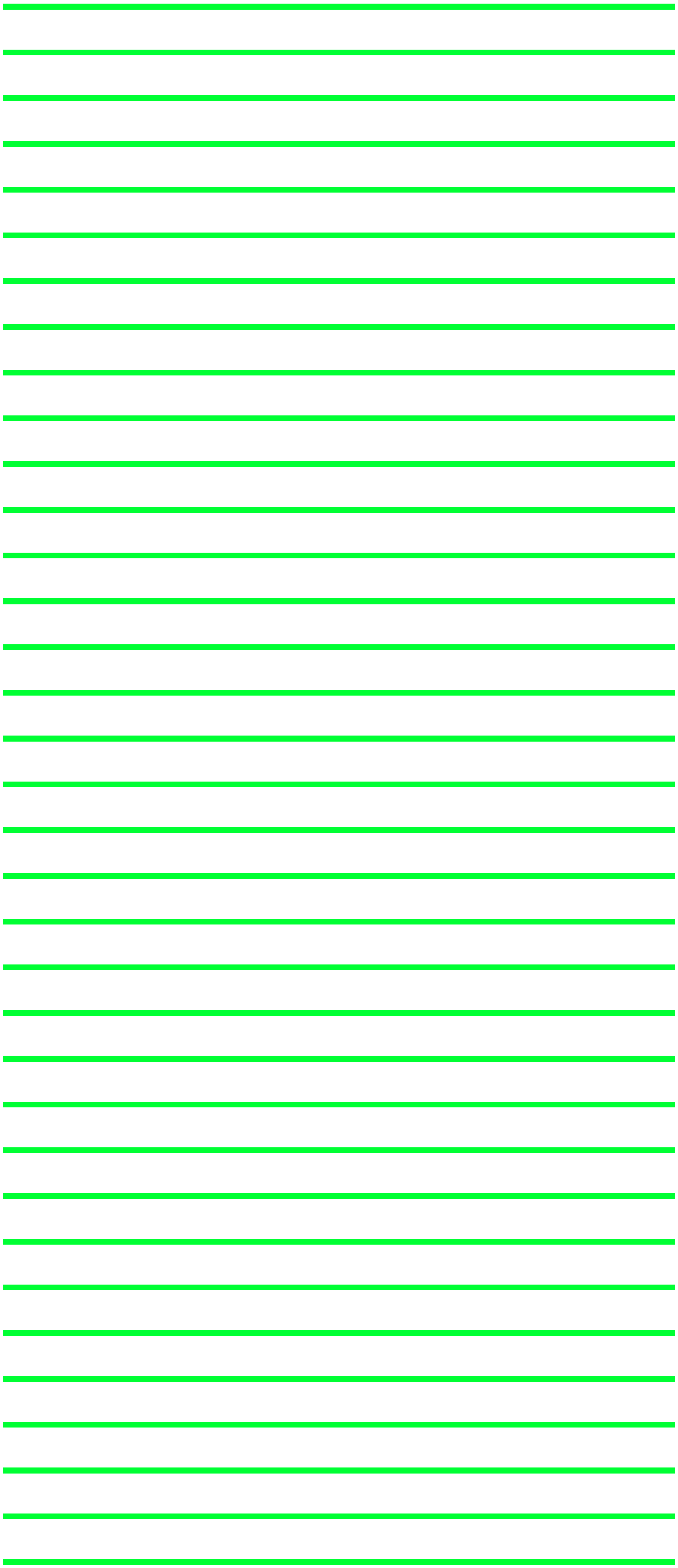
Show Conserved Domains

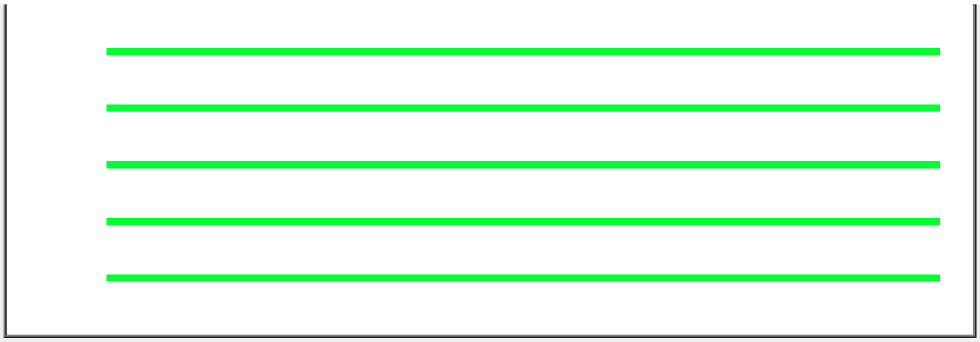
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|194390586|BAG62052.1
☐	TPA: cadherin-5 precursor [Bos taurus]	54.9	54.9	100%	2e-07	100%	gi|296477907|DAA20022.1
☐	Cadherin-5 [Tupaia chinensis]	54.9	54.9	100%	2e-07	100%	gi|444715905|ELW56766.1
☐	PREDICTED: cadherin-5 isoform X1 [Pongo abelii]	54.9	54.9	100%	2e-07	100%	gi|686750801|XP_009249057.1
☐	PREDICTED: cadherin-5 [Tupaia chinensis]	54.9	54.9	100%	2e-07	100%	gi|562854134|XP_006155681.1
☐	unnamed protein product [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|194390842|BAG62180.1
☐	PREDICTED: cadherin-5 [Macaca mulatta]	54.9	54.9	100%	2e-07	100%	gi|297284162|XP_002802558.1
☐	PREDICTED: cadherin-5 [Ovis aries]	54.9	54.9	100%	2e-07	100%	gi|426242469|XP_004015095.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-5 [Felis catus]	54.9	54.9	100%	2e-07	100%	gi|587014936|XP_006941627.1
☐	cadherin-5 [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|29593|CAA42468.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-5 [Vicugna paco	54.9	54.9	100%	2e-07	100%	gi|560962576|XP_006203720.1
☐	PREDICTED: cadherin-5 [Camelus ferus]	54.9	54.9	100%	2e-07	100%	gi|560908802|XP_006180715.1
☐	VE cadherin [Sus scrofa]	54.9	54.9	100%	2e-07	100%	gi|18146997|BAB82983.1
☐	cadherin-5 precursor [Sus scrofa]	54.9	54.9	100%	2e-07	100%	gi|48976065|NP_001001649.2
☐	PREDICTED: cadherin-5 isoform X1 [Bubalus bubalis]	54.9	54.9	100%	2e-07	100%	gi|594098001|XP_006072178.1
☐	PREDICTED: cadherin-5 [Pantholops hodgsonii]	54.9	54.9	100%	2e-07	100%	gi|556727010|XP_005959261.1
☐	PREDICTED: cadherin-5 isoform X2 [Capra hircus]	54.9	54.9	100%	2e-07	100%	gi|548503374|XP_005692159.1
☐	PREDICTED: cadherin-5 [Bos mutus]	54.9	54.9	100%	2e-07	100%	gi|555969230|XP_005896642.1
☐	cadherin-5 precursor [Bos taurus]	54.9	54.9	100%	2e-07	100%	gi|48675381|NP_001001601.1
☐	PREDICTED: cadherin-5 [Rhinopithecus roxellana]	54.9	54.9	100%	2e-07	100%	gi|724956739|XP_010353493.1
☐	cadherin-5 preproprotein [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|166362713|NP_001786.2
☐	PREDICTED: cadherin-5 isoform X1 [Capra hircus]	54.9	54.9	100%	2e-07	100%	gi|548503369|XP_005692158.1
☐	PREDICTED: cadherin-5 [Gorilla gorilla gorilla]	54.9	54.9	100%	2e-07	100%	gi|426382415|XP_004057800.1
☐	VE-cadherin [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|599834|CAA56306.1
☐	PREDICTED: cadherin-5 [Pan troglodytes]	54.9	54.9	100%	2e-07	100%	gi|332846093|XP_523383.3
☐	PREDICTED: cadherin-5 isoform X2 [Pongo abelii]	54.9	54.9	100%	2e-07	100%	gi|686750804|XP_009249058.1
☐	PREDICTED: cadherin-5 [Saimiri boliviensis boliviensis]	54.9	54.9	100%	2e-07	100%	gi|725587922|XP_010345034.1
☐	PREDICTED: cadherin-5 [Callithrix jacchus]	54.9	54.9	100%	2e-07	100%	gi|675751676|XP_008984237.1
☐							

	PREDICTED: cadherin-5 [Chlorocebus sabaeus]	54.9	54.9	100%	2e-07	100%	gi|635032884|XP_007991751.1
☐	PREDICTED: cadherin-5 [Papio anubis]	54.9	54.9	100%	2e-07	100%	gi|402908616|XP_003917032.1
☐	PREDICTED: cadherin-5 isoform 3 [Macaca mulatta]	54.9	54.9	100%	2e-07	100%	gi|109128804|XP_001082641.1
☐	cadherin-5 precursor [Camelus ferus]	54.9	54.9	100%	2e-07	100%	gi|528764579|EPY84238.1
☐	PREDICTED: cadherin-5 [Nomascus leucogenys]	54.9	54.9	100%	2e-07	100%	gi|441597734|XP_003263044.2
☐	cadherin 5, type 2 preproprotein variant [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|62089402|BAD93145.1
☐	PREDICTED: cadherin-5 [Panthera tigris altaica]	54.9	54.9	100%	2e-07	100%	gi|591329126|XP_007090445.1
☐	cadherin-5 [Mustela putorius furo]	52.8	52.8	100%	9e-07	93%	gi|226875148|ACO88922.1
☐	PREDICTED: cadherin-5-like [Leptonychotes weddellii]	52.8	52.8	100%	1e-06	93%	gi|585197558|XP_006749826.1
☐	PREDICTED: cadherin-5 [Sarcophilus harrisii]	52.8	52.8	100%	1e-06	93%	gi|395508265|XP_003758433.1
☐	PREDICTED: cadherin-5 [Canis lupus familiaris]	52.8	52.8	100%	1e-06	93%	gi|73957557|XP_546894.2
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-5 [Ursus maritim	52.8	52.8	100%	1e-06	93%	gi|671019829|XP_008700743.1
☐	PREDICTED: cadherin-5-like [Ailuropoda melanoleuca]	52.8	52.8	100%	1e-06	93%	gi|301766044|XP_002918443.1
☐	PREDICTED: cadherin-5 [Equus caballus]	52.8	52.8	100%	1e-06	93%	gi|194208672|XP_001495945.2
☐	PREDICTED: cadherin-5 [Mustela putorius furo]	52.8	52.8	100%	1e-06	93%	gi|511839697|XP_004744358.1
☐	PREDICTED: cadherin-5 [Erinaceus europaeus]	52.8	52.8	100%	1e-06	93%	gi|617578262|XP_007517858.1
☐	PREDICTED: cadherin-5 [Odobenus rosmarus divergens]	52.8	52.8	100%	1e-06	93%	gi|472347531|XP_004393487.1
☐	PREDICTED: cadherin-5 [Equus przewalskii]	52.8	52.8	100%	1e-06	93%	gi|664707002|XP_008507790.1
☐	PREDICTED: cadherin-5 [Trichechus manatus latirostris]	52.8	52.8	100%	1e-06	93%	gi|471362314|XP_004371717.1
☐	PREDICTED: cadherin-5 [Chrysochloris asiatica]	52.8	52.8	100%	1e-06	93%	gi|586466154|XP_006863694.1
☐	PREDICTED: cadherin-5 [Sorex araneus]	51.5	51.5	100%	3e-06	93%	gi|505770491|XP_004600986.1
☐	PREDICTED: cadherin-5 [Condylura cristata]	51.5	51.5	100%	3e-06	93%	gi|507970985|XP_004690559.1
☐	PREDICTED: cadherin-5 [Pteropus alecto]	51.1	51.1	100%	4e-06	93%	gi|586549436|XP_006909789.1
☐	PREDICTED: cadherin-5 [Orycteropus afer afer]	51.1	51.1	100%	4e-06	93%	gi|634846452|XP_007938408.1
☐	PREDICTED: cadherin-5 [Tarsius syrichta]	51.1	51.1	100%	4e-06	93%	gi|640786228|XP_008048850.1
☐	PREDICTED: cadherin-5 [Oryctolagus cuniculus]	50.7	50.7	100%	5e-06	93%	gi|655787380|XP_008255604.1
☐	PREDICTED: cadherin-5 [Ictidomys tridecemlineatus]	50.7	50.7	100%	5e-06	93%	gi|532064908|XP_005318316.1
☐	PREDICTED: cadherin-5 isoform X1 [Monodelphis domestica]	50.7	50.7	100%	5e-06	87%	gi|611983494|XP_007477155.1
☐	PREDICTED: cadherin-5 isoform X2 [Fukomys damarensis]	49.4	49.4	100%	1e-05	87%	gi|731283855|XP_010610445.1
☐	PREDICTED: cadherin-5 isoform X1 [Fukomys damarensis]	49.4	49.4	100%	1e-05	87%	gi|731283852|XP_010610444.1
☐	PREDICTED: cadherin-5 [Chinchilla lanigera]	49.4	49.4	100%	1e-05	87%	gi|533148306|XP_005388518.1
☐	PREDICTED: cadherin-5 [Ceratotherium simum simum]	49.4	49.4	100%	1e-05	87%	gi|478514976|XP_004431736.1
☐	PREDICTED: cadherin-5 [Jaculus jaculus]	49.4	49.4	100%	1e-05	87%	gi|507559632|XP_004663539.1
☐	Cadherin-5 [Fukomys damarensis]	49.4	49.4	100%	1e-05	87%	gi|676263212|KFO19951.1
☐	PREDICTED: cadherin-5 [Orcinus orca]	49.0	49.0	100%	2e-05	93%	gi|466063942|XP_004280947.1
☐	PREDICTED: cadherin-5 [Lipotes vexillifer]	49.0	49.0	100%	2e-05	93%	gi|602690374|XP_007457381.1
☐	PREDICTED: cadherin-5 isoform X1 [Balaenoptera acutorostrata sc	49.0	49.0	100%	2e-05	93%	gi|594627004|XP_007198115.1
☐	PREDICTED: cadherin-5 [Physeter catodon]	49.0	49.0	100%	2e-05	93%	gi|593728968|XP_007110305.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-5 [Tursiops trunc	49.0	49.0	100%	2e-05	93%	gi|470599892|XP_004312079.1
☐	PREDICTED: cadherin-5 [Dasypus novemcinctus]	48.6	48.6	100%	3e-05	87%	gi|488538668|XP_004460971.1
☐	PREDICTED: cadherin-5 [Otolemur garnettii]	48.6	48.6	100%	3e-05	87%	gi|395853972|XP_003799472.1
☐	PREDICTED: cadherin-5 [Eptesicus fuscus]	48.1	48.1	100%	4e-05	93%	gi|641699668|XP_008138341.1
☐	PREDICTED: cadherin-5-like [Myotis lucifugus]	48.1	48.1	100%	4e-05	93%	gi|558214330|XP_006108333.1
☐	PREDICTED: cadherin-5 [Echinops telfairi]	48.1	48.1	100%	4e-05	87%	gi|507654772|XP_004704918.1
☐	Cadherin-5 [Myotis davidii]	48.1	48.1	100%	4e-05	93%	gi|432093659|ELK25641.1

☐	PREDICTED: cadherin-5 [Myotis brandtii]	48.1	48.1	100%	4e-05	93%	gi|554564388|XP_005876511.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-5 [Myotis davidii	48.1	48.1	100%	4e-05	93%	gi|584050367|XP_006769887.1
☐	PREDICTED: cadherin-5 [Ochotona princeps]	45.2	45.2	100%	4e-04	87%	gi|504143531|XP_004584199.1
☐	PREDICTED: cadherin-5 [Cavia porcellus]	43.9	43.9	100%	0.001	80%	gi|348572421|XP_003471991.1
☐	PREDICTED: cadherin-5 [Nannospalax galili]	43.9	43.9	100%	0.001	80%	gi|674058723|XP_008835942.1
☐	PREDICTED: cadherin-5 isoform X2 [Heterocephalus glaber]	43.9	43.9	100%	0.001	80%	gi|512961812|XP_004843169.1
☐	PREDICTED: cadherin-5 isoform X1 [Heterocephalus glaber]	43.9	43.9	100%	0.001	80%	gi|512961810|XP_004843168.1
☐	PREDICTED: cadherin-5 [Heterocephalus glaber]	43.9	43.9	100%	0.001	80%	gi|512867808|XP_004891539.1
☐	Cadherin-5 [Heterocephalus glaber]	43.9	43.9	100%	0.001	80%	gi|351704405|EHB07324.1
☐	cadherin:ISOTYPE=VE [Mus musculus]	43.1	43.1	100%	0.002	80%	gi|1588293|2208309A
☐	unnamed protein product [Mus musculus]	43.1	43.1	100%	0.002	80%	gi|74198375|BAE39672.1
☐	cadherin-5 precursor [Mus musculus]	43.1	43.1	100%	0.002	80%	gi|38490561|NP_033998.2
☐	PREDICTED: cadherin-5 [Octodon degus]	42.2	42.2	100%	0.004	80%	gi|507624164|XP_004626098.1
☐	PREDICTED: cadherin-5 [Peromyscus maniculatus bairdii]	41.8	41.8	100%	0.005	80%	gi|589931486|XP_006978546.1
☐	Cadherin-5 [Cricetulus griseus]	39.7	39.7	100%	0.026	73%	gi|344242493|EGV98596.1
☐	PREDICTED: cadherin-5 isoform X2 [Cricetulus griseus]	39.7	39.7	100%	0.026	73%	gi|625281830|XP_007632574.1
☐	PREDICTED: cadherin-5 isoform X1 [Cricetulus griseus]	39.7	39.7	100%	0.026	73%	gi|354475023|XP_003499729.1
☐	cadherin-5 [Rattus norvegicus]	37.5	37.5	100%	0.13	73%	gi|157817743|NP_001100877.1
☐	PREDICTED: cadherin-5 [Microtus ochrogaster]	37.5	37.5	100%	0.13	73%	gi|532002685|XP_005345597.1
☐	PREDICTED: cadherin-5 [Mesocricetus auratus]	37.5	37.5	100%	0.13	73%	gi|524957484|XP_005078704.1
☐	unnamed protein product [Mus musculus]	33.3	33.3	100%	2.8	73%	gi|74203863|BAE28530.1
☐	mCG130451 [Mus musculus]	33.3	33.3	100%	2.9	73%	gi|148707891|EDL39838.1
☐	Cadherin 19, type 2 [Mus musculus]	33.3	33.3	100%	2.9	73%	gi|187957174|AAI57928.1
☐	cadherin-19 precursor [Mus musculus]	33.3	33.3	100%	2.9	73%	gi|124487065|NP_001074855.1
☐	PREDICTED: cadherin-19 [Loxodonta africana]	33.3	33.3	100%	2.9	73%	gi|344268920|XP_003406304.1
☐	ATP-binding region, ATPase-like protein [Actinokineospora sp. EG	32.9	32.9	80%	3.8	77%	gi|583003441|EWC62912.1
☐	peptidase M24 [Halalkalicoccus jeotgali]	32.9	32.9	100%	3.9	67%	gi|495693044|WP_008417623.1

⊟ Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194390586|dbj|BAG62052.1| **Length:** 525 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 176 to 190 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.9 bits(122)	2e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    REVYPWYNLTVEAKE  15
            REVYPWYNLTVEAKE
Sbjct  176  REVYPWYNLTVEAKE  190
```

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TPA: cadherin-5 precursor [Bos taurus]

Sequence ID: gi|296477907|tpg|DAA20022.1| **Length:** 618 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 434 to 448 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.9 bits(122)	2e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    REVYPWYNLTVEAKE  15
```

```
                REVYPWYNLTVEAKE
Sbjct  434  REVYPWYNLTVEAKE  448
```

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Cadherin-5 [Tupaia chinensis]

Sequence ID: gi|444715905|gb|ELW56766.1| **Length:** 684 **Number of Matches:** 1

Related Information

Range 1: 489 to 503 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.9 bits(122)	2e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    REVYPWYNLTVEAKE  15
            REVYPWYNLTVEAKE
Sbjct  489  REVYPWYNLTVEAKE  503
```

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PREDICTED: cadherin-5 isoform X1 [Pongo abelii]

Sequence ID: gi|686750801|ref|XP_009249057.1| **Length:** 706 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 435 to 449 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.9 bits(122)	2e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    REVYPWYNLTVEAKE  15
            REVYPWYNLTVEAKE
Sbjct  435  REVYPWYNLTVEAKE  449
```

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PREDICTED: cadherin-5 [Tupaia chinensis]

Sequence ID: gi|562854134|ref|XP_006155681.1| **Length:** 715 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 432 to 446 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.9 bits(122)	2e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    REVYPWYNLTVEAKE  15
            REVYPWYNLTVEAKE
Sbjct  432  REVYPWYNLTVEAKE  446
```

NCBI/ BLAST/ blastp suite/ Formatting Results - BTG0ZY8T013

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

CDHR5_RVEEDTKVDSTVIPETQLQAEDRD_Mod

RID BTG0ZY8T013 (Expires on 01-20 15:28 pm)

Query ID	lcl|29927	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	24		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

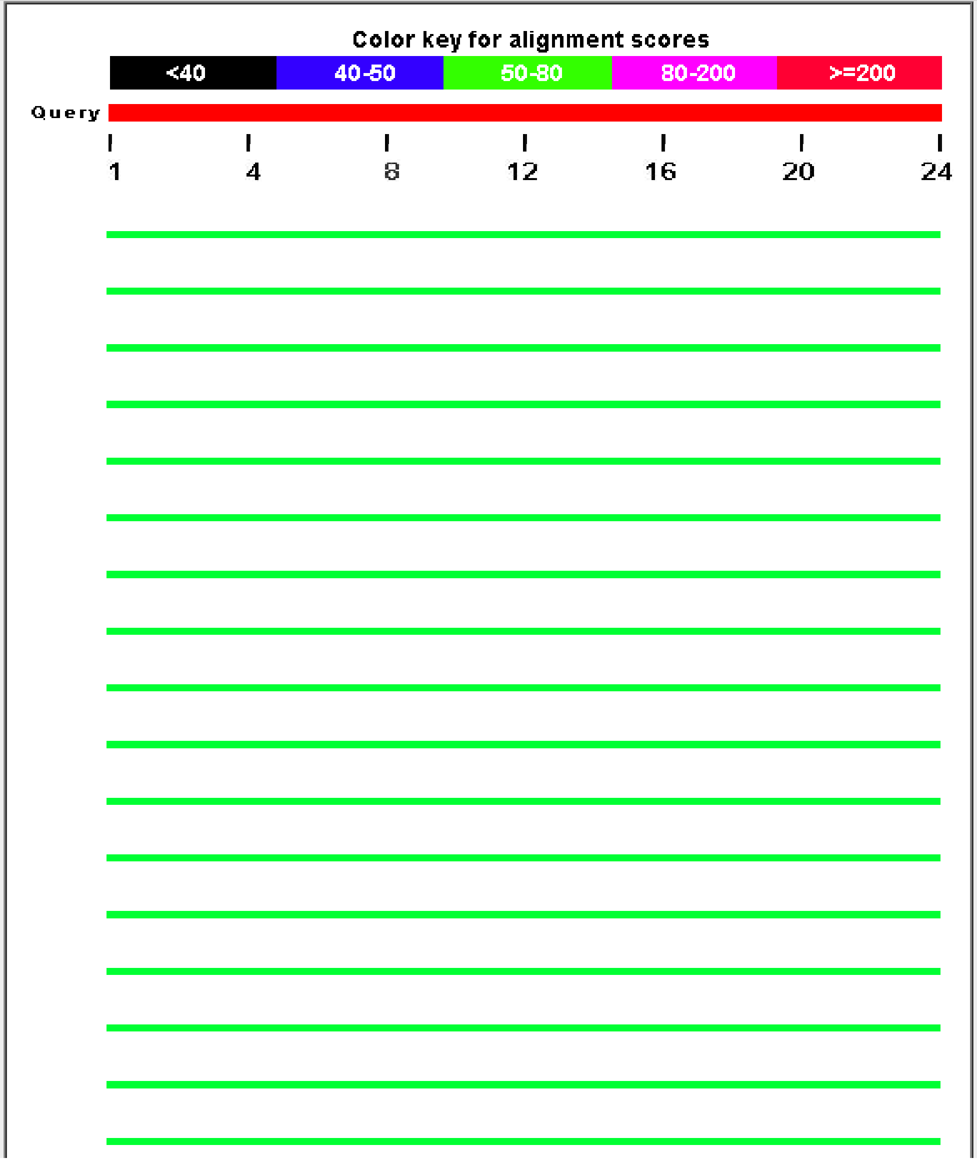
Graphic Summary

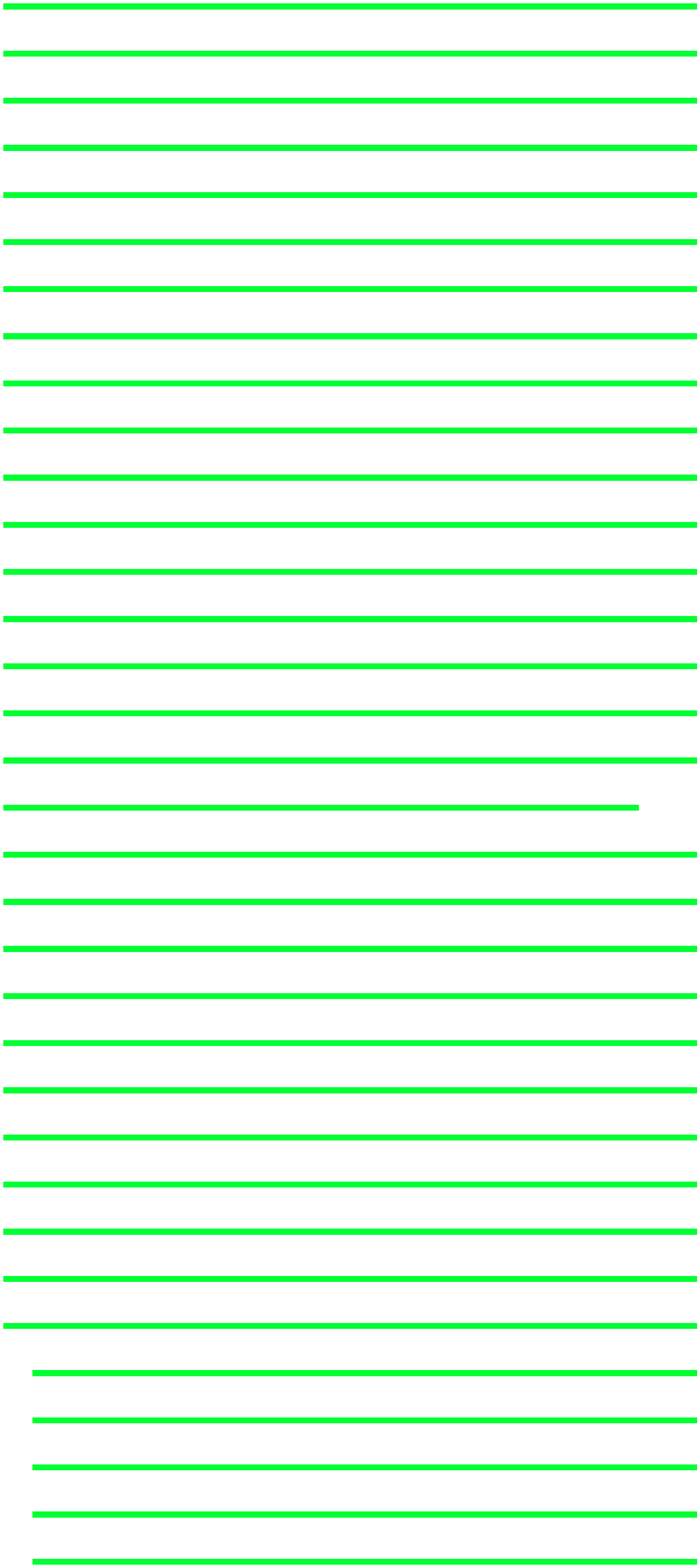
Show Conserved Domains

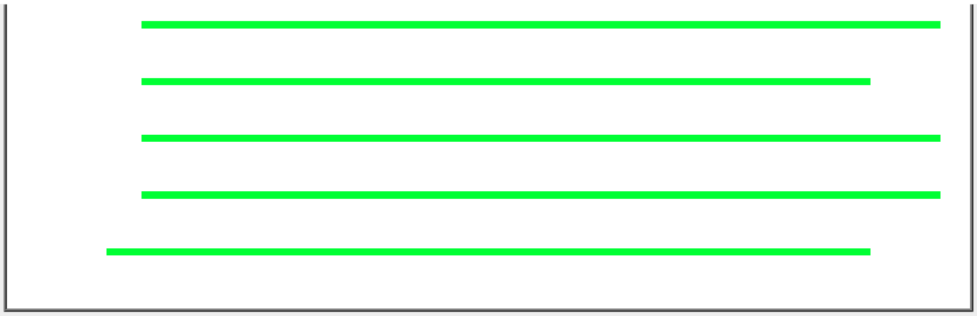
No putative conserved domains have been detected

Distribution of 105 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	mucin and cadherin-like, isoform CRA_f [Homo sapiens]	77.0	77.0	100%	2e-14	96%	gi|119622771|EAX02366.1
☐	MUCDHL-ALT [Homo sapiens]	77.0	77.0	100%	2e-14	96%	gi|10334769|AAG16730.1
☐	MUCDHL-ALT [Homo sapiens]	77.0	77.0	100%	2e-14	96%	gi|10334772|AAG16732.1
☐	mucin and cadherin-like, isoform CRA_d [Homo sapiens]	77.0	77.0	100%	2e-14	96%	gi|119622769|EAX02364.1
☐	PREDICTED: cadherin-related family member 5 isoform X4 [Hc	77.0	77.0	100%	2e-14	96%	gi|578839861|XP_005253047.2
☐	unnamed protein product [Homo sapiens]	77.0	77.0	100%	2e-14	96%	gi|194374995|BAG62610.1
☐	cadherin-related family member 5 isoform 3 precursor [Homo sa	77.0	77.0	100%	2e-14	96%	gi|110618250|NP_112554.2
☐	unnamed protein product [Homo sapiens]	77.0	77.0	100%	2e-14	96%	gi|7020438|BAA91130.1
☐	PREDICTED: cadherin-related family member 5 [Gorilla gorilla	77.0	77.0	100%	2e-14	96%	gi|426366755|XP_004050412.1
☐	mucin and cadherin-like, isoform CRA_c [Homo sapiens]	77.0	77.0	100%	2e-14	96%	gi|119622768|EAX02363.1
☐	PREDICTED: cadherin-related family member 5 isoform X3 [Hc	77.0	77.0	100%	2e-14	96%	gi|578839859|XP_005253046.2
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Hc	77.0	77.0	100%	2e-14	96%	gi|578839857|XP_005253045.2
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Hc	77.0	77.0	100%	2e-14	96%	gi|578839855|XP_005253044.2
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Hc	77.0	77.0	100%	2e-14	96%	gi|578820616|XP_006718316.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-related famil	77.0	77.0	100%	2e-14	96%	gi|397468758|XP_003806038.1
☐	cadherin-related family member 5 isoform 4 precursor [Homo sa	77.0	77.0	100%	2e-14	96%	gi|285002199|NP_001165439.1
☐	MUCDHL [Homo sapiens]	77.0	77.0	100%	2e-14	96%	gi|37181861|AAQ88734.1
☐	mu-protocadherin [Homo sapiens]	77.0	77.0	100%	2e-14	96%	gi|11245187|AAG33495.1
☐	MUCDHL-FL [Homo sapiens]	77.0	77.0	100%	2e-14	96%	gi|10334770|AAG16731.1
☐	MUCDHL-FL [Homo sapiens]	77.0	77.0	100%	2e-14	96%	gi|10334774|AAG16733.1
☐	RecName: Full=Cadherin-related family member 5; AltName: F	77.0	77.0	100%	2e-14	96%	gi|296439399|Q9HBB8.3
☐	mucin and cadherin-like, isoform CRA_b [Homo sapiens]	77.0	77.0	100%	2e-14	96%	gi|119622767|EAX02362.1
☐	cadherin-related family member 5 isoform 1 precursor [Homo sa	77.0	77.0	100%	2e-14	96%	gi|110618248|NP_068743.2
☐	PREDICTED: cadherin-related family member 5 isoform X6 [Ch	70.6	70.6	100%	3e-12	88%	gi|635011025|XP_007988108.1
☐	PREDICTED: cadherin-related family member 5 isoform X5 [Pa	70.6	70.6	100%	3e-12	88%	gi|685584291|XP_009183489.1
☐	PREDICTED: cadherin-related family member 5 isoform X4 [Pa	70.6	70.6	100%	3e-12	88%	gi|685584289|XP_009183488.1
☐	PREDICTED: cadherin-related family member 5 isoform X5 [Ch	70.6	70.6	100%	3e-12	88%	gi|635011023|XP_007987388.1
☐	PREDICTED: cadherin-related family member 5 isoform X3 [Pa	70.6	70.6	100%	3e-12	88%	gi|685584287|XP_009183487.1
☐	PREDICTED: cadherin-related family member 5 isoform X4 [Ch	70.6	70.6	100%	3e-12	88%	gi|635011021|XP_007986645.1

☐	PREDICTED: cadherin-related family member 5 isoform X2 [Pa	70.6	70.6	100%	3e-12	88%	gi|685584285|XP_009183486.1
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Pa	70.6	70.6	100%	3e-12	88%	gi|685584283|XP_009183484.1
☐	PREDICTED: cadherin-related family member 5 isoform X3 [Ch	70.6	70.6	100%	3e-12	88%	gi|635011019|XP_007986020.1
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Ch	70.6	70.6	100%	3e-12	88%	gi|635011017|XP_007985338.1
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Ch	70.6	70.6	100%	3e-12	88%	gi|635011015|XP_007984693.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-related famil	70.2	70.2	91%	4e-12	95%	gi|441665990|XP_003281373.2
☐	PREDICTED: cadherin-related family member 5 isoform X5 [Rh	68.5	68.5	100%	2e-11	83%	gi|724796233|XP_010387931.1
☐	PREDICTED: cadherin-related family member 5 isoform X4 [Rh	68.5	68.5	100%	2e-11	83%	gi|724796230|XP_010387851.1
☐	PREDICTED: cadherin-related family member 5 isoform X3 [Rh	68.5	68.5	100%	2e-11	83%	gi|724796227|XP_010387784.1
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Rh	68.5	68.5	100%	2e-11	83%	gi|724796224|XP_010387726.1
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Rh	68.5	68.5	100%	2e-11	83%	gi|724796221|XP_010387653.1
☐	PREDICTED: cadherin-related family member 5 isoform X5 [Ma	65.5	65.5	100%	2e-10	83%	gi|544483429|XP_005576826.1
☐	PREDICTED: cadherin-related family member 5 isoform 2 [Mac	65.5	65.5	100%	2e-10	83%	gi|109104860|XP_001086363.1
☐	PREDICTED: cadherin-related family member 5 isoform X4 [Ma	65.5	65.5	100%	2e-10	83%	gi|544483427|XP_005576825.1
☐	PREDICTED: cadherin-related family member 5 isoform X3 [Ma	65.5	65.5	100%	2e-10	83%	gi|544483425|XP_005576824.1
☐	PREDICTED: cadherin-related family member 5 isoform 1 [Mac	65.5	65.5	100%	2e-10	83%	gi|297267104|XP_001086239.2
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Ma	65.5	65.5	100%	2e-10	83%	gi|544483421|XP_005576822.1
☐	PREDICTED: cadherin-related family member 5-like [Galeopter	62.1	62.1	95%	2e-09	83%	gi|667346400|XP_008563564.1
☐	PREDICTED: cadherin-related family member 5 [Ictidomys tride	58.3	58.3	95%	5e-08	78%	gi|532114016|XP_005341679.1
☐	PREDICTED: cadherin-related family member 5 [Otolemur garr	57.5	57.5	95%	9e-08	78%	gi|395861133|XP_003802848.1
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Sa	54.9	54.9	95%	6e-07	78%	gi|725605770|XP_010329489.1
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Sa	54.9	54.9	95%	6e-07	78%	gi|725605768|XP_010329488.1
☐	PREDICTED: cadherin-related family member 5 isoform X3 [Sa	54.9	54.9	95%	6e-07	78%	gi|403305644|XP_003943368.1
☐	PREDICTED: cadherin-related family member 5 [Tupaia chiner	54.5	54.5	87%	8e-07	81%	gi|562873172|XP_006164495.1
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Su	54.1	54.1	95%	1e-06	74%	gi|545805609|XP_005652842.1
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Su	54.1	54.1	95%	1e-06	74%	gi|545805606|XP_005652841.1
☐	PREDICTED: cadherin-related family member 5 [Ceratotherium	53.7	53.7	91%	2e-06	68%	gi|478534060|XP_004441167.1
☐	PREDICTED: cadherin-related family member 5 [Galeopterus v	52.8	52.8	87%	3e-06	76%	gi|667327847|XP_008590353.1
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Ma	52.4	52.4	83%	4e-06	80%	gi|544483423|XP_005576823.1
☐	PREDICTED: cadherin-related family member 5 [Equus przewa	52.0	52.0	91%	5e-06	73%	gi|664777361|XP_008507976.1
☐	PREDICTED: cadherin-related family member 5 [Equus caballu	52.0	52.0	91%	6e-06	73%	gi|545182188|XP_005598543.1
☐	PREDICTED: cadherin-related family member 5 [Callithrix jacch	50.7	50.7	95%	2e-05	74%	gi|675704132|XP_009007036.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-related famil	50.3	50.3	87%	2e-05	71%	gi|504181561|XP_004600071.1
☐	PREDICTED: cadherin-related family member 5 [Ursus maritim	50.3	50.3	87%	2e-05	67%	gi|671014096|XP_008697888.1
☐	PREDICTED: cadherin-related family member 5 [Chrysochloris	50.3	50.3	87%	2e-05	76%	gi|586493238|XP_006877066.1
☐	Mucin and cadherin-like protein [Pteropus alecto]	49.8	49.8	95%	3e-05	62%	gi|431910097|ELK13170.1
☐	PREDICTED: cadherin-related family member 5 [Pteropus alec	49.8	49.8	95%	3e-05	62%	gi|586552614|XP_006911325.1
☐	PREDICTED: cadherin-related family member 5 [Lipotes vexillif	49.8	49.8	91%	3e-05	73%	gi|602711484|XP_007465981.1
☐	mucin and cadherin like, isoform CRA_b [Mus musculus]	49.0	70.8	100%	5e-05	74%	gi|148686086|EDL18033.1
☐	PREDICTED: cadherin-related family member 5 [Jaculus jaculu	49.0	49.0	95%	5e-05	70%	gi|507539897|XP_004653954.1
☐	cadherin-related family member 5 isoform 2 precursor [Mus mu	49.0	70.8	100%	5e-05	74%	gi|21312502|NP_082345.1
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Mu	49.0	70.8	100%	5e-05	74%	gi|568952506|XP_006536323.1
☐	cadherin-related family member 5 isoform 1 precursor [Mus mu	49.0	70.8	100%	5e-05	74%	gi|167004347|NP_001107794.1
☐	RecName: Full=Cadherin-related family member 5; AltName: F	49.0	70.8	100%	5e-05	74%	gi|45477152|Q8VHF2.1
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Ca	47.7	47.7	87%	1e-04	67%	gi|744621423|XP_010997521.1

☐ PREDICTED: cadherin-related family member 5 isoform X5 [Ca	47.7	47.7	87%	1e-04	67%	gi|743697761|XP_010954426.1
☐ PREDICTED: cadherin-related family member 5 isoform X4 [Ca	47.7	47.7	87%	1e-04	67%	gi|743697759|XP_010954420.1
☐ PREDICTED: cadherin-related family member 5 isoform X3 [Ca	47.7	47.7	87%	1e-04	67%	gi|743697757|XP_010954413.1
☐ PREDICTED: cadherin-related family member 5 [Camelus ferus	47.7	47.7	87%	1e-04	67%	gi|560909593|XP_006181104.1
☐ PREDICTED: cadherin-related family member 5 [Vicugna paco	47.7	47.7	87%	1e-04	67%	gi|560994295|XP_006219255.1
☐ PREDICTED: cadherin-related family member 5 isoform X1 [Ca	47.7	47.7	87%	1e-04	67%	gi|744621420|XP_010997520.1
☐ PREDICTED: cadherin-related family member 5 isoform X2 [Ca	47.7	47.7	87%	1e-04	67%	gi|743697755|XP_010954403.1
☐ PREDICTED: cadherin-related family member 5 isoform X1 [Ca	47.7	47.7	87%	1e-04	67%	gi|743697753|XP_010954393.1
☐ PREDICTED: LOW QUALITY PROTEIN: cadherin-related famil	47.7	47.7	87%	1e-04	71%	gi|471415885|XP_004389467.1
☐ cadherin-related family member 5 precursor [Camelus ferus]	47.7	47.7	87%	1e-04	67%	gi|528764226|EPY83885.1
☐ PREDICTED: cadherin-related family member 5 [Loxodonta afr	47.7	47.7	87%	1e-04	71%	gi|344309231|XP_003423280.1
☐ PREDICTED: cadherin-related family member 5 [Leptonychotes	47.3	47.3	87%	2e-04	71%	gi|585180394|XP_006741861.1
☐ PREDICTED: cadherin-related family member 5 [Orcinus orca]	47.3	47.3	91%	2e-04	68%	gi|466050257|XP_004278199.1
☐ PREDICTED: cadherin-related family member 5 [Echinops telfa	46.9	46.9	87%	3e-04	71%	gi|507709657|XP_004717252.1
☐ PREDICTED: cadherin-related family member 5 [Cavia porcellu	46.4	46.4	95%	4e-04	70%	gi|514443851|XP_003461333.2
☐ PREDICTED: cadherin-related family member 5 [Orycteropus a	46.0	46.0	95%	5e-04	65%	gi|634871909|XP_007947550.1
☐ PREDICTED: cadherin-related family member 5 isoform X4 [Ch	45.6	45.6	95%	7e-04	65%	gi|533177179|XP_005401888.1
☐ PREDICTED: cadherin-related family member 5 isoform X3 [Ch	45.6	45.6	95%	7e-04	65%	gi|533177177|XP_005401887.1
☐ PREDICTED: cadherin-related family member 5 isoform X2 [Ch	45.6	45.6	95%	7e-04	65%	gi|533177175|XP_005401886.1
☐ PREDICTED: cadherin-related family member 5 [Physeter cato	45.6	45.6	95%	7e-04	65%	gi|593725286|XP_007108751.1
☐ PREDICTED: cadherin-related family member 5 isoform X1 [Ch	45.6	45.6	95%	7e-04	65%	gi|533177173|XP_005401885.1
☐ PREDICTED: cadherin-related family member 5 isoform X2 [Bu	45.2	45.2	95%	0.001	61%	gi|594042619|XP_006045841.1
☐ PREDICTED: cadherin-related family member 5 [Octodon degu	45.2	45.2	95%	0.001	70%	gi|507671995|XP_004638095.1
☐ PREDICTED: cadherin-related family member 5 [Bison bison bi	45.2	45.2	95%	0.001	61%	gi|742077964|XP_010835550.1
☐ PREDICTED: cadherin-related family member 5 [Odobenus ros	45.2	45.2	79%	0.001	68%	gi|472368599|XP_004403824.1
☐ Cadherin-related family member 5 [Bos mutus]	45.2	45.2	95%	0.001	61%	gi|440906581|ELR56829.1

Alignments

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mucin and cadherin-like, isoform CRA_f [Homo sapiens]

Sequence ID: gi|119622771|gb|EAX02366.1| **Length:** 485 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 132 to 155 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.0 bits(174)	2e-14	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    RVEEDTKVDSTVIPETQLQAEDRD  24
            RVEEDTKV+STVIPETQLQAEDRD
Sbjct  132  RVEEDTKVNSTVIPETQLQAEDRD  155
```

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MUCDHL-ALT [Homo sapiens]

Sequence ID: gi|10334769|gb|AAG16730.1| **Length:** 487 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 132 to 155 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.0 bits(174)	2e-14	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    RVEEDTKVDSTVIPETQLQAEDRD  24
            RVEEDTKV+STVIPETQLQAEDRD
Sbjct  132  RVEEDTKVNSTVIPETQLQAEDRD  155
```

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MUCDHL-ALT [Homo sapiens]

Sequence ID: gi|10334772|gb|AAG16732.1|AF258675_1 **Length:** 487 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 132 to 155 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.0 bits(174)	2e-14	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    RVEEDTKVDSTVIPETQLQAEDRD  24
            RVEEDTKV+STVIPETQLQAEDRD
Sbjct  132  RVEEDTKVNSTVIPETQLQAEDRD  155
```

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mucin and cadherin-like, isoform CRA_d, partial [Homo sapiens]

Sequence ID: gi|119622769|gb|EAX02364.1| **Length:** 493 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 132 to 155 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.0 bits(174)	2e-14	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    RVEEDTKVDSTVIPETQLQAEDRD  24
            RVEEDTKV+STVIPETQLQAEDRD
Sbjct  132  RVEEDTKVNSTVIPETQLQAEDRD  155
```

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PREDICTED: cadherin-related family member 5 isoform X4 [Homo sapiens]

Sequence ID: gi|578839861|ref|XP_005253047.2| **Length:** 551 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 132 to 155 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.0 bits(174)	2e-14	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    RVEEDTKVDSTVIPETQLQAEDRD  24
            RVEEDTKV+STVIPETQLQAEDRD
Sbjct  132  RVEEDTKVNSTVIPETQLQAEDRD  155
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - B92KKENH01R

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How to read this page | Blast report description

CDHR5_RVEEDTKVNSTVIPETQLQAEDRD_NonMod

RID	B92KKENH01R (Expires on 01-14 10:01 am)		
Query ID	lcl|328478	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	24		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

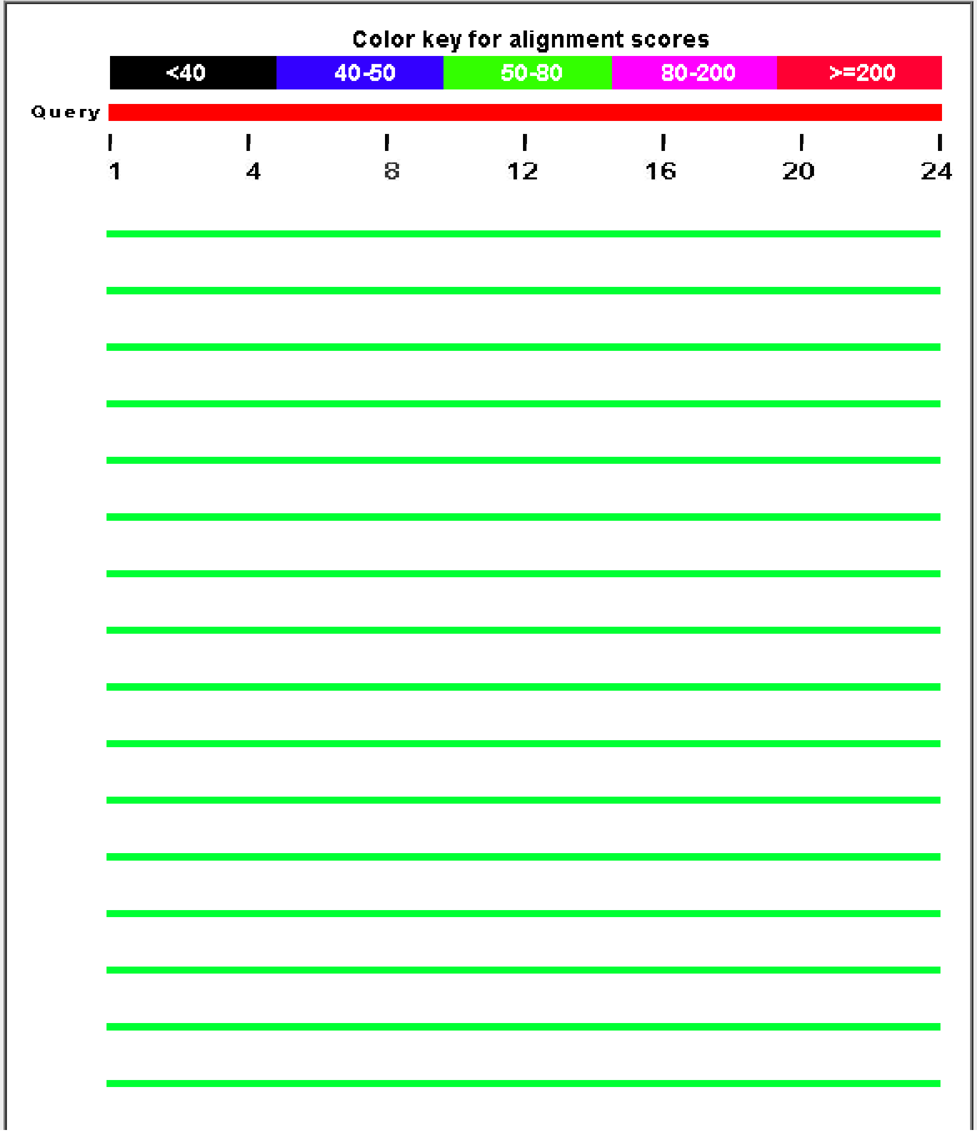
Graphic Summary

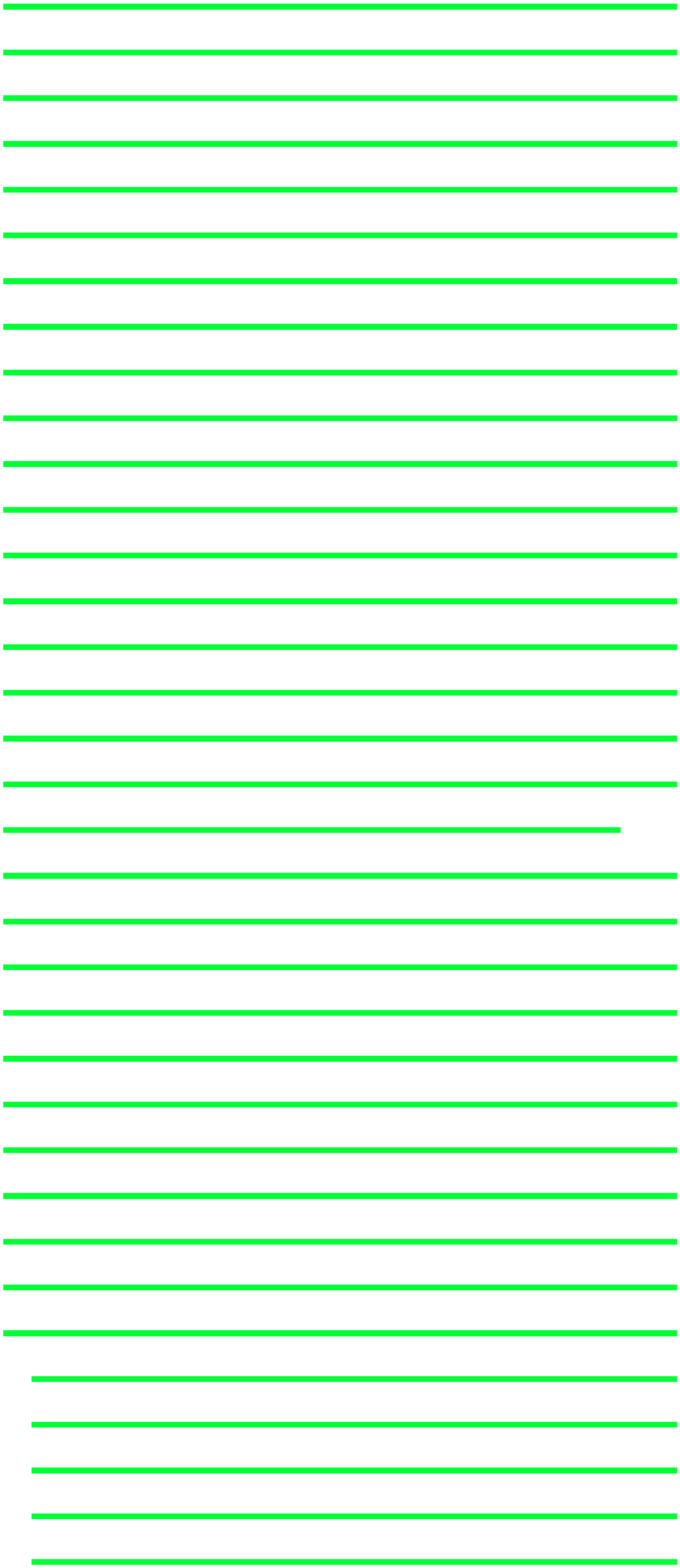
Show Conserved Domains

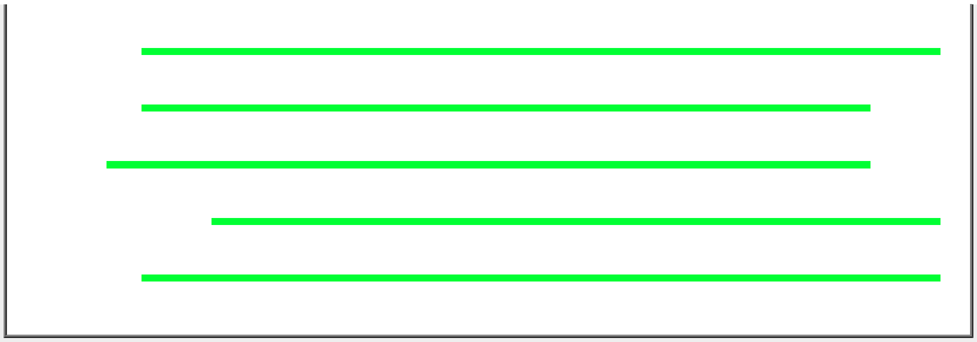
No putative conserved domains have been detected

Distribution of 106 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	mucin and cadherin-like, isoform CRA_f [Homo sapiens]	79.5	79.5	100%	3e-15	100%	gi|119622771|EAX02366.1
☐	MUCDHL-ALT [Homo sapiens]	79.5	79.5	100%	3e-15	100%	gi|10334769|AAG16730.1
☐	MUCDHL-ALT [Homo sapiens]	79.5	79.5	100%	3e-15	100%	gi|10334772|AAG16732.1
☐	mucin and cadherin-like, isoform CRA_d [Homo sapiens]	79.5	79.5	100%	3e-15	100%	gi|119622769|EAX02364.1
☐	PREDICTED: cadherin-related family member 5 isoform X4 [Homo	79.5	79.5	100%	3e-15	100%	gi|578839861|XP_005253047.2
☐	unnamed protein product [Homo sapiens]	79.5	79.5	100%	3e-15	100%	gi|194374995|BAG62610.1
☐	cadherin-related family member 5 isoform 3 precursor [Homo sapie	79.5	79.5	100%	3e-15	100%	gi|110618250|NP_112554.2
☐	unnamed protein product [Homo sapiens]	79.5	79.5	100%	3e-15	100%	gi|7020438|BAA91130.1
☐	PREDICTED: cadherin-related family member 5 [Gorilla gorilla goril	79.5	79.5	100%	3e-15	100%	gi|426366755|XP_004050412.1
☐	mucin and cadherin-like, isoform CRA_c [Homo sapiens]	79.5	79.5	100%	3e-15	100%	gi|119622768|EAX02363.1
☐	PREDICTED: cadherin-related family member 5 isoform X3 [Homo	79.5	79.5	100%	3e-15	100%	gi|578839859|XP_005253046.2
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Homo	79.5	79.5	100%	3e-15	100%	gi|578839857|XP_005253045.2
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Homo	79.5	79.5	100%	3e-15	100%	gi|578839855|XP_005253044.2
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Homo	79.5	79.5	100%	3e-15	100%	gi|578820616|XP_006718316.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-related family m	79.5	79.5	100%	3e-15	100%	gi|397468758|XP_003806038.1
☐	cadherin-related family member 5 isoform 4 precursor [Homo sapie	79.5	79.5	100%	3e-15	100%	gi|285002199|NP_001165439.1
☐	MUCDHL [Homo sapiens]	79.5	79.5	100%	3e-15	100%	gi|37181861|AAQ88734.1
☐	mu-protocadherin [Homo sapiens]	79.5	79.5	100%	3e-15	100%	gi|11245187|AAG33495.1
☐	MUCDHL-FL [Homo sapiens]	79.5	79.5	100%	3e-15	100%	gi|10334770|AAG16731.1
☐	MUCDHL-FL [Homo sapiens]	79.5	79.5	100%	3e-15	100%	gi|10334774|AAG16733.1
☐	RecName: Full=Cadherin-related family member 5; AltName: Full=l	79.5	79.5	100%	3e-15	100%	gi|296439399|Q9HBB8.3
☐	mucin and cadherin-like, isoform CRA_b [Homo sapiens]	79.5	79.5	100%	3e-15	100%	gi|119622767|EAX02362.1
☐	cadherin-related family member 5 isoform 1 precursor [Homo sapie	79.5	79.5	100%	3e-15	100%	gi|110618248|NP_068743.2
☐	PREDICTED: cadherin-related family member 5 isoform X6 [Chloro	73.2	73.2	100%	4e-13	92%	gi|635011025|XP_007988108.1
☐	PREDICTED: cadherin-related family member 5 isoform X5 [Papio	73.2	73.2	100%	4e-13	92%	gi|685584291|XP_009183489.1
☐	PREDICTED: cadherin-related family member 5 isoform X4 [Papio	73.2	73.2	100%	4e-13	92%	gi|685584289|XP_009183488.1
☐	PREDICTED: cadherin-related family member 5 isoform X5 [Chloro	73.2	73.2	100%	4e-13	92%	gi|635011023|XP_007987388.1
☐	PREDICTED: cadherin-related family member 5 isoform X3 [Papio	73.2	73.2	100%	4e-13	92%	gi|685584287|XP_009183487.1
☐							

	PREDICTED: cadherin-related family member 5 isoform X4 [Chloro	73.2	73.2	100%	4e-13	92%	gi|635011021|XP_007986645.1
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Papio	73.2	73.2	100%	4e-13	92%	gi|685584285|XP_009183486.1
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Papio	73.2	73.2	100%	4e-13	92%	gi|685584283|XP_009183484.1
☐	PREDICTED: cadherin-related family member 5 isoform X3 [Chloro	73.2	73.2	100%	4e-13	92%	gi|635011019|XP_007986020.1
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Chloro	73.2	73.2	100%	4e-13	92%	gi|635011017|XP_007985338.1
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Chloro	73.2	73.2	100%	4e-13	92%	gi|635011015|XP_007984693.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-related family m	72.7	72.7	91%	6e-13	100%	gi|441665990|XP_003281373.2
☐	PREDICTED: cadherin-related family member 5 isoform X5 [Rhinop	71.0	71.0	100%	2e-12	88%	gi|724796233|XP_010387931.1
☐	PREDICTED: cadherin-related family member 5 isoform X4 [Rhinop	71.0	71.0	100%	2e-12	88%	gi|724796230|XP_010387851.1
☐	PREDICTED: cadherin-related family member 5 isoform X3 [Rhinop	71.0	71.0	100%	2e-12	88%	gi|724796227|XP_010387784.1
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Rhinop	71.0	71.0	100%	2e-12	88%	gi|724796224|XP_010387726.1
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Rhinop	71.0	71.0	100%	2e-12	88%	gi|724796221|XP_010387653.1
☐	PREDICTED: cadherin-related family member 5 isoform X5 [Macac	68.1	68.1	100%	2e-11	88%	gi|544483429|XP_005576826.1
☐	PREDICTED: cadherin-related family member 5 isoform 2 [Macaca	68.1	68.1	100%	2e-11	88%	gi|109104860|XP_001086363.1
☐	PREDICTED: cadherin-related family member 5 isoform X4 [Macac	68.1	68.1	100%	2e-11	88%	gi|544483427|XP_005576825.1
☐	PREDICTED: cadherin-related family member 5 isoform X3 [Macac	68.1	68.1	100%	2e-11	88%	gi|544483425|XP_005576824.1
☐	PREDICTED: cadherin-related family member 5 isoform 1 [Macaca	68.1	68.1	100%	2e-11	88%	gi|297267104|XP_001086239.2
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Macac	68.1	68.1	100%	2e-11	88%	gi|544483421|XP_005576822.1
☐	PREDICTED: cadherin-related family member 5-like [Galeopterus v	64.7	64.7	95%	3e-10	87%	gi|667346400|XP_008563564.1
☐	PREDICTED: cadherin-related family member 5 [Ictidomys tridecen	60.9	60.9	95%	6e-09	83%	gi|532114016|XP_005341679.1
☐	PREDICTED: cadherin-related family member 5 [Otolemur garnettii	60.0	60.0	95%	1e-08	83%	gi|395861133|XP_003802848.1
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Saimir	56.6	56.6	95%	2e-07	78%	gi|725605770|XP_010329489.1
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Saimir	56.6	56.6	95%	2e-07	78%	gi|725605768|XP_010329488.1
☐	PREDICTED: cadherin-related family member 5 isoform X3 [Saimir	56.6	56.6	95%	2e-07	78%	gi|403305644|XP_003943368.1
☐	PREDICTED: cadherin-related family member 5 [Tupaia chinensis]	56.2	56.2	87%	2e-07	81%	gi|562873172|XP_006164495.1
☐	PREDICTED: cadherin-related family member 5 [Ceratotherium sim	56.2	56.2	91%	2e-07	72%	gi|478534060|XP_004441167.1
☐	PREDICTED: cadherin-related family member 5 [Galeopterus varie	55.4	55.4	87%	4e-07	81%	gi|667327847|XP_008590353.1
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Sus sc	55.4	55.4	95%	4e-07	74%	gi|545805609|XP_005652842.1
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Sus sc	55.4	55.4	95%	4e-07	74%	gi|545805606|XP_005652841.1
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Macac	54.9	54.9	83%	6e-07	85%	gi|544483423|XP_005576823.1
☐	PREDICTED: cadherin-related family member 5 [Equus przewalskii	54.5	54.5	91%	7e-07	77%	gi|664777361|XP_008507976.1
☐	PREDICTED: cadherin-related family member 5 [Equus caballus]	54.5	54.5	91%	8e-07	77%	gi|545182188|XP_005598543.1
☐	PREDICTED: cadherin-related family member 5 [Ursus maritimus]	52.8	52.8	87%	3e-06	71%	gi|671014096|XP_008697888.1
☐	PREDICTED: cadherin-related family member 5 [Chrysochloris asia	52.8	52.8	87%	3e-06	81%	gi|586493238|XP_006877066.1
☐	Mucin and cadherin-like protein [Pteropus alecto]	52.4	52.4	95%	4e-06	65%	gi|431910097|ELK13170.1
☐	PREDICTED: cadherin-related family member 5 [Pteropus alecto]	52.4	52.4	95%	4e-06	65%	gi|586552614|XP_006911325.1
☐	PREDICTED: cadherin-related family member 5 [Callithrix jacchus]	52.0	52.0	95%	6e-06	74%	gi|675704132|XP_009007036.1
☐	mucin and cadherin like, isoform CRA_b [Mus musculus]	51.5	73.4	100%	7e-06	78%	gi|148686086|EDL18033.1
☐	PREDICTED: cadherin-related family member 5 [Jaculus jaculus]	51.5	51.5	95%	8e-06	74%	gi|507539897|XP_004653954.1
☐	cadherin-related family member 5 isoform 2 precursor [Mus muscul	51.5	73.4	100%	8e-06	78%	gi|21312502|NP_082345.1
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Mus m	51.5	73.4	100%	8e-06	78%	gi|568952506|XP_006536323.1
☐	cadherin-related family member 5 isoform 1 precursor [Mus muscul	51.5	73.4	100%	8e-06	78%	gi|167004347|NP_001107794.1
☐	RecName: Full=Cadherin-related family member 5; AltName: Full=I	51.5	73.4	100%	8e-06	78%	gi|45477152|Q8VHF2.1
☐	PREDICTED: cadherin-related family member 5 [Camelus ferus]	50.3	50.3	87%	2e-05	71%	gi|560909593|XP_006181104.1
☐	PREDICTED: cadherin-related family member 5 [Vicugna pacos]	50.3	50.3	87%	2e-05	71%	gi|560994295|XP_006219255.1

☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-related family m	50.3	50.3	87%	2e-05	76%	gi|471415885|XP_004389467.1
☐	cadherin-related family member 5 precursor [Camelus ferus]	50.3	50.3	87%	2e-05	71%	gi|528764226|EPY83885.1
☐	PREDICTED: cadherin-related family member 5 [Loxodonta african	50.3	50.3	87%	2e-05	76%	gi|344309231|XP_003423280.1
☐	PREDICTED: cadherin-related family member 5 [Leptonychotes we	49.8	49.8	87%	3e-05	76%	gi|585180394|XP_006741861.1
☐	PREDICTED: cadherin-related family member 5 [Orcinus orca]	49.8	49.8	91%	3e-05	73%	gi|466050257|XP_004278199.1
☐	PREDICTED: cadherin-related family member 5 [Echinops telfairi]	49.4	49.4	87%	4e-05	76%	gi|507709657|XP_004717252.1
☐	PREDICTED: cadherin-related family member 5 [Cavia porcellus]	49.0	49.0	95%	5e-05	74%	gi|514443851|XP_003461333.2
☐	PREDICTED: cadherin-related family member 5 isoform X4 [Chinch	48.1	48.1	95%	9e-05	70%	gi|533177179|XP_005401888.1
☐	PREDICTED: cadherin-related family member 5 isoform X3 [Chinch	48.1	48.1	95%	1e-04	70%	gi|533177177|XP_005401887.1
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Chinch	48.1	48.1	95%	1e-04	70%	gi|533177175|XP_005401886.1
☐	PREDICTED: cadherin-related family member 5 [Physeter catodon]	48.1	48.1	95%	1e-04	70%	gi|593725286|XP_007108751.1
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Chinch	48.1	48.1	95%	1e-04	70%	gi|533177173|XP_005401885.1
☐	PREDICTED: cadherin-related family member 5 isoform X2 [Bubalu	47.7	47.7	95%	1e-04	65%	gi|594042619|XP_006045841.1
☐	PREDICTED: cadherin-related family member 5 [Octodon degus]	47.7	47.7	95%	1e-04	74%	gi|507671995|XP_004638095.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-related family m	47.7	47.7	87%	1e-04	67%	gi|504181561|XP_004600071.1
☐	PREDICTED: cadherin-related family member 5 [Orycteropus afer a	47.7	47.7	95%	1e-04	65%	gi|634871909|XP_007947550.1
☐	PREDICTED: cadherin-related family member 5 [Odobenus rosmar	47.7	47.7	79%	1e-04	74%	gi|472368599|XP_004403824.1
☐	Cadherin-related family member 5 [Bos mutus]	47.7	47.7	95%	1e-04	65%	gi|440906581|ELR56829.1
☐	TPA: mucin and cadherin-like [Bos taurus]	47.7	47.7	95%	1e-04	65%	gi|296471403|DAA13518.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-related family m	47.7	47.7	87%	1e-04	67%	gi|301788244|XP_002929539.1
☐	PREDICTED: LOW QUALITY PROTEIN: cadherin-related family m	47.7	47.7	95%	1e-04	65%	gi|555966244|XP_005895175.1
☐	PREDICTED: cadherin-related family member 5 isoform X1 [Bubalu	47.7	47.7	95%	1e-04	65%	gi|594042617|XP_006045840.1
☐	cadherin-related family member 5 precursor [Bos taurus]	47.7	47.7	95%	1e-04	65%	gi|157074164|NP_001096796.1
☐	PREDICTED: cadherin-related family member 5 [Lipotes vexillifer]	47.3	47.3	91%	2e-04	68%	gi|602711484|XP_007465981.1
☐	mucin and cadherin like, isoform CRA_c [Mus musculus]	46.9	68.7	100%	2e-04	80%	gi|148686087|EDL18034.1
☐	PREDICTED: cadherin-related family member 5 [Balaenoptera acut	46.0	46.0	91%	5e-04	68%	gi|594635661|XP_007171249.1
☐	PREDICTED: cadherin-related family member 5 [Ovis aries]	45.2	45.2	95%	9e-04	61%	gi|426252672|XP_004020028.1

⊟ Alignments

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mucin and cadherin-like, isoform CRA_f [Homo sapiens]

Sequence ID: gi|119622771|gb|EAX02366.1| **Length:** 485 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 132 to 155 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	3e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    RVEEDTKVNSTVIPETQLQAEDRD  24
            RVEEDTKVNSTVIPETQLQAEDRD
Sbjct  132  RVEEDTKVNSTVIPETQLQAEDRD  155
```

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MUCDHL-ALT [Homo sapiens]

Sequence ID: gi|10334769|gb|AAG16730.1| **Length:** 487 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 132 to 155 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	3e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    RVEEDTKVNSTVIPETQLQAEDRD  24
```

```
                 RVEEDTKVNSTVIPETQLQAEDRD
Sbjct  132  RVEEDTKVNSTVIPETQLQAEDRD  155
```

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MUCDHL-ALT [Homo sapiens]

Sequence ID: gi|10334772|gb|AAG16732.1|AF258675_1 **Length:** 487 **Number of Matches:** 1

Range 1: 132 to 155 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	3e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    RVEEDTKVNSTVIPETQLQAEDRD  24
            RVEEDTKVNSTVIPETQLQAEDRD
Sbjct  132  RVEEDTKVNSTVIPETQLQAEDRD  155
```

Related Information

Gene - associated gene details

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mucin and cadherin-like, isoform CRA_d, partial [Homo sapiens]

Sequence ID: gi|119622769|gb|EAX02364.1| **Length:** 493 **Number of Matches:** 1

Range 1: 132 to 155 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	3e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    RVEEDTKVNSTVIPETQLQAEDRD  24
            RVEEDTKVNSTVIPETQLQAEDRD
Sbjct  132  RVEEDTKVNSTVIPETQLQAEDRD  155
```

Related Information

Gene - associated gene details

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PREDICTED: cadherin-related family member 5 isoform X4 [Homo sapiens]

Sequence ID: gi|578839861|ref|XP_005253047.2| **Length:** 551 **Number of Matches:** 1

Range 1: 132 to 155 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	3e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    RVEEDTKVNSTVIPETQLQAEDRD  24
            RVEEDTKVNSTVIPETQLQAEDRD
Sbjct  132  RVEEDTKVNSTVIPETQLQAEDRD  155
```

Related Information

Gene - associated gene details

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

CFHR3_KLGYNADTSILSFQAVCRE_Mod

RID BTG1CZ7M016 (Expires on 01-20 15:28 pm)

Query ID lcl|39824
Description None
Molecule type amino acid
Query Length 19

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

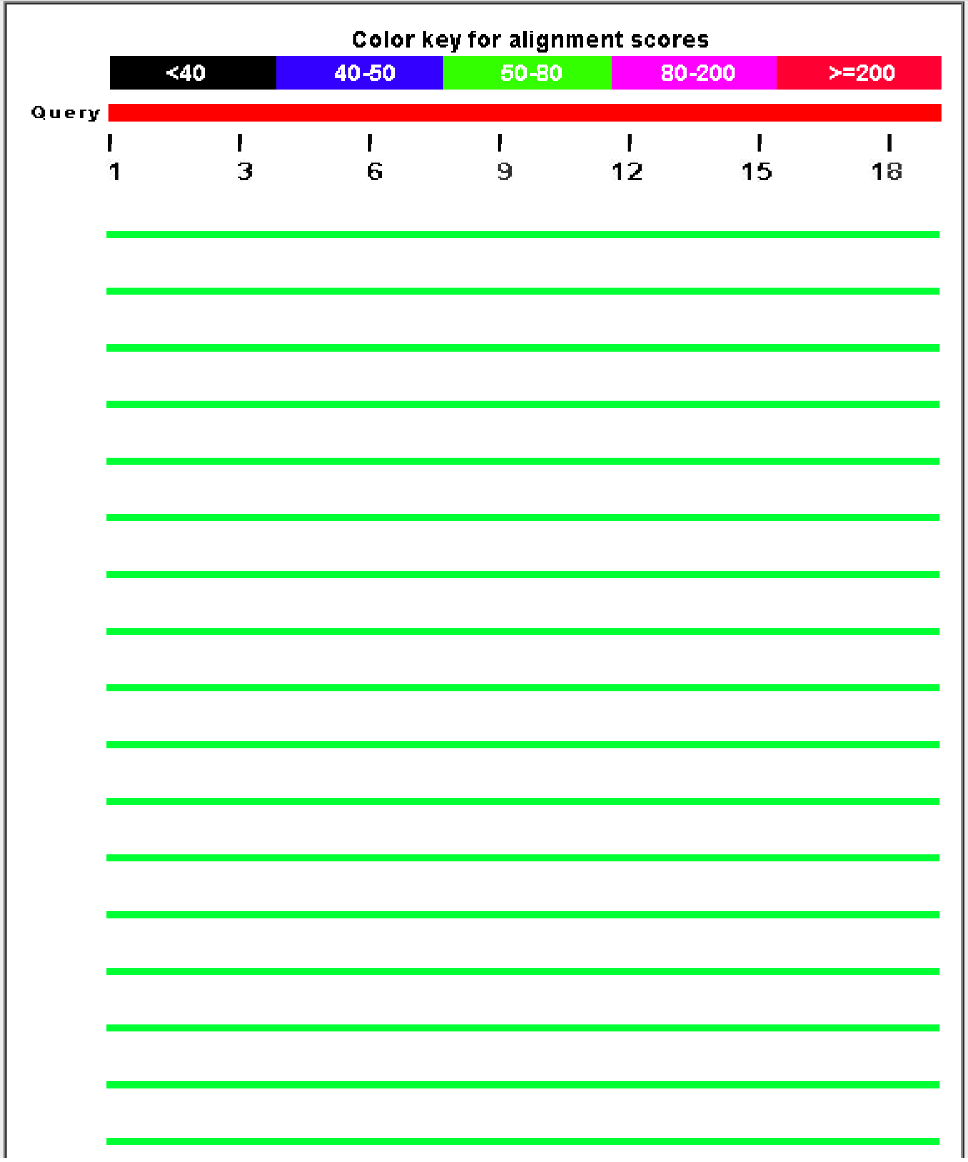
Graphic Summary

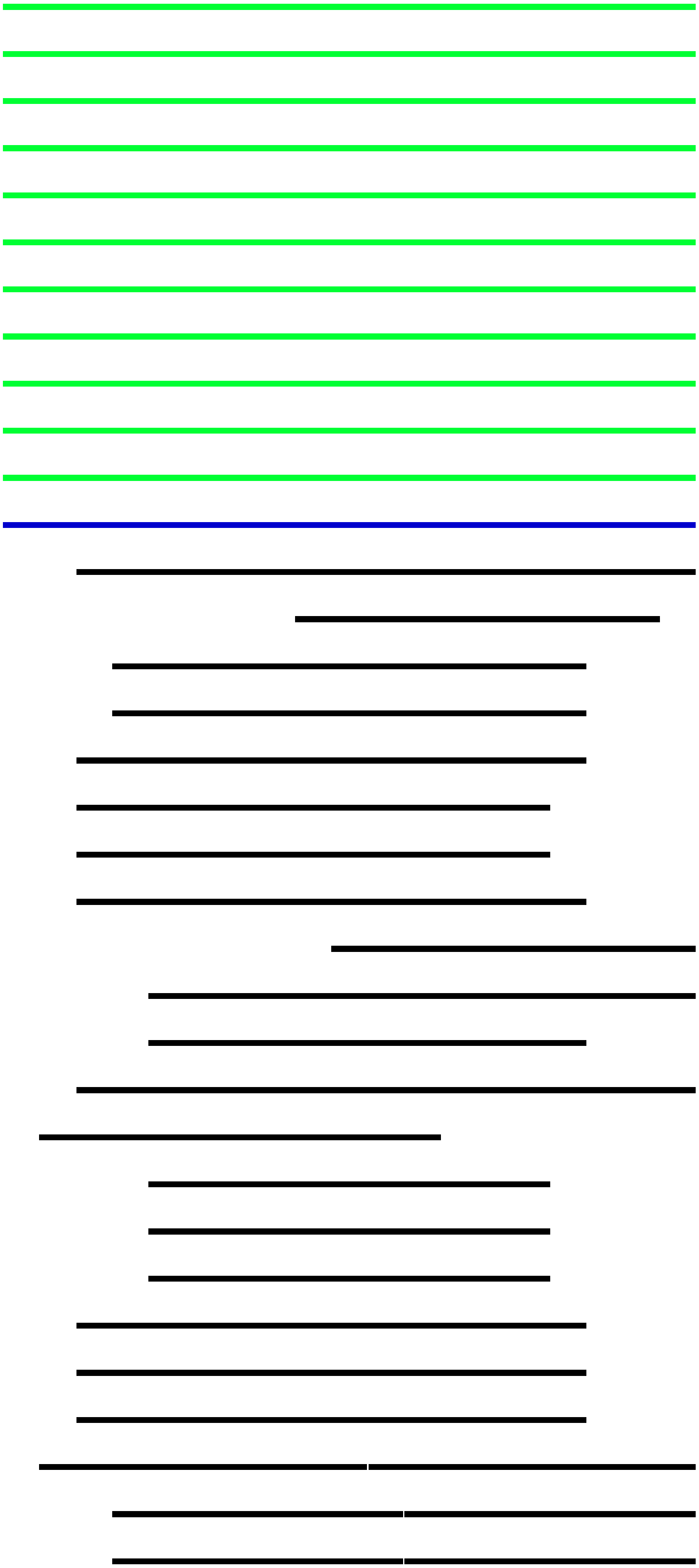
Show Conserved Domains

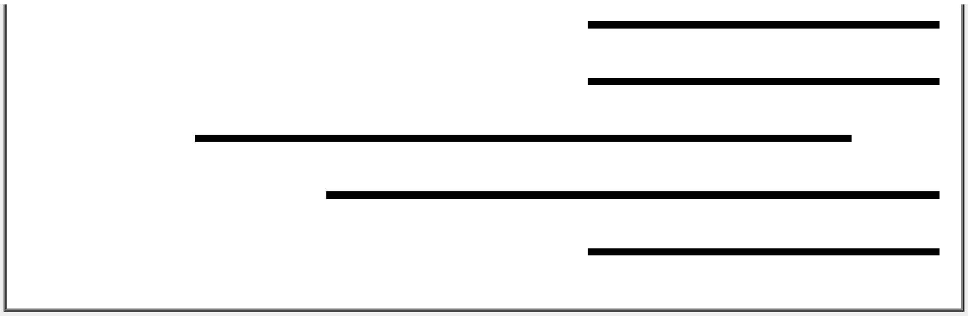
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: complement factor H-related protein 3-like [Pan t	60.9	60.9	100%	1e-09	95%	gi|694890843|XP_009438422.1
☐	complement factor H-related protein 3 isoform 2 precursor [Hon	60.9	60.9	100%	3e-09	95%	gi|262231791|NP_001160096.1
☐	complement factor H-related protein 3 isoform 1 precursor [Hon	60.9	60.9	100%	3e-09	95%	gi|54792787|NP_066303.2
☐	PREDICTED: complement factor H-related protein 4 isoform X3	60.9	60.9	100%	3e-09	95%	gi|686700699|XP_009238037.1
☐	PREDICTED: complement factor H-related protein 4 [Gorilla go	60.9	60.9	100%	3e-09	95%	gi|426333125|XP_004028135.1
☐	FHR-3; complement Factor H-related Protein 3 [Homo sapiens]	60.9	60.9	100%	3e-09	95%	gi|30870|CAA48639.1
☐	PREDICTED: complement factor H-related protein 4 isoform X2	60.9	60.9	100%	3e-09	95%	gi|686700697|XP_009238034.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1	60.9	60.9	100%	3e-09	95%	gi|297662444|XP_002809716.1
☐	complement factor H-related protein 4 [Homo sapiens]	58.3	58.3	100%	2e-08	89%	gi|1524058|CAA66980.1
☐	complement factor H-related protein 4 isoform 3 precursor [Hon	58.3	58.3	100%	2e-08	89%	gi|117320518|NP_006675.2
☐	PREDICTED: complement factor H-related protein 4 isoform X6	58.3	58.3	100%	2e-08	89%	gi|578800460|XP_006711196.1
☐	PREDICTED: complement factor H-related protein 4 isoform X5	58.3	58.3	100%	2e-08	89%	gi|578800458|XP_006711195.1
☐	PREDICTED: complement factor H-related protein 4 isoform X4	58.3	58.3	100%	2e-08	89%	gi|578800456|XP_006711194.1
☐	PREDICTED: complement factor H-related protein 4 isoform X3	58.3	58.3	100%	2e-08	89%	gi|578800454|XP_006711193.1
☐	PREDICTED: complement factor H-related protein 4 isoform X2	58.3	58.3	100%	2e-08	89%	gi|578800452|XP_006711192.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1	58.3	58.3	100%	2e-08	89%	gi|578800450|XP_006711191.1
☐	complement factor H-related protein 4 isoform 2 precursor [Hon	58.3	58.3	100%	2e-08	89%	gi|320089550|NP_001188480.1
☐	unnamed protein product [Homo sapiens]	58.3	58.3	100%	2e-08	89%	gi|158258941|BAF85441.1
☐	complement factor H-related protein 4 isoform 1 precursor [Hon	58.3	58.3	100%	2e-08	89%	gi|320089548|NP_001188479.1
☐	complement factor H-related 4, isoform CRA_a [Homo sapiens]	58.3	58.3	100%	2e-08	89%	gi|119611671|EAW91265.1
☐	complement factor H-related protein 4A precursor [Homo sapie	58.3	58.3	100%	2e-08	89%	gi|60417192|CAG26679.2
☐	hypothetical protein EGK_01829 [Macaca mulatta]	56.6	56.6	100%	8e-08	89%	gi|355558923|EHH15703.1
☐	hypothetical protein EGM_21015 [Macaca fascicularis]	56.6	56.6	100%	8e-08	89%	gi|355767342|EHH62602.1
☐	PREDICTED: complement factor H-related protein 4 [Rhinopith	56.6	56.6	100%	9e-08	89%	gi|724956788|XP_010353520.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1	56.6	56.6	100%	9e-08	89%	gi|685520468|XP_009189240.1
☐	PREDICTED: complement factor H-related protein 4 isoform X2	50.7	50.7	100%	9e-06	84%	gi|635131791|XP_007987278.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1	50.7	50.7	100%	9e-06	84%	gi|635131789|XP_007987277.1
☐	PREDICTED: complement factor H-related protein 4 isoform X3	50.7	50.7	100%	1e-05	84%	gi|635131793|XP_007987280.1
☐	PREDICTED: complement factor H-related protein 4-like [Galec	42.6	42.6	100%	0.004	68%	gi|667317955|XP_008586983.1

☐	PREDICTED: LOW QUALITY PROTEIN: complement factor H-	35.0	35.0	89%	1.1	65%	gi|395863185|XP_003803783.1
☐	hypothetical protein F775_03153 [Aegilops tauschii]	31.2	31.2	52%	18	90%	gi|475509050|EMT05155.1
☐	6-phosphogluconolactonase [Listeria grayi]	30.8	30.8	68%	25	71%	gi|738150575|WP_036107982.1
☐	hypothetical protein [Listeria grayi]	30.8	30.8	68%	25	71%	gi|489854279|WP_003757946.1
☐	aminotransferase DegT [Legionella fairfieldensis]	30.8	30.8	73%	25	71%	gi|737954707|WP_035918220.1
☐	putative ABC transport system [Corynebacterium casei LMG S-	30.8	30.8	68%	25	63%	gi|582017243|AHI20589.1
☐	ABC transporter, ATPase and permease components [Coryneb	30.8	30.8	68%	25	63%	gi|493876585|WP_006822974.1
☐	hypothetical protein A370_03188 [Clostridium sp. Maddingley M	30.8	30.8	73%	26	71%	gi|410599826|EKQ54365.1
☐	hypothetical protein [Oryza sativa Japonica Group]	30.3	30.3	52%	30	90%	gi|51535724|BAD37741.1
☐	hypothetical protein [Neisseria sicca]	30.3	30.3	78%	34	67%	gi|489862389|WP_003766012.1
☐	hypothetical protein [Photobacterium halotolerans]	30.3	30.3	63%	35	75%	gi|652998808|WP_027251054.1
☐	PREDICTED: complement factor H-like [Otolemur garnettii]	30.3	30.3	89%	35	65%	gi|395839039|XP_003792410.1
☐	hypothetical protein [Flectobacillus major]	30.3	30.3	57%	35	82%	gi|652618855|WP_026994381.1
☐	PREDICTED: DNA-binding protein inhibitor ID-2 [Tursiops trunc	29.9	29.9	57%	45	82%	gi|470595421|XP_004310676.1
☐	PREDICTED: DNA-binding protein inhibitor ID-2 [Orcinus orca]	29.9	29.9	57%	45	82%	gi|466034088|XP_004274954.1
☐	PREDICTED: DNA-binding protein inhibitor ID-2 [Ornithorhynch	29.9	29.9	57%	45	82%	gi|149448519|XP_001509293.1
☐	aminotransferase DegT [Vibrio tasmaniensis]	29.9	29.9	73%	47	64%	gi|515669795|WP_017102395.1
☐	aminotransferase DegT [Vibrio tasmaniensis]	29.9	29.9	73%	47	64%	gi|515667578|WP_017100178.1
☐	aminotransferase DegT [Vibrio tasmaniensis]	29.9	29.9	73%	47	64%	gi|515664772|WP_017097372.1
☐	hypothetical protein [Methylobacterium sp. 77]	29.9	29.9	47%	48	89%	gi|518747471|WP_019905760.1
☐	putative uncharacterized protein [Eubacterium eligens CAG:72]	29.5	29.5	42%	63	100%	gi|547480816|WP_022098743.1
☐	DNA mismatch repair protein MutT [[Eubacterium eligens]	29.5	29.5	42%	63	100%	gi|502246835|WP_012740632.1
☐	PREDICTED: complement factor H-related protein 4-like [Eptes	29.5	29.5	42%	63	100%	gi|641732931|XP_008156854.1
☐	dethiobiotin synthetase [Selenomonas ruminantium]	29.5	29.5	42%	64	100%	gi|739504320|WP_037364005.1
☐	PREDICTED: complement factor H-related protein 3-like [Eptes	29.5	29.5	78%	64	73%	gi|641736903|XP_008159089.1
☐	phage minor capsid protein 2 [Eggerthella sp. CAG:1427]	29.5	29.5	73%	64	64%	gi|546864462|WP_021899188.1
☐	PREDICTED: complement factor H-related protein 3-like [Myoti	29.5	29.5	42%	65	100%	gi|554549152|XP_005869111.1
☐	Complement factor H [Myotis brandtii]	29.5	29.5	42%	65	100%	gi|521027702|EPQ09490.1
☐	hypothetical protein HELRODRAFT_182568 [Helobdella robust	29.5	29.5	73%	65	71%	gi|675891122|XP_009031063.1
☐	hypothetical protein PFL1_04598 [Pseudozyma flocculosa PF-1	29.5	29.5	73%	66	64%	gi|630967814|XP_007880315.1
☐	DEHA2D09988p [Debaryomyces hansenii CBS767]	29.5	29.5	52%	66	80%	gi|294656603|XP_002770293.1
☐	hypothetical protein [Pseudomonas fluorescens]	29.1	29.1	52%	82	80%	gi|734952209|WP_034151885.1
☐	hypothetical protein [Helicobacter pametensis]	29.1	29.1	68%	85	65%	gi|736571822|WP_034583474.1
☐	chemotaxis protein CheY [Helicobacter rodentium]	29.1	29.1	52%	88	80%	gi|652549882|WP_026943532.1
☐	hypothetical protein ACD_50C00316G0007 [uncultured bacteri	29.1	29.1	52%	88	80%	gi|406929036|EKD64720.1
☐	PREDICTED: complement factor H-related protein 2 [Panthera	29.1	29.1	73%	88	64%	gi|591341448|XP_007096167.1
☐	PREDICTED: complement factor H-related protein 2 [Felis catu	29.1	29.1	73%	88	64%	gi|410986188|XP_003999394.1
☐	hypothetical protein DDB_G0278071 [Dictyostelium discoideum	29.1	29.1	63%	89	75%	gi|111226698|XP_642103.2
☐	hypothetical protein GGTG_03117 [Gaeumannomyces graminis	29.1	29.1	42%	90	100%	gi|685400597|XP_009219159.1
☐	alanyl-tRNA synthetase [alpha proteobacterium SCGC AAA280	29.1	29.1	57%	90	71%	gi|516596938|WP_017971961.1
☐	transcript cleavage factor [Parachlamydia acanthamoebae]	29.1	29.1	52%	90	80%	gi|738856889|WP_036745875.1
☐	transcript cleavage factor [Parachlamydia acanthamoebae]	29.1	29.1	52%	90	80%	gi|503690232|WP_013924308.1
☐	hypothetical protein pah_c005o031 [Parachlamydia acanthamo	29.1	29.1	52%	90	80%	gi|281500219|EFB42500.1
☐	CRISPR-associated protein Cas9 [Coprobacter sp. 177]	29.1	29.1	73%	91	71%	gi|733789567|KHM44152.1
☐	PREDICTED: myosin-IIIa-like [Xiphophorus maculatus]	29.1	29.1	63%	91	75%	gi|551508520|XP_005805789.1

☐	hypothetical protein [Bradyrhizobium elkanii]	28.6	28.6	42%	122	100%	gi|654711331|WP_028169225.1
☐	endonuclease [Chryseobacterium sp. CTM]	28.6	28.6	57%	123	75%	gi|736677382|WP_034683764.1
☐	hypothetical protein CNE04810 [Cryptococcus neoformans var.	28.6	28.6	52%	123	90%	gi|58267682|XP_570997.1
☐	hypothetical protein [Peptococcaceae bacterium BIC-A1/1_c8]	28.6	28.6	68%	123	71%	gi|734899322|WP_034132529.1
☐	Mob1/phocein family protein [Cryptosporidium muris RN66]	28.6	28.6	68%	123	77%	gi|209878001|XP_002140442.1
☐	hypothetical protein CNBE4810 [Cryptococcus neoformans var.	28.6	28.6	52%	124	90%	gi|134112465|XP_775208.1
☐	PREDICTED: E3 ubiquitin-protein ligase TRIM39-like [Stegaste	28.6	28.6	68%	124	69%	gi|657574654|XP_008291043.1
☐	chemotaxis protein [Mesorhizobium sp. WSM4349]	28.6	28.6	42%	124	100%	gi|517265644|WP_018454462.1
☐	AMP-binding enzyme family protein [Neisseria cinerea]	28.6	28.6	84%	124	57%	gi|489773904|WP_003677803.1
☐	AMP-binding enzyme family protein [Neisseria lactamica]	28.6	28.6	84%	124	57%	gi|518102455|WP_019272663.1
☐	hypothetical protein AURDEDRAFT_109663 [Auricularia delica	28.6	28.6	47%	125	89%	gi|598009353|XP_007336597.1
☐	hypothetical protein H072_8051 [Dactylellina haptotyla CBS 20	28.6	28.6	63%	125	64%	gi|526196835|EPS38168.1
☐	hemagluttinin domain containing protein [Acanthamoeba castel	28.6	28.6	47%	125	89%	gi|470404656|XP_004335814.1
☐	peptidase S8/S53 family [Eubacterium sp. CAG:161]	28.6	28.6	68%	125	69%	gi|547212177|WP_021952779.1
☐	type III secretion chaperone, CesT family [Succinatimonas hipp	28.2	28.2	68%	165	62%	gi|496435125|WP_009143972.1
☐	hypothetical protein [Salmonella enterica]	28.2	28.2	57%	169	82%	gi|446682240|WP_000759586.1
☐	PREDICTED: charged multivesicular body protein 4c [Pantholo	28.2	28.2	47%	169	89%	gi|556774019|XP_005982153.1
☐	MULTISPECIES: UDP pyrophosphate phosphatase [Thauera]	28.2	28.2	94%	169	44%	gi|490450797|WP_004321679.1
☐	UDP pyrophosphate phosphatase [Thauera terpenica]	28.2	28.2	94%	169	44%	gi|544832433|WP_021248217.1
☐	undecaprenyl pyrophosphate phosphatase [Thauera phenylace	28.2	28.2	94%	169	44%	gi|490512323|WP_004377930.1
☐	undecaprenyl pyrophosphate phosphatase [Thauera linaloolent	28.2	28.2	94%	169	44%	gi|490474503|WP_004344932.1
☐	MULTISPECIES: undecaprenyl pyrophosphate phosphatase [T	28.2	28.2	94%	169	44%	gi|489022592|WP_002933072.1
☐	undecaprenyl pyrophosphate phosphatase [Thauera sp. 63]	28.2	28.2	94%	169	44%	gi|490419422|WP_004291725.1
☐	putative aldose 1-epimerase [Epulopiscium sp. 'N.t. morphotype	28.2	28.2	57%	170	75%	gi|497854140|WP_010168296.1
☐	FAD-dependent oxidoreductase [Leptospirillum ferrooxidans]	28.2	28.2	57%	170	73%	gi|504262420|WP_014449522.1
☐	ATPase [Salmonella enterica]	28.2	28.2	57%	170	82%	gi|566075054|WP_023994444.1

Alignments

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PREDICTED: complement factor H-related protein 3-like, partial [Pan troglodytes]

Sequence ID: gi|694890843|ref|XP_009438422.1| **Length:** 78 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 53 to 71 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.9 bits(136)	1e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1   KLGYNADTSILSFQAVCRE  19
           KLGYNA+TSILSFQAVCRE
Sbjct  53  KLGYNANTSILSFQAVCRE  71
```

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complement factor H-related protein 3 isoform 2 precursor [Homo sapiens]

Sequence ID: gi|262231791|ref|NP_001160096.1| **Length:** 269 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic

Range 1: 242 to 260 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.9 bits(136)	3e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNADTSILSFQAVCRE  19
            KLGYNA+TSILSFQAVCRE
Sbjct  242  KLGYNANTSILSFQAVCRE  260
```

context

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

complement factor H-related protein 3 isoform 1 precursor [Homo sapiens]

Sequence ID: gi|54792787|ref|NP_066303.2| **Length:** 330 **Number of Matches:** 1

See 5 more title(s)

Range 1: 303 to 321 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.9 bits(136)	3e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNADTSILSFQAVCRE  19
            KLGYNA+TSILSFQAVCRE
Sbjct  303  KLGYNANTSILSFQAVCRE  321
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: complement factor H-related protein 4 isoform X3 [Pongo abelii]

Sequence ID: gi|686700699|ref|XP_009238037.1| **Length:** 331 **Number of Matches:** 1

Range 1: 304 to 322 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.9 bits(136)	3e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNADTSILSFQAVCRE  19
            KLGYNA+TSILSFQAVCRE
Sbjct  304  KLGYNANTSILSFQAVCRE  322
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: complement factor H-related protein 4 [Gorilla gorilla gorilla]

Sequence ID: gi|426333125|ref|XP_004028135.1| **Length:** 331 **Number of Matches:** 1

Range 1: 304 to 322 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.9 bits(136)	3e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNADTSILSFQAVCRE  19
            KLGYNA+TSILSFQAVCRE
Sbjct  304  KLGYNANTSILSFQAVCRE  322
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Your search parameters were adjusted to search for a short input sequence.

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CFHR3_KLGYNANTSILSFQAVCRE_NonMod

RID B92KVY2D01R (Expires on 01-14 10:01 am)

Query ID	lcl|256154	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	19		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

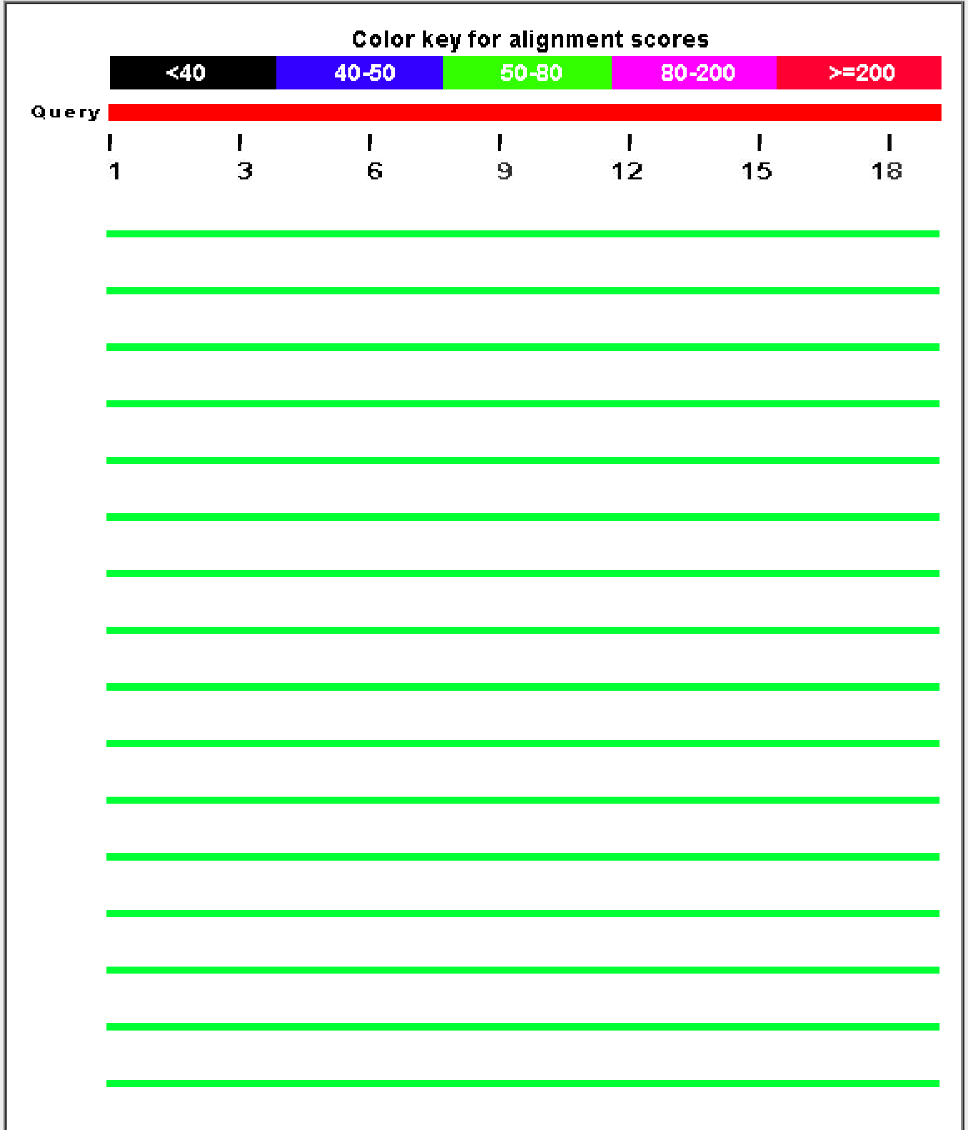
Graphic Summary

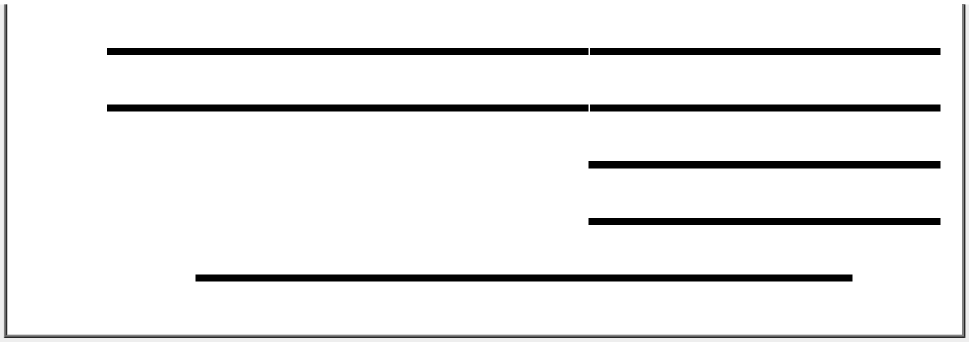
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: complement factor H-related protein 3-like [Pan trogl	63.4	63.4	100%	1e-10	100%	gi|694890843|XP_009438422.1
☐	complement factor H-related protein 3 isoform 2 precursor [Homo s	63.4	63.4	100%	4e-10	100%	gi|262231791|NP_001160096.1
☐	complement factor H-related protein 3 isoform 1 precursor [Homo s	63.4	63.4	100%	4e-10	100%	gi|54792787|NP_066303.2
☐	PREDICTED: complement factor H-related protein 4 isoform X3 [Po	63.4	63.4	100%	4e-10	100%	gi|686700699|XP_009238037.1
☐	PREDICTED: complement factor H-related protein 4 [Gorilla gorilla	63.4	63.4	100%	4e-10	100%	gi|426333125|XP_004028135.1
☐	FHR-3; complement Factor H-related Protein 3 [Homo sapiens]	63.4	63.4	100%	4e-10	100%	gi|30870|CAA48639.1
☐	PREDICTED: complement factor H-related protein 4 isoform X2 [Po	63.4	63.4	100%	4e-10	100%	gi|686700697|XP_009238034.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1 [Po	63.4	63.4	100%	4e-10	100%	gi|297662444|XP_002809716.1
☐	complement factor H-related protein 4 [Homo sapiens]	60.9	60.9	100%	3e-09	95%	gi|1524058|CAA66980.1
☐	complement factor H-related protein 4 isoform 3 precursor [Homo s	60.9	60.9	100%	3e-09	95%	gi|117320518|NP_006675.2
☐	PREDICTED: complement factor H-related protein 4 isoform X6 [Ho	60.9	60.9	100%	3e-09	95%	gi|578800460|XP_006711196.1
☐	PREDICTED: complement factor H-related protein 4 isoform X5 [Ho	60.9	60.9	100%	3e-09	95%	gi|578800458|XP_006711195.1
☐	PREDICTED: complement factor H-related protein 4 isoform X4 [Ho	60.9	60.9	100%	3e-09	95%	gi|578800456|XP_006711194.1
☐	PREDICTED: complement factor H-related protein 4 isoform X3 [Ho	60.9	60.9	100%	3e-09	95%	gi|578800454|XP_006711193.1
☐	PREDICTED: complement factor H-related protein 4 isoform X2 [Ho	60.9	60.9	100%	3e-09	95%	gi|578800452|XP_006711192.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1 [Ho	60.9	60.9	100%	3e-09	95%	gi|578800450|XP_006711191.1
☐	complement factor H-related protein 4 isoform 2 precursor [Homo s	60.9	60.9	100%	3e-09	95%	gi|320089550|NP_001188480.1
☐	unnamed protein product [Homo sapiens]	60.9	60.9	100%	3e-09	95%	gi|158258941|BAF85441.1
☐	complement factor H-related protein 4 isoform 1 precursor [Homo s	60.9	60.9	100%	3e-09	95%	gi|320089548|NP_001188479.1
☐	complement factor H-related 4, isoform CRA_a [Homo sapiens]	60.9	60.9	100%	3e-09	95%	gi|119611671|EAW91265.1
☐	complement factor H-related protein 4A precursor [Homo sapiens]	60.9	60.9	100%	3e-09	95%	gi|60417192|CAG26679.2
☐	hypothetical protein EGK_01829 [Macaca mulatta]	59.2	59.2	100%	1e-08	95%	gi|355558923|EHH15703.1
☐	hypothetical protein EGM_21015 [Macaca fascicularis]	59.2	59.2	100%	1e-08	95%	gi|355767342|EHH62602.1
☐	PREDICTED: complement factor H-related protein 4 [Rhinopithecus	59.2	59.2	100%	1e-08	95%	gi|724956788|XP_010353520.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1 [Pa	59.2	59.2	100%	1e-08	95%	gi|685520468|XP_009189240.1
☐	PREDICTED: complement factor H-related protein 4 isoform X2 [Ch	53.2	53.2	100%	1e-06	89%	gi|635131791|XP_007987278.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1 [Ch	53.2	53.2	100%	1e-06	89%	gi|635131789|XP_007987277.1
☐	PREDICTED: complement factor H-related protein 4 isoform X3 [Ch	53.2	53.2	100%	1e-06	89%	gi|635131793|XP_007987280.1
☐							

PREDICTED: complement factor H-related protein 4-like [Galeopter	45.2	45.2	100%	5e-04	74%	gi|667317955|XP_008586983.1
☐ PREDICTED: LOW QUALITY PROTEIN: complement factor H-relat	34.6	34.6	89%	1.4	65%	gi|395863185|XP_003803783.1
☐ hypothetical protein [Clostridium sp. Maddingley MBC34-26]	33.3	33.3	73%	3.8	79%	gi|495699764|WP_008424343.1
☐ PREDICTED: complement factor H-related protein 2 [Panthera tigris	31.6	31.6	73%	12	71%	gi|591341448|XP_007096167.1
☐ PREDICTED: complement factor H-related protein 2 [Felis catus]	31.6	31.6	73%	12	71%	gi|410986188|XP_003999394.1
☐ hypothetical protein F775_03153 [Aegilops tauschii]	31.2	31.2	52%	17	90%	gi|475509050|EMT05155.1
☐ hemagluttinin domain containing protein [Acanthamoeba castellanii	31.2	31.2	47%	18	100%	gi|470404656|XP_004335814.1
☐ PREDICTED: charged multivesicular body protein 4c [Pantholops h	30.8	30.8	47%	23	100%	gi|556774019|XP_005982153.1
☐ TonB-dependent receptor [Sphingobacterium antarcticus 4BY]	30.8	30.8	57%	24	91%	gi|662330546|KEQ29330.1
☐ TonB-denpendent receptor [Pedobacter heparinus]	30.8	30.8	57%	24	91%	gi|502416040|WP_012780400.1
☐ TonB-denpendent receptor [Pedobacter sp. BAL39]	30.8	30.8	57%	24	91%	gi|495515274|WP_008239919.1
☐ hypothetical protein [Oryza sativa Japonica Group]	30.3	30.3	52%	29	90%	gi|51535724|BAD37741.1
☐ hypothetical protein HELRODRAFT_166585 [Helobdella robusta]	30.3	30.3	84%	31	57%	gi|675849010|XP_009010065.1
☐ PREDICTED: charged multivesicular body protein 7-like [Larimichth	30.3	30.3	63%	32	75%	gi|734645724|XP_010751967.1
☐ aminotransferase [Chlamydia trachomatis]	29.9	29.9	63%	45	75%	gi|499644114|WP_011324848.1
☐ aminotransferase [Chlamydia trachomatis]	29.9	29.9	63%	45	75%	gi|497559140|WP_009873324.1
☐ aminotransferase [Chlamydia trachomatis]	29.9	29.9	63%	45	75%	gi|497558693|WP_009872877.1
☐ aminotransferase [Chlamydia trachomatis]	29.9	29.9	63%	45	75%	gi|497557913|WP_009872097.1
☐ cysteine sulfinate desulfinase [Vibrio coralliilyticus]	29.9	29.9	63%	45	75%	gi|694160560|AIS53989.1
☐ cysteine sulfinate desulfinase [Vibrio sp. B183]	29.9	29.9	63%	45	75%	gi|672867461|KFI10261.1
☐ cysteine sulfinate desulfinase [Vibrio coralliilyticus]	29.9	29.9	63%	45	75%	gi|494015608|WP_006957963.1
☐ Tripeptide permease tppB, putative [Perkinsus marinus ATCC 5098	29.9	29.9	78%	45	67%	gi|294893760|XP_002774633.1
☐ PREDICTED: complement factor H-like [Otolemur garnettii]	29.9	29.9	89%	45	65%	gi|395839039|XP_003792410.1
☐ hypothetical protein [Methylobacterium sp. 77]	29.9	29.9	47%	45	89%	gi|518747471|WP_019905760.1
☐ alpha-2-macroglobulin family N-terminal region [Microscilla marina]	29.9	29.9	57%	46	82%	gi|488781502|WP_002693909.1
☐ putative uncharacterized protein [Eubacterium eligens CAG:72]	29.5	29.5	42%	59	100%	gi|547480816|WP_022098743.1
☐ DNA mismatch repair protein MutT [[Eubacterium eligens]	29.5	29.5	42%	59	100%	gi|502246835|WP_012740632.1
☐ PREDICTED: complement factor H-related protein 4-like [Eptesicus	29.5	29.5	42%	60	100%	gi|641732931|XP_008156854.1
☐ dethiobiotin synthetase [Selenomonas ruminantium]	29.5	29.5	42%	60	100%	gi|652371003|WP_026767006.1
☐ PREDICTED: complement factor H-related protein 3-like [Eptesicus	29.5	29.5	78%	61	73%	gi|641736903|XP_008159089.1
☐ hypothetical protein CAPTEDRAFT_110011 [Capitella teleta]	29.5	29.5	73%	61	54%	gi|443710050|ELU04431.1
☐ PREDICTED: complement factor H-related protein 3-like [Myotis bra	29.5	29.5	42%	61	100%	gi|554549152|XP_005869111.1
☐ Complement factor H [Myotis brandtii]	29.5	29.5	42%	62	100%	gi|521027702|EPQ09490.1
☐ hypothetical protein [Clostridium hydrogeniformans]	29.5	29.5	68%	63	59%	gi|653621594|WP_027631917.1
☐ DEHA2D09988p [Debaryomyces hansenii CBS767]	29.5	29.5	52%	63	80%	gi|294656603|XP_002770293.1
☐ hypothetical protein [Acinetobacter sp. NIPH 973]	29.1	29.1	57%	82	82%	gi|490837251|WP_004699327.1
☐ hypothetical protein ACD_50C00316G0007 [uncultured bacterium]	29.1	29.1	52%	84	80%	gi|406929036|EKD64720.1
☐ hypothetical protein Ecym_7413 [Eremothecium cymbalariae DBVP	29.1	29.1	57%	85	82%	gi|363755680|XP_003648055.1
☐ hypothetical protein NEMVEDRAFT_v1g224817 [Nematostella vect	29.1	29.1	84%	85	53%	gi|156603150|XP_001618784.1
☐ RNA pseudouridylate synthase domain-containing protein 2 [Zooter	29.1	29.1	63%	85	75%	gi|646721122|KDR22592.1
☐ hypothetical protein GGTG_03117 [Gaeumannomyces graminis var	29.1	29.1	42%	85	100%	gi|685400597|XP_009219159.1
☐ hypothetical protein HELRODRAFT_108261 [Helobdella robusta]	29.1	29.1	89%	85	65%	gi|675887632|XP_009029318.1
☐ LORF2 [synthetic construct]	29.1	29.1	68%	86	62%	gi|237626215|ACR02738.1
☐ LORF2 [Gallid herpesvirus 2]	29.1	29.1	68%	86	62%	gi|392497295|AFM74559.1
☐ orf-1 [Gallid herpesvirus 2]	29.1	29.1	68%	86	62%	gi|632856|AAB30933.1

☐	v-lipase [synthetic construct]	29.1	29.1	68%	86	62%	gi|237626170|ACR02693.1
☐	lipase [Gallid herpesvirus 2]	29.1	29.1	68%	86	62%	gi|125745049|YP_001033926.1
☐	lipase [Gallid herpesvirus 2]	29.1	29.1	68%	86	62%	gi|392497294|AFM74558.1
☐	membrane protein [Bacillus cereus]	28.6	28.6	73%	115	69%	gi|446377531|WP_000455386.1
☐	serine proteinase isoform 11 [Sistrurus catenatus edwardsi]	28.6	28.6	73%	116	71%	gi|109254958|ABG26977.1
☐	hypothetical protein [Flavobacteriaceae bacterium S85]	28.6	28.6	73%	116	58%	gi|657688926|WP_029489377.1
☐	putative 8-amino-7-oxononanoate synthase [Bacteroides fragilis 3_	28.6	28.6	78%	117	67%	gi|313134892|EFR52252.1
☐	MULTISPECIES: 8-amino-7-oxononanoate synthase [Bacteroides]	28.6	28.6	78%	117	67%	gi|547279488|WP_022013034.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|492356497|WP_005819256.1
☐	MULTISPECIES: 8-amino-7-oxononanoate synthase [Bacteroides]	28.6	28.6	78%	117	67%	gi|496043771|WP_008768278.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|695484637|WP_032575181.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|695430276|WP_032561108.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|695481996|WP_032573987.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|695552986|WP_032598057.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|695447183|WP_032564620.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|695518014|WP_032589697.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|695399375|WP_032556467.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|695545142|WP_032596772.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|695486286|WP_032576022.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|695331358|WP_032529385.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|695336295|WP_032533939.1
☐	MULTISPECIES: 8-amino-7-oxononanoate synthase [Bacteroides]	28.6	28.6	78%	117	67%	gi|547946592|WP_022347591.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|499301826|WP_010992601.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|499515854|WP_011202494.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|492345939|WP_005816880.1
☐	8-amino-7-oxononanoate synthase [Bacteroides sp. 2_1_56FAA]	28.6	28.6	78%	117	67%	gi|496601943|WP_009291977.1
☐	8-amino-7-oxononanoate synthase [Bacteroides fragilis]	28.6	28.6	78%	117	67%	gi|504064609|WP_014298603.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: complement factor H-related protein 3-like, partial [Pan troglodytes]

Sequence ID: gi|694890843|ref|XP_009438422.1| **Length:** 78 **Number of Matches:** 1

Range 1: 53 to 71 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.4 bits(142)	1e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1   KLGYNANTSILSFQAVCRE  19
           KLGYNANTSILSFQAVCRE
Sbjct  53  KLGYNANTSILSFQAVCRE  71
```

Related Information

Gene - associated gene details

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

complement factor H-related protein 3 isoform 2 precursor [Homo sapiens]

Sequence ID: gi|262231791|ref|NP_001160096.1| **Length:** 269 **Number of Matches:** 1

See 1 more title(s)

Range 1: 242 to 260 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.4 bits(142)	4e-10	19/19(100%)	19/19(100%)	0/19(0%)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

```
Query  1    KLGYNANTSILSFQAVCRE  19
            KLGYNANTSILSFQAVCRE
Sbjct  242  KLGYNANTSILSFQAVCRE  260
```

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

complement factor H-related protein 3 isoform 1 precursor [Homo sapiens]

Sequence ID: gi|54792787|ref|NP_066303.2| **Length:** 330 **Number of Matches:** 1

See 5 more title(s)

Range 1: 303 to 321 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.4 bits(142)	4e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNANTSILSFQAVCRE  19
            KLGYNANTSILSFQAVCRE
Sbjct  303  KLGYNANTSILSFQAVCRE  321
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: complement factor H-related protein 4 isoform X3 [Pongo abelii]

Sequence ID: gi|686700699|ref|XP_009238037.1| **Length:** 331 **Number of Matches:** 1

Range 1: 304 to 322 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.4 bits(142)	4e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNANTSILSFQAVCRE  19
            KLGYNANTSILSFQAVCRE
Sbjct  304  KLGYNANTSILSFQAVCRE  322
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: complement factor H-related protein 4 [Gorilla gorilla gorilla]

Sequence ID: gi|426333125|ref|XP_004028135.1| **Length:** 331 **Number of Matches:** 1

Range 1: 304 to 322 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.4 bits(142)	4e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNANTSILSFQAVCRE  19
            KLGYNANTSILSFQAVCRE
Sbjct  304  KLGYNANTSILSFQAVCRE  322
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

CFHR4_KLGYNADTSVLSFQAVCRE_Mod

RID	BTG1S5YX013 (Expires on 01-20 15:28 pm)		
Query ID	lcl|41843	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	19	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

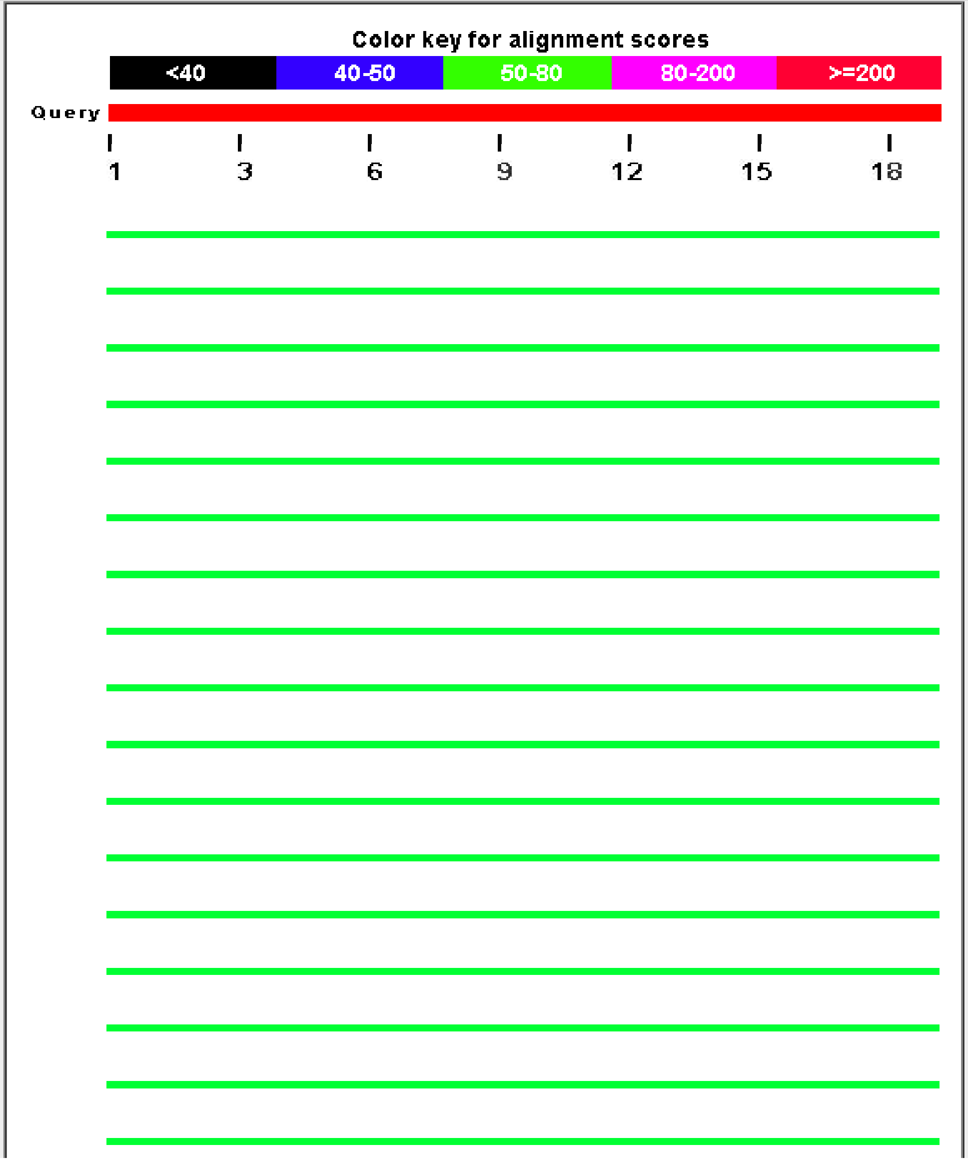
Graphic Summary

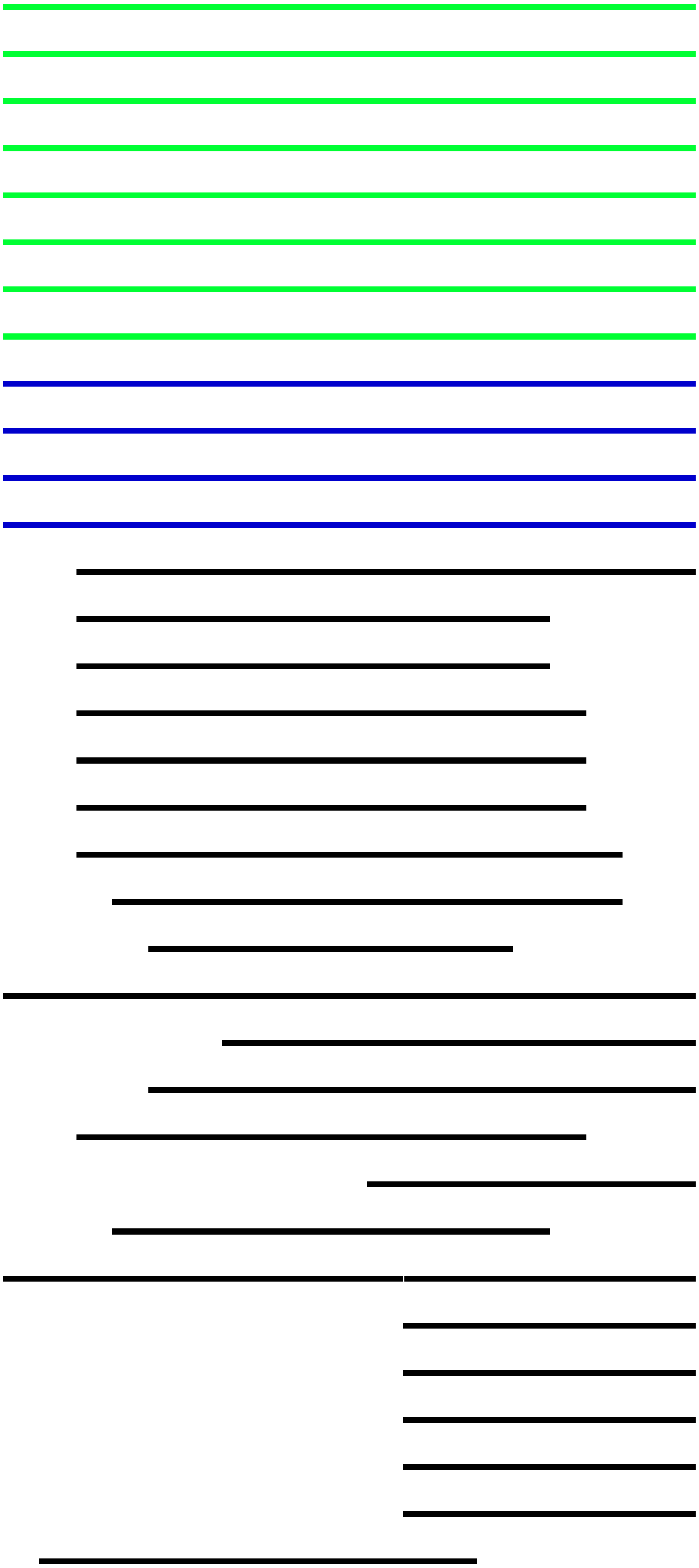
Show Conserved Domains

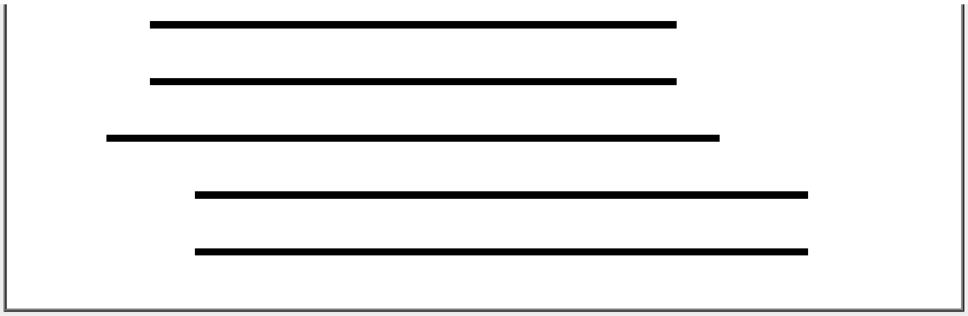
No putative conserved domains have been detected

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	complement factor H-related protein 4 [Homo sapiens]	60.4	60.4	100%	4e-09	95%	gi|1524058|CAA66980.1
☐	complement factor H-related protein 4 isoform 3 precursor [Hon	60.4	60.4	100%	4e-09	95%	gi|117320518|NP_006675.2
☐	PREDICTED: complement factor H-related protein 4 isoform X6	60.4	60.4	100%	5e-09	95%	gi|578800460|XP_006711196.1
☐	PREDICTED: complement factor H-related protein 4 isoform X5	60.4	60.4	100%	5e-09	95%	gi|578800458|XP_006711195.1
☐	PREDICTED: complement factor H-related protein 4 isoform X4	60.4	60.4	100%	5e-09	95%	gi|578800456|XP_006711194.1
☐	PREDICTED: complement factor H-related protein 4 isoform X3	60.4	60.4	100%	5e-09	95%	gi|578800454|XP_006711193.1
☐	PREDICTED: complement factor H-related protein 4 isoform X2	60.4	60.4	100%	5e-09	95%	gi|578800452|XP_006711192.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1	60.4	60.4	100%	5e-09	95%	gi|578800450|XP_006711191.1
☐	complement factor H-related protein 4 isoform 2 precursor [Hon	60.4	60.4	100%	5e-09	95%	gi|320089550|NP_001188480.1
☐	unnamed protein product [Homo sapiens]	60.4	60.4	100%	5e-09	95%	gi|158258941|BAF85441.1
☐	complement factor H-related protein 4 isoform 1 precursor [Hon	60.4	60.4	100%	5e-09	95%	gi|320089548|NP_001188479.1
☐	complement factor H-related 4, isoform CRA_a [Homo sapiens]	60.4	60.4	100%	5e-09	95%	gi|119611671|EAW91265.1
☐	complement factor H-related protein 4A precursor [Homo sapie	60.4	60.4	100%	5e-09	95%	gi|60417192|CAG26679.2
☐	PREDICTED: complement factor H-related protein 3-like [Pan t	58.3	58.3	100%	8e-09	89%	gi|694890843|XP_009438422.1
☐	complement factor H-related protein 3 isoform 2 precursor [Hon	58.3	58.3	100%	2e-08	89%	gi|262231791|NP_001160096.1
☐	complement factor H-related protein 3 isoform 1 precursor [Hon	58.3	58.3	100%	2e-08	89%	gi|54792787|NP_066303.2
☐	PREDICTED: complement factor H-related protein 4 isoform X3	58.3	58.3	100%	2e-08	89%	gi|686700699|XP_009238037.1
☐	PREDICTED: complement factor H-related protein 4 [Gorilla go	58.3	58.3	100%	2e-08	89%	gi|426333125|XP_004028135.1
☐	FHR-3; complement Factor H-related Protein 3 [Homo sapiens]	58.3	58.3	100%	2e-08	89%	gi|30870|CAA48639.1
☐	PREDICTED: complement factor H-related protein 4 isoform X2	58.3	58.3	100%	2e-08	89%	gi|686700697|XP_009238034.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1	58.3	58.3	100%	2e-08	89%	gi|297662444|XP_002809716.1
☐	hypothetical protein EGK_01829 [Macaca mulatta]	54.1	54.1	100%	6e-07	84%	gi|355558923|EHH15703.1
☐	hypothetical protein EGM_21015 [Macaca fascicularis]	54.1	54.1	100%	6e-07	84%	gi|355767342|EHH62602.1
☐	PREDICTED: complement factor H-related protein 4 [Rhinopith	54.1	54.1	100%	7e-07	84%	gi|724956788|XP_010353520.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1	54.1	54.1	100%	7e-07	84%	gi|685520468|XP_009189240.1
☐	PREDICTED: complement factor H-related protein 4 isoform X2	48.1	48.1	100%	7e-05	79%	gi|635131791|XP_007987278.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1	48.1	48.1	100%	7e-05	79%	gi|635131789|XP_007987277.1
☐	PREDICTED: complement factor H-related protein 4 isoform X3	48.1	48.1	100%	7e-05	79%	gi|635131793|XP_007987280.1
☐	PREDICTED: complement factor H-related protein 4-like [Galec	42.6	42.6	100%	0.004	68%	gi|667317955|XP_008586983.1

☐	PREDICTED: LOW QUALITY PROTEIN: complement factor H-	37.1	37.1	89%	0.24	71%	gi|395863185|XP_003803783.1
☐	putative ABC transport system [Corynebacterium casei LMG S-	32.9	32.9	68%	5.4	69%	gi|582017243|AHI20589.1
☐	ABC transporter, ATPase and permease components [Coryneb	32.9	32.9	68%	5.4	69%	gi|493876585|WP_006822974.1
☐	aminotransferase DegT [Vibrio tasmaniensis]	32.0	32.0	73%	9.8	71%	gi|515669795|WP_017102395.1
☐	aminotransferase DegT [Vibrio tasmaniensis]	32.0	32.0	73%	9.8	71%	gi|515667578|WP_017100178.1
☐	aminotransferase DegT [Vibrio tasmaniensis]	32.0	32.0	73%	9.8	71%	gi|515664772|WP_017097372.1
☐	PREDICTED: complement factor H-related protein 3-like [Eptes	31.6	31.6	78%	13	80%	gi|641736903|XP_008159089.1
☐	hypothetical protein PFL1_04598 [Pseudozyma flocculosa PF-1	31.6	31.6	73%	14	71%	gi|630967814|XP_007880315.1
☐	hypothetical protein [Pseudomonas fluorescens]	31.2	31.2	52%	16	90%	gi|734952209|WP_034151885.1
☐	transglutaminase [Rhodobacteraceae bacterium PD-2]	30.8	30.8	100%	25	46%	gi|564608082|WP_023849349.1
☐	PREDICTED: E3 ubiquitin-protein ligase TRIM39-like [Stegaste	30.8	30.8	68%	25	75%	gi|657574654|XP_008291043.1
☐	hypothetical protein [Neisseria sicca]	30.3	30.3	78%	34	67%	gi|489862389|WP_003766012.1
☐	aminotransferase DegT [Dechloromonas agitata]	30.3	30.3	73%	34	71%	gi|653253558|WP_027458964.1
☐	hypothetical protein [Methylobacterium sp. 77]	29.9	29.9	47%	48	89%	gi|518747471|WP_019905760.1
☐	SwmA-cell surface protein required for swimming motility [Syne	29.9	29.9	63%	48	75%	gi|499439499|WP_011126963.1
☐	putative uncharacterized protein [Eubacterium eligens CAG:72]	29.5	29.5	42%	63	100%	gi|547480816|WP_022098743.1
☐	DNA mismatch repair protein MutT [[Eubacterium eligens]	29.5	29.5	42%	63	100%	gi|502246835|WP_012740632.1
☐	PREDICTED: complement factor H-related protein 4-like [Eptes	29.5	29.5	42%	63	100%	gi|641732931|XP_008156854.1
☐	dethiobiotin synthetase [Selenomonas ruminantium]	29.5	29.5	42%	64	100%	gi|739504320|WP_037364005.1
☐	PREDICTED: complement factor H-related protein 3-like [Myoti	29.5	29.5	42%	65	100%	gi|554549152|XP_005869111.1
☐	Complement factor H [Myotis brandtii]	29.5	29.5	42%	65	100%	gi|521027702|EPQ09490.1
☐	cysteine sulfinate desulfinase [Vibrio coralliilyticus]	29.5	29.5	63%	65	75%	gi|740724577|WP_038509863.1
☐	cysteine sulfinate desulfinase [Vibrio sp. B183]	29.5	29.5	63%	65	75%	gi|740326507|WP_038163522.1
☐	cysteine sulfinate desulfinase [Vibrio coralliilyticus]	29.5	29.5	63%	65	75%	gi|494015608|WP_006957963.1
☐	tyrosinase [Lyngbya aestuarii]	29.5	29.5	73%	65	73%	gi|553732390|WP_023067053.1
☐	aminotransferase DegT [Campylobacter curvus]	29.1	29.1	73%	89	64%	gi|500772039|WP_011992428.1
☐	hypothetical protein HELRODRAFT_182568 [Helobdella robust	29.1	29.1	73%	89	71%	gi|675891122|XP_009031063.1
☐	PREDICTED: immunoglobulin superfamily member 5-like [Steg	29.1	29.1	68%	90	52%	gi|657552971|XP_008280877.1
☐	invasin [Pantoea sp. PSNIH1]	29.1	29.1	57%	90	82%	gi|723258150|AIX52171.1
☐	PREDICTED: complement factor H-like [Otolemur garnettii]	29.1	29.1	89%	90	65%	gi|395839039|XP_003792410.1
☐	Uncharacterized ABC transporter ATP-binding protein y4gM [M	29.1	29.1	68%	90	69%	gi|685109776|CDX63100.1
☐	ABC transporter ATP-binding protein [Mesorhizobium sp. WSM	29.1	29.1	68%	90	69%	gi|738306835|WP_036259860.1
☐	Uncharacterized ABC transporter ATP-binding protein y4gM [M	29.1	29.1	68%	90	69%	gi|685117947|CDX27594.1
☐	Uncharacterized ABC transporter ATP-binding protein y4gM [M	29.1	29.1	68%	90	69%	gi|685098267|CDX37427.1
☐	hypothetical protein [Flexithrix dorotheae]	29.1	29.1	78%	91	55%	gi|522018255|WP_020529526.1
☐	D-lactate dehydrogenase [Oceanimonas sp. GK1]	28.6	28.6	68%	123	67%	gi|504056525|WP_014290519.1
☐	polyketide synthase [Burkholderia thailandensis]	28.6	28.6	52%	123	90%	gi|497586475|WP_009900659.1
☐	hypothetical protein [Burkholderia thailandensis]	28.6	28.6	52%	123	90%	gi|740922590|WP_038707751.1
☐	1,2-diacylglycerol 3-glucosyltransferase [Lactobacillus fabiferme	28.6	28.6	57%	123	82%	gi|639445784|WP_024624314.1
☐	cysteine sulfinate desulfinase [Vibrio ichthyoenteri]	28.6	28.6	63%	124	75%	gi|745638899|KIE20425.1
☐	cysteine sulfinate desulfinase [Vibrio sinaloensis]	28.6	28.6	63%	124	75%	gi|741156892|KHT49024.1
☐	cysteine sulfinate desulfinase [Vibrio sinaloensis]	28.6	28.6	63%	124	75%	gi|741153139|KHT45358.1
☐	cysteine sulfinate desulfinase [Vibrio sp. N384]	28.6	28.6	63%	124	75%	gi|740302209|WP_038139625.1
☐	cysteine sulfinate desulfinase [Vibrio variabilis]	28.6	28.6	63%	124	75%	gi|740380775|WP_038215628.1
☐	cysteine sulfinate desulfinase [Vibrio sinaloensis]	28.6	28.6	63%	124	75%	gi|740354451|WP_038190786.1

☐ cysteine sulfinate desulfinase [Vibrio sp. 16]	28.6	28.6	63%	124	75%	gi|491616019|WP_005473574.1
☐ hypothetical protein F775_03153 [Aegilops tauschii]	28.6	28.6	52%	124	80%	gi|475509050|EMT05155.1
☐ Transcription factor kayak [Trichuris trichiura]	28.6	28.6	68%	124	71%	gi|669223612|CDW55099.1
☐ hypothetical protein CPXG_00120 [Cyanophage P-RSM6]	28.6	48.4	63%	126	75%	gi|472341641|YP_007675157.1
☐ polyketide synthase [Burkholderia thailandensis]	28.6	28.6	52%	126	90%	gi|497583450|WP_009897634.1
☐ polyketide synthase [Burkholderia thailandensis]	28.6	28.6	52%	126	90%	gi|499720622|WP_011401356.1
☐ beta-ketoacyl-acyl-carrier-protein synthase II [Burkholderia thail	28.6	28.6	52%	126	90%	gi|695926079|AIT23281.1
☐ beta-ketoacyl-acyl-carrier-protein synthase II [Burkholderia thail	28.6	28.6	52%	126	90%	gi|695183164|AIS98946.1
☐ beta-ketoacyl-acyl-carrier-protein synthase II [Burkholderia thail	28.6	28.6	52%	126	90%	gi|685784685|AIP65843.1
☐ beta-ketoacyl-acyl-carrier-protein synthase II [Burkholderia thail	28.6	28.6	52%	126	90%	gi|655542764|AIC91228.1
☐ beta-ketoacyl-acyl-carrier-protein synthase II [Burkholderia thail	28.6	28.6	52%	126	90%	gi|584110125|AHI81736.1
☐ beta-ketoacyl-acyl-carrier-protein synthase II [Burkholderia thail	28.6	28.6	52%	126	90%	gi|584096752|AHI68319.1
☐ hypothetical protein AW09_003464 [Candidatus Accumulibacte	28.2	28.2	73%	163	67%	gi|668676831|KFB71395.1
☐ hypothetical protein MELLADRAFT_113382 [Melampsora larici-	28.2	28.2	63%	167	75%	gi|599427138|XP_007418119.1
☐ hypothetical protein [Salmonella enterica]	28.2	28.2	57%	169	82%	gi|446682240|WP_000759586.1
☐ ATPase [Salmonella enterica]	28.2	28.2	57%	170	82%	gi|566075054|WP_023994444.1
☐ hypothetical protein [Enterobacter cloacae]	28.2	28.2	57%	170	82%	gi|556453881|WP_023313998.1
☐ cobQ/CobB/MinD/ParA nucleotide binding domain protein [Escl	28.2	28.2	57%	170	82%	gi|487682790|WP_001767473.1
☐ ATPase [Salmonella enterica]	28.2	28.2	57%	170	82%	gi|446682239|WP_000759585.1
☐ ATPase [Enterobacter aerogenes]	28.2	28.2	57%	170	82%	gi|505807971|WP_015705723.1
☐ hypothetical protein [Roseburia inulinivorans]	28.2	28.2	52%	170	90%	gi|495160822|WP_007885623.1
☐ 6-phosphogluconolactonase [Listeria grayi]	28.2	28.2	68%	170	64%	gi|738150575|WP_036107982.1
☐ hypothetical protein [Listeria grayi]	28.2	28.2	68%	170	64%	gi|489854279|WP_003757946.1
☐ cytochrome b [Amazona versicolor]	28.2	28.2	78%	171	61%	gi|37574968|AAQ93411.1
☐ ATPase [Salmonella enterica subsp. enterica serovar Cerro FS	28.2	28.2	57%	171	82%	gi|627373969|KCU91242.1
☐ ATPase domain protein [Escherichia coli 908675]	28.2	28.2	57%	171	82%	gi|553697628|ESE13481.1

Alignments

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complement factor H-related protein 4 [Homo sapiens]

Sequence ID: gi|1524058|emb|CAA66980.1| **Length:** 331 **Number of Matches:** 1

▷ See 2 more title(s)

Range 1: 304 to 322 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	4e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNADTSVLSFQAVCRE  19
            KLGYNA+TSVLSFQAVCRE
Sbjct  304  KLGYNANTSVLSFQAVCRE  322
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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complement factor H-related protein 4 isoform 3 precursor [Homo sapiens]

Sequence ID: gi|117320518|ref|NP_006675.2| **Length:** 331 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 304 to 322 GenPept Graphics ▼ Next Match ▲ Previous Match

Related Information

Gene - associated gene details

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	4e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNADTSVLSFQAVCRE  19
            KLGYNA+TSVLSFQAVCRE
Sbjct  304  KLGYNANTSVLSFQAVCRE  322
```

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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PREDICTED: complement factor H-related protein 4 isoform X6 [Homo sapiens]

Sequence ID: gi|578800460|ref|XP_006711196.1| **Length:** 519 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 492 to 510 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	5e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNADTSVLSFQAVCRE  19
            KLGYNA+TSVLSFQAVCRE
Sbjct  492  KLGYNANTSVLSFQAVCRE  510
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: complement factor H-related protein 4 isoform X5 [Homo sapiens]

Sequence ID: gi|578800458|ref|XP_006711195.1| **Length:** 523 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 496 to 514 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	5e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNADTSVLSFQAVCRE  19
            KLGYNA+TSVLSFQAVCRE
Sbjct  496  KLGYNANTSVLSFQAVCRE  514
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: complement factor H-related protein 4 isoform X4 [Homo sapiens]

Sequence ID: gi|578800456|ref|XP_006711194.1| **Length:** 533 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 506 to 524 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	5e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNADTSVLSFQAVCRE  19
            KLGYNA+TSVLSFQAVCRE
Sbjct  506  KLGYNANTSVLSFQAVCRE  524
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - B92M7GCE01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download

How to read this page | Blast report description

CFHR4_KLGYNANTSVLSFQAVCRE_NonMod

RID B92M7GCE01R (Expires on 01-14 10:01 am)

Query ID	lcl|339182	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	19		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

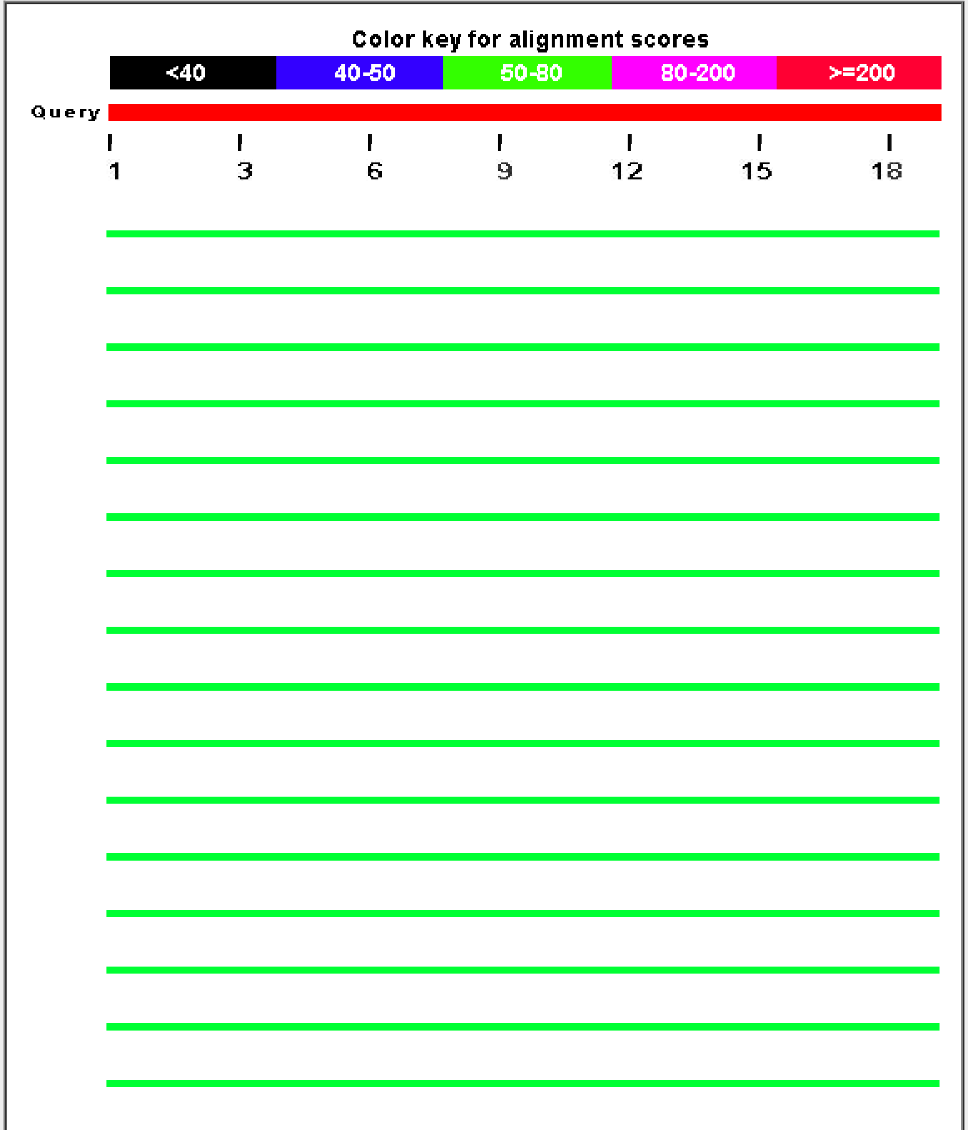
Graphic Summary

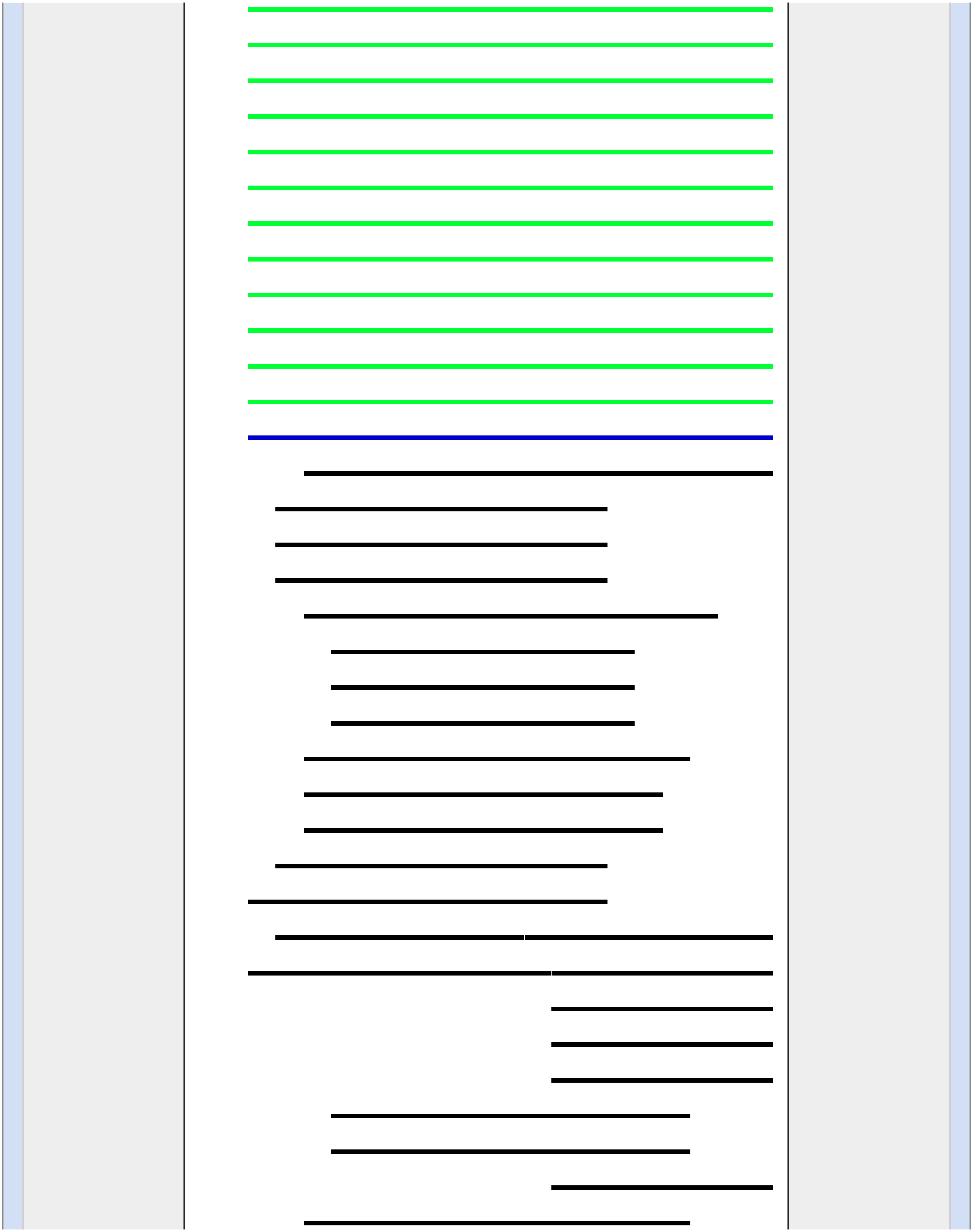
Show Conserved Domains

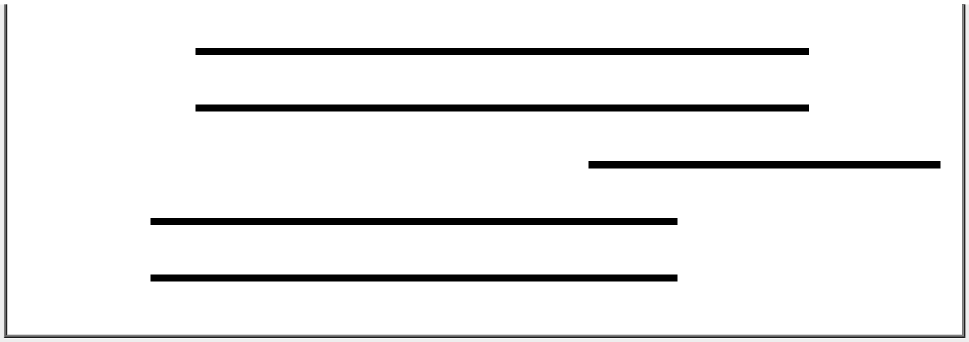
No putative conserved domains have been detected

Distribution of 102 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊖ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	complement factor H-related protein 4 [Homo sapiens]	63.0	63.0	100%	5e-10	100%	gi|1524058|CAA66980.1
☐	complement factor H-related protein 4 isoform 3 precursor [Homo sa	63.0	63.0	100%	5e-10	100%	gi|117320518|NP_006675.2
☐	PREDICTED: complement factor H-related protein 4 isoform X6 [Ho	63.0	63.0	100%	6e-10	100%	gi|578800460|XP_006711196.1
☐	PREDICTED: complement factor H-related protein 4 isoform X5 [Ho	63.0	63.0	100%	6e-10	100%	gi|578800458|XP_006711195.1
☐	PREDICTED: complement factor H-related protein 4 isoform X4 [Ho	63.0	63.0	100%	6e-10	100%	gi|578800456|XP_006711194.1
☐	PREDICTED: complement factor H-related protein 4 isoform X3 [Ho	63.0	63.0	100%	6e-10	100%	gi|578800454|XP_006711193.1
☐	PREDICTED: complement factor H-related protein 4 isoform X2 [Ho	63.0	63.0	100%	6e-10	100%	gi|578800452|XP_006711192.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1 [Ho	63.0	63.0	100%	6e-10	100%	gi|578800450|XP_006711191.1
☐	complement factor H-related protein 4 isoform 2 precursor [Homo sa	63.0	63.0	100%	6e-10	100%	gi|320089550|NP_001188480.1
☐	unnamed protein product [Homo sapiens]	63.0	63.0	100%	6e-10	100%	gi|158258941|BAF85441.1
☐	complement factor H-related protein 4 isoform 1 precursor [Homo sa	63.0	63.0	100%	6e-10	100%	gi|320089548|NP_001188479.1
☐	complement factor H-related 4, isoform CRA_a [Homo sapiens]	63.0	63.0	100%	6e-10	100%	gi|119611671|EAW91265.1
☐	complement factor H-related protein 4A precursor [Homo sapiens]	63.0	63.0	100%	6e-10	100%	gi|60417192|CAG26679.2
☐	PREDICTED: complement factor H-related protein 3-like [Pan troglo	60.9	60.9	100%	1e-09	95%	gi|694890843|XP_009438422.1
☐	complement factor H-related protein 3 isoform 2 precursor [Homo sa	60.9	60.9	100%	3e-09	95%	gi|262231791|NP_001160096.1
☐	complement factor H-related protein 3 isoform 1 precursor [Homo sa	60.9	60.9	100%	3e-09	95%	gi|54792787|NP_066303.2
☐	PREDICTED: complement factor H-related protein 4 isoform X3 [Po	60.9	60.9	100%	3e-09	95%	gi|686700699|XP_009238037.1
☐	PREDICTED: complement factor H-related protein 4 [Gorilla gorilla	60.9	60.9	100%	3e-09	95%	gi|426333125|XP_004028135.1
☐	FHR-3; complement Factor H-related Protein 3 [Homo sapiens]	60.9	60.9	100%	3e-09	95%	gi|30870|CAA48639.1
☐	PREDICTED: complement factor H-related protein 4 isoform X2 [Po	60.9	60.9	100%	3e-09	95%	gi|686700697|XP_009238034.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1 [Po	60.9	60.9	100%	3e-09	95%	gi|297662444|XP_002809716.1
☐	hypothetical protein EGK_01829 [Macaca mulatta]	56.6	56.6	100%	8e-08	89%	gi|355558923|EHH15703.1
☐	hypothetical protein EGM_21015 [Macaca fascicularis]	56.6	56.6	100%	8e-08	89%	gi|355767342|EHH62602.1
☐	PREDICTED: complement factor H-related protein 4 [Rhinopithecus	56.6	56.6	100%	9e-08	89%	gi|724956788|XP_010353520.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1 [Pa	56.6	56.6	100%	9e-08	89%	gi|685520468|XP_009189240.1
☐	PREDICTED: complement factor H-related protein 4 isoform X2 [Ch	50.7	50.7	100%	9e-06	84%	gi|635131791|XP_007987278.1
☐	PREDICTED: complement factor H-related protein 4 isoform X1 [Ch	50.7	50.7	100%	9e-06	84%	gi|635131789|XP_007987277.1
☐	PREDICTED: complement factor H-related protein 4 isoform X3 [Ch	50.7	50.7	100%	9e-06	84%	gi|635131793|XP_007987280.1
☐							

	PREDICTED: complement factor H-related protein 4-like [Galeopter	45.2	45.2	100%	5e-04	74%	gi|667317955|XP_008586983.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor H-relat	36.7	36.7	89%	0.31	71%	gi|395863185|XP_003803783.1
☐	cysteine sulfinate desulfinase [Vibrio coralliilyticus]	32.0	32.0	63%	9.3	83%	gi|694160560|AIS53989.1
☐	cysteine sulfinate desulfinase [Vibrio sp. B183]	32.0	32.0	63%	9.3	83%	gi|672867461|KFI10261.1
☐	cysteine sulfinate desulfinase [Vibrio coralliilyticus]	32.0	32.0	63%	9.3	83%	gi|494015608|WP_006957963.1
☐	PREDICTED: complement factor H-related protein 3-like [Eptesicus	31.6	31.6	78%	12	80%	gi|641736903|XP_008159089.1
☐	TonB-dependent receptor [Sphingobacterium antarcticus 4BY]	30.8	30.8	57%	24	91%	gi|662330546|KEQ29330.1
☐	TonB-denpendent receptor [Pedobacter heparinus]	30.8	30.8	57%	24	91%	gi|502416040|WP_012780400.1
☐	TonB-denpendent receptor [Pedobacter sp. BAL39]	30.8	30.8	57%	24	91%	gi|495515274|WP_008239919.1
☐	hypothetical protein [Clostridium sp. Maddingley MBC34-26]	30.8	30.8	73%	24	71%	gi|495699764|WP_008424343.1
☐	putative ABC transport system [Corynebacterium casei LMG S-192	30.3	30.3	68%	33	63%	gi|582017243|AHI20589.1
☐	ABC transporter, ATPase and permease components [Corynebacte	30.3	30.3	68%	33	63%	gi|493876585|WP_006822974.1
☐	hypothetical protein CPXG_00120 [Cyanophage P-RSM6]	30.3	72.3	63%	33	75%	gi|472341641|YP_007675157.1
☐	hypothetical protein [Streptococcus merionis]	29.9	29.9	68%	45	77%	gi|517185092|WP_018373910.1
☐	hypothetical protein [Methylobacterium sp. 77]	29.9	29.9	47%	45	89%	gi|518747471|WP_019905760.1
☐	alpha-2-macroglobulin family N-terminal region [Microscilla marina]	29.9	29.9	57%	46	82%	gi|488781502|WP_002693909.1
☐	putative uncharacterized protein [Eubacterium eligens CAG:72]	29.5	29.5	42%	59	100%	gi|547480816|WP_022098743.1
☐	DNA mistmatch repair protein MutT [[Eubacterium eligens]	29.5	29.5	42%	59	100%	gi|502246835|WP_012740632.1
☐	PREDICTED: complement factor H-related protein 4-like [Eptesicus	29.5	29.5	42%	60	100%	gi|641732931|XP_008156854.1
☐	dethiobiotin synthetase [Selenomonas ruminantium]	29.5	29.5	42%	60	100%	gi|652371003|WP_026767006.1
☐	uracil-DNA glycosylase [Azorhizobium doebereinerae]	29.5	29.5	68%	60	63%	gi|655960432|WP_029003187.1
☐	uracil-DNA glycosylase, family 4 [Afipia felis]	29.5	29.5	68%	60	63%	gi|488803136|WP_002715542.1
☐	PREDICTED: complement factor H-related protein 3-like [Myotis bra	29.5	29.5	42%	61	100%	gi|554549152|XP_005869111.1
☐	aminotransferase DegT [Vibrio tasmaniensis]	29.5	29.5	73%	61	64%	gi|515669795|WP_017102395.1
☐	aminotransferase DegT [Vibrio tasmaniensis]	29.5	29.5	73%	61	64%	gi|515667578|WP_017100178.1
☐	aminotransferase DegT [Vibrio tasmaniensis]	29.5	29.5	73%	61	64%	gi|515664772|WP_017097372.1
☐	Complement factor H [Myotis brandtii]	29.5	29.5	42%	62	100%	gi|521027702|EPQ09490.1
☐	cysteine sulfinate desulfinase [Vibrio navarrensis]	29.5	29.5	63%	62	75%	gi|694876636|KGK20568.1
☐	cysteine sulfinate desulfinase [Vibrio navarrensis]	29.5	29.5	63%	62	75%	gi|694864623|KGK09043.1
☐	cysteine sulfinate desulfinase [Vibrio parahaemolyticus]	29.5	29.5	63%	62	75%	gi|646482819|WP_025541596.1
☐	Ser/Thr protein phosphatase [Alcanivorax dieselolei]	29.5	29.5	57%	62	73%	gi|504808478|WP_014995580.1
☐	PREDICTED: complement factor H-related protein 2 [Panthera tigris	29.1	29.1	73%	84	64%	gi|591341448|XP_007096167.1
☐	PREDICTED: complement factor H-related protein 2 [Felis catus]	29.1	29.1	73%	84	64%	gi|410986188|XP_003999394.1
☐	cysteine sulfinate desulfinase [Vibrio coralliilyticus]	29.1	29.1	63%	85	75%	gi|703567374|AIW19751.1
☐	cysteine sulfinate desulfinase [Vibrio coralliilyticus]	29.1	29.1	63%	85	75%	gi|545088181|WP_021457971.1
☐	cysteine sulfinate desulfinase [Vibrio coralliilyticus]	29.1	29.1	63%	85	75%	gi|518104313|WP_019274521.1
☐	ABC transporter, permease/ATP-binding protein [Acholeplasma ocu	29.1	29.1	68%	85	69%	gi|644984528|CDR31023.1
☐	hypothetical protein PFL1_04598 [Pseudozyma flocculosa PF-1]	29.1	29.1	73%	86	64%	gi|630967814|XP_007880315.1
☐	hypothetical protein [Pseudomonas fluorescens]	28.6	28.6	52%	108	80%	gi|734952209|WP_034151885.1
☐	hypothetical protein WIVsmall_58 [Mycobacterium phage WIVsmall]	28.6	28.6	52%	113	80%	gi|509141068|YP_008059959.1
☐	hypothetical protein MFLO_02598 [Listeriaceae bacterium FSL S10	28.6	28.6	84%	114	57%	gi|577772450|EUJ33408.1
☐	hypothetical protein [Escherichia coli]	28.6	28.6	52%	115	80%	gi|693132514|WP_032276586.1
☐	polyketide cyclase [Cupriavidus metallidurans]	28.6	28.6	73%	116	64%	gi|658504234|WP_029700341.1
☐	polyketide cyclase [Cupriavidus metallidurans]	28.6	28.6	73%	117	64%	gi|657065825|WP_029307857.1
☐	activator of HSP90 ATPase [Cupriavidus metallidurans]	28.6	28.6	73%	117	64%	gi|499835793|WP_011516527.1

☐	hypothetical protein [Cupriavidus sp. HMR-1]	28.6	28.6	73%	117	64%	gi|495927146|WP_008651725.1
☐	hypothetical protein [Corynebacterium massiliense]	28.6	28.6	73%	117	71%	gi|652660992|WP_027018828.1
☐	hypothetical protein [Pseudomonas fluorescens]	28.6	28.6	52%	117	80%	gi|502153488|WP_012721608.1
☐	hypothetical protein [Serratia sp. M24T3]	28.6	28.6	52%	117	80%	gi|497320983|WP_009635196.1
☐	hypothetical protein [Enterobacter cloacae]	28.6	28.6	52%	117	80%	gi|695711419|WP_032643881.1
☐	hypothetical protein [Enterobacter cloacae]	28.6	28.6	52%	117	80%	gi|527039551|WP_020885375.1
☐	hypothetical protein F775_03153 [Aegilops tauschii]	28.6	28.6	52%	117	80%	gi|475509050|EMT05155.1
☐	PREDICTED: complement factor H-like [Otolemur garnettii]	28.6	28.6	89%	118	65%	gi|395839039|XP_003792410.1
☐	LORF2 [synthetic construct]	28.6	28.6	68%	118	62%	gi|237626215|ACR02738.1
☐	LORF2 [Gallid herpesvirus 2]	28.6	28.6	68%	118	62%	gi|392497295|AFM74559.1
☐	orf-1 [Gallid herpesvirus 2]	28.6	28.6	68%	118	62%	gi|632856|AAB30933.1
☐	v-lipase [synthetic construct]	28.6	28.6	68%	118	62%	gi|237626170|ACR02693.1
☐	lipase [Gallid herpesvirus 2]	28.6	28.6	68%	118	62%	gi|125745049|YP_001033926.1
☐	lipase [Gallid herpesvirus 2]	28.6	28.6	68%	118	62%	gi|392497294|AFM74558.1
☐	hemagluttinin domain containing protein [Acanthamoeba castellanii	28.6	28.6	47%	119	89%	gi|470404656|XP_004335814.1
☐	TonB-denpendent receptor [Asticcacaulis excentricus]	28.6	28.6	68%	119	71%	gi|503244073|WP_013478734.1
☐	serine/threonine kinase [Acanthamoeba castellanii str. Neff]	28.6	28.6	78%	119	73%	gi|470395773|XP_004335110.1
☐	polyketide synthase [Burkholderia thailandensis]	28.6	28.6	52%	120	90%	gi|497583450|WP_009897634.1
☐	polyketide synthase [Burkholderia thailandensis]	28.6	28.6	52%	120	90%	gi|499720622|WP_011401356.1
☐	beta-ketoacyl-acyl-carrier-protein synthase II [Burkholderia thailand	28.6	28.6	52%	120	90%	gi|695926079|AIT23281.1
☐	beta-ketoacyl-acyl-carrier-protein synthase II [Burkholderia thailand	28.6	28.6	52%	120	90%	gi|695183164|AIS98946.1
☐	beta-ketoacyl-acyl-carrier-protein synthase II [Burkholderia thailand	28.6	28.6	52%	120	90%	gi|685784685|AIP65843.1
☐	beta-ketoacyl-acyl-carrier-protein synthase II [Burkholderia thailand	28.6	28.6	52%	120	90%	gi|655542764|AIC91228.1
☐	beta-ketoacyl-acyl-carrier-protein synthase II [Burkholderia thailand	28.6	28.6	52%	120	90%	gi|584110125|AHI81736.1
☐	beta-ketoacyl-acyl-carrier-protein synthase II [Burkholderia thailand	28.6	28.6	52%	120	90%	gi|584096752|AHI68319.1
☐	hypothetical protein [Psychrobacter lutiphocae]	28.2	28.2	68%	158	69%	gi|518502112|WP_019672319.1
☐	hypothetical protein [Salmonella enterica]	28.2	28.2	57%	160	82%	gi|446682240|WP_000759586.1

⊟ Alignments

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complement factor H-related protein 4 [Homo sapiens]

Sequence ID: gi|1524058|emb|CAA66980.1| **Length:** 331 **Number of Matches:** 1

▷ See 2 more title(s)

Range 1: 304 to 322 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	5e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNANTSVLSFQAVCRE  19
            KLGYNANTSVLSFQAVCRE
Sbjct  304  KLGYNANTSVLSFQAVCRE  322
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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complement factor H-related protein 4 isoform 3 precursor [Homo sapiens]

Sequence ID: gi|117320518|ref|NP_006675.2| **Length:** 331 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 304 to 322 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps

Related Information

Gene - associated gene details

Map Viewer - aligned genomic

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	5e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNANTSVLSFQAVCRE  19
            KLGYNANTSVLSFQAVCRE
Sbjct  304  KLGYNANTSVLSFQAVCRE  322
```

context
Identical Proteins - Proteins identical to the subject

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PREDICTED: complement factor H-related protein 4 isoform X6 [Homo sapiens]

Sequence ID: gi|578800460|ref|XP_006711196.1| **Length:** 519 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 492 to 510 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	6e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNANTSVLSFQAVCRE  19
            KLGYNANTSVLSFQAVCRE
Sbjct  492  KLGYNANTSVLSFQAVCRE  510
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: complement factor H-related protein 4 isoform X5 [Homo sapiens]

Sequence ID: gi|578800458|ref|XP_006711195.1| **Length:** 523 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 496 to 514 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	6e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNANTSVLSFQAVCRE  19
            KLGYNANTSVLSFQAVCRE
Sbjct  496  KLGYNANTSVLSFQAVCRE  514
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: complement factor H-related protein 4 isoform X4 [Homo sapiens]

Sequence ID: gi|578800456|ref|XP_006711194.1| **Length:** 533 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 506 to 524 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	6e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLGYNANTSVLSFQAVCRE  19
            KLGYNANTSVLSFQAVCRE
Sbjct  506  KLGYNANTSVLSFQAVCRE  524
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BTG1ZVB7016

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

CFHR5_REQFCPPPPQIPNAQDMTTTVNYQDGEKV_Mod

RID BTG1ZVB7016 (Expires on 01-20 15:28 pm)

Query ID lcl|15590
Description None
Molecule type amino acid
Query Length 29

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

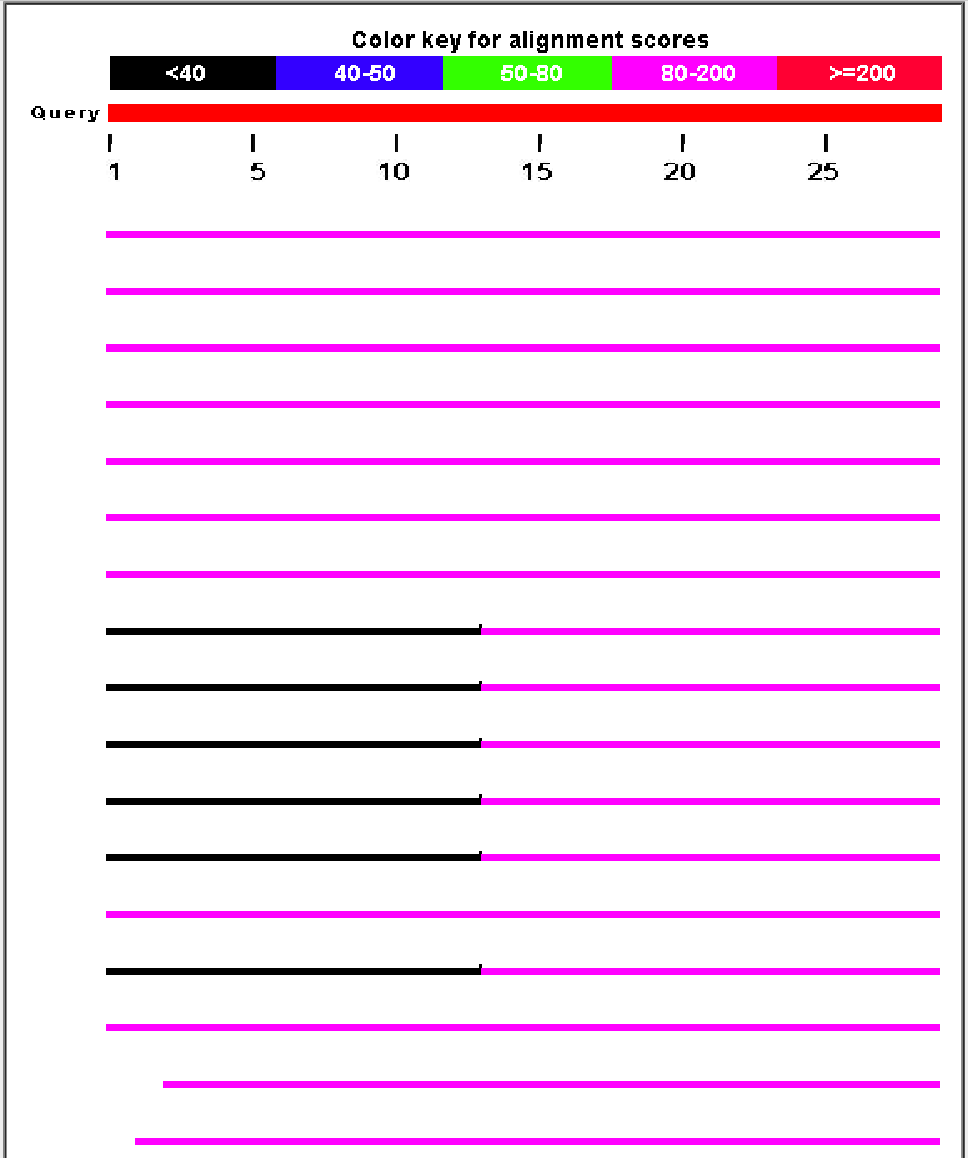
Graphic Summary

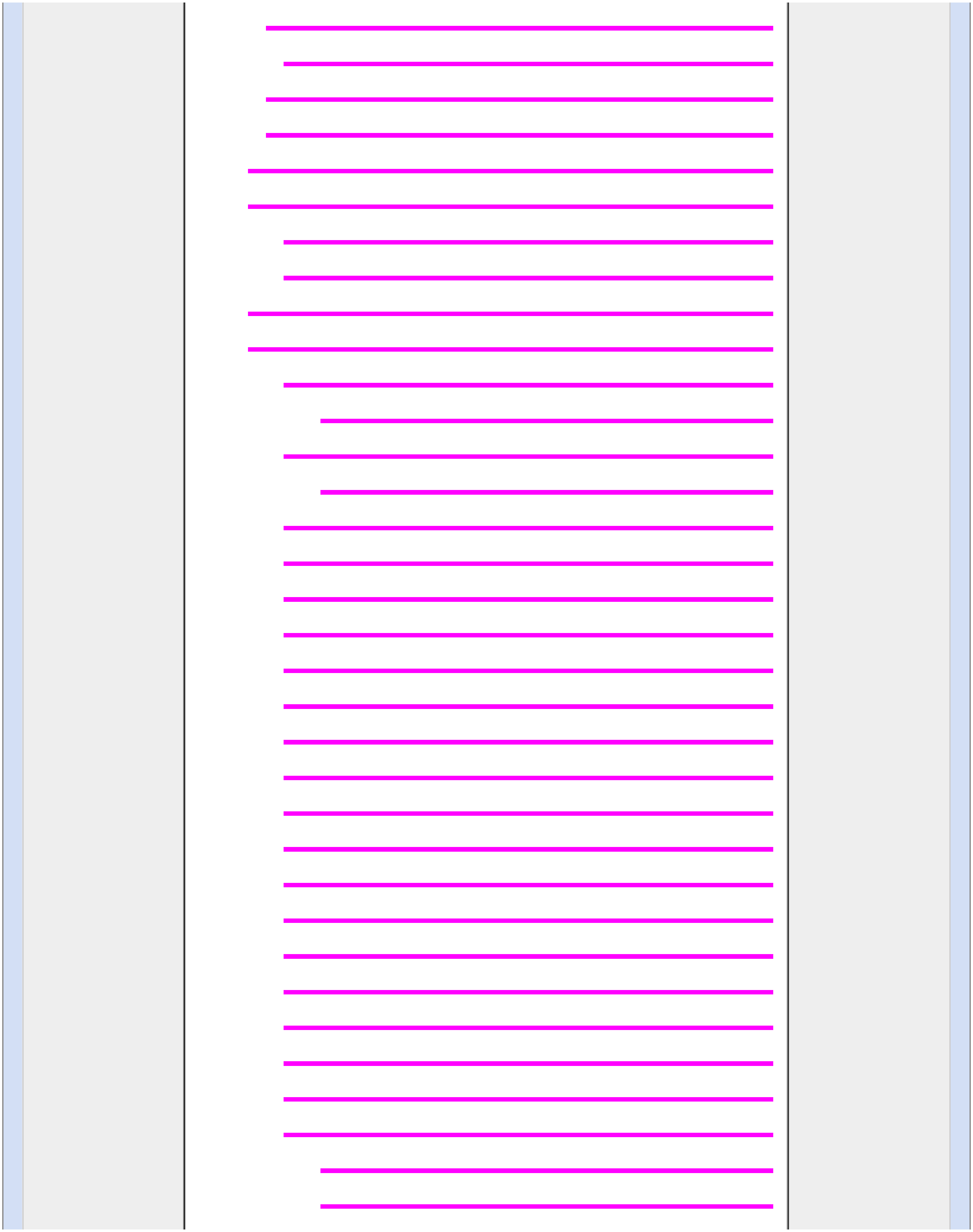
Show Conserved Domains

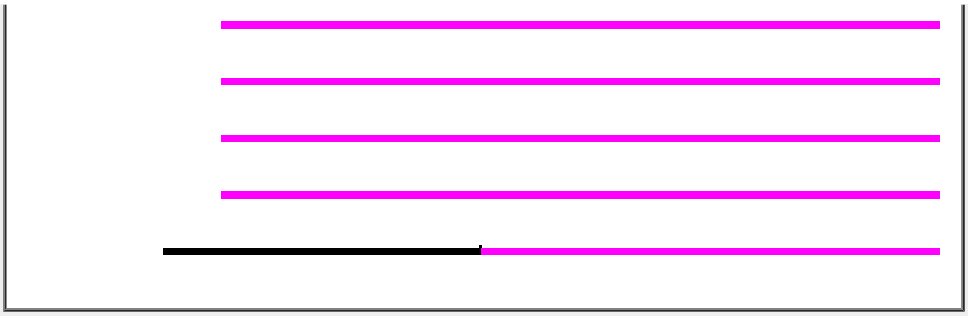
No putative conserved domains have been detected

Distribution of 150 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	CFHR5 protein [Homo sapiens]	98.2	118	100%	2e-21	97%	gi|116283370|AAH26282.1
☐	PREDICTED: complement factor H-related protein 5 isoform X2	98.2	139	100%	2e-21	97%	gi|694890880|XP_009438538.1
☐	unnamed protein product [Homo sapiens]	98.2	118	100%	2e-21	97%	gi|189054216|BAG36736.1
☐	PREDICTED: complement factor H-related protein 5 [Gorilla go	98.2	118	100%	2e-21	97%	gi|426333131|XP_004028138.1
☐	complement factor H-related protein 5 precursor [Homo sapiens	98.2	118	100%	2e-21	97%	gi|13540563|NP_110414.1
☐	PREDICTED: complement factor H-related protein 5 [Pan panis	98.2	139	100%	2e-21	97%	gi|397505136|XP_003823129.1
☐	PREDICTED: complement factor H-related protein 5 isoform X1	98.2	139	100%	2e-21	97%	gi|332811564|XP_514078.3
☐	PREDICTED: complement factor H-related protein 5 [Rhinopith	94.8	117	100%	3e-20	96%	gi|724966978|XP_010356756.1
☐	PREDICTED: complement factor H-related protein 5-like isofor	94.8	117	100%	3e-20	96%	gi|544399121|XP_005540361.1
☐	PREDICTED: complement factor H-related protein 5 [Chlorocel	94.8	117	100%	3e-20	96%	gi|635131776|XP_007987271.1
☐	PREDICTED: complement factor H-related protein 5-like isofor	94.8	117	100%	3e-20	96%	gi|544399119|XP_005540360.1
☐	PREDICTED: complement factor H-related protein 5 [Papio anu	94.8	117	100%	3e-20	96%	gi|402857751|XP_003893408.1
☐	PREDICTED: complement factor H-related protein 5 isoform 1 |	93.5	93.5	100%	9e-20	93%	gi|332230725|XP_003264546.1
☐	hypothetical protein EGM_01566 [Macaca fascicularis]	91.4	113	100%	5e-19	93%	gi|355746073|EHH50698.1
☐	PREDICTED: complement factor H [Ursus maritimus]	87.6	87.6	100%	1e-17	90%	gi|671013917|XP_008697795.1
☐	PREDICTED: complement factor H-like [Equus przewalskii]	86.7	111	93%	2e-17	93%	gi|664780060|XP_008509345.1
☐	PREDICTED: complement factor H-related protein 5 isoform X2	86.7	86.7	96%	2e-17	89%	gi|675747013|XP_008983384.1
☐	PREDICTED: complement factor H-related protein 5 isoform X2	86.7	86.7	96%	2e-17	89%	gi|403294474|XP_003938210.1
☐	PREDICTED: complement factor H [Equus caballus]	86.7	111	93%	2e-17	93%	gi|545210836|XP_005608148.1
☐	PREDICTED: complement factor H isoform X3 [Saimiri bolivien	86.7	155	96%	2e-17	89%	gi|725592697|XP_010347049.1
☐	PREDICTED: complement factor H isoform X4 [Callithrix jacchu	86.7	175	96%	2e-17	89%	gi|675747020|XP_008983387.1
☐	Complement factor H-related protein 5 [Tupaia chinensis]	86.3	86.3	100%	2e-17	84%	gi|444515052|ELV10720.1
☐	PREDICTED: complement factor H-related protein 5-like [Tupai	86.3	167	100%	3e-17	84%	gi|562882019|XP_006168581.1
☐	PREDICTED: complement factor H-like [Tupaia chinensis]	84.6	84.6	93%	3e-17	93%	gi|562888444|XP_006171583.1
☐	PREDICTED: complement factor H-like [Tupaia chinensis]	84.6	84.6	93%	3e-17	93%	gi|562879073|XP_006167236.1
☐	hypothetical protein PANDA_019683 [Ailuropoda melanoleuca]	85.9	85.9	100%	4e-17	90%	gi|281343750|EFB19334.1
☐	PREDICTED: complement factor H-like [Ailuropoda melanoleuc	85.9	85.9	100%	4e-17	90%	gi|301788162|XP_002929497.1
☐	Complement factor H [Tupaia chinensis]	84.6	106	93%	1e-16	93%	gi|444727587|ELW68070.1
☐	PREDICTED: complement factor H-like [Ailuropoda melanoleuc	84.6	84.6	86%	1e-16	96%	gi|301761648|XP_002916246.1

☐	PREDICTED: complement factor H-like [Tupaia chinensis]	84.6	106	93%	1e-16	93%	gi|562833386|XP_006146097.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor H-	84.6	84.6	86%	1e-16	96%	gi|670979575|XP_008695918.1
☐	PREDICTED: complement factor H-like isoform X3 [Tupaia chir	84.6	84.6	93%	1e-16	93%	gi|562853709|XP_006155484.1
☐	PREDICTED: complement factor H-like isoform X2 [Tupaia chir	84.6	84.6	93%	1e-16	93%	gi|562853707|XP_006155483.1
☐	PREDICTED: complement factor H-like isoform X1 [Tupaia chir	84.6	84.6	93%	1e-16	93%	gi|562853705|XP_006155482.1
☐	Complement factor H [Tupaia chinensis]	84.6	84.6	93%	1e-16	93%	gi|444717040|ELW57876.1
☐	PREDICTED: complement factor H isoform X2 [Equus caballus	84.2	109	93%	2e-16	89%	gi|545210671|XP_005608090.1
☐	PREDICTED: complement factor H isoform X1 [Equus caballus	84.2	109	93%	2e-16	89%	gi|338722817|XP_001491754.3
☐	PREDICTED: complement factor H [Galeopterus variegatus]	82.5	108	93%	6e-16	93%	gi|667324753|XP_008589310.1
☐	PREDICTED: complement factor H-like [Leptonychotes weddel	81.7	81.7	93%	1e-15	89%	gi|585151741|XP_006728299.1
☐	PREDICTED: complement factor H-like isoform X5 [Mustela pu	81.7	81.7	93%	1e-15	89%	gi|511939033|XP_004788345.1
☐	PREDICTED: complement factor H-like isoform X5 [Mustela pu	81.7	81.7	93%	1e-15	89%	gi|511872177|XP_004756532.1
☐	PREDICTED: complement factor H-like isoform X4 [Mustela pu	81.7	81.7	93%	1e-15	89%	gi|511939031|XP_004788344.1
☐	PREDICTED: complement factor H-like isoform X4 [Mustela pu	81.7	81.7	93%	1e-15	89%	gi|511872174|XP_004756531.1
☐	PREDICTED: complement factor H-like isoform X3 [Mustela pu	81.7	81.7	93%	1e-15	89%	gi|511939029|XP_004788343.1
☐	PREDICTED: complement factor H-like isoform X3 [Mustela pu	81.7	81.7	93%	1e-15	89%	gi|511872171|XP_004756530.1
☐	PREDICTED: complement factor H-like isoform X2 [Mustela pu	81.7	81.7	93%	1e-15	89%	gi|511939027|XP_004788342.1
☐	PREDICTED: complement factor H-like isoform X2 [Mustela pu	81.7	81.7	93%	1e-15	89%	gi|511872168|XP_004756529.1
☐	PREDICTED: complement factor H-like isoform X1 [Mustela pu	81.7	81.7	93%	1e-15	89%	gi|511939025|XP_004788341.1
☐	PREDICTED: complement factor H-like isoform X1 [Mustela pu	81.7	81.7	93%	1e-15	89%	gi|511872165|XP_004756528.1
☐	PREDICTED: complement factor H-related protein 5-like isofori	80.8	80.8	86%	2e-15	92%	gi|511872183|XP_004756534.1
☐	PREDICTED: complement factor H-related protein 5-like isofori	80.8	80.8	86%	2e-15	92%	gi|511872180|XP_004756533.1
☐	PREDICTED: complement factor H-related protein 5 [Ochotona	80.8	105	86%	2e-15	92%	gi|504132482|XP_004578857.1
☐	PREDICTED: complement factor H isoform X7 [Oryctolagus cu	80.8	105	86%	2e-15	92%	gi|655861296|XP_008266941.1
☐	factor H [Ovis aries]	80.8	80.8	86%	2e-15	92%	gi|294991863|ADF57191.1
☐	PREDICTED: complement factor H-like [Mustela putorius furo]	80.8	80.8	86%	2e-15	92%	gi|511872156|XP_004756526.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor H-	80.4	106	93%	3e-15	92%	gi|488582023|XP_004476425.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor H	80.4	80.4	93%	3e-15	85%	gi|488582009|XP_004485294.1
☐	complement factor H precursor [Sus scrofa]	80.0	80.0	86%	4e-15	92%	gi|47523636|NP_999446.1
☐	PREDICTED: complement factor H-related protein 5 [Echinops	79.5	79.5	86%	5e-15	92%	gi|507633996|XP_004699836.1
☐	PREDICTED: complement factor H-like [Ictidomys tridecemline	79.5	79.5	89%	6e-15	88%	gi|532099560|XP_005335418.1
☐	PREDICTED: complement factor H [Jaculus jaculus]	79.1	79.1	89%	8e-15	88%	gi|507551420|XP_004659511.1
☐	PREDICTED: complement factor H-like [Odobenus rosmarus d	78.7	103	100%	1e-14	83%	gi|472346387|XP_004392923.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor H-	78.7	101	93%	1e-14	85%	gi|591334492|XP_007092940.1
☐	PREDICTED: complement factor H-related protein 5 isoform X1	78.3	100	96%	1e-14	86%	gi|545504211|XP_005622354.1
☐	PREDICTED: complement factor H-related protein 5 isoform X3	78.3	100	96%	1e-14	86%	gi|359319938|XP_547381.3
☐	PREDICTED: complement factor H-like isoform X2 [Equus prze	78.3	105	93%	2e-14	85%	gi|664733497|XP_008523962.1
☐	PREDICTED: complement factor H-like isoform X1 [Equus prze	78.3	105	93%	2e-14	85%	gi|664733495|XP_008523961.1
☐	PREDICTED: complement factor H-like [Equus caballus]	78.3	105	93%	2e-14	85%	gi|545210838|XP_005608149.1
☐	PREDICTED: complement factor H-related protein 5 isoform X3	77.8	100	93%	2e-14	85%	gi|594082716|XP_006064951.1
☐	PREDICTED: complement factor H-related protein 5 [Panthalor	77.8	99.3	93%	2e-14	85%	gi|556769080|XP_005979750.1
☐	PREDICTED: complement factor H-related protein 5 isoform X3	77.8	99.3	93%	2e-14	85%	gi|548499622|XP_005691107.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor H-	77.8	77.8	93%	2e-14	85%	gi|426240147|XP_004013975.1
☐	PREDICTED: complement factor H-related protein 5 isoform X2	77.8	100	93%	2e-14	85%	gi|594082714|XP_006064950.1
☐	PREDICTED: complement factor H-related protein 5 isoform X2	77.8	99.3	93%	2e-14	85%	gi|548499620|XP_005691106.1

☐	PREDICTED: complement factor H-related protein 5 isoform X1	77.8	100	93%	2e-14	85%	gi|594082712|XP_006064949.1
☐	PREDICTED: complement factor H-related protein 5 isoform X1	77.8	99.3	93%	2e-14	85%	gi|548499618|XP_005691105.1
☐	PREDICTED: complement factor H isoform X2 [Equus przewals	77.4	103	93%	3e-14	88%	gi|664733501|XP_008523965.1
☐	PREDICTED: complement factor H isoform X1 [Equus przewals	77.4	103	93%	3e-14	88%	gi|664733499|XP_008523964.1
☐	PREDICTED: complement factor H-related protein 4 [Erinaceus	77.4	98.4	100%	3e-14	78%	gi|617559171|XP_007539820.1
☐	PREDICTED: complement factor H-like [Otolemur garnettii]	77.4	77.4	93%	3e-14	89%	gi|395862888|XP_003803652.1
☐	PREDICTED: complement factor H-like [Sarcophilus harrisii]	77.0	77.0	86%	4e-14	88%	gi|395537227|XP_003770605.1
☐	PREDICTED: complement factor H-like [Elephantulus edwardii]	77.0	77.0	86%	4e-14	88%	gi|585682096|XP_006892182.1
☐	PREDICTED: complement factor H-like [Bos taurus]	76.6	76.6	86%	5e-14	88%	gi|741909329|XP_010798105.1
☐	hypothetical protein M91_20038 [Bos mutus]	76.6	76.6	86%	5e-14	88%	gi|440903747|ELR54366.1
☐	PREDICTED: complement factor H-like [Felis catus]	76.1	99.3	93%	6e-14	85%	gi|587022555|XP_006944335.1
☐	PREDICTED: complement factor H isoform X8 [Bos taurus]	76.6	76.6	86%	6e-14	88%	gi|741953647|XP_010811369.1
☐	PREDICTED: complement factor H isoform X7 [Bos taurus]	76.6	76.6	86%	6e-14	88%	gi|741953645|XP_010811368.1
☐	PREDICTED: complement factor H isoform X6 [Bos taurus]	76.6	76.6	86%	6e-14	88%	gi|528979321|XP_002693921.3
☐	PREDICTED: complement factor H-like [Bos mutus]	76.6	76.6	86%	6e-14	88%	gi|555973258|XP_005898627.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor H	76.6	76.6	86%	6e-14	88%	gi|741953665|XP_010811375.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor H	76.6	76.6	86%	6e-14	88%	gi|741891379|XP_010821343.1
☐	PREDICTED: complement factor H isoform X5 [Bos taurus]	76.6	76.6	86%	6e-14	88%	gi|741953642|XP_010811367.1
☐	PREDICTED: complement factor H-related protein 5 isoform X4	76.6	76.6	86%	6e-14	88%	gi|528979319|XP_005216787.1
☐	TPA: complement factor H-like [Bos taurus]	76.6	76.6	86%	6e-14	88%	gi|296479358|DAA21473.1
☐	TPA: complement factor H-like [Bos taurus]	76.6	76.6	86%	6e-14	88%	gi|296479412|DAA21527.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor H-	76.6	76.6	86%	6e-14	88%	gi|742179883|XP_010852545.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor H-	76.6	76.6	86%	6e-14	88%	gi|426240233|XP_004014017.1
☐	PREDICTED: complement factor H-like [Felis catus]	76.1	99.3	93%	6e-14	85%	gi|587022553|XP_006944334.1
☐	hypothetical protein EGK_01830 [Macaca mulatta]	76.1	76.1	93%	8e-14	81%	gi|355558924|EHH15704.1
☐	PREDICTED: complement factor H-related protein 5 [Nannospa	75.7	98.0	96%	1e-13	88%	gi|674047442|XP_008829796.1

⊟ Alignments

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CFHR5 protein, partial [Homo sapiens]

Sequence ID: gi|116283370|gb|AAH26282.1| **Length:** 434 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 385 to 413 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
98.2 bits(224)	2e-21	28/29(97%)	29/29(100%)	0/29(0%)

```
Query  1    REQFCPPPPQIPNAQDMTTTVNYQDGEKV  29
            REQFCPPPPQIPNAQ+MTTTVNYQDGEKV
Sbjct  385  REQFCPPPPQIPNAQNMTTTVNYQDGEKV  413
```

Range 2: 208 to 216 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
20.6 bits(41)	198530	6/9(67%)	6/9(66%)	0/9(0%)

```
Query  5    CPPPPQIPN  13
            C PPPQ  N
Sbjct  208  CGPPPQLSN  216
```

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PREDICTED: complement factor H-related protein 5 isoform X2 [Pan troglodytes]

Sequence ID: gi|694890880|ref|XP_009438538.1| **Length:** 565 **Number of Matches:** 3

Related Information

Gene - associated gene details

Range 1: 381 to 409 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
98.2 bits(224)	2e-21	28/29(97%)	29/29(100%)	0/29(0%)

```
Query  1    REQFCPPPPQIPNAQDMTTTVNYQDGEKV  29
            REQFCPPPPQIPNAQ+MTTTVNYQDGEKV
Sbjct  381  REQFCPPPPQIPNAQNMTTTVNYQDGEKV  409
```

Range 2: 204 to 212 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
20.6 bits(41)	199550	6/9(67%)	6/9(66%)	0/9(0%)

```
Query  5    CPPPPQIPN  13
            C PPPQ  N
Sbjct  204  CGPPPQLSN  212
```

Range 3: 444 to 472 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
20.6 bits(41)	199550	11/30(37%)	12/30(40%)	11/30(36%)

```
Query  4    FCPPPPQIPNAQDMT----------TTVNY  23
            +C PPP I N  D T          TV Y
Sbjct  444  YCGPPPSISNG-DTTSFPLSVYPPGSTVTY  472
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|189054216|dbj|BAG36736.1| **Length:** 569 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 385 to 413 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
98.2 bits(224)	2e-21	28/29(97%)	29/29(100%)	0/29(0%)

```
Query  1    REQFCPPPPQIPNAQDMTTTVNYQDGEKV  29
            REQFCPPPPQIPNAQ+MTTTVNYQDGEKV
Sbjct  385  REQFCPPPPQIPNAQNMTTTVNYQDGEKV  413
```

Range 2: 208 to 216 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
20.6 bits(41)	199574	6/9(67%)	6/9(66%)	0/9(0%)

```
Query  5    CPPPPQIPN  13
            C PPPQ  N
Sbjct  208  CGPPPQLSN  216
```

Download ⌄ GenPept Graphics Sort by: E value ▼ Next ▲ Previous ▲ Descriptions

PREDICTED: complement factor H-related protein 5 [Gorilla gorilla gorilla]

Sequence ID: gi|426333131|ref|XP_004028138.1| **Length:** 569 **Number of Matches:** 2

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 385 to 413 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
98.2 bits(224)	2e-21	28/29(97%)	29/29(100%)	0/29(0%)

```
Query  1    REQFCPPPPQIPNAQDMTTTVNYQDGEKV  29
            REQFCPPPPQIPNAQ+MTTTVNYQDGEKV
Sbjct  385  REQFCPPPPQIPNAQNMTTTVNYQDGEKV  413
```

Range 2: 208 to 216 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
20.6 bits(41)	199574	6/9(67%)	6/9(66%)	0/9(0%)

```
Query  5    CPPPPQIPN  13
            C PPPQ  N
Sbjct  208  CGPPPQLSN  216
```

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complement factor H-related protein 5 precursor [Homo sapiens]

Sequence ID: gi|13540563|ref|NP_110414.1| **Length:** 569 **Number of Matches:** 2

See 6 more title(s)

Range 1: 385 to 413 GenPept Graphics

Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
98.2 bits(224)	2e-21	28/29(97%)	29/29(100%)	0/29(0%)

```
Query  1    REQFCPPPPQIPNAQDMTTTVNYQDGEKV  29
            REQFCPPPPQIPNAQ+MTTTVNYQDGEKV
Sbjct  385  REQFCPPPPQIPNAQNMTTTVNYQDGEKV  413
```

Range 2: 208 to 216 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Identities	Positives	Gaps
20.6 bits(41)	199574	6/9(67%)	6/9(66%)	0/9(0%)

```
Query  5    CPPPPQIPN  13
            C PPPQ  N
Sbjct  208  CGPPPQLSN  216
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download

How to read this page   Blast report description

CFHR5_REQFCPPPPQIPNAQNMTTTVNYQDGEKV_NonMod

RID	B92PDFE501R (Expires on 01-14 10:02 am)		
Query ID	lcl|278651	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	29		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

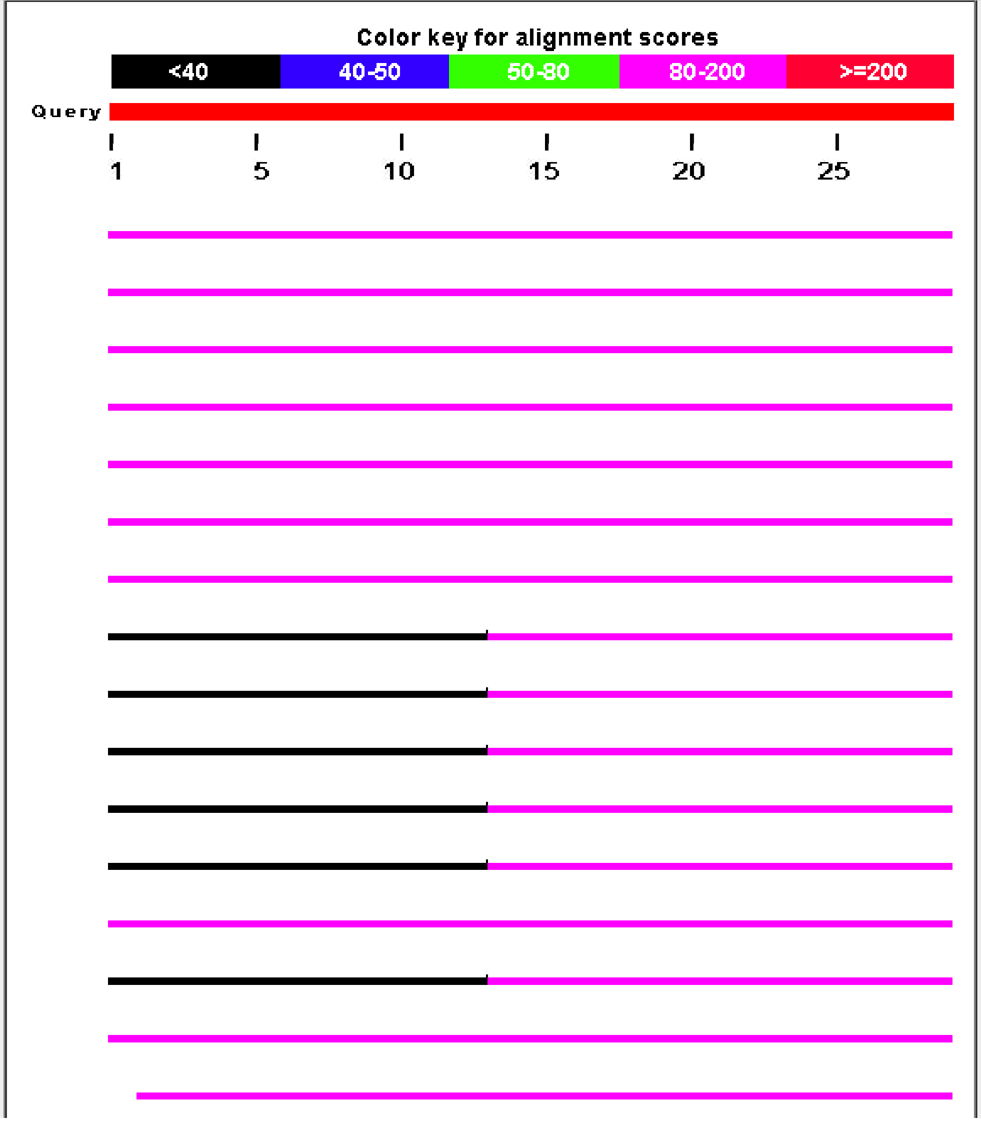
Graphic Summary

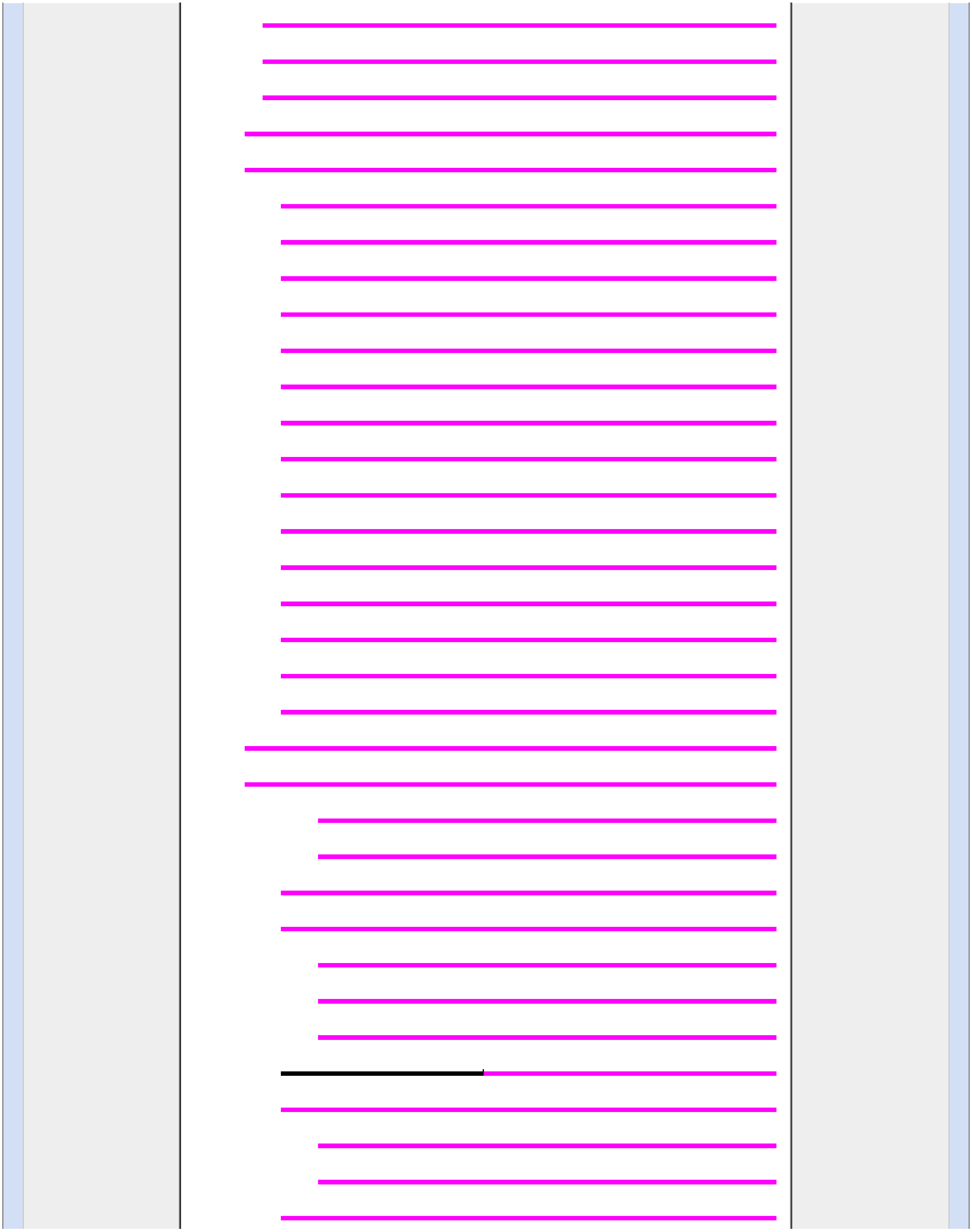
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 155 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	CFHR5 protein [Homo sapiens]	100	121	100%	3e-22	100%	gi|116283370|AAH26282.1
☐	PREDICTED: complement factor I	100	121	100%	3e-22	100%	gi|694890880|XP_009438538.1
☐	unnamed protein product [Homo s	100	121	100%	3e-22	100%	gi|189054216|BAG36736.1
☐	PREDICTED: complement factor I	100	121	100%	3e-22	100%	gi|426333131|XP_004028138.1
☐	complement factor H-related prote	100	121	100%	3e-22	100%	gi|13540563|NP_110414.1
☐	PREDICTED: complement factor I	100	121	100%	3e-22	100%	gi|397505136|XP_003823129.1
☐	PREDICTED: complement factor I	100	121	100%	3e-22	100%	gi|332811564|XP_514078.3
☐	PREDICTED: complement factor I	97.3	119	100%	4e-21	100%	gi|724966978|XP_010356756.1
☐	PREDICTED: complement factor I	97.3	119	100%	4e-21	100%	gi|544399121|XP_005540361.1
☐	PREDICTED: complement factor I	97.3	119	100%	4e-21	100%	gi|635131776|XP_007987271.1
☐	PREDICTED: complement factor I	97.3	119	100%	4e-21	100%	gi|544399119|XP_005540360.1
☐	PREDICTED: complement factor I	97.3	119	100%	4e-21	100%	gi|402857751|XP_003893408.1
☐	PREDICTED: complement factor I	96.1	96.1	100%	1e-20	97%	gi|332230725|XP_003264546.1
☐	hypothetical protein EGM_01566 [	94.0	116	100%	6e-20	96%	gi|355746073|EHH50698.1
☐	PREDICTED: complement factor I	90.1	90.1	100%	1e-18	93%	gi|671013917|XP_008697795.1
☐	PREDICTED: complement factor I	89.3	89.3	96%	2e-18	93%	gi|675747013|XP_008983384.1
☐	PREDICTED: complement factor I	89.3	89.3	96%	2e-18	93%	gi|403294474|XP_003938210.1
☐	PREDICTED: complement factor I	89.3	160	96%	3e-18	93%	gi|725592697|XP_010347049.1
☐	PREDICTED: complement factor I	89.3	180	96%	3e-18	93%	gi|675747020|XP_008983387.1
☐	hypothetical protein PANDA_0196	88.4	88.4	100%	5e-18	93%	gi|281343750|EFB19334.1
☐	PREDICTED: complement factor I	88.4	88.4	100%	5e-18	93%	gi|301788162|XP_002929497.1
☐	PREDICTED: complement factor I	86.7	111	93%	2e-17	93%	gi|545210671|XP_005608090.1
☐	PREDICTED: complement factor I	86.7	111	93%	2e-17	93%	gi|338722817|XP_001491754.3
☐	PREDICTED: complement factor I	84.2	109	93%	1e-16	89%	gi|664780060|XP_008509345.1

☐	PREDICTED: complement factor H	84.2	84.2	93%	1e-16	93%	gi|585151741|XP_006728299.1
☐	PREDICTED: complement factor H	84.2	84.2	93%	1e-16	93%	gi|511939033|XP_004788345.1
☐	PREDICTED: complement factor H	84.2	84.2	93%	1e-16	93%	gi|511872177|XP_004756532.1
☐	PREDICTED: complement factor H	84.2	84.2	93%	1e-16	93%	gi|511939031|XP_004788344.1
☐	PREDICTED: complement factor H	84.2	84.2	93%	1e-16	93%	gi|511872174|XP_004756531.1
☐	PREDICTED: complement factor H	84.2	84.2	93%	1e-16	93%	gi|511939029|XP_004788343.1
☐	PREDICTED: complement factor H	84.2	84.2	93%	1e-16	93%	gi|511872171|XP_004756530.1
☐	PREDICTED: complement factor H	84.2	84.2	93%	1e-16	93%	gi|511939027|XP_004788342.1
☐	PREDICTED: complement factor H	84.2	84.2	93%	1e-16	93%	gi|511872168|XP_004756529.1
☐	PREDICTED: complement factor H	84.2	84.2	93%	1e-16	93%	gi|511939025|XP_004788341.1
☐	PREDICTED: complement factor H	84.2	84.2	93%	1e-16	93%	gi|511872165|XP_004756528.1
☐	PREDICTED: complement factor H	84.2	109	93%	1e-16	89%	gi|545210836|XP_005608148.1
☐	Complement factor H-related prote	83.8	83.8	100%	2e-16	81%	gi|444515052|ELV10720.1
☐	PREDICTED: complement factor H	83.8	162	100%	2e-16	81%	gi|562882019|XP_006168581.1
☐	PREDICTED: complement factor H	83.3	83.3	86%	2e-16	96%	gi|511872183|XP_004756534.1
☐	PREDICTED: complement factor H	83.3	83.3	86%	2e-16	96%	gi|511872180|XP_004756533.1
☐	PREDICTED: complement factor H	82.1	82.1	93%	2e-16	89%	gi|562888444|XP_006171583.1
☐	PREDICTED: complement factor H	82.1	82.1	93%	2e-16	89%	gi|562879073|XP_006167236.1
☐	PREDICTED: complement factor H	83.3	108	86%	3e-16	96%	gi|504132482|XP_004578857.1
☐	PREDICTED: complement factor H	83.3	108	86%	3e-16	96%	gi|655861296|XP_008266941.1
☐	PREDICTED: complement factor H	83.3	83.3	86%	3e-16	96%	gi|511872156|XP_004756526.1
☐	PREDICTED: LOW QUALITY PRO	82.9	108	93%	4e-16	96%	gi|488582023|XP_004476425.1
☐	Complement factor H [Tupaia chin	82.1	103	93%	7e-16	89%	gi|444727587|ELW68070.1
☐	PREDICTED: complement factor H	82.1	82.1	86%	7e-16	96%	gi|507633996|XP_004699836.1
☐	PREDICTED: complement factor H	82.1	82.1	86%	7e-16	92%	gi|301761648|XP_002916246.1
☐	PREDICTED: complement factor H	82.1	103	93%	7e-16	89%	gi|562833386|XP_006146097.1
☐	PREDICTED: LOW QUALITY PRO	82.1	82.1	86%	7e-16	92%	gi|670979575|XP_008695918.1
☐	PREDICTED: complement factor H	82.1	82.1	93%	7e-16	89%	gi|562853709|XP_006155484.1
☐	PREDICTED: complement factor H	82.1	82.1	93%	8e-16	89%	gi|562853707|XP_006155483.1
☐	PREDICTED: complement factor H	82.1	82.1	93%	8e-16	89%	gi|562853705|XP_006155482.1
☐	Complement factor H [Tupaia chin	82.1	82.1	93%	8e-16	89%	gi|444717040|ELW57876.1
☐	PREDICTED: complement factor H	81.2	105	100%	1e-15	86%	gi|472346387|XP_004392923.1
☐	PREDICTED: LOW QUALITY PRO	81.2	104	93%	1e-15	89%	gi|591334492|XP_007092940.1
☐	PREDICTED: complement factor H	80.8	102	96%	2e-15	89%	gi|545504211|XP_005622354.1
☐	PREDICTED: complement factor H	80.8	102	96%	2e-15	89%	gi|359319938|XP_547381.3
☐	PREDICTED: complement factor H	80.4	101	93%	3e-15	89%	gi|594082716|XP_006064951.1
☐	PREDICTED: complement factor H	80.4	100	93%	3e-15	89%	gi|556769080|XP_005979750.1
☐	PREDICTED: complement factor H	80.4	101	93%	3e-15	89%	gi|548499622|XP_005691107.1
☐	PREDICTED: LOW QUALITY PRO	80.4	80.4	93%	3e-15	89%	gi|426240147|XP_004013975.1
☐	PREDICTED: complement factor H	80.4	101	93%	3e-15	89%	gi|594082714|XP_006064950.1
☐	PREDICTED: complement factor H	80.4	101	93%	3e-15	89%	gi|548499620|XP_005691106.1

☐	PREDICTED: complement factor H	80.4	101	93%	3e-15	89%	gi|594082712|XP_006064949.1
☐	PREDICTED: complement factor H	80.4	101	93%	3e-15	89%	gi|548499618|XP_005691105.1
☐	PREDICTED: complement factor H	80.0	106	93%	4e-15	89%	gi|667324753|XP_008589310.1
☐	PREDICTED: complement factor H	80.0	80.0	93%	4e-15	93%	gi|395862888|XP_003803652.1
☐	hypothetical protein EGK_01830 [I	78.7	78.7	93%	1e-14	85%	gi|355558924|EHH15704.1
☐	PREDICTED: complement factor H	78.3	100	96%	1e-14	92%	gi|674047442|XP_008829796.1
☐	PREDICTED: complement factor H	78.3	100	93%	1e-14	92%	gi|555970510|XP_005897276.1
☐	PREDICTED: complement factor H	78.3	99.7	93%	1e-14	92%	gi|528981178|XP_003587159.2
☐	PREDICTED: complement factor H	78.3	100	93%	1e-14	92%	gi|528917598|XP_003583321.2
☐	PREDICTED: complement factor H	78.3	99.7	93%	1e-14	92%	gi|528981176|XP_005217472.1
☐	PREDICTED: complement factor H	78.3	100	93%	1e-14	92%	gi|528917596|XP_005192693.1
☐	hypothetical protein M91_03590 [E	78.3	100	93%	1e-14	92%	gi|440904871|ELR55328.1
☐	PREDICTED: complement factor H	78.3	78.3	93%	2e-14	85%	gi|402857760|XP_003893412.1
☐	PREDICTED: complement factor H	78.3	78.3	93%	2e-14	81%	gi|488582015|XP_004476421.1
☐	factor H [Ovis aries]	78.3	78.3	86%	2e-14	88%	gi|294991863|ADF57191.1
☐	PREDICTED: complement factor H	78.3	78.3	93%	2e-14	85%	gi|544399111|XP_005540356.1
☐	PREDICTED: complement factor H	78.3	78.3	93%	2e-14	85%	gi|544399109|XP_005540355.1
☐	hypothetical protein EGM_01567 [	78.3	78.3	93%	2e-14	85%	gi|355746074|EHH50699.1
☐	PREDICTED: complement factor H	78.3	78.3	93%	2e-14	85%	gi|544399107|XP_005540354.1
☐	PREDICTED: complement factor H	78.3	78.3	93%	2e-14	85%	gi|109019000|XP_001111875.1
☐	PREDICTED: complement factor H	77.4	100	93%	2e-14	85%	gi|587022555|XP_006944335.1
☐	PREDICTED: LOW QUALITY PRO	77.8	77.8	93%	2e-14	81%	gi|488582009|XP_004485294.1
☐	PREDICTED: complement factor H	77.4	100	93%	2e-14	85%	gi|587022553|XP_006944334.1
☐	PREDICTED: complement factor H	77.4	98.4	93%	3e-14	85%	gi|594625544|XP_007167345.1
☐							

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - BTG6MF7J016

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

CFI_KFLNDGTCTAEGKF_Mod

RID BTG6MF7J016 (Expires on 01-20 15:31 pm)

Query ID lcl|57140
Description None
Molecule type amino acid
Query Length 14

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

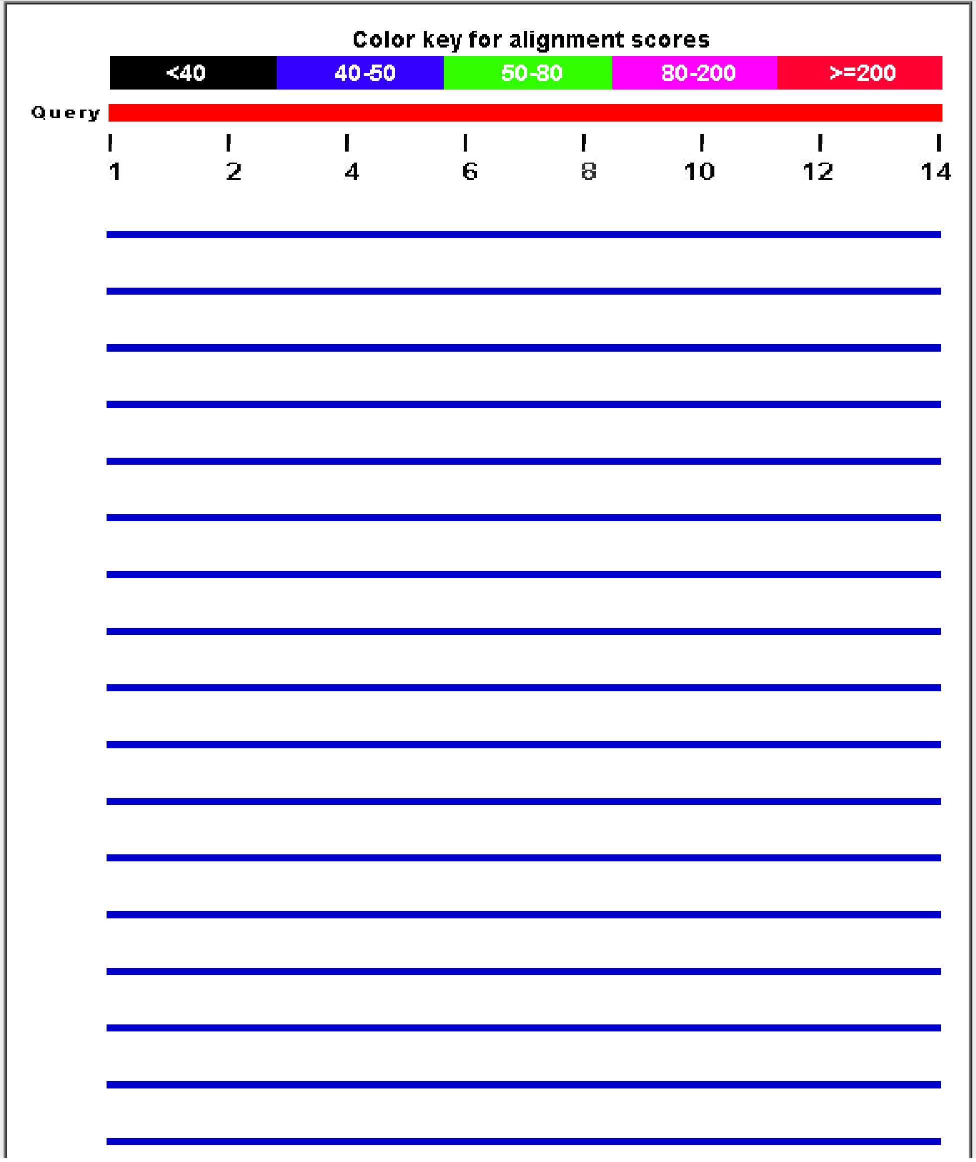
Graphic Summary

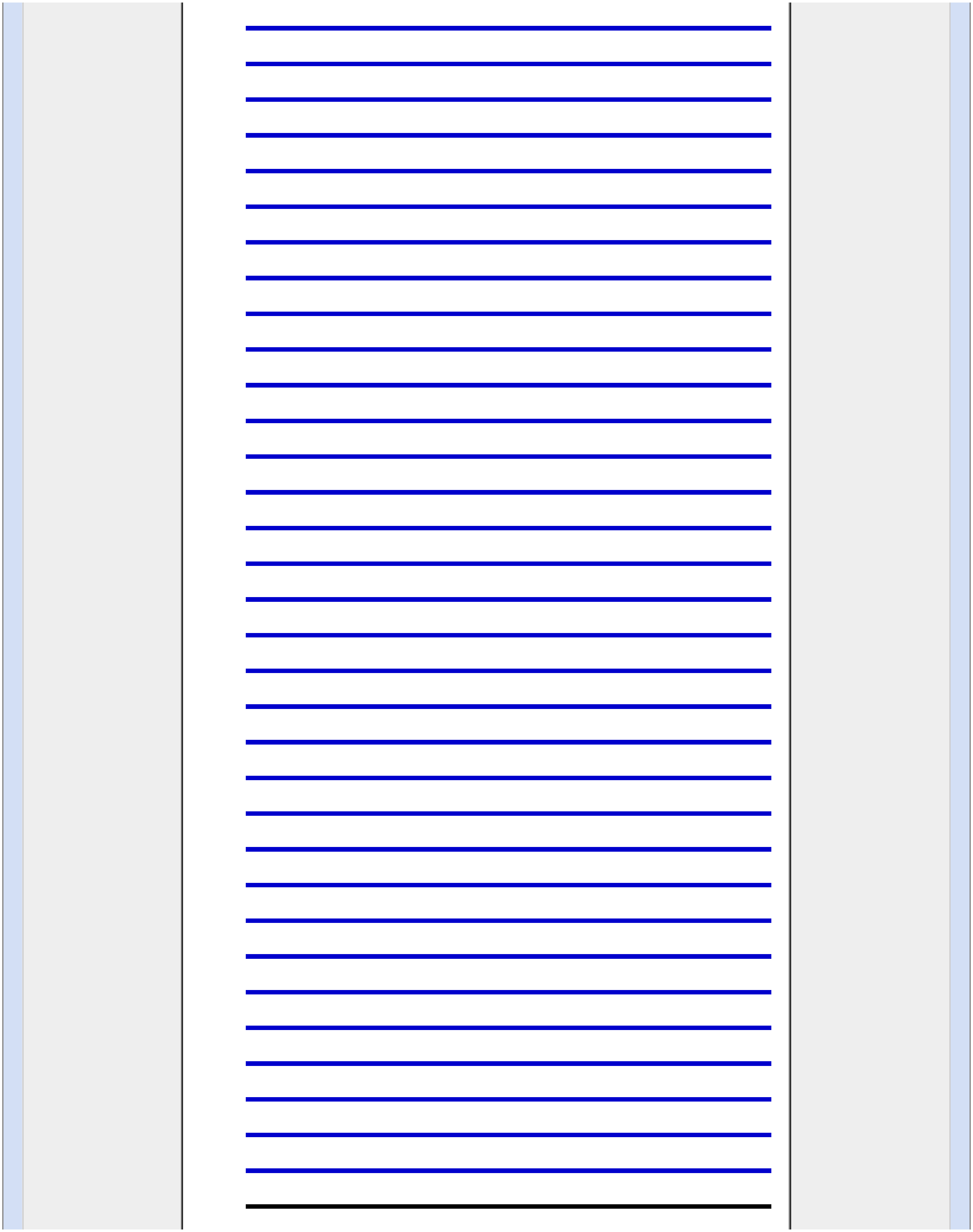
Show Conserved Domains

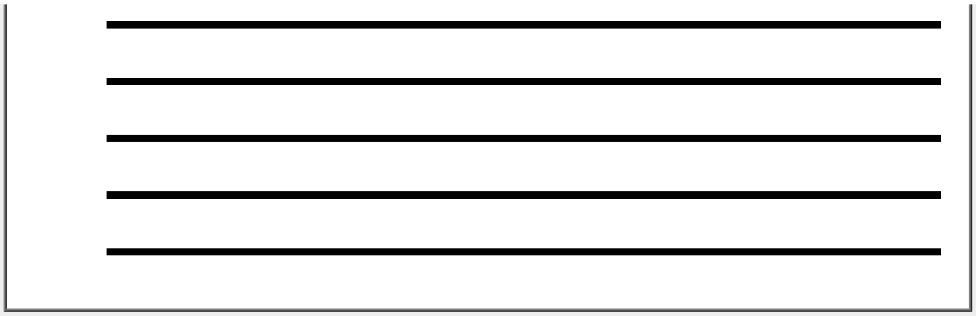
No putative conserved domains have been detected

Distribution of 105 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: complement factor I-like [Gorilla gorilla gorilla]	45.2	45.2	100%	3e-04	93%	gi|426345243|XP_004040330.1
☐	unnamed protein product [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|1335055|CAA68417.1
☐	CFI protein [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|18089117|AAH20718.1
☐	complement factor I, isoform CRA_a [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|119626655|EAX06250.1
☐	PREDICTED: complement factor I isoform X6 [Pan troglodytes]	45.2	45.2	100%	3e-04	93%	gi|694908492|XP_009446407.1
☐	PREDICTED: complement factor I isoform X6 [Pan paniscus]	45.2	45.2	100%	3e-04	93%	gi|675793799|XP_008953634.1
☐	PREDICTED: complement factor I isoform X5 [Pan troglodytes]	45.2	45.2	100%	3e-04	93%	gi|694908490|XP_009446406.1
☐	PREDICTED: complement factor I isoform X5 [Pan paniscus]	45.2	45.2	100%	3e-04	93%	gi|675793797|XP_008953633.1
☐	PREDICTED: complement factor I isoform X4 [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|578809103|XP_006714273.1
☐	Chain A, Human Complement Factor I [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|339961198|2XRC_A
☐	PREDICTED: complement factor I isoform X4 [Pan troglodytes]	45.2	45.2	100%	3e-04	93%	gi|694908488|XP_009446405.1
☐	PREDICTED: complement factor I isoform X4 [Pan paniscus]	45.2	45.2	100%	3e-04	93%	gi|675793795|XP_008953632.1
☐	PREDICTED: complement factor I isoform X2 [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|530377647|XP_005263033.1
☐	PREDICTED: complement factor I isoform X2 [Saimiri boliviens	45.2	45.2	100%	3e-04	93%	gi|725571753|XP_010338379.1
☐	PREDICTED: complement factor I [Callithrix jacchus]	45.2	45.2	100%	3e-04	93%	gi|675648222|XP_002745538.3
☐	PREDICTED: complement factor I [Nomascus leucogenys]	45.2	45.2	100%	3e-04	93%	gi|332240463|XP_003269405.1
☐	prepro-C3b/C4B inactivator [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|182607|AAA52455.1
☐	complement factor I preproprotein [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|119392081|NP_000195.2
☐	complement factor I precursor [Pongo abelii]	45.2	45.2	100%	3e-04	93%	gi|197098986|NP_001127624.1
☐	PREDICTED: complement factor I isoform X3 [Pan paniscus]	45.2	45.2	100%	3e-04	93%	gi|397519838|XP_003830060.1
☐	RecName: Full=Complement factor I; AltName: Full=C3B/C4B i	45.2	45.2	100%	3e-04	93%	gi|317373341|P05156.2
☐	unnamed protein product [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|158254682|BAF83314.1
☐	PREDICTED: complement factor I isoform X3 [Pan troglodytes]	45.2	45.2	100%	3e-04	93%	gi|114595644|XP_526653.2
☐	PREDICTED: complement factor I [Callithrix jacchus]	45.2	45.2	100%	3e-04	93%	gi|675752511|XP_008984405.1
☐	PREDICTED: complement factor I isoform X2 [Nannospalax ga	45.2	45.2	100%	3e-04	93%	gi|674034950|XP_008841698.1
☐	PREDICTED: complement factor I isoform X2 [Pan troglodytes]	45.2	45.2	100%	3e-04	93%	gi|694908485|XP_009446404.1
☐	PREDICTED: complement factor I isoform X2 [Pan paniscus]	45.2	45.2	100%	3e-04	93%	gi|675793792|XP_008953631.1
☐	PREDICTED: complement factor I isoform X1 [Nannospalax ga	45.2	45.2	100%	3e-04	93%	gi|674034948|XP_008841690.1
☐	PREDICTED: complement factor I isoform X3 [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|578809101|XP_006714272.1

☐	unnamed protein product [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|194387702|BAG61264.1
☐	PREDICTED: complement factor I isoform X1 [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|530377645|XP_005263032.1
☐	PREDICTED: complement factor I isoform X1 [Pan paniscus]	45.2	45.2	100%	3e-04	93%	gi|397519840|XP_003830061.1
☐	PREDICTED: complement factor I isoform X1 [Pan troglodytes]	45.2	45.2	100%	3e-04	93%	gi|332820084|XP_003310493.1
☐	PREDICTED: complement factor I isoform X1 [Saimiri boliviens	45.2	45.2	100%	4e-04	93%	gi|725571751|XP_010338378.1
☐	PREDICTED: complement factor I isoform X2 [Equus przewals	41.4	41.4	100%	0.006	86%	gi|664769275|XP_008542181.1
☐	PREDICTED: complement factor I isoform X1 [Equus przewals	41.4	41.4	100%	0.006	86%	gi|664769273|XP_008542180.1
☐	PREDICTED: complement factor I isoform X2 [Equus caballus]	41.4	41.4	100%	0.007	86%	gi|545210264|XP_005607952.1
☐	PREDICTED: complement factor I isoform X1 [Equus caballus]	41.4	41.4	100%	0.007	86%	gi|545210262|XP_005607951.1
☐	PREDICTED: complement factor I isoform X5 [Canis lupus fam	40.9	60.2	100%	0.009	86%	gi|545552244|XP_005639326.1
☐	PREDICTED: complement factor I isoformX3 [Canis lupus fami	40.9	60.2	100%	0.009	86%	gi|74002140|XP_863506.1
☐	PREDICTED: complement factor I isoform X4 [Canis lupus fam	40.9	60.2	100%	0.009	86%	gi|545552242|XP_005639325.1
☐	PREDICTED: complement factor I [Otolemur garnettii]	40.5	40.5	100%	0.012	86%	gi|395851346|XP_003798222.1
☐	Complement factor I [Fukomys damarensis]	40.5	40.5	100%	0.012	86%	gi|676270629|KFO25832.1
☐	Complement factor I [Heterocephalus glaber]	40.5	40.5	100%	0.013	86%	gi|351696416|EHA99334.1
☐	PREDICTED: complement factor I isoform X2 [Fukomys damar	40.5	40.5	100%	0.013	86%	gi|731254237|XP_010639824.1
☐	PREDICTED: complement factor I isoform X2 [Heterocephalus	40.5	40.5	100%	0.013	86%	gi|512818622|XP_004878889.1
☐	PREDICTED: complement factor I isoform X1 [Fukomys damar	40.5	40.5	100%	0.013	86%	gi|731254235|XP_010639823.1
☐	PREDICTED: complement factor I isoform X1 [Heterocephalus	40.5	40.5	100%	0.013	86%	gi|512818618|XP_004878888.1
☐	PREDICTED: complement factor I [Rhinopithecus roxellana]	40.1	40.1	100%	0.017	86%	gi|724946291|XP_010387365.1
☐	PREDICTED: complement factor I [Papio anubis]	40.1	40.1	100%	0.017	86%	gi|685542561|XP_009205631.1
☐	PREDICTED: complement factor I isoform X2 [Ictidomys tridec	39.7	39.7	100%	0.024	86%	gi|532088899|XP_005330149.1
☐	PREDICTED: complement factor I isoform X1 [Ictidomys tridec	39.7	39.7	100%	0.024	86%	gi|532088897|XP_005330148.1
☐	PREDICTED: complement factor I [Ceratotherium simum simu	38.4	38.4	100%	0.063	86%	gi|478504685|XP_004426641.1
☐	PREDICTED: complement factor I isoform X2 [Cavia porcellus]	38.0	38.0	100%	0.087	79%	gi|514457647|XP_005002957.1
☐	PREDICTED: complement factor I isoform X1 [Cavia porcellus]	38.0	38.0	100%	0.087	79%	gi|514457649|XP_003468099.2
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	37.5	37.5	100%	0.12	79%	gi|585149528|XP_006727262.1
☐	PREDICTED: complement factor I [Octodon degus]	37.5	56.8	100%	0.12	79%	gi|507626946|XP_004626817.1
☐	PREDICTED: complement factor I isoform X2 [Oryctolagus cun	37.5	37.5	100%	0.12	79%	gi|655856777|XP_008265709.1
☐	PREDICTED: complement factor I isoform X1 [Oryctolagus cun	37.5	37.5	100%	0.12	79%	gi|655856775|XP_002717177.2
☐	PREDICTED: complement factor I [Ochotona princeps]	37.1	37.1	100%	0.16	79%	gi|504169976|XP_004594584.1
☐	PREDICTED: complement factor I [Tarsius syrichta]	37.1	37.1	100%	0.16	86%	gi|640813983|XP_008063707.1
☐	PREDICTED: complement factor I [Loxodonta africana]	37.1	37.1	100%	0.16	79%	gi|731479219|XP_010588889.1
☐	PREDICTED: complement factor I isoform X6 [Panthera tigris a	36.7	36.7	100%	0.22	79%	gi|591346160|XP_007098330.1
☐	PREDICTED: complement factor I isoform X2 [Chlorocebus sa	36.7	36.7	100%	0.23	79%	gi|635044269|XP_007997719.1
☐	PREDICTED: complement factor I isoform X1 [Chlorocebus sa	36.7	36.7	100%	0.23	79%	gi|635044267|XP_007997718.1
☐	PREDICTED: complement factor I [Orycteropus afer afer]	36.7	36.7	100%	0.23	79%	gi|634848033|XP_007938975.1
☐	PREDICTED: complement factor I isoform X5 [Panthera tigris a	36.7	36.7	100%	0.23	79%	gi|591346158|XP_007098329.1
☐	PREDICTED: complement factor I isoform X4 [Panthera tigris a	36.7	36.7	100%	0.23	79%	gi|591346156|XP_007098328.1
☐	PREDICTED: complement factor I isoform X2 [Panthera tigris a	36.7	36.7	100%	0.23	79%	gi|591346152|XP_007098326.1
☐	PREDICTED: complement factor I isoform X1 [Panthera tigris a	36.7	36.7	100%	0.23	79%	gi|591346150|XP_007098325.1
☐	PREDICTED: complement factor I-like [Macaca mulatta]	36.3	36.3	100%	0.30	79%	gi|297293220|XP_001087512.2
☐	uncharacterized protein LOC101866929 precursor [Macaca fas	36.3	36.3	100%	0.31	79%	gi|548961885|NP_001271714.1
☐	hypothetical protein EGK_16010 [Macaca mulatta]	36.3	36.3	100%	0.31	79%	gi|355687535|EHH26119.1
☐	complement factor I-like protein [Cricetulus griseus]	35.4	35.4	100%	0.58	79%	gi|537261801|ERE90152.1

☐	PREDICTED: complement factor I [Cricetulus griseus]	35.4	35.4	100%	0.59	79%	gi|625241505|XP_007611983.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	35.4	35.4	100%	0.59	79%	gi|625222421|XP_007651009.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	35.0	35.0	100%	0.80	79%	gi|472383864|XP_004411307.1
☐	complement factor I precursor [Rattus norvegicus]	34.6	34.6	100%	1.1	79%	gi|13162353|NP_077071.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	34.6	34.6	100%	1.1	79%	gi|586984171|XP_006930977.1
☐	PREDICTED: complement factor I isoform X1 [Rattus norvegicu	34.6	34.6	100%	1.1	79%	gi|672044321|XP_008759748.1
☐	PREDICTED: complement factor I [Jaculus jaculus]	34.1	34.1	100%	1.5	71%	gi|507549735|XP_004658680.1
☐	PREDICTED: complement factor I [Trichechus manatus latirost	33.3	33.3	100%	2.8	71%	gi|471391575|XP_004380312.1
☐	PREDICTED: complement factor I [Mesocricetus auratus]	32.5	32.5	100%	5.3	79%	gi|524965961|XP_005082885.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	32.0	32.0	100%	7.1	71%	gi|511847748|XP_004748251.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	32.0	32.0	100%	7.2	71%	gi|511991360|XP_004813365.1
☐	PREDICTED: complement factor I isoform X4 [Mus musculus]	32.0	32.0	100%	7.2	71%	gi|568921717|XP_006501026.1
☐	PREDICTED: complement factor I isoform X3 [Mus musculus]	32.0	32.0	100%	7.2	71%	gi|568921715|XP_006501025.1
☐	PREDICTED: complement factor I isoform X2 [Mus musculus]	32.0	32.0	100%	7.2	71%	gi|568921713|XP_006501024.1
☐	complement factor I precursor [Mus musculus]	32.0	32.0	100%	7.2	71%	gi|110347406|NP_031712.2
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	31.2	50.5	100%	13	71%	gi|533186455|XP_005406244.1
☐	PREDICTED: complement factor I [Chrysochloris asiatica]	30.8	30.8	100%	18	71%	gi|586477731|XP_006869402.1
☐	PREDICTED: complement factor I [Sarcophilus harrisii]	30.3	30.3	100%	25	64%	gi|395542057|XP_003772951.1
☐	hypothetical protein C404_13575 [Ralstonia sp. AU12-08]	29.9	29.9	71%	34	91%	gi|528186626|EPX97543.1
☐	hypothetical protein [Ralstonia sp. AU12-08]	29.9	29.9	71%	34	91%	gi|739147048|WP_037011702.1
☐	hypothetical protein [Ralstonia sp. UNC404CL21Col]	29.9	29.9	71%	34	91%	gi|653774958|WP_027680912.1
☐	hypothetical protein [Ralstonia pickettii]	29.9	29.9	71%	34	91%	gi|640543007|WP_024975163.1
☐	PREDICTED: complement factor I [Peromyscus maniculatus ba	29.9	29.9	100%	34	71%	gi|589914217|XP_006970447.1
☐	Putative disease resistance protein RXW24L [Aegilops tauschii	29.5	29.5	57%	46	100%	gi|475506332|EMT04834.1
☐	molecular chaperone DnaJ [Desulfovibrio putealis]	29.1	29.1	85%	61	83%	gi|652937116|WP_027190715.1
☐	PREDICTED: complement factor I [Myotis davidii]	29.1	29.1	100%	62	71%	gi|584046382|XP_006767995.1

⊟ Alignments

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PREDICTED: complement factor I-like, partial [Gorilla gorilla gorilla]

Sequence ID: gi|426345243|ref|XP_004040330.1| **Length:** 309 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 99 to 112 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.2 bits(99)	3e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KFLNDGTCTAEGKF  14
            KFLN+GTCTAEGKF
Sbjct  99   KFLNNGTCTAEGKF  112
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|1335055|emb|CAA68417.1| **Length:** 321 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 81 to 94 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.2 bits(99)	3e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1   KFLNDGTCTAEGKF  14
           KFLN+GTCTAEGKF
Sbjct  81  KFLNNGTCTAEGKF  94
```

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CFI protein [Homo sapiens]

Sequence ID: gi|18089117|gb|AAH20718.1| **Length:** 377 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details
Identical Proteins - Proteins identical to the subject

Range 1: 99 to 112 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.2 bits(99)	3e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KFLNDGTCTAEGKF  14
            KFLN+GTCTAEGKF
Sbjct  99   KFLNNGTCTAEGKF  112
```

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complement factor I, isoform CRA_a, partial [Homo sapiens]

Sequence ID: gi|119626655|gb|EAX06250.1| **Length:** 378 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 99 to 112 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.2 bits(99)	3e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KFLNDGTCTAEGKF  14
            KFLN+GTCTAEGKF
Sbjct  99   KFLNNGTCTAEGKF  112
```

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PREDICTED: complement factor I isoform X6 [Pan troglodytes]

Sequence ID: gi|694908492|ref|XP_009446407.1| **Length:** 516 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 99 to 112 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.2 bits(99)	3e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KFLNDGTCTAEGKF  14
            KFLN+GTCTAEGKF
Sbjct  99   KFLNNGTCTAEGKF  112
```

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Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

CFI_KFLNDGTCTAEGKFSVSLKH_Mod

RID BTG7JCWX013 (Expires on 01-20 15:31 pm)

Query ID lcl|81263
Description None
Molecule type amino acid
Query Length 20

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

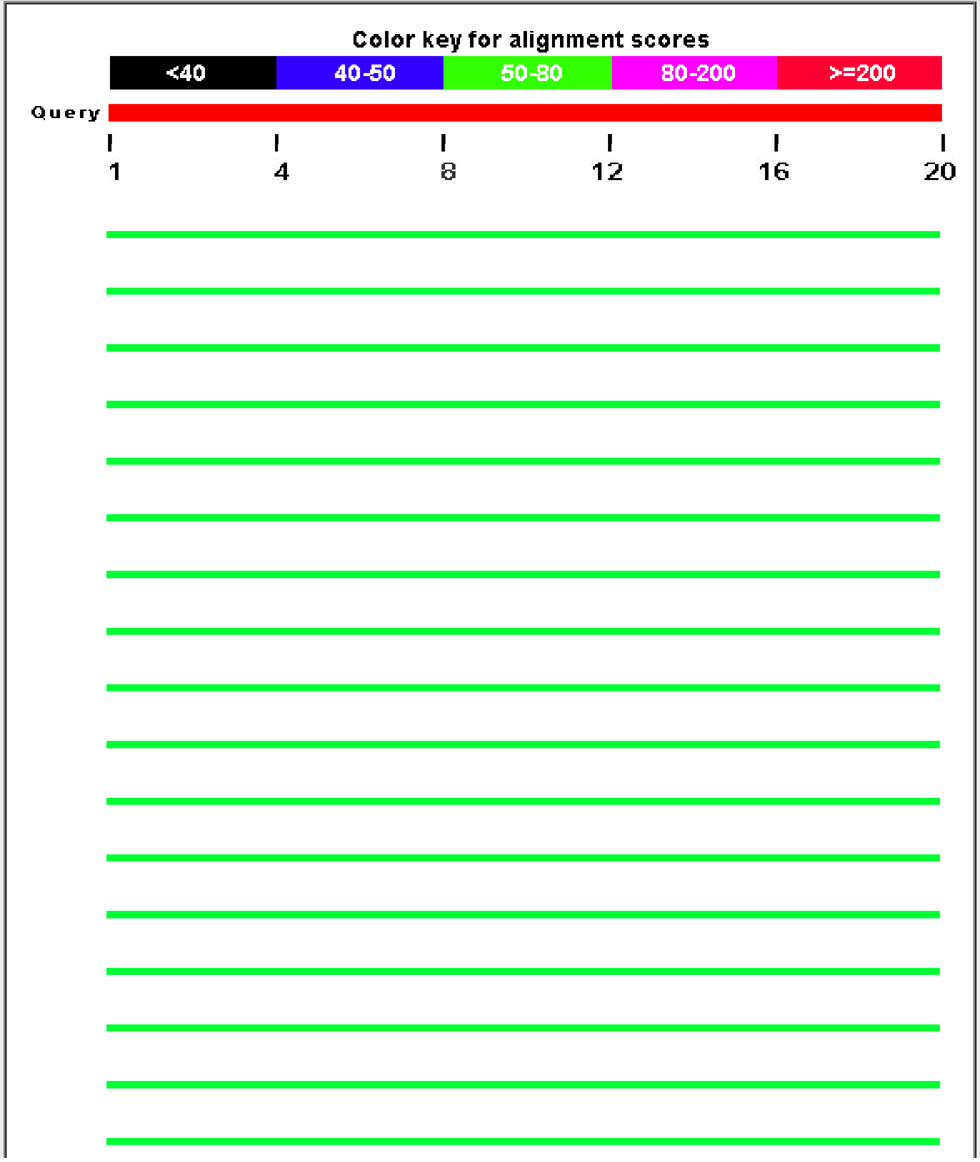
Graphic Summary

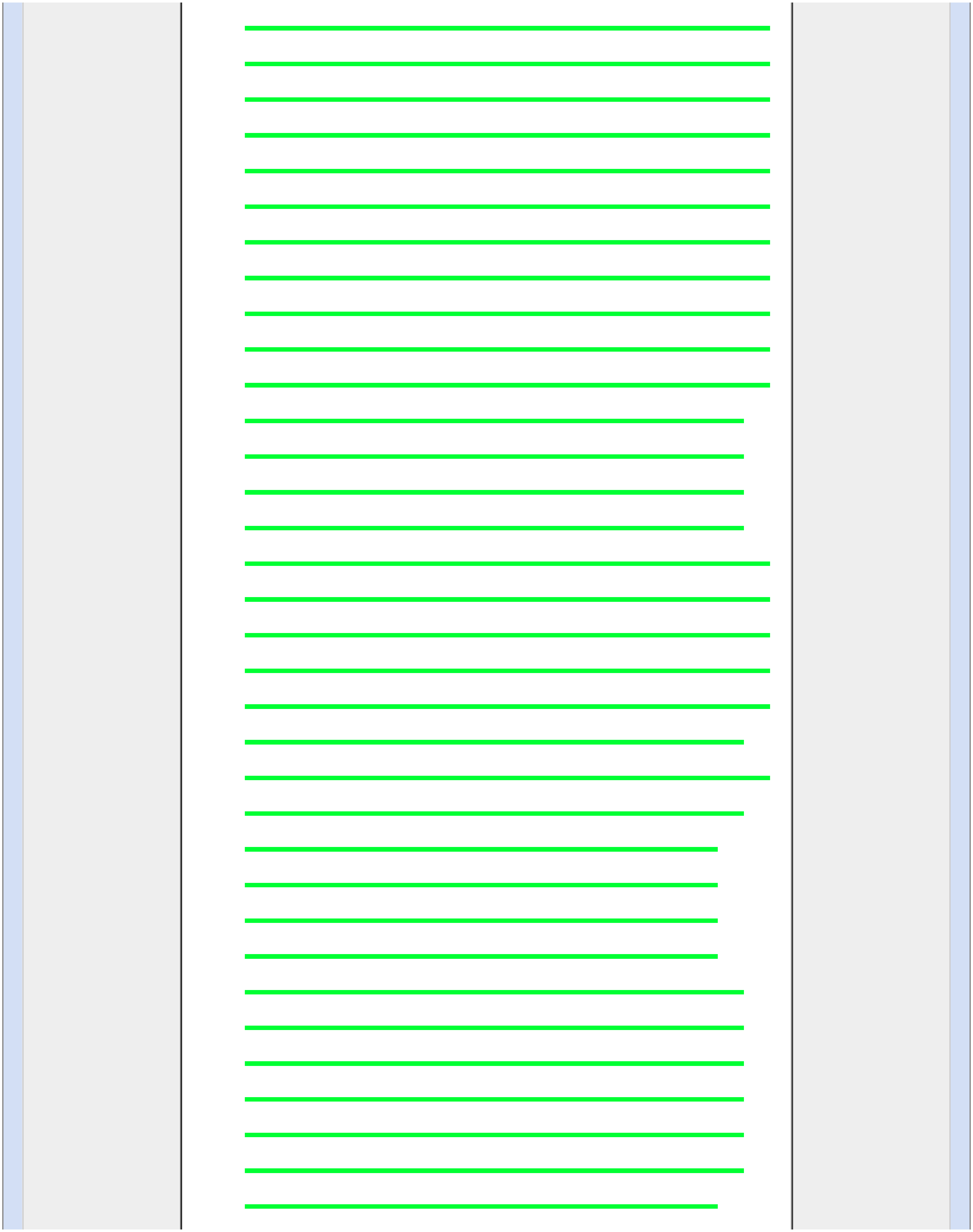
Show Conserved Domains

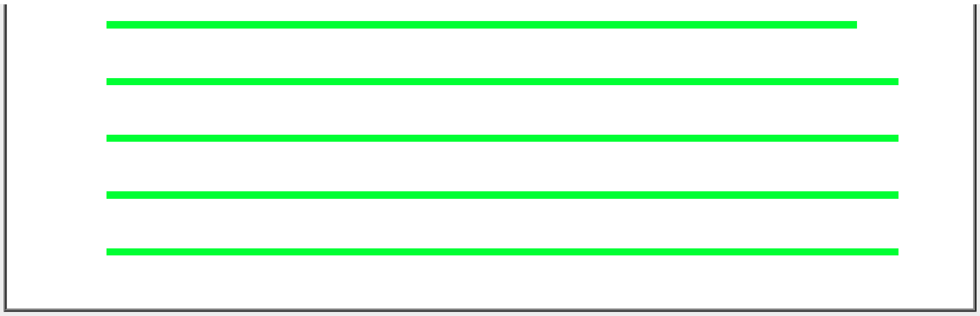
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: complement factor I-like [Gorilla gorilla gorilla]	63.0	63.0	100%	6e-10	95%	gi|426345243|XP_004040330.1
☐	unnamed protein product [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|1335055|CAA68417.1
☐	CFI protein [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|18089117|AAH20718.1
☐	complement factor I, isoform CRA_a [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|119626655|EAX06250.1
☐	PREDICTED: complement factor I isoform X6 [Pan troglodytes]	63.0	63.0	100%	7e-10	95%	gi|694908492|XP_009446407.1
☐	PREDICTED: complement factor I isoform X6 [Pan paniscus]	63.0	63.0	100%	7e-10	95%	gi|675793799|XP_008953634.1
☐	PREDICTED: complement factor I isoform X5 [Pan troglodytes]	63.0	63.0	100%	7e-10	95%	gi|694908490|XP_009446406.1
☐	PREDICTED: complement factor I isoform X5 [Pan paniscus]	63.0	63.0	100%	7e-10	95%	gi|675793797|XP_008953633.1
☐	PREDICTED: complement factor I isoform X4 [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|578809103|XP_006714273.1
☐	Chain A, Human Complement Factor I [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|339961198|2XRC_A
☐	PREDICTED: complement factor I isoform X4 [Pan troglodytes]	63.0	63.0	100%	7e-10	95%	gi|694908488|XP_009446405.1
☐	PREDICTED: complement factor I isoform X4 [Pan paniscus]	63.0	63.0	100%	7e-10	95%	gi|675793795|XP_008953632.1
☐	PREDICTED: complement factor I isoform X2 [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|530377647|XP_005263033.1
☐	PREDICTED: complement factor I [Nomascus leucogenys]	63.0	63.0	100%	7e-10	95%	gi|332240463|XP_003269405.1
☐	prepro-C3b/C4B inactivator [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|182607|AAA52455.1
☐	complement factor I preproprotein [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|119392081|NP_000195.2
☐	complement factor I precursor [Pongo abelii]	63.0	63.0	100%	7e-10	95%	gi|197098986|NP_001127624.1
☐	PREDICTED: complement factor I isoform X3 [Pan paniscus]	63.0	63.0	100%	7e-10	95%	gi|397519838|XP_003830060.1
☐	RecName: Full=Complement factor I; AltName: Full=C3B/C4B i	63.0	63.0	100%	7e-10	95%	gi|317373341|P05156.2
☐	unnamed protein product [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|158254682|BAF83314.1
☐	PREDICTED: complement factor I isoform X3 [Pan troglodytes]	63.0	63.0	100%	7e-10	95%	gi|114595644|XP_526653.2
☐	PREDICTED: complement factor I isoform X2 [Pan troglodytes]	63.0	63.0	100%	7e-10	95%	gi|694908485|XP_009446404.1
☐	PREDICTED: complement factor I isoform X2 [Pan paniscus]	63.0	63.0	100%	7e-10	95%	gi|675793792|XP_008953631.1
☐	PREDICTED: complement factor I isoform X3 [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|578809101|XP_006714272.1
☐	unnamed protein product [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|194387702|BAG61264.1
☐	PREDICTED: complement factor I isoform X1 [Homo sapiens]	63.0	63.0	100%	7e-10	95%	gi|530377645|XP_005263032.1
☐	PREDICTED: complement factor I isoform X1 [Pan paniscus]	63.0	63.0	100%	7e-10	95%	gi|397519840|XP_003830061.1
☐	PREDICTED: complement factor I isoform X1 [Pan troglodytes]	63.0	63.0	100%	7e-10	95%	gi|332820084|XP_003310493.1
☐	PREDICTED: complement factor I isoform X2 [Saimiri boliviens	59.2	59.2	95%	1e-08	95%	gi|725571753|XP_010338379.1

☐	PREDICTED: complement factor I [Callithrix jacchus]	59.2	59.2	95%	1e-08	95%	gi|675648222|XP_002745538.3
☐	PREDICTED: complement factor I [Callithrix jacchus]	59.2	59.2	95%	1e-08	95%	gi|675752511|XP_008984405.1
☐	PREDICTED: complement factor I isoform X1 [Saimiri boliviens	59.2	59.2	95%	1e-08	95%	gi|725571751|XP_010338378.1
☐	PREDICTED: complement factor I [Papio anubis]	57.9	57.9	100%	4e-08	90%	gi|685542561|XP_009205631.1
☐	PREDICTED: complement factor I isoform X2 [Chlorocebus sal	54.5	54.5	100%	5e-07	85%	gi|635044269|XP_007997719.1
☐	PREDICTED: complement factor I isoform X1 [Chlorocebus sal	54.5	54.5	100%	5e-07	85%	gi|635044267|XP_007997718.1
☐	PREDICTED: complement factor I-like [Macaca mulatta]	54.1	54.1	100%	7e-07	85%	gi|297293220|XP_001087512.2
☐	uncharacterized protein LOC101866929 precursor [Macaca fas	54.1	54.1	100%	7e-07	85%	gi|548961885|NP_001271714.1
☐	PREDICTED: complement factor I [Rhinopithecus roxellana]	54.1	54.1	95%	7e-07	89%	gi|724946291|XP_010387365.1
☐	hypothetical protein EGK_16010 [Macaca mulatta]	54.1	54.1	100%	7e-07	85%	gi|355687535|EHH26119.1
☐	PREDICTED: complement factor I [Ceratotherium simum simur	52.4	52.4	95%	3e-06	89%	gi|478504685|XP_004426641.1
☐	PREDICTED: complement factor I [Otolemur garnettii]	51.5	51.5	90%	5e-06	89%	gi|395851346|XP_003798222.1
☐	Complement factor I [Heterocephalus glaber]	51.5	51.5	90%	5e-06	89%	gi|351696416|EHA99334.1
☐	PREDICTED: complement factor I isoform X2 [Heterocephalus	51.5	51.5	90%	5e-06	89%	gi|512818622|XP_004878889.1
☐	PREDICTED: complement factor I isoform X1 [Heterocephalus	51.5	51.5	90%	5e-06	89%	gi|512818618|XP_004878888.1
☐	PREDICTED: complement factor I isoform X2 [Equus przewalsl	51.1	51.1	95%	7e-06	84%	gi|664769275|XP_008542181.1
☐	PREDICTED: complement factor I isoform X1 [Equus przewalsl	51.1	51.1	95%	7e-06	84%	gi|664769273|XP_008542180.1
☐	PREDICTED: complement factor I [Tarsius syrichta]	51.1	51.1	95%	7e-06	89%	gi|640813983|XP_008063707.1
☐	PREDICTED: complement factor I isoform X2 [Equus caballus]	51.1	51.1	95%	7e-06	84%	gi|545210264|XP_005607952.1
☐	PREDICTED: complement factor I isoform X1 [Equus caballus]	51.1	51.1	95%	7e-06	84%	gi|545210262|XP_005607951.1
☐	PREDICTED: complement factor I isoform X6 [Panthera tigris a	50.7	50.7	95%	1e-05	84%	gi|591346160|XP_007098330.1
☐	PREDICTED: complement factor I isoform X2 [Nannospalax ga	50.7	50.7	90%	1e-05	89%	gi|674034950|XP_008841698.1
☐	PREDICTED: complement factor I isoform X1 [Nannospalax ga	50.7	50.7	90%	1e-05	89%	gi|674034948|XP_008841690.1
☐	PREDICTED: complement factor I isoform X5 [Panthera tigris a	50.7	50.7	95%	1e-05	84%	gi|591346158|XP_007098329.1
☐	PREDICTED: complement factor I isoform X4 [Panthera tigris a	50.7	50.7	95%	1e-05	84%	gi|591346156|XP_007098328.1
☐	PREDICTED: complement factor I isoform X2 [Panthera tigris a	50.7	50.7	95%	1e-05	84%	gi|591346152|XP_007098326.1
☐	PREDICTED: complement factor I isoform X1 [Panthera tigris a	50.7	50.7	95%	1e-05	84%	gi|591346150|XP_007098325.1
☐	PREDICTED: complement factor I isoform X5 [Canis lupus fam	49.8	49.8	90%	2e-05	83%	gi|545552244|XP_005639326.1
☐	PREDICTED: complement factor I isoformX3 [Canis lupus famil	49.8	49.8	90%	2e-05	83%	gi|74002140|XP_863506.1
☐	PREDICTED: complement factor I isoform X4 [Canis lupus fam	49.8	49.8	90%	2e-05	83%	gi|545552242|XP_005639325.1
☐	PREDICTED: complement factor I isoform X2 [Oryctolagus cun	49.0	49.0	95%	4e-05	79%	gi|655856777|XP_008265709.1
☐	PREDICTED: complement factor I isoform X1 [Oryctolagus cun	49.0	49.0	95%	4e-05	79%	gi|655856775|XP_002717177.2
☐	Complement factor I [Fukomys damarensis]	48.6	48.6	85%	5e-05	88%	gi|676270629|KFO25832.1
☐	PREDICTED: complement factor I isoform X2 [Ictidomys tridece	48.6	48.6	90%	5e-05	83%	gi|532088899|XP_005330149.1
☐	PREDICTED: complement factor I isoform X1 [Ictidomys tridece	48.6	48.6	90%	5e-05	83%	gi|532088897|XP_005330148.1
☐	PREDICTED: complement factor I isoform X2 [Fukomys damar	48.6	48.6	85%	5e-05	88%	gi|731254237|XP_010639824.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [I	48.6	48.6	95%	5e-05	84%	gi|586984171|XP_006930977.1
☐	PREDICTED: complement factor I isoform X1 [Fukomys damar	48.6	48.6	85%	5e-05	88%	gi|731254235|XP_010639823.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [I	48.1	48.1	95%	7e-05	79%	gi|585149528|XP_006727262.1
☐	PREDICTED: complement factor I [Octodon degus]	46.0	46.0	90%	4e-04	78%	gi|507626946|XP_004626817.1
☐	PREDICTED: complement factor I [Loxodonta africana]	46.0	46.0	90%	4e-04	78%	gi|731479219|XP_010588889.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [(	45.6	45.6	95%	5e-04	79%	gi|472383864|XP_004411307.1
☐	PREDICTED: complement factor I [Orycteropus afer afer]	45.6	45.6	95%	5e-04	79%	gi|634848033|XP_007938975.1
☐	PREDICTED: complement factor I [Chrysochloris asiatica]	44.8	44.8	95%	0.001	79%	gi|586477731|XP_006869402.1
☐	PREDICTED: complement factor I [Ochotona princeps]	43.9	43.9	90%	0.002	78%	gi|504169976|XP_004594584.1

☐	complement factor I-like protein [Cricetulus griseus]	43.9	43.9	90%	0.002	78%	gi|537261801|ERE90152.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	43.9	43.9	90%	0.002	78%	gi|625241505|XP_007611983.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	43.9	43.9	90%	0.002	78%	gi|625222421|XP_007651009.1
☐	complement factor I precursor [Rattus norvegicus]	43.1	43.1	90%	0.003	78%	gi|13162353|NP_077071.1
☐	PREDICTED: complement factor I isoform X1 [Rattus norvegicu	43.1	43.1	90%	0.003	78%	gi|672044321|XP_008759748.1
☐	PREDICTED: complement factor I [Jaculus jaculus]	42.6	42.6	90%	0.004	72%	gi|507549735|XP_004658680.1
☐	PREDICTED: complement factor I [Myotis davidii]	42.2	42.2	100%	0.006	70%	gi|584046382|XP_006767995.1
☐	PREDICTED: complement factor I [Trichechus manatus latirost	41.4	41.4	85%	0.012	76%	gi|471391575|XP_004380312.1
☐	PREDICTED: complement factor I isoform X2 [Cavia porcellus]	40.9	40.9	90%	0.016	72%	gi|514457647|XP_005002957.1
☐	PREDICTED: complement factor I isoform X1 [Cavia porcellus]	40.9	40.9	90%	0.016	72%	gi|514457649|XP_003468099.2
☐	PREDICTED: complement factor I [Mesocricetus auratus]	40.9	40.9	90%	0.016	78%	gi|524965961|XP_005082885.1
☐	complement factor I precursor [Camelus ferus]	40.5	40.5	95%	0.021	74%	gi|528758403|EPY78062.1
☐	PREDICTED: complement factor I isoform X2 [Camelus drome	40.5	40.5	95%	0.022	74%	gi|744567503|XP_010979382.1
☐	PREDICTED: complement factor I isoform X2 [Camelus bactria	40.5	40.5	95%	0.022	74%	gi|743716645|XP_010951976.1
☐	PREDICTED: complement factor I isoform X1 [Camelus drome	40.5	40.5	95%	0.022	74%	gi|744567500|XP_010979381.1
☐	PREDICTED: complement factor I isoform X1 [Camelus bactria	40.5	40.5	95%	0.022	74%	gi|743716643|XP_010951975.1
☐	PREDICTED: complement factor I isoform X4 [Mus musculus]	40.5	40.5	90%	0.022	72%	gi|568921717|XP_006501026.1
☐	PREDICTED: complement factor I isoform X3 [Mus musculus]	40.5	40.5	90%	0.022	72%	gi|568921715|XP_006501025.1
☐	PREDICTED: complement factor I isoform X2 [Mus musculus]	40.5	40.5	90%	0.022	72%	gi|568921713|XP_006501024.1
☐	complement factor I precursor [Mus musculus]	40.5	40.5	90%	0.022	72%	gi|110347406|NP_031712.2
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	40.5	40.5	95%	0.022	74%	gi|560925633|XP_006188998.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	40.5	40.5	95%	0.022	74%	gi|560979761|XP_006212132.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	39.7	39.7	90%	0.040	72%	gi|533186455|XP_005406244.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	38.8	38.8	95%	0.075	68%	gi|511847748|XP_004748251.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	38.8	38.8	95%	0.075	68%	gi|511991360|XP_004813365.1
☐	PREDICTED: complement factor I isoform X2 [Myotis brandtii]	38.8	38.8	100%	0.075	65%	gi|554556058|XP_005872468.1

Alignments

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PREDICTED: complement factor I-like, partial [Gorilla gorilla gorilla]

Sequence ID: gi|426345243|ref|XP_004040330.1| **Length:** 309 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 99 to 118 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	6e-10	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1     KFLNDGTCTAEGKFSVSLKH  20
             KFLN+GTCTAEGKFSVSLKH
Sbjct  99    KFLNNGTCTAEGKFSVSLKH  118
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|1335055|emb|CAA68417.1| **Length:** 321 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 81 to 100 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	7e-10	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1   KFLNDGTCTAEGKFSVSLKH  20
           KFLN+GTCTAEGKFSVSLKH
Sbjct  81  KFLNNGTCTAEGKFSVSLKH  100
```

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CFI protein [Homo sapiens]

Sequence ID: gi|18089117|gb|AAH20718.1| **Length:** 377 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 99 to 118 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	7e-10	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KFLNDGTCTAEGKFSVSLKH  20
            KFLN+GTCTAEGKFSVSLKH
Sbjct  99   KFLNNGTCTAEGKFSVSLKH  118
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

complement factor I, isoform CRA_a, partial [Homo sapiens]

Sequence ID: gi|119626655|gb|EAX06250.1| **Length:** 378 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 99 to 118 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	7e-10	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KFLNDGTCTAEGKFSVSLKH  20
            KFLN+GTCTAEGKFSVSLKH
Sbjct  99   KFLNNGTCTAEGKFSVSLKH  118
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: complement factor I isoform X6 [Pan troglodytes]

Sequence ID: gi|694908492|ref|XP_009446407.1| **Length:** 516 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 99 to 118 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	7e-10	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KFLNDGTCTAEGKFSVSLKH  20
            KFLN+GTCTAEGKFSVSLKH
Sbjct  99   KFLNNGTCTAEGKFSVSLKH  118
```

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CFI_KFLNNGTCTAEGKF_NonMod

RID	B93R6MBC01R (Expires on 01-14 10:20 am)
Query ID	lcl|301892
Description	None
Molecule type	amino acid
Query Length	14

Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

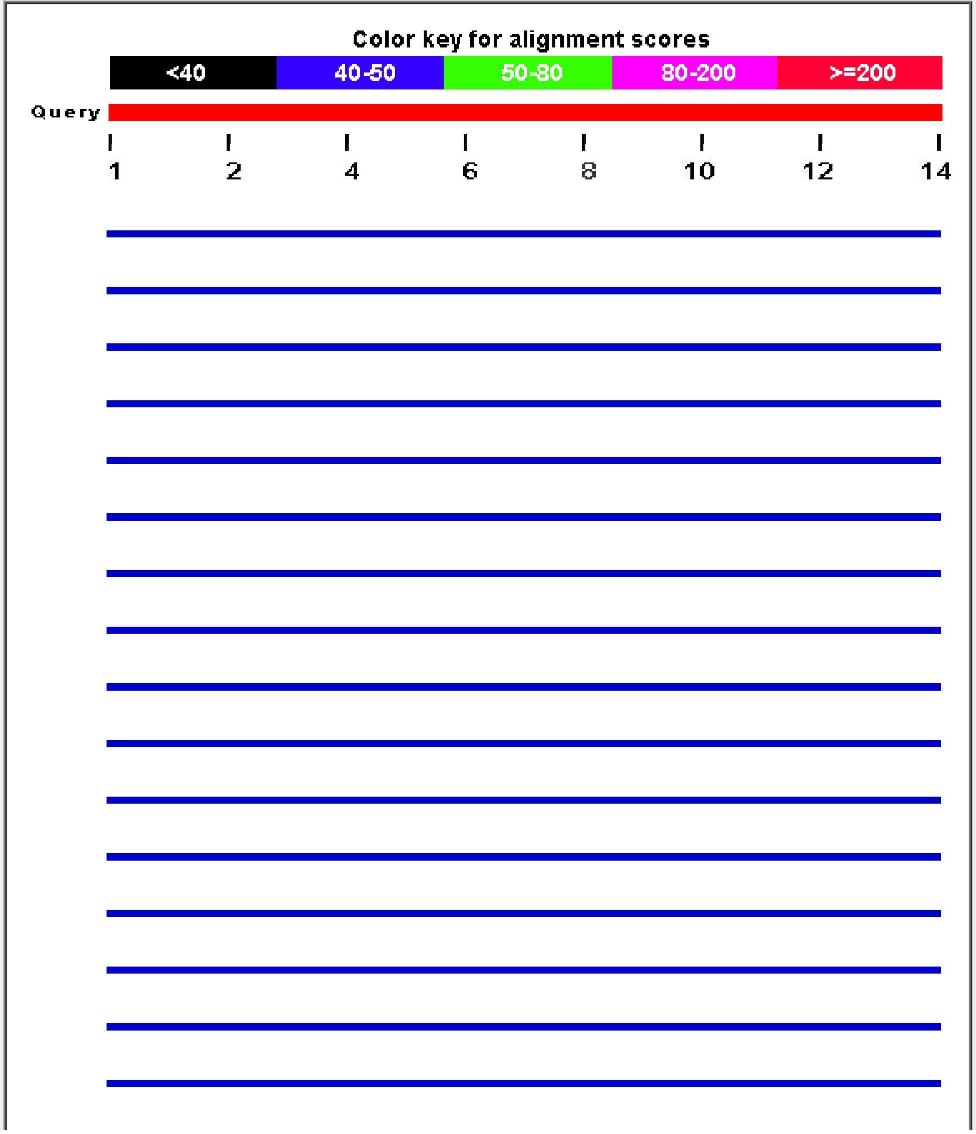
Graphic Summary

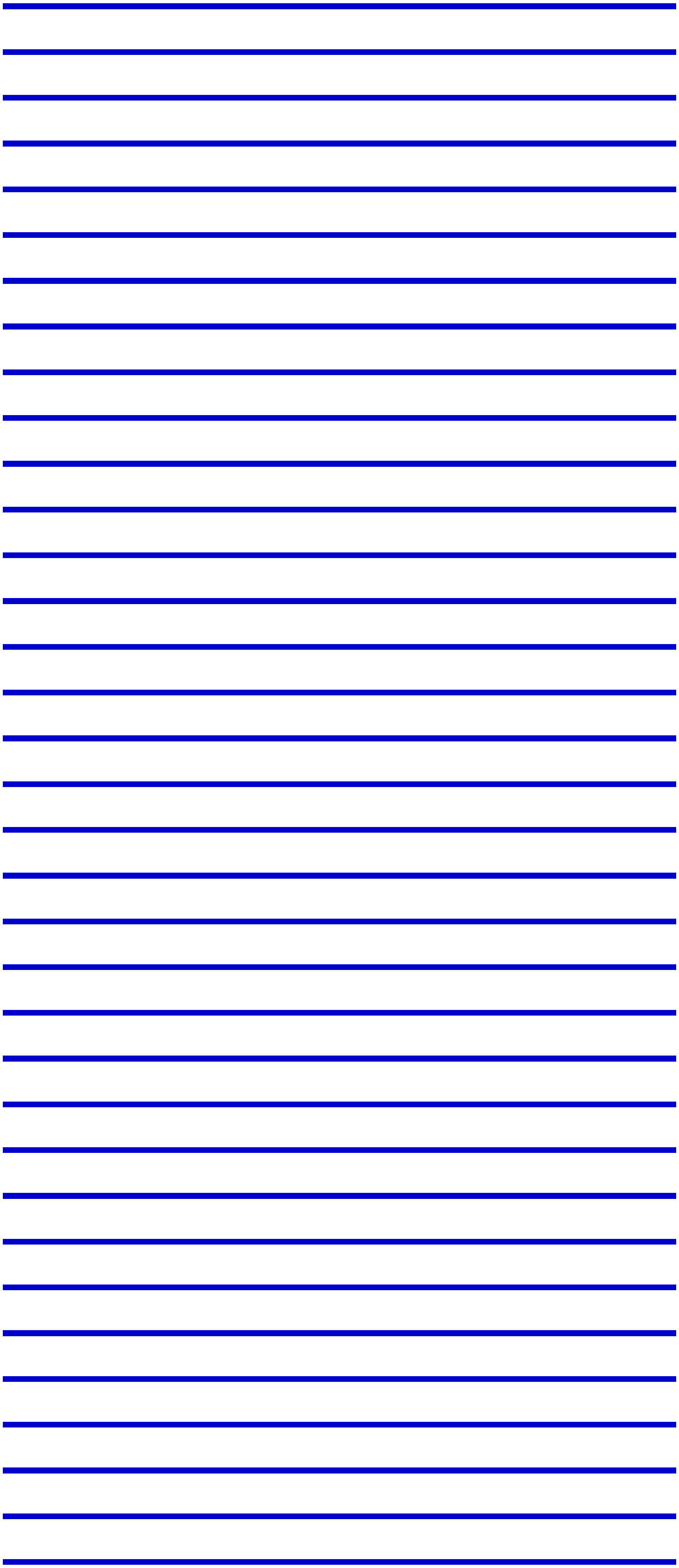
Show Conserved Domains

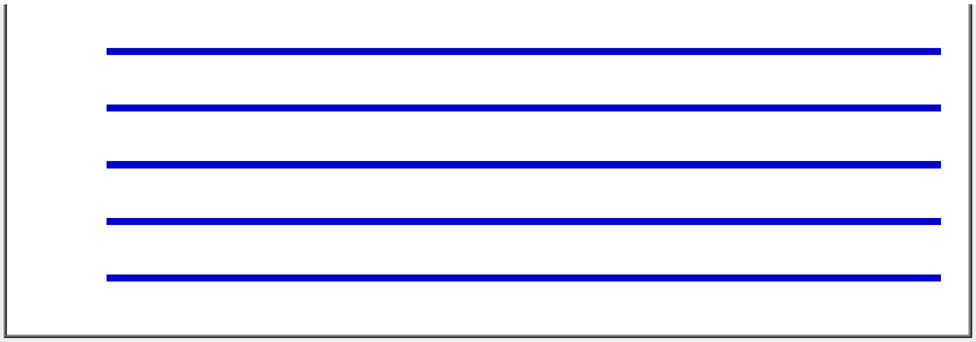
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: complement factor I-like [Gorilla gorilla gorilla]	47.7	47.7	100%	4e-05	100%	gi|426345243|XP_004040330.1
☐	unnamed protein product [Homo sapiens]	47.7	47.7	100%	4e-05	100%	gi|1335055|CAA68417.1
☐	CFI protein [Homo sapiens]	47.7	47.7	100%	4e-05	100%	gi|18089117|AAH20718.1
☐	complement factor I, isoform CRA_a [Homo sapiens]	47.7	47.7	100%	4e-05	100%	gi|119626655|EAX06250.1
☐	PREDICTED: complement factor I isoform X6 [Pan troglodytes]	47.7	47.7	100%	5e-05	100%	gi|694908492|XP_009446407.1
☐	PREDICTED: complement factor I isoform X6 [Pan paniscus]	47.7	47.7	100%	5e-05	100%	gi|675793799|XP_008953634.1
☐	PREDICTED: complement factor I isoform X5 [Pan troglodytes]	47.7	47.7	100%	5e-05	100%	gi|694908490|XP_009446406.1
☐	PREDICTED: complement factor I isoform X5 [Pan paniscus]	47.7	47.7	100%	5e-05	100%	gi|675793797|XP_008953633.1
☐	PREDICTED: complement factor I isoform X4 [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|578809103|XP_006714273.1
☐	Chain A, Human Complement Factor I [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|339961198|2XRC_A
☐	PREDICTED: complement factor I isoform X4 [Pan troglodytes]	47.7	47.7	100%	5e-05	100%	gi|694908488|XP_009446405.1
☐	PREDICTED: complement factor I isoform X4 [Pan paniscus]	47.7	47.7	100%	5e-05	100%	gi|675793795|XP_008953632.1
☐	PREDICTED: complement factor I isoform X2 [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|530377647|XP_005263033.1
☐	PREDICTED: complement factor I isoform X2 [Saimiri boliviensis bo	47.7	47.7	100%	5e-05	100%	gi|725571753|XP_010338379.1
☐	PREDICTED: complement factor I [Callithrix jacchus]	47.7	47.7	100%	5e-05	100%	gi|675648222|XP_002745538.3
☐	PREDICTED: complement factor I [Nomascus leucogenys]	47.7	47.7	100%	5e-05	100%	gi|332240463|XP_003269405.1
☐	prepro-C3b/C4B inactivator [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|182607|AAA52455.1
☐	complement factor I preproprotein [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|119392081|NP_000195.2
☐	complement factor I precursor [Pongo abelii]	47.7	47.7	100%	5e-05	100%	gi|197098986|NP_001127624.1
☐	PREDICTED: complement factor I isoform X3 [Pan paniscus]	47.7	47.7	100%	5e-05	100%	gi|397519838|XP_003830060.1
☐	RecName: Full=Complement factor I; AltName: Full=C3B/C4B inact	47.7	47.7	100%	5e-05	100%	gi|317373341|P05156.2
☐	unnamed protein product [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|158254682|BAF83314.1
☐	PREDICTED: complement factor I isoform X3 [Pan troglodytes]	47.7	47.7	100%	5e-05	100%	gi|114595644|XP_526653.2
☐	PREDICTED: complement factor I [Callithrix jacchus]	47.7	47.7	100%	5e-05	100%	gi|675752511|XP_008984405.1
☐	PREDICTED: complement factor I isoform X2 [Nannospalax galili]	47.7	47.7	100%	5e-05	100%	gi|674034950|XP_008841698.1
☐	PREDICTED: complement factor I isoform X2 [Pan troglodytes]	47.7	47.7	100%	5e-05	100%	gi|694908485|XP_009446404.1
☐	PREDICTED: complement factor I isoform X2 [Pan paniscus]	47.7	47.7	100%	5e-05	100%	gi|675793792|XP_008953631.1
☐	PREDICTED: complement factor I isoform X1 [Nannospalax galili]	47.7	47.7	100%	5e-05	100%	gi|674034948|XP_008841690.1
☐							

	PREDICTED: complement factor I isoform X3 [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|578809101|XP_006714272.1
☐	unnamed protein product [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|194387702|BAG61264.1
☐	PREDICTED: complement factor I isoform X1 [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|530377645|XP_005263032.1
☐	PREDICTED: complement factor I isoform X1 [Pan paniscus]	47.7	47.7	100%	5e-05	100%	gi|397519840|XP_003830061.1
☐	PREDICTED: complement factor I isoform X1 [Pan troglodytes]	47.7	47.7	100%	5e-05	100%	gi|332820084|XP_003310493.1
☐	PREDICTED: complement factor I isoform X1 [Saimiri boliviensis bo	47.7	47.7	100%	5e-05	100%	gi|725571751|XP_010338378.1
☐	PREDICTED: complement factor I isoform X2 [Equus przewalskii]	43.9	43.9	100%	8e-04	93%	gi|664769275|XP_008542181.1
☐	PREDICTED: complement factor I isoform X1 [Equus przewalskii]	43.9	43.9	100%	9e-04	93%	gi|664769273|XP_008542180.1
☐	PREDICTED: complement factor I isoform X2 [Equus caballus]	43.9	43.9	100%	9e-04	93%	gi|545210264|XP_005607952.1
☐	PREDICTED: complement factor I isoform X1 [Equus caballus]	43.9	43.9	100%	9e-04	93%	gi|545210262|XP_005607951.1
☐	PREDICTED: complement factor I isoform X5 [Canis lupus familiari	43.5	43.5	100%	0.001	93%	gi|545552244|XP_005639326.1
☐	PREDICTED: complement factor I isoformX3 [Canis lupus familiaris	43.5	43.5	100%	0.001	93%	gi|74002140|XP_863506.1
☐	PREDICTED: complement factor I isoform X4 [Canis lupus familiari	43.5	43.5	100%	0.001	93%	gi|545552242|XP_005639325.1
☐	PREDICTED: complement factor I [Otolemur garnettii]	43.1	43.1	100%	0.002	93%	gi|395851346|XP_003798222.1
☐	Complement factor I [Fukomys damarensis]	43.1	43.1	100%	0.002	93%	gi|676270629|KFO25832.1
☐	Complement factor I [Heterocephalus glaber]	43.1	43.1	100%	0.002	93%	gi|351696416|EHA99334.1
☐	PREDICTED: complement factor I isoform X2 [Fukomys damarensi	43.1	43.1	100%	0.002	93%	gi|731254237|XP_010639824.1
☐	PREDICTED: complement factor I isoform X2 [Heterocephalus glab	43.1	43.1	100%	0.002	93%	gi|512818622|XP_004878889.1
☐	PREDICTED: complement factor I isoform X1 [Fukomys damarensi	43.1	43.1	100%	0.002	93%	gi|731254235|XP_010639823.1
☐	PREDICTED: complement factor I isoform X1 [Heterocephalus glab	43.1	43.1	100%	0.002	93%	gi|512818618|XP_004878888.1
☐	PREDICTED: complement factor I [Rhinopithecus roxellana]	42.6	42.6	100%	0.002	93%	gi|724946291|XP_010387365.1
☐	PREDICTED: complement factor I [Papio anubis]	42.6	42.6	100%	0.002	93%	gi|685542561|XP_009205631.1
☐	PREDICTED: complement factor I isoform X2 [Ictidomys tridecemlir	42.2	42.2	100%	0.003	93%	gi|532088899|XP_005330149.1
☐	PREDICTED: complement factor I isoform X1 [Ictidomys tridecemlir	42.2	42.2	100%	0.003	93%	gi|532088897|XP_005330148.1
☐	PREDICTED: complement factor I isoform X2 [Cavia porcellus]	40.5	40.5	100%	0.012	86%	gi|514457647|XP_005002957.1
☐	PREDICTED: complement factor I isoform X1 [Cavia porcellus]	40.5	40.5	100%	0.012	86%	gi|514457649|XP_003468099.2
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Lept	40.1	40.1	100%	0.016	86%	gi|585149528|XP_006727262.1
☐	PREDICTED: complement factor I [Octodon degus]	40.1	40.1	100%	0.016	86%	gi|507626946|XP_004626817.1
☐	PREDICTED: complement factor I isoform X2 [Oryctolagus cuniculu	40.1	40.1	100%	0.016	86%	gi|655856777|XP_008265709.1
☐	PREDICTED: complement factor I [Ceratotherium simum simum]	40.1	40.1	100%	0.016	86%	gi|478504685|XP_004426641.1
☐	PREDICTED: complement factor I isoform X1 [Oryctolagus cuniculu	40.1	40.1	100%	0.016	86%	gi|655856775|XP_002717177.2
☐	PREDICTED: complement factor I [Ochotona princeps]	39.7	39.7	100%	0.023	86%	gi|504169976|XP_004594584.1
☐	PREDICTED: complement factor I [Loxodonta africana]	39.7	39.7	100%	0.023	86%	gi|731479219|XP_010588889.1
☐	PREDICTED: complement factor I isoform X6 [Panthera tigris altaic	39.2	39.2	100%	0.031	86%	gi|591346160|XP_007098330.1
☐	PREDICTED: complement factor I isoform X2 [Chlorocebus sabaeu	39.2	39.2	100%	0.031	86%	gi|635044269|XP_007997719.1
☐	PREDICTED: complement factor I isoform X1 [Chlorocebus sabaeu	39.2	39.2	100%	0.031	86%	gi|635044267|XP_007997718.1
☐	PREDICTED: complement factor I [Orycteropus afer afer]	39.2	39.2	100%	0.031	86%	gi|634848033|XP_007938975.1
☐	PREDICTED: complement factor I isoform X5 [Panthera tigris altaic	39.2	39.2	100%	0.031	86%	gi|591346158|XP_007098329.1
☐	PREDICTED: complement factor I isoform X4 [Panthera tigris altaic	39.2	39.2	100%	0.031	86%	gi|591346156|XP_007098328.1
☐	PREDICTED: complement factor I isoform X2 [Panthera tigris altaic	39.2	39.2	100%	0.031	86%	gi|591346152|XP_007098326.1
☐	PREDICTED: complement factor I isoform X1 [Panthera tigris altaic	39.2	39.2	100%	0.031	86%	gi|591346150|XP_007098325.1
☐	PREDICTED: complement factor I-like [Macaca mulatta]	38.8	38.8	100%	0.042	86%	gi|297293220|XP_001087512.2
☐	uncharacterized protein LOC101866929 precursor [Macaca fascicul	38.8	38.8	100%	0.043	86%	gi|548961885|NP_001271714.1
☐	PREDICTED: complement factor I [Tarsius syrichta]	38.8	38.8	100%	0.043	86%	gi|640813983|XP_008063707.1
☐	hypothetical protein EGK_16010 [Macaca mulatta]	38.8	38.8	100%	0.043	86%	gi|355687535|EHH26119.1

☐	complement factor I-like protein [Cricetulus griseus]	38.0	38.0	100%	0.082	86%	gi|537261801|ERE90152.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	38.0	38.0	100%	0.082	86%	gi|625241505|XP_007611983.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	38.0	38.0	100%	0.082	86%	gi|625222421|XP_007651009.1
☐	complement factor I precursor [Rattus norvegicus]	37.1	37.1	100%	0.16	86%	gi|13162353|NP_077071.1
☐	PREDICTED: complement factor I isoform X1 [Rattus norvegicus]	37.1	37.1	100%	0.16	86%	gi|672044321|XP_008759748.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Odol	36.7	36.7	100%	0.21	79%	gi|472383864|XP_004411307.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Felis	36.3	36.3	100%	0.29	79%	gi|586984171|XP_006930977.1
☐	PREDICTED: complement factor I [Trichechus manatus latirostris]	35.8	35.8	100%	0.41	79%	gi|471391575|XP_004380312.1
☐	PREDICTED: complement factor I isoform X4 [Mus musculus]	34.6	34.6	100%	1.0	79%	gi|568921717|XP_006501026.1
☐	PREDICTED: complement factor I isoform X3 [Mus musculus]	34.6	34.6	100%	1.0	79%	gi|568921715|XP_006501025.1
☐	PREDICTED: complement factor I isoform X2 [Mus musculus]	34.6	34.6	100%	1.0	79%	gi|568921713|XP_006501024.1
☐	complement factor I precursor [Mus musculus]	34.6	34.6	100%	1.0	79%	gi|110347406|NP_031712.2
☐	PREDICTED: complement factor I [Mesocricetus auratus]	34.1	34.1	100%	1.4	79%	gi|524965961|XP_005082885.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	33.7	33.7	100%	1.9	71%	gi|511847748|XP_004748251.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	33.7	33.7	100%	2.0	71%	gi|511991360|XP_004813365.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Chin	33.7	33.7	100%	2.0	79%	gi|533186455|XP_005406244.1
☐	PREDICTED: complement factor I [Chrysochloris asiatica]	33.3	33.3	100%	2.7	79%	gi|586477731|XP_006869402.1
☐	PREDICTED: complement factor I [Sarcophilus harrisii]	32.9	32.9	100%	3.6	71%	gi|395542057|XP_003772951.1
☐	PREDICTED: complement factor I [Peromyscus maniculatus bairdii	32.5	32.5	100%	5.0	79%	gi|589914217|XP_006970447.1
☐	PREDICTED: complement factor I [Jaculus jaculus]	31.6	31.6	100%	9.3	64%	gi|507549735|XP_004658680.1
☐	complement factor I [Mus musculus]	31.2	31.2	100%	13	71%	gi|1322034|AAB00438.1
☐	PREDICTED: complement factor I [Myotis davidii]	30.8	30.8	100%	17	71%	gi|584046382|XP_006767995.1
☐	PREDICTED: complement factor I [Eptesicus fuscus]	30.8	30.8	100%	17	71%	gi|641717977|XP_008148531.1
☐	molecular chaperone DnaJ [Desulfovibrio putealis]	29.9	29.9	85%	31	83%	gi|652937116|WP_027190715.1
☐	hypothetical protein PI87_11065 [Ralstonia sp. A12]	29.9	29.9	71%	32	91%	gi|733381272|KHK56250.1
☐	PREDICTED: complement factor I isoform X4 [Monodelphis domes	29.5	29.5	57%	43	100%	gi|612030135|XP_007496055.1
☐	PREDICTED: complement factor I isoform X3 [Monodelphis domes	29.5	29.5	57%	43	100%	gi|612030133|XP_007496054.1

Alignments

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PREDICTED: complement factor I-like, partial [Gorilla gorilla gorilla]

Sequence ID: gi|426345243|ref|XP_004040330.1| **Length:** 309 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 99 to 112 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	4e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KFLNNGTCTAEGKF  14
            KFLNNGTCTAEGKF
Sbjct  99   KFLNNGTCTAEGKF  112
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|1335055|emb|CAA68417.1| **Length:** 321 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 81 to 94 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	4e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1   KFLNNGTCTAEGKF  14
```

```
             KFLNNGTCTAEGKF
Sbjct  81  KFLNNGTCTAEGKF  94
```

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CFI protein [Homo sapiens]

Sequence ID: gi|18089117|gb|AAH20718.1| **Length:** 377 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 99 to 112 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	4e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KFLNNGTCTAEGKF  14
            KFLNNGTCTAEGKF
Sbjct  99   KFLNNGTCTAEGKF  112
```

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complement factor I, isoform CRA_a, partial [Homo sapiens]

Sequence ID: gi|119626655|gb|EAX06250.1| **Length:** 378 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 99 to 112 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	4e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KFLNNGTCTAEGKF  14
            KFLNNGTCTAEGKF
Sbjct  99   KFLNNGTCTAEGKF  112
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: complement factor I isoform X6 [Pan troglodytes]

Sequence ID: gi|694908492|ref|XP_009446407.1| **Length:** 516 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 99 to 112 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	5e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KFLNNGTCTAEGKF  14
            KFLNNGTCTAEGKF
Sbjct  99   KFLNNGTCTAEGKF  112
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - B93Y75X901R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download

How to read this page Blast report description

CFI_KFLNNGTCTAEGKFSVSLKH_NonMod

RID B93Y75X901R (Expires on 01-14 10:23 am)

Query ID	lcl|26369	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	20		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

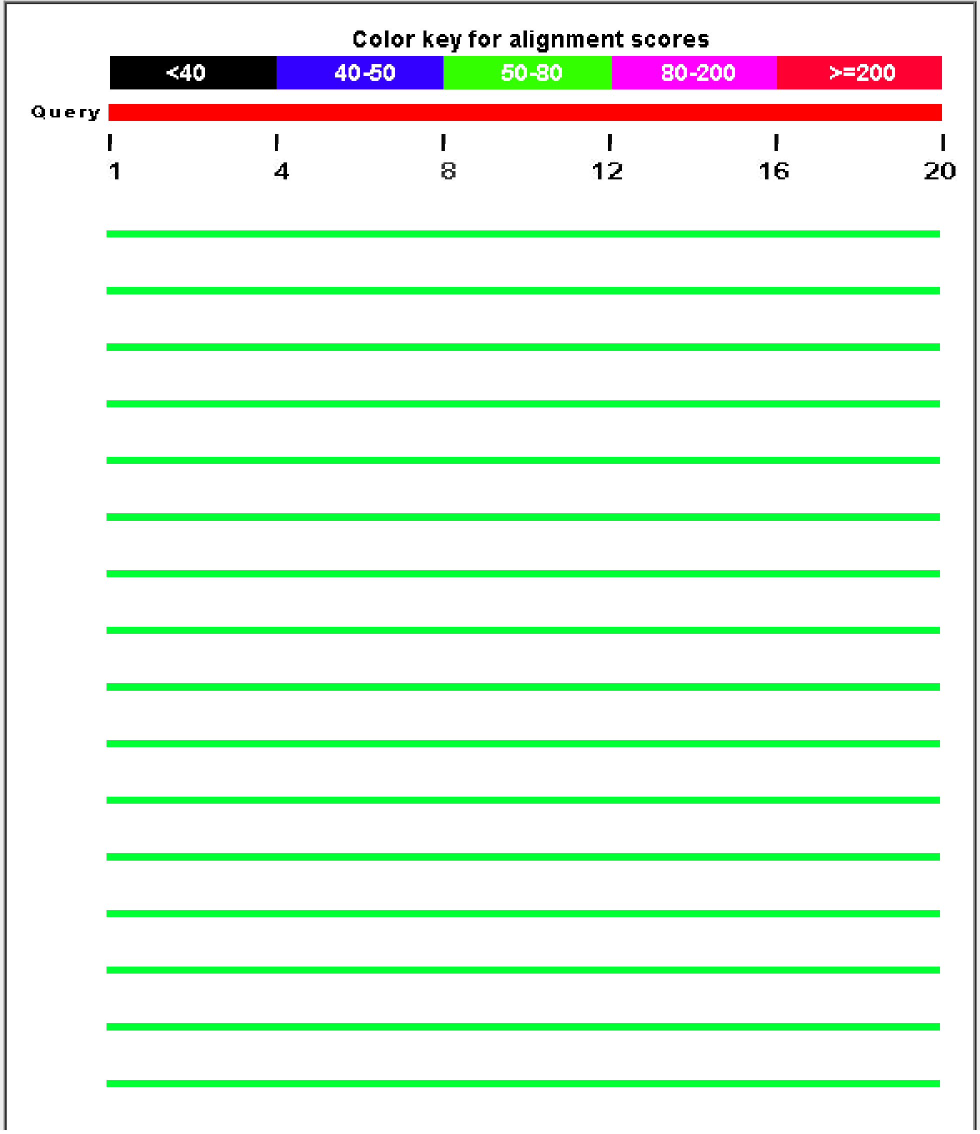
Graphic Summary

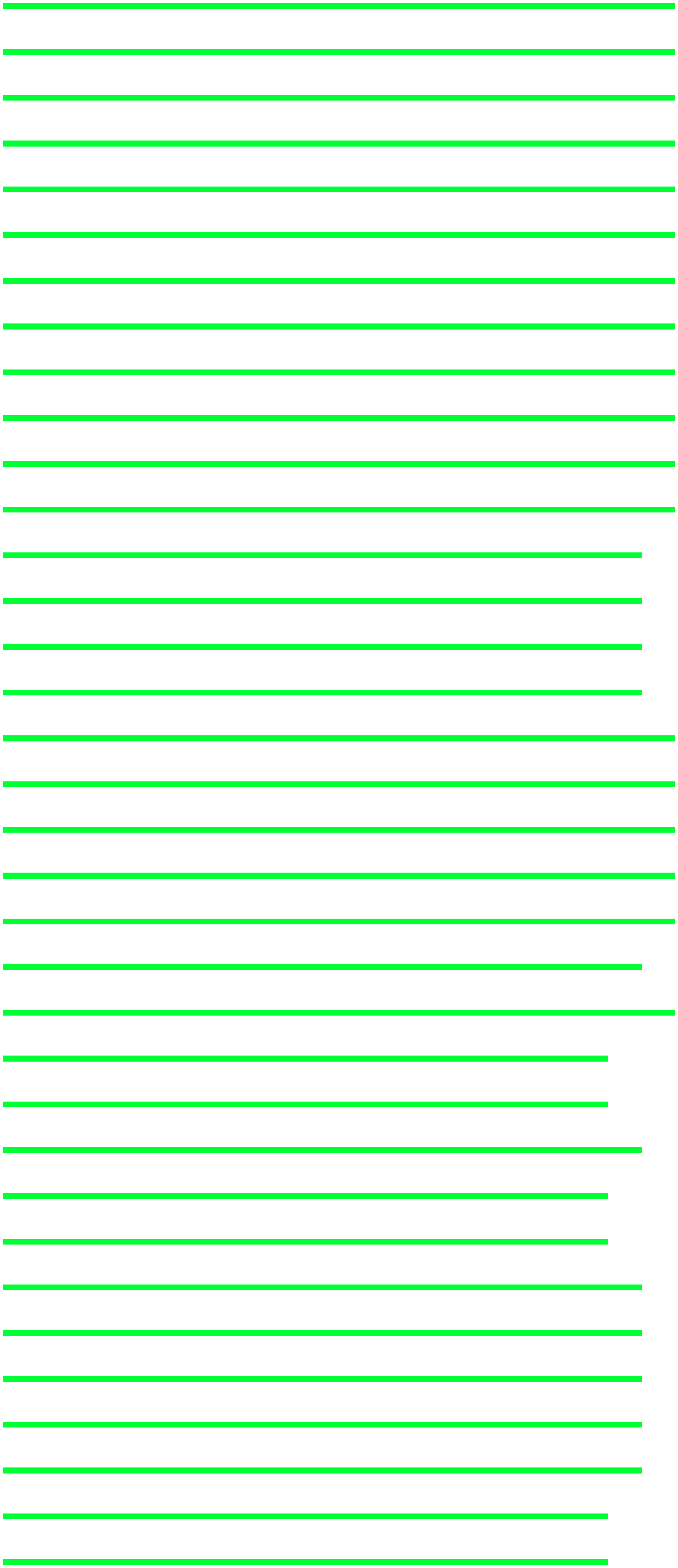
Show Conserved Domains

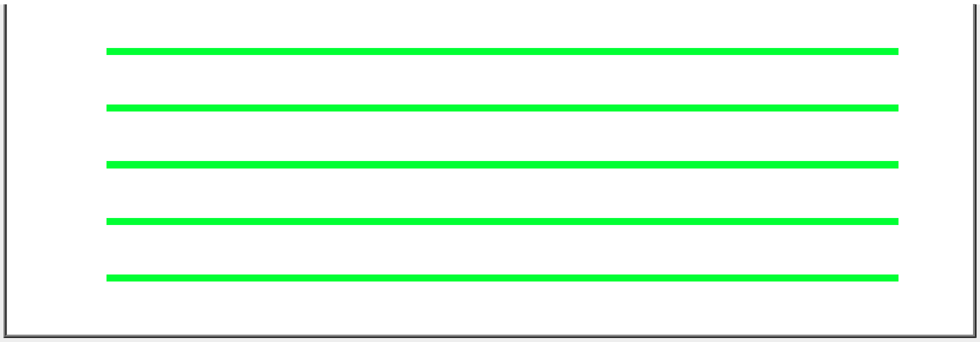
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: complement factor I-like [Gorilla gorilla gorilla]	65.5	65.5	100%	8e-11	100%	gi|426345243|XP_004040330.1
☐	unnamed protein product [Homo sapiens]	65.5	65.5	100%	8e-11	100%	gi|1335055|CAA68417.1
☐	CFI protein [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|18089117|AAH20718.1
☐	complement factor I, isoform CRA_a [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|119626655|EAX06250.1
☐	PREDICTED: complement factor I isoform X6 [Pan troglodytes]	65.5	65.5	100%	9e-11	100%	gi|694908492|XP_009446407.1
☐	PREDICTED: complement factor I isoform X6 [Pan paniscus]	65.5	65.5	100%	9e-11	100%	gi|675793799|XP_008953634.1
☐	PREDICTED: complement factor I isoform X5 [Pan troglodytes]	65.5	65.5	100%	9e-11	100%	gi|694908490|XP_009446406.1
☐	PREDICTED: complement factor I isoform X5 [Pan paniscus]	65.5	65.5	100%	9e-11	100%	gi|675793797|XP_008953633.1
☐	PREDICTED: complement factor I isoform X4 [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|578809103|XP_006714273.1
☐	Chain A, Human Complement Factor I [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|339961198|2XRC_A
☐	PREDICTED: complement factor I isoform X4 [Pan troglodytes]	65.5	65.5	100%	9e-11	100%	gi|694908488|XP_009446405.1
☐	PREDICTED: complement factor I isoform X4 [Pan paniscus]	65.5	65.5	100%	9e-11	100%	gi|675793795|XP_008953632.1
☐	PREDICTED: complement factor I isoform X2 [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|530377647|XP_005263033.1
☐	PREDICTED: complement factor I [Nomascus leucogenys]	65.5	65.5	100%	9e-11	100%	gi|332240463|XP_003269405.1
☐	prepro-C3b/C4B inactivator [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|182607|AAA52455.1
☐	complement factor I preproprotein [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|119392081|NP_000195.2
☐	complement factor I precursor [Pongo abelii]	65.5	65.5	100%	9e-11	100%	gi|197098986|NP_001127624.1
☐	PREDICTED: complement factor I isoform X3 [Pan paniscus]	65.5	65.5	100%	9e-11	100%	gi|397519838|XP_003830060.1
☐	RecName: Full=Complement factor I; AltName: Full=C3B/C4B inact	65.5	65.5	100%	9e-11	100%	gi|317373341|P05156.2
☐	unnamed protein product [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|158254682|BAF83314.1
☐	PREDICTED: complement factor I isoform X3 [Pan troglodytes]	65.5	65.5	100%	9e-11	100%	gi|114595644|XP_526653.2
☐	PREDICTED: complement factor I isoform X2 [Pan troglodytes]	65.5	65.5	100%	9e-11	100%	gi|694908485|XP_009446404.1
☐	PREDICTED: complement factor I isoform X2 [Pan paniscus]	65.5	65.5	100%	9e-11	100%	gi|675793792|XP_008953631.1
☐	PREDICTED: complement factor I isoform X3 [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|578809101|XP_006714272.1
☐	unnamed protein product [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|194387702|BAG61264.1
☐	PREDICTED: complement factor I isoform X1 [Homo sapiens]	65.5	65.5	100%	9e-11	100%	gi|530377645|XP_005263032.1
☐	PREDICTED: complement factor I isoform X1 [Pan paniscus]	65.5	65.5	100%	9e-11	100%	gi|397519840|XP_003830061.1
☐	PREDICTED: complement factor I isoform X1 [Pan troglodytes]	65.5	65.5	100%	9e-11	100%	gi|332820084|XP_003310493.1
☐							

	PREDICTED: complement factor I isoform X2 [Saimiri boliviensis bo	61.7	61.7	95%	2e-09	100%	gi|725571753|XP_010338379.1
☐	PREDICTED: complement factor I [Callithrix jacchus]	61.7	61.7	95%	2e-09	100%	gi|675648222|XP_002745538.3
☐	PREDICTED: complement factor I [Callithrix jacchus]	61.7	61.7	95%	2e-09	100%	gi|675752511|XP_008984405.1
☐	PREDICTED: complement factor I isoform X1 [Saimiri boliviensis bo	61.7	61.7	95%	2e-09	100%	gi|725571751|XP_010338378.1
☐	PREDICTED: complement factor I [Papio anubis]	60.4	60.4	100%	5e-09	95%	gi|685542561|XP_009205631.1
☐	PREDICTED: complement factor I isoform X2 [Chlorocebus sabaeu	57.1	57.1	100%	7e-08	90%	gi|635044269|XP_007997719.1
☐	PREDICTED: complement factor I isoform X1 [Chlorocebus sabaeu	57.1	57.1	100%	7e-08	90%	gi|635044267|XP_007997718.1
☐	PREDICTED: complement factor I-like [Macaca mulatta]	56.6	56.6	100%	9e-08	90%	gi|297293220|XP_001087512.2
☐	uncharacterized protein LOC101866929 precursor [Macaca fascicul	56.6	56.6	100%	1e-07	90%	gi|548961885|NP_001271714.1
☐	PREDICTED: complement factor I [Rhinopithecus roxellana]	56.6	56.6	95%	1e-07	95%	gi|724946291|XP_010387365.1
☐	hypothetical protein EGK_16010 [Macaca mulatta]	56.6	56.6	100%	1e-07	90%	gi|355687535|EHH26119.1
☐	PREDICTED: complement factor I [Otolemur garnettii]	54.1	54.1	90%	7e-07	94%	gi|395851346|XP_003798222.1
☐	Complement factor I [Heterocephalus glaber]	54.1	54.1	90%	7e-07	94%	gi|351696416|EHA99334.1
☐	PREDICTED: complement factor I [Ceratotherium simum simum]	54.1	54.1	95%	7e-07	89%	gi|478504685|XP_004426641.1
☐	PREDICTED: complement factor I isoform X2 [Heterocephalus glab	54.1	54.1	90%	7e-07	94%	gi|512818622|XP_004878889.1
☐	PREDICTED: complement factor I isoform X1 [Heterocephalus glab	54.1	54.1	90%	7e-07	94%	gi|512818618|XP_004878888.1
☐	PREDICTED: complement factor I isoform X2 [Equus przewalskii]	53.7	53.7	95%	9e-07	89%	gi|664769275|XP_008542181.1
☐	PREDICTED: complement factor I isoform X1 [Equus przewalskii]	53.7	53.7	95%	9e-07	89%	gi|664769273|XP_008542180.1
☐	PREDICTED: complement factor I isoform X2 [Equus caballus]	53.7	53.7	95%	1e-06	89%	gi|545210264|XP_005607952.1
☐	PREDICTED: complement factor I isoform X1 [Equus caballus]	53.7	53.7	95%	1e-06	89%	gi|545210262|XP_005607951.1
☐	PREDICTED: complement factor I isoform X6 [Panthera tigris altaic	53.2	53.2	95%	1e-06	89%	gi|591346160|XP_007098330.1
☐	PREDICTED: complement factor I isoform X2 [Nannospalax galili]	53.2	53.2	90%	1e-06	94%	gi|674034950|XP_008841698.1
☐	PREDICTED: complement factor I isoform X1 [Nannospalax galili]	53.2	53.2	90%	1e-06	94%	gi|674034948|XP_008841690.1
☐	PREDICTED: complement factor I isoform X5 [Panthera tigris altaic	53.2	53.2	95%	1e-06	89%	gi|591346158|XP_007098329.1
☐	PREDICTED: complement factor I isoform X4 [Panthera tigris altaic	53.2	53.2	95%	1e-06	89%	gi|591346156|XP_007098328.1
☐	PREDICTED: complement factor I isoform X2 [Panthera tigris altaic	53.2	53.2	95%	1e-06	89%	gi|591346152|XP_007098326.1
☐	PREDICTED: complement factor I isoform X1 [Panthera tigris altaic	53.2	53.2	95%	1e-06	89%	gi|591346150|XP_007098325.1
☐	PREDICTED: complement factor I [Tarsius syrichta]	52.8	52.8	95%	2e-06	89%	gi|640813983|XP_008063707.1
☐	PREDICTED: complement factor I isoform X5 [Canis lupus familiari	52.4	52.4	90%	3e-06	89%	gi|545552244|XP_005639326.1
☐	PREDICTED: complement factor I isoformX3 [Canis lupus familiaris	52.4	52.4	90%	3e-06	89%	gi|74002140|XP_863506.1
☐	PREDICTED: complement factor I isoform X4 [Canis lupus familiari	52.4	52.4	90%	3e-06	89%	gi|545552242|XP_005639325.1
☐	PREDICTED: complement factor I isoform X2 [Oryctolagus cuniculu	51.5	51.5	95%	5e-06	84%	gi|655856777|XP_008265709.1
☐	PREDICTED: complement factor I isoform X1 [Oryctolagus cuniculu	51.5	51.5	95%	5e-06	84%	gi|655856775|XP_002717177.2
☐	Complement factor I [Fukomys damarensis]	51.1	51.1	85%	7e-06	94%	gi|676270629|KFO25832.1
☐	PREDICTED: complement factor I isoform X2 [Ictidomys tridecemlir	51.1	51.1	90%	7e-06	89%	gi|532088899|XP_005330149.1
☐	PREDICTED: complement factor I isoform X1 [Ictidomys tridecemlir	51.1	51.1	90%	7e-06	89%	gi|532088897|XP_005330148.1
☐	PREDICTED: complement factor I isoform X2 [Fukomys damarensi	51.1	51.1	85%	7e-06	94%	gi|731254237|XP_010639824.1
☐	PREDICTED: complement factor I isoform X1 [Fukomys damarensi	51.1	51.1	85%	7e-06	94%	gi|731254235|XP_010639823.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Lept	50.7	50.7	95%	1e-05	84%	gi|585149528|XP_006727262.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Felis	50.3	50.3	95%	1e-05	84%	gi|586984171|XP_006930977.1
☐	PREDICTED: complement factor I [Octodon degus]	48.6	48.6	90%	5e-05	83%	gi|507626946|XP_004626817.1
☐	PREDICTED: complement factor I [Loxodonta africana]	48.6	48.6	90%	5e-05	83%	gi|731479219|XP_010588889.1
☐	PREDICTED: complement factor I [Orycteropus afer afer]	48.1	48.1	95%	7e-05	84%	gi|634848033|XP_007938975.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Odol	47.3	47.3	95%	1e-04	79%	gi|472383864|XP_004411307.1
☐	PREDICTED: complement factor I [Chrysochloris asiatica]	47.3	47.3	95%	1e-04	84%	gi|586477731|XP_006869402.1

☐	PREDICTED: complement factor I [Ochotona princeps]	46.4	46.4	90%	2e-04	83%	gi|504169976|XP_004594584.1
☐	complement factor I-like protein [Cricetulus griseus]	46.4	46.4	90%	2e-04	83%	gi|537261801|ERE90152.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	46.4	46.4	90%	2e-04	83%	gi|625241505|XP_007611983.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	46.4	46.4	90%	2e-04	83%	gi|625222421|XP_007651009.1
☐	complement factor I precursor [Rattus norvegicus]	45.6	45.6	90%	5e-04	83%	gi|13162353|NP_077071.1
☐	PREDICTED: complement factor I isoform X1 [Rattus norvegicus]	45.6	45.6	90%	5e-04	83%	gi|672044321|XP_008759748.1
☐	PREDICTED: complement factor I [Myotis davidii]	43.9	43.9	100%	0.002	70%	gi|584046382|XP_006767995.1
☐	PREDICTED: complement factor I [Trichechus manatus latirostris]	43.9	43.9	85%	0.002	82%	gi|471391575|XP_004380312.1
☐	PREDICTED: complement factor I isoform X2 [Cavia porcellus]	43.5	43.5	90%	0.002	78%	gi|514457647|XP_005002957.1
☐	PREDICTED: complement factor I isoform X1 [Cavia porcellus]	43.5	43.5	90%	0.002	78%	gi|514457649|XP_003468099.2
☐	PREDICTED: complement factor I isoform X4 [Mus musculus]	43.1	43.1	90%	0.003	78%	gi|568921717|XP_006501026.1
☐	PREDICTED: complement factor I isoform X3 [Mus musculus]	43.1	43.1	90%	0.003	78%	gi|568921715|XP_006501025.1
☐	PREDICTED: complement factor I isoform X2 [Mus musculus]	43.1	43.1	90%	0.003	78%	gi|568921713|XP_006501024.1
☐	complement factor I precursor [Mus musculus]	43.1	43.1	90%	0.003	78%	gi|110347406|NP_031712.2
☐	PREDICTED: complement factor I [Mesocricetus auratus]	42.6	42.6	90%	0.004	78%	gi|524965961|XP_005082885.1
☐	complement factor I precursor [Camelus ferus]	42.2	42.2	95%	0.006	74%	gi|528758403|EPY78062.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Chin	42.2	42.2	90%	0.006	78%	gi|533186455|XP_005406244.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Cam	42.2	42.2	95%	0.006	74%	gi|560925633|XP_006188998.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Vicu	42.2	42.2	95%	0.006	74%	gi|560979761|XP_006212132.1
☐	PREDICTED: complement factor I [Peromyscus maniculatus bairdii	40.9	40.9	90%	0.015	78%	gi|589914217|XP_006970447.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	40.5	40.5	95%	0.020	68%	gi|511847748|XP_004748251.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	40.5	40.5	95%	0.020	68%	gi|511991360|XP_004813365.1
☐	PREDICTED: complement factor I isoform X2 [Myotis brandtii]	40.5	40.5	100%	0.021	65%	gi|554556058|XP_005872468.1
☐	PREDICTED: complement factor I [Pantholops hodgsonii]	40.5	40.5	90%	0.021	72%	gi|556750321|XP_005970578.1
☐	PREDICTED: complement factor I isoform X2 [Capra hircus]	40.5	40.5	90%	0.021	72%	gi|548469406|XP_005681373.1
☐	PREDICTED: complement factor I isoform X1 [Capra hircus]	40.5	40.5	90%	0.021	72%	gi|548469399|XP_005681372.1
☐	PREDICTED: complement factor I [Ovis aries]	40.5	40.5	90%	0.021	72%	gi|426231287|XP_004009671.1

⊟ Alignments

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PREDICTED: complement factor I-like, partial [Gorilla gorilla gorilla]

Sequence ID: gi|426345243|ref|XP_004040330.1| **Length:** 309 **Number of Matches:** 1

Range 1: 99 to 118 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	8e-11	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KFLNNGTCTAEGKFSVSLKH  20
            KFLNNGTCTAEGKFSVSLKH
Sbjct  99   KFLNNGTCTAEGKFSVSLKH  118
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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unnamed protein product [Homo sapiens]

Sequence ID: gi|1335055|emb|CAA68417.1| **Length:** 321 **Number of Matches:** 1

Range 1: 81 to 100 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	8e-11	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1   KFLNNGTCTAEGKFSVSLKH  20
```

Related Information

Gene - associated gene details

```
           KFLNNGTCTAEGKFSVSLKH
Sbjct  81  KFLNNGTCTAEGKFSVSLKH  100
```

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CFI protein [Homo sapiens]

Sequence ID: gi|18089117|gb|AAH20718.1| **Length:** 377 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 99 to 118 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	9e-11	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KFLNNGTCTAEGKFSVSLKH  20
            KFLNNGTCTAEGKFSVSLKH
Sbjct  99   KFLNNGTCTAEGKFSVSLKH  118
```

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complement factor I, isoform CRA_a, partial [Homo sapiens]

Sequence ID: gi|119626655|gb|EAX06250.1| **Length:** 378 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 99 to 118 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	9e-11	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KFLNNGTCTAEGKFSVSLKH  20
            KFLNNGTCTAEGKFSVSLKH
Sbjct  99   KFLNNGTCTAEGKFSVSLKH  118
```

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PREDICTED: complement factor I isoform X6 [Pan troglodytes]

Sequence ID: gi|694908492|ref|XP_009446407.1| **Length:** 516 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 99 to 118 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	9e-11	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KFLNNGTCTAEGKFSVSLKH  20
            KFLNNGTCTAEGKFSVSLKH
Sbjct  99   KFLNNGTCTAEGKFSVSLKH  118
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BTG7XKUN013

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | ▷Formatting options | ▷Download | How to read this page | Blast report description

CFI_KLISDCSKFYGNRF_Mod

RID BTG7XKUN013 (Expires on 01-20 15:31 pm)

Query ID lcl|97559
Description None
Molecule type amino acid
Query Length 14

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

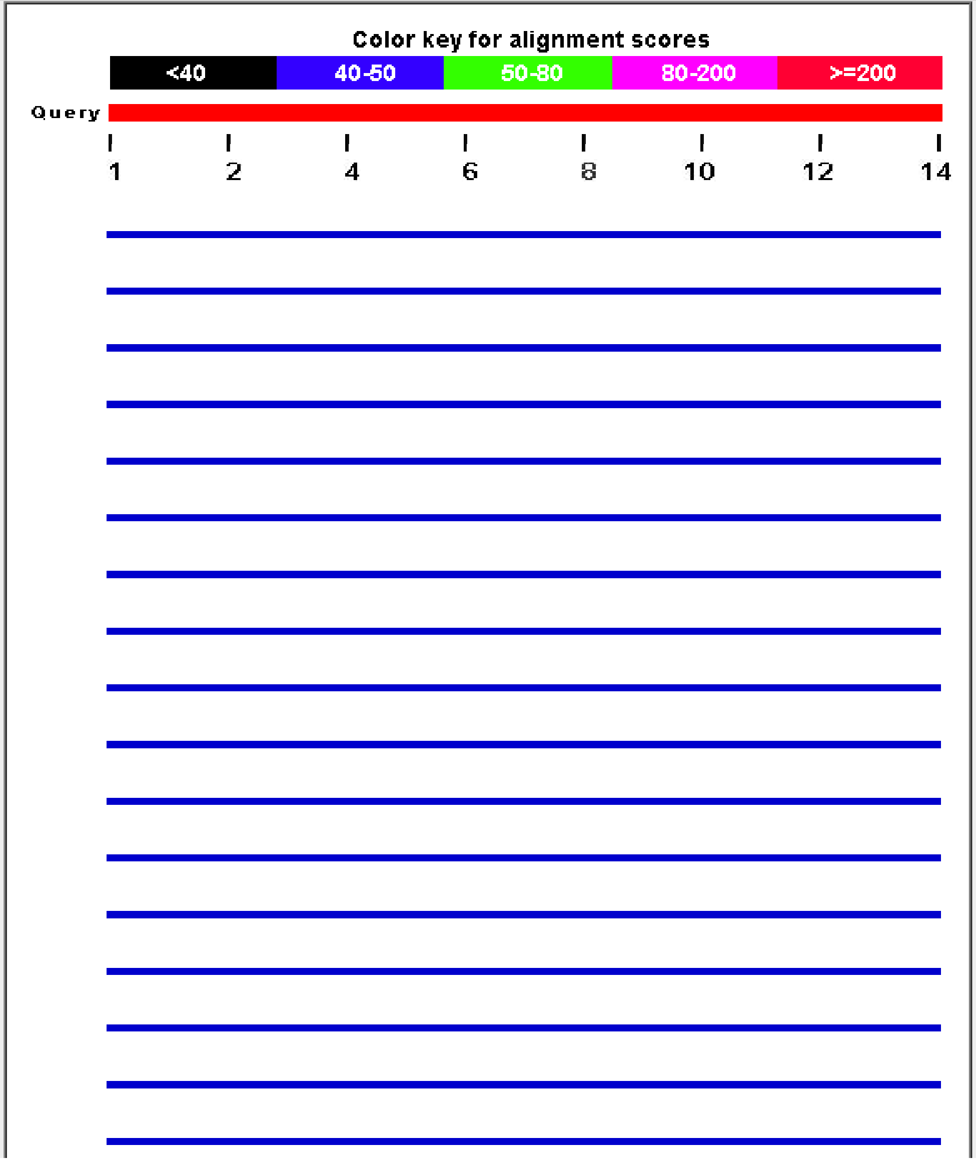
⊟ Graphic Summary

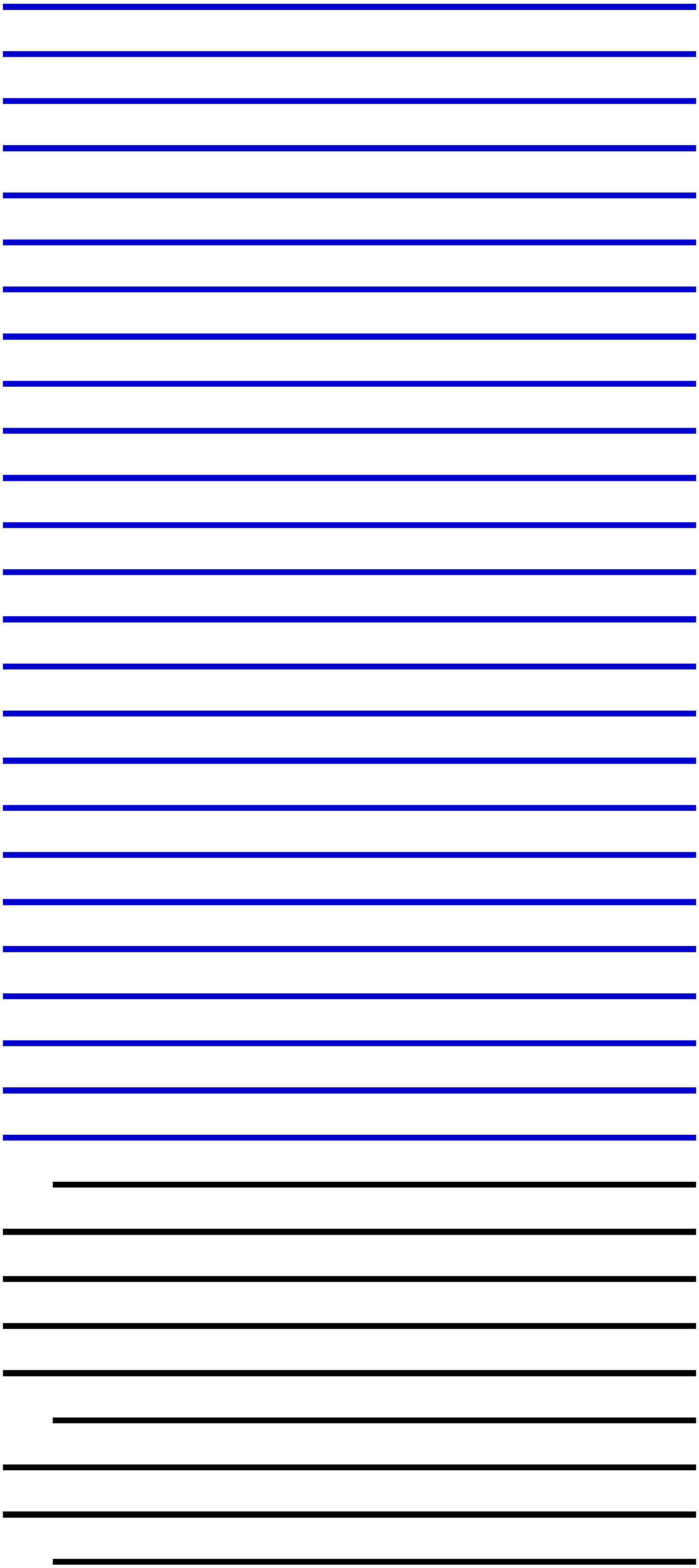
⊟ Show Conserved Domains

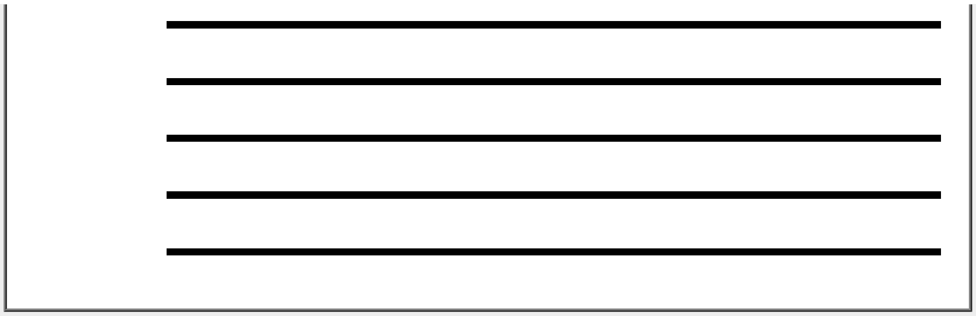
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	complement factor I light chain [Homo sapiens]	46.9	46.9	100%	8e-05	93%	gi|224798|1202205A
☐	PREDICTED: complement factor I-like [Macaca mulatta]	46.9	46.9	100%	8e-05	93%	gi|297293864|XP_002804336.1
☐	unnamed protein product [Homo sapiens]	46.9	46.9	100%	8e-05	93%	gi|1335056|CAA68418.1
☐	PREDICTED: complement factor I-like [Gorilla gorilla gorilla]	46.9	46.9	100%	9e-05	93%	gi|426345227|XP_004040322.1
☐	PREDICTED: complement factor I-like [Macaca fascicularis]	46.9	46.9	100%	9e-05	93%	gi|544524397|XP_005595214.1
☐	PREDICTED: complement factor I isoform X3 [Chlorocebus sal	46.9	46.9	100%	9e-05	93%	gi|635044271|XP_007997720.1
☐	complement factor I [Pongo abelii]	46.9	46.9	100%	9e-05	93%	gi|207080120|NP_001128776.1
☐	PREDICTED: complement factor I isoform X6 [Pan troglodytes]	46.9	46.9	100%	9e-05	93%	gi|694908492|XP_009446407.1
☐	PREDICTED: complement factor I isoform X6 [Pan paniscus]	46.9	46.9	100%	9e-05	93%	gi|675793799|XP_008953634.1
☐	uncharacterized protein LOC101866929 precursor [Macaca fas	46.9	46.9	100%	9e-05	93%	gi|548961885|NP_001271714.1
☐	PREDICTED: complement factor I isoform X5 [Pan troglodytes]	46.9	46.9	100%	9e-05	93%	gi|694908490|XP_009446406.1
☐	PREDICTED: complement factor I isoform X5 [Pan paniscus]	46.9	46.9	100%	9e-05	93%	gi|675793797|XP_008953633.1
☐	PREDICTED: complement factor I isoform X4 [Homo sapiens]	46.9	46.9	100%	9e-05	93%	gi|578809103|XP_006714273.1
☐	Chain A, Human Complement Factor I [Homo sapiens]	46.9	46.9	100%	9e-05	93%	gi|339961198|2XRC_A
☐	PREDICTED: complement factor I isoform X4 [Pan troglodytes]	46.9	46.9	100%	9e-05	93%	gi|694908488|XP_009446405.1
☐	PREDICTED: complement factor I isoform X4 [Pan paniscus]	46.9	46.9	100%	9e-05	93%	gi|675793795|XP_008953632.1
☐	PREDICTED: complement factor I isoform X2 [Chlorocebus sal	46.9	46.9	100%	9e-05	93%	gi|635044269|XP_007997719.1
☐	PREDICTED: complement factor I isoform X2 [Homo sapiens]	46.9	46.9	100%	9e-05	93%	gi|530377647|XP_005263033.1
☐	PREDICTED: complement factor I isoform X2 [Saimiri boliviens	46.9	46.9	100%	9e-05	93%	gi|725571753|XP_010338379.1
☐	PREDICTED: complement factor I [Callithrix jacchus]	46.9	46.9	100%	9e-05	93%	gi|675648222|XP_002745538.3
☐	PREDICTED: complement factor I [Nomascus leucogenys]	46.9	46.9	100%	9e-05	93%	gi|332240463|XP_003269405.1
☐	PREDICTED: complement factor I [Rhinopithecus roxellana]	46.9	46.9	100%	9e-05	93%	gi|724946291|XP_010387365.1
☐	PREDICTED: complement factor I isoform X1 [Chlorocebus sal	46.9	46.9	100%	9e-05	93%	gi|635044267|XP_007997718.1
☐	prepro-C3b/C4B inactivator [Homo sapiens]	46.9	46.9	100%	9e-05	93%	gi|182607|AAA52455.1
☐	complement factor I preproprotein [Homo sapiens]	46.9	46.9	100%	9e-05	93%	gi|119392081|NP_000195.2
☐	complement factor I precursor [Pongo abelii]	46.9	46.9	100%	9e-05	93%	gi|197098986|NP_001127624.1
☐	PREDICTED: complement factor I isoform X3 [Pan paniscus]	46.9	46.9	100%	9e-05	93%	gi|397519838|XP_003830060.1
☐	RecName: Full=Complement factor I; AltName: Full=C3B/C4B i	46.9	46.9	100%	9e-05	93%	gi|317373341|P05156.2
☐	unnamed protein product [Homo sapiens]	46.9	46.9	100%	9e-05	93%	gi|158254682|BAF83314.1

☐	PREDICTED: complement factor I isoform X3 [Pan troglodytes]	46.9	46.9	100%	9e-05	93%	gi|114595644|XP_526653.2
☐	PREDICTED: complement factor I [Callithrix jacchus]	46.9	46.9	100%	9e-05	93%	gi|675752511|XP_008984405.1
☐	PREDICTED: complement factor I isoform X2 [Pan troglodytes]	46.9	46.9	100%	9e-05	93%	gi|694908485|XP_009446404.1
☐	PREDICTED: complement factor I isoform X2 [Pan paniscus]	46.9	46.9	100%	9e-05	93%	gi|675793792|XP_008953631.1
☐	PREDICTED: complement factor I isoform X3 [Homo sapiens]	46.9	46.9	100%	9e-05	93%	gi|578809101|XP_006714272.1
☐	unnamed protein product [Homo sapiens]	46.9	46.9	100%	9e-05	93%	gi|194387702|BAG61264.1
☐	PREDICTED: complement factor I isoform X1 [Homo sapiens]	46.9	46.9	100%	9e-05	93%	gi|530377645|XP_005263032.1
☐	PREDICTED: complement factor I isoform X1 [Pan paniscus]	46.9	46.9	100%	9e-05	93%	gi|397519840|XP_003830061.1
☐	hypothetical protein EGK_16010 [Macaca mulatta]	46.9	46.9	100%	9e-05	93%	gi|355687535|EHH26119.1
☐	PREDICTED: complement factor I isoform X1 [Pan troglodytes]	46.9	46.9	100%	9e-05	93%	gi|332820084|XP_003310493.1
☐	PREDICTED: complement factor I [Papio anubis]	46.9	46.9	100%	9e-05	93%	gi|685542561|XP_009205631.1
☐	PREDICTED: complement factor I isoform X1 [Saimiri boliviens	46.9	46.9	100%	9e-05	93%	gi|725571751|XP_010338378.1
☐	PREDICTED: complement factor I isoform X1 [Pongo abelii]	43.5	43.5	100%	0.001	86%	gi|686716760|XP_009238531.1
☐	PREDICTED: complement factor I-like [Neolamprologus bricha	37.5	37.5	92%	0.12	77%	gi|584028791|XP_006808922.1
☐	PREDICTED: complement factor I isoform X4 [Monodelphis do	37.1	37.1	100%	0.16	71%	gi|612030135|XP_007496055.1
☐	PREDICTED: complement factor I isoform X3 [Monodelphis do	37.1	37.1	100%	0.16	71%	gi|612030133|XP_007496054.1
☐	PREDICTED: complement factor I isoform X2 [Monodelphis do	37.1	37.1	100%	0.16	71%	gi|612030131|XP_007496053.1
☐	PREDICTED: complement factor I isoform X1 [Monodelphis do	37.1	37.1	100%	0.16	71%	gi|612030129|XP_007496052.1
☐	PREDICTED: complement factor I [Sus scrofa]	37.1	37.1	92%	0.16	85%	gi|545846437|XP_005656603.1
☐	PREDICTED: complement factor I [Microtus ochrogaster]	37.1	37.1	100%	0.16	71%	gi|532029058|XP_005357485.1
☐	PREDICTED: complement factor I [Dasypus novemcinctus]	36.7	36.7	100%	0.22	71%	gi|488581726|XP_004476284.1
☐	PREDICTED: complement factor I isoform X2 [Oryctolagus cun	36.7	36.7	92%	0.23	77%	gi|655856777|XP_008265709.1
☐	PREDICTED: complement factor I isoform X1 [Oryctolagus cun	36.7	36.7	92%	0.23	77%	gi|655856775|XP_002717177.2
☐	PREDICTED: complement factor I-like [Galeopterus variegatus	35.8	35.8	92%	0.42	77%	gi|667268997|XP_008570201.1
☐	PREDICTED: complement factor I-like [Oreochromis niloticus]	35.8	35.8	92%	0.43	77%	gi|542244580|XP_005459189.1
☐	PREDICTED: complement factor I [Tarsius syrichta]	35.4	35.4	92%	0.58	77%	gi|640813983|XP_008063707.1
☐	PREDICTED: complement factor I [Otolemur garnettii]	35.0	35.0	92%	0.80	77%	gi|395851346|XP_003798222.1
☐	PREDICTED: complement factor I [Chrysochloris asiatica]	35.0	35.0	92%	0.80	69%	gi|586477731|XP_006869402.1
☐	PREDICTED: complement factor I [Sarcophilus harrisii]	34.1	34.1	92%	1.5	69%	gi|395542057|XP_003772951.1
☐	complement factor I precursor [Camelus ferus]	33.3	33.3	92%	2.8	69%	gi|528758403|EPY78062.1
☐	PREDICTED: complement factor I-like [Maylandia zebra]	33.3	33.3	92%	2.8	69%	gi|499048737|XP_004574910.1
☐	PREDICTED: complement factor I-like [Pundamilia nyererei]	33.3	33.3	92%	2.8	69%	gi|548538438|XP_005752638.1
☐	PREDICTED: complement factor I isoform X2 [Camelus drome	33.3	33.3	92%	2.8	69%	gi|744567503|XP_010979382.1
☐	PREDICTED: complement factor I isoform X2 [Camelus bactria	33.3	33.3	92%	2.8	69%	gi|743716645|XP_010951976.1
☐	PREDICTED: complement factor I-like [Haplochromis burtoni]	33.3	33.3	92%	2.8	69%	gi|554881320|XP_005950423.1
☐	PREDICTED: complement factor I isoform X1 [Camelus drome	33.3	33.3	92%	2.8	69%	gi|744567500|XP_010979381.1
☐	PREDICTED: complement factor I isoform X1 [Camelus bactria	33.3	33.3	92%	2.8	69%	gi|743716643|XP_010951975.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	33.3	33.3	92%	2.8	69%	gi|560925633|XP_006188998.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	33.3	33.3	92%	2.8	69%	gi|560979761|XP_006212132.1
☐	PREDICTED: complement factor I-like [Equus przewalskii]	32.9	32.9	92%	3.7	69%	gi|664780387|XP_008509513.1
☐	PREDICTED: complement factor I [Jaculus jaculus]	32.9	32.9	92%	3.8	69%	gi|507549735|XP_004658680.1
☐	PREDICTED: complement factor I isoform X2 [Equus caballus]	32.9	32.9	92%	3.9	69%	gi|545210264|XP_005607952.1
☐	PREDICTED: complement factor I isoform X1 [Equus caballus]	32.9	32.9	92%	3.9	69%	gi|545210262|XP_005607951.1
☐	PREDICTED: complement factor I [Trichechus manatus latirost	32.5	32.5	100%	5.3	64%	gi|471391575|XP_004380312.1
☐	PREDICTED: complement factor I [Ornithorhynchus anatinus]	31.6	31.6	92%	9.8	62%	gi|620978285|XP_007668373.1

☐	PREDICTED: complement factor I isoform X2 [Ictidomys tridece	31.6	31.6	92%	9.8	69%	gi|532088899|XP_005330149.1
☐	PREDICTED: complement factor I isoform X1 [Ictidomys tridece	31.6	31.6	92%	9.8	69%	gi|532088897|XP_005330148.1
☐	Complement factor I [Fukomys damarensis]	31.2	31.2	92%	13	69%	gi|676270629|KFO25832.1
☐	Complement factor I [Heterocephalus glaber]	31.2	31.2	92%	13	69%	gi|351696416|EHA99334.1
☐	complement factor I-like protein [Cricetulus griseus]	31.2	31.2	100%	13	64%	gi|537261801|ERE90152.1
☐	PREDICTED: complement factor I [Ceratotherium simum simur	31.2	31.2	92%	13	62%	gi|478504685|XP_004426641.1
☐	PREDICTED: complement factor I isoform X2 [Fukomys damar	31.2	31.2	92%	13	69%	gi|731254237|XP_010639824.1
☐	PREDICTED: complement factor I isoform X2 [Heterocephalus	31.2	31.2	92%	13	69%	gi|512818622|XP_004878889.1
☐	PREDICTED: complement factor I isoform X1 [Fukomys damar	31.2	31.2	92%	13	69%	gi|731254235|XP_010639823.1
☐	PREDICTED: complement factor I isoform X2 [Cavia porcellus]	31.2	31.2	92%	13	69%	gi|514457647|XP_005002957.1
☐	PREDICTED: complement factor I isoform X1 [Heterocephalus	31.2	31.2	92%	13	69%	gi|512818618|XP_004878888.1
☐	PREDICTED: complement factor I isoform X1 [Cavia porcellus]	31.2	31.2	92%	13	69%	gi|514457649|XP_003468099.2
☐	PREDICTED: complement factor I [Cricetulus griseus]	31.2	31.2	100%	13	64%	gi|625241505|XP_007611983.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	31.2	31.2	100%	13	64%	gi|625222421|XP_007651009.1
☐	PREDICTED: complement factor I [Tursiops truncatus]	30.8	30.8	92%	18	62%	gi|470636247|XP_004323514.1
☐	PREDICTED: complement factor I [Ochotona princeps]	30.8	30.8	92%	18	62%	gi|504169976|XP_004594584.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [(	30.8	30.8	92%	18	69%	gi|533186455|XP_005406244.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [(	30.8	30.8	92%	18	62%	gi|466008566|XP_004269732.1
☐	PREDICTED: GTPase IMAP family member 7-like [Danio rerio]	30.3	30.3	100%	23	71%	gi|688540502|XP_009293412.1
☐	phosphonate C-P lyase system protein PhnK [Rhizobium legum	30.3	30.3	78%	24	82%	gi|739199265|WP_037062723.1
☐	PREDICTED: GTPase IMAP family member 8-like [Danio rerio]	30.3	30.3	100%	25	71%	gi|688540491|XP_009292350.1
☐	PREDICTED: complement factor I isoform X5 [Canis lupus fam	29.9	29.9	100%	34	64%	gi|545552244|XP_005639326.1
☐	PREDICTED: complement factor I isoformX3 [Canis lupus famil	29.9	29.9	100%	34	64%	gi|74002140|XP_863506.1
☐	PREDICTED: complement factor I isoform X4 [Canis lupus fam	29.9	29.9	100%	34	64%	gi|545552242|XP_005639325.1
☐	PREDICTED: probable cysteine proteinase At3g19400 [Malus (	29.5	29.5	78%	42	56%	gi|658064694|XP_008368290.1
☐	hypothetical protein [Gallibacterium anatis]	29.5	29.5	64%	44	89%	gi|517156972|WP_018345790.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

complement factor I light chain

Sequence ID: gi|224798|prf||1202205A **Length:** 200 **Number of Matches:** 1

Related Information

Range 1: 108 to 121 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	8e-05	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KLISDCSKFYGNRF  14
            KLIS+CSKFYGNRF
Sbjct  108  KLISNCSKFYGNRF  121
```

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PREDICTED: complement factor I-like, partial [Macaca mulatta]

Sequence ID: gi|297293864|ref|XP_002804336.1| **Length:** 214 **Number of Matches:** 1

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Range 1: 121 to 134 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	8e-05	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KLISDCSKFYGNRF  14
            KLIS+CSKFYGNRF
Sbjct  121  KLISNCSKFYGNRF  134
```

Map Viewer - aligned genomic context

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unnamed protein product [Homo sapiens]

Sequence ID: gi|1335056|emb|CAA68418.1| **Length:** 244 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 151 to 164 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	8e-05	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KLISDCSKFYGNRF  14
            KLIS+CSKFYGNRF
Sbjct  151  KLISNCSKFYGNRF  164
```

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PREDICTED: complement factor I-like, partial [Gorilla gorilla gorilla]

Sequence ID: gi|426345227|ref|XP_004040322.1| **Length:** 281 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 188 to 201 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	9e-05	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KLISDCSKFYGNRF  14
            KLIS+CSKFYGNRF
Sbjct  188  KLISNCSKFYGNRF  201
```

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PREDICTED: complement factor I-like, partial [Macaca fascicularis]

Sequence ID: gi|544524397|ref|XP_005595214.1| **Length:** 314 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 221 to 234 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	9e-05	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KLISDCSKFYGNRF  14
            KLIS+CSKFYGNRF
Sbjct  221  KLISNCSKFYGNRF  234
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - B94H58KR01R

Your search parameters were adjusted to search for a short input sequence.

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How to read this page   Blast report description

CFI_KLISNCSKFYGNRF_NonMod

RID	B94H58KR01R (Expires on 01-14 10:33 am)
Query ID	lcl|237167
Description	None
Molecule type	amino acid
Query Length	14

Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

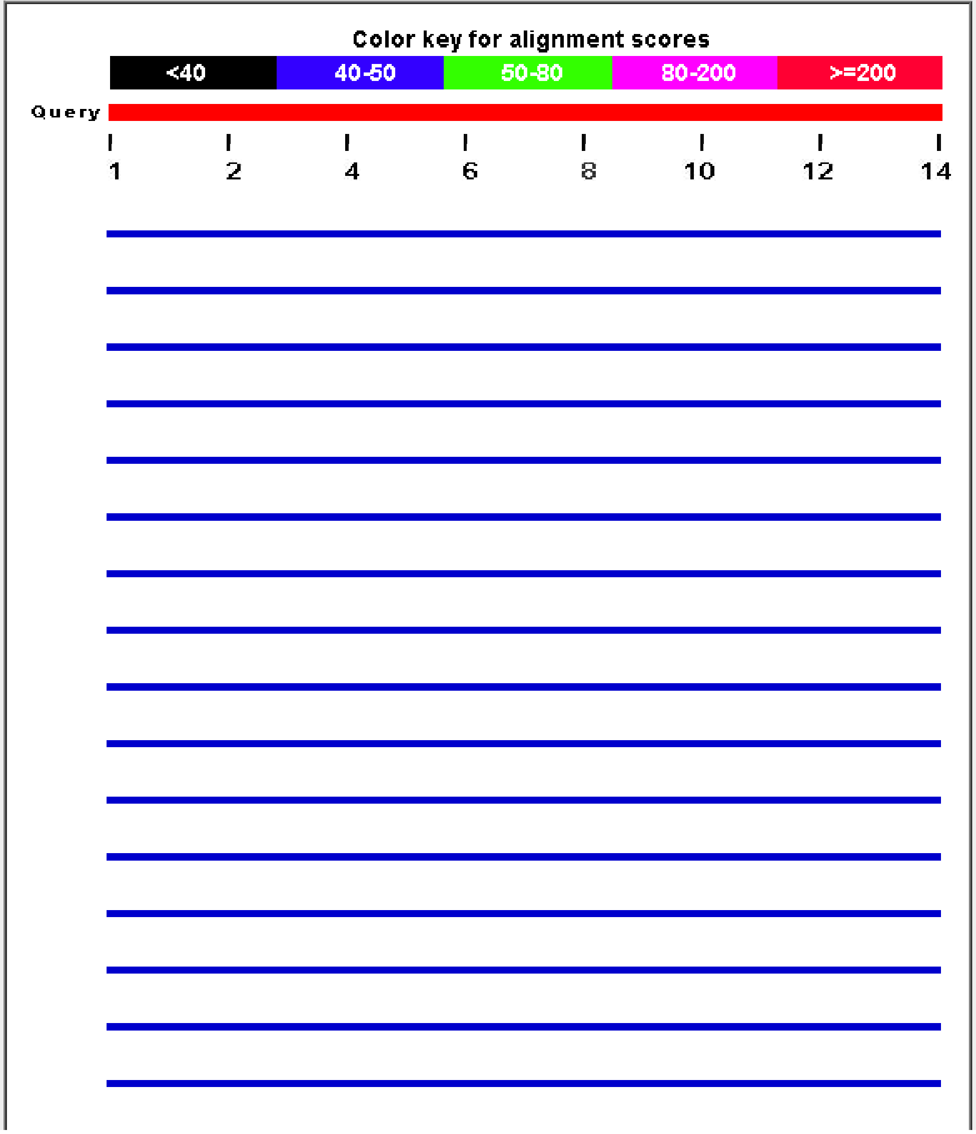
Graphic Summary

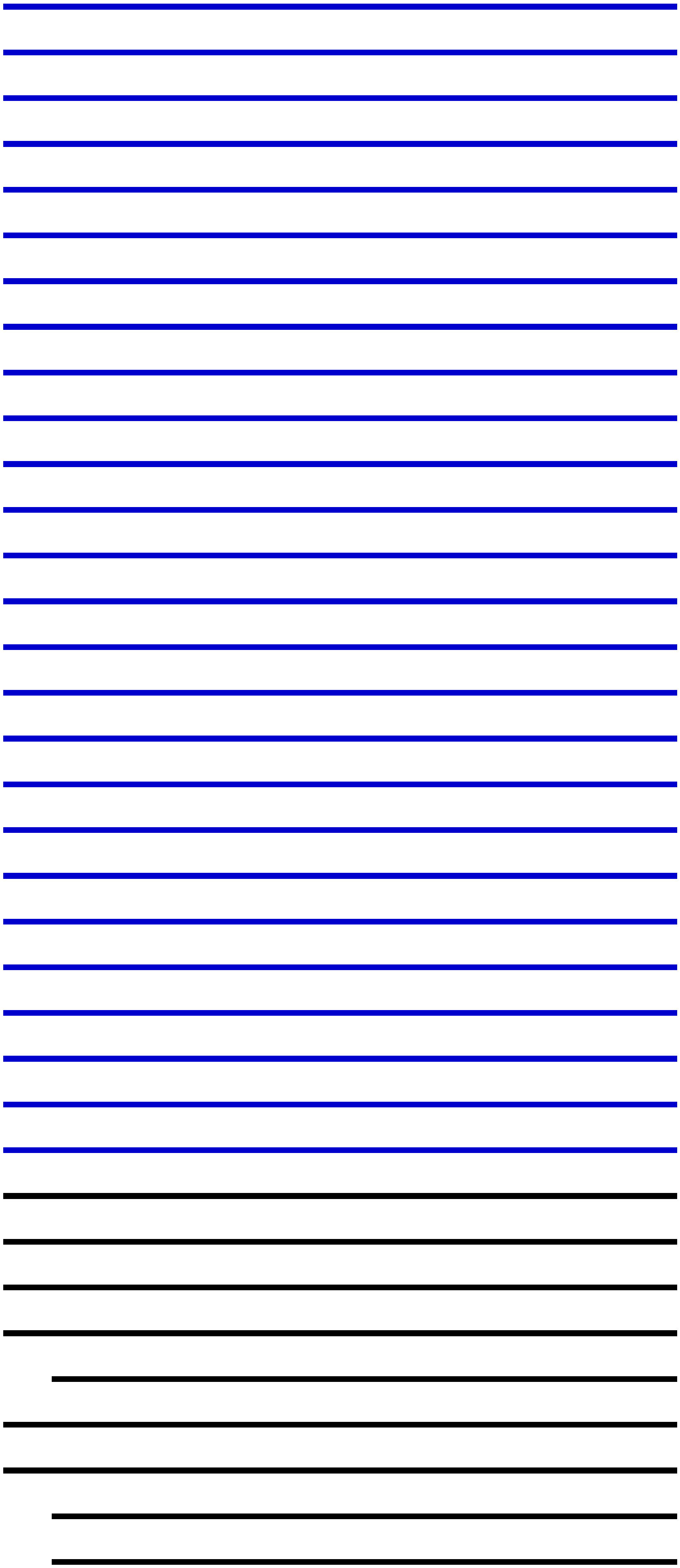
Show Conserved Domains

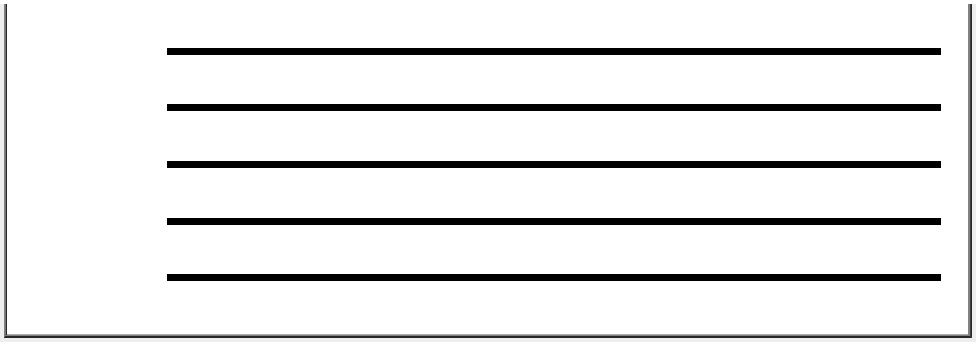
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	complement factor I light chain [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|224798|1202205A
☐	PREDICTED: complement factor I-like [Macaca mulatta]	49.4	49.4	100%	1e-05	100%	gi|297293864|XP_002804336.1
☐	unnamed protein product [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|1335056|CAA68418.1
☐	PREDICTED: complement factor I-like [Gorilla gorilla gorilla]	49.4	49.4	100%	1e-05	100%	gi|426345227|XP_004040322.1
☐	PREDICTED: complement factor I-like [Macaca fascicularis]	49.4	49.4	100%	1e-05	100%	gi|544524397|XP_005595214.1
☐	PREDICTED: complement factor I isoform X3 [Chlorocebus sabaeu	49.4	49.4	100%	1e-05	100%	gi|635044271|XP_007997720.1
☐	complement factor I [Pongo abelii]	49.4	49.4	100%	1e-05	100%	gi|207080120|NP_001128776.1
☐	PREDICTED: complement factor I isoform X6 [Pan troglodytes]	49.4	49.4	100%	1e-05	100%	gi|694908492|XP_009446407.1
☐	PREDICTED: complement factor I isoform X6 [Pan paniscus]	49.4	49.4	100%	1e-05	100%	gi|675793799|XP_008953634.1
☐	uncharacterized protein LOC101866929 precursor [Macaca fascicul	49.4	49.4	100%	1e-05	100%	gi|548961885|NP_001271714.1
☐	PREDICTED: complement factor I isoform X5 [Pan troglodytes]	49.4	49.4	100%	1e-05	100%	gi|694908490|XP_009446406.1
☐	PREDICTED: complement factor I isoform X5 [Pan paniscus]	49.4	49.4	100%	1e-05	100%	gi|675793797|XP_008953633.1
☐	PREDICTED: complement factor I isoform X4 [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|578809103|XP_006714273.1
☐	Chain A, Human Complement Factor I [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|339961198|2XRC_A
☐	PREDICTED: complement factor I isoform X4 [Pan troglodytes]	49.4	49.4	100%	1e-05	100%	gi|694908488|XP_009446405.1
☐	PREDICTED: complement factor I isoform X4 [Pan paniscus]	49.4	49.4	100%	1e-05	100%	gi|675793795|XP_008953632.1
☐	PREDICTED: complement factor I isoform X2 [Chlorocebus sabaeu	49.4	49.4	100%	1e-05	100%	gi|635044269|XP_007997719.1
☐	PREDICTED: complement factor I isoform X2 [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|530377647|XP_005263033.1
☐	PREDICTED: complement factor I isoform X2 [Saimiri boliviensis bo	49.4	49.4	100%	1e-05	100%	gi|725571753|XP_010338379.1
☐	PREDICTED: complement factor I [Callithrix jacchus]	49.4	49.4	100%	1e-05	100%	gi|675648222|XP_002745538.3
☐	PREDICTED: complement factor I [Nomascus leucogenys]	49.4	49.4	100%	1e-05	100%	gi|332240463|XP_003269405.1
☐	PREDICTED: complement factor I [Rhinopithecus roxellana]	49.4	49.4	100%	1e-05	100%	gi|724946291|XP_010387365.1
☐	PREDICTED: complement factor I isoform X1 [Chlorocebus sabaeu	49.4	49.4	100%	1e-05	100%	gi|635044267|XP_007997718.1
☐	prepro-C3b/C4B inactivator [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|182607|AAA52455.1
☐	complement factor I preproprotein [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|119392081|NP_000195.2
☐	complement factor I precursor [Pongo abelii]	49.4	49.4	100%	1e-05	100%	gi|197098986|NP_001127624.1
☐	PREDICTED: complement factor I isoform X3 [Pan paniscus]	49.4	49.4	100%	1e-05	100%	gi|397519838|XP_003830060.1
☐	RecName: Full=Complement factor I; AltName: Full=C3B/C4B inact	49.4	49.4	100%	1e-05	100%	gi|317373341|P05156.2
☐							

	unnamed protein product [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|158254682|BAF83314.1
☐	PREDICTED: complement factor I isoform X3 [Pan troglodytes]	49.4	49.4	100%	1e-05	100%	gi|114595644|XP_526653.2
☐	PREDICTED: complement factor I [Callithrix jacchus]	49.4	49.4	100%	1e-05	100%	gi|675752511|XP_008984405.1
☐	PREDICTED: complement factor I isoform X2 [Pan troglodytes]	49.4	49.4	100%	1e-05	100%	gi|694908485|XP_009446404.1
☐	PREDICTED: complement factor I isoform X2 [Pan paniscus]	49.4	49.4	100%	1e-05	100%	gi|675793792|XP_008953631.1
☐	PREDICTED: complement factor I isoform X3 [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|578809101|XP_006714272.1
☐	unnamed protein product [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|194387702|BAG61264.1
☐	PREDICTED: complement factor I isoform X1 [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|530377645|XP_005263032.1
☐	PREDICTED: complement factor I isoform X1 [Pan paniscus]	49.4	49.4	100%	1e-05	100%	gi|397519840|XP_003830061.1
☐	hypothetical protein EGK_16010 [Macaca mulatta]	49.4	49.4	100%	1e-05	100%	gi|355687535|EHH26119.1
☐	PREDICTED: complement factor I isoform X1 [Pan troglodytes]	49.4	49.4	100%	1e-05	100%	gi|332820084|XP_003310493.1
☐	PREDICTED: complement factor I [Papio anubis]	49.4	49.4	100%	1e-05	100%	gi|685542561|XP_009205631.1
☐	PREDICTED: complement factor I isoform X1 [Saimiri boliviensis b	49.4	49.4	100%	1e-05	100%	gi|725571751|XP_010338378.1
☐	PREDICTED: complement factor I isoform X1 [Pongo abelii]	46.0	46.0	100%	2e-04	93%	gi|686716760|XP_009238531.1
☐	PREDICTED: complement factor I isoform X4 [Monodelphis domes	39.7	39.7	100%	0.023	79%	gi|612030135|XP_007496055.1
☐	PREDICTED: complement factor I isoform X3 [Monodelphis domes	39.7	39.7	100%	0.023	79%	gi|612030133|XP_007496054.1
☐	PREDICTED: complement factor I isoform X2 [Monodelphis domes	39.7	39.7	100%	0.023	79%	gi|612030131|XP_007496053.1
☐	PREDICTED: complement factor I isoform X1 [Monodelphis domes	39.7	39.7	100%	0.023	79%	gi|612030129|XP_007496052.1
☐	PREDICTED: complement factor I [Sus scrofa]	39.7	39.7	92%	0.023	92%	gi|545846437|XP_005656603.1
☐	PREDICTED: complement factor I [Microtus ochrogaster]	39.7	39.7	100%	0.023	79%	gi|532029058|XP_005357485.1
☐	PREDICTED: complement factor I [Dasypus novemcinctus]	39.2	39.2	100%	0.031	79%	gi|488581726|XP_004476284.1
☐	PREDICTED: complement factor I isoform X2 [Oryctolagus cunicul	39.2	39.2	92%	0.031	85%	gi|655856777|XP_008265709.1
☐	PREDICTED: complement factor I isoform X1 [Oryctolagus cunicul	39.2	39.2	92%	0.031	85%	gi|655856775|XP_002717177.2
☐	PREDICTED: complement factor I-like [Galeopterus variegatus]	38.4	38.4	92%	0.059	85%	gi|667268997|XP_008570201.1
☐	PREDICTED: complement factor I [Tarsius syrichta]	38.0	38.0	92%	0.082	85%	gi|640813983|XP_008063707.1
☐	PREDICTED: complement factor I [Otolemur garnettii]	37.5	37.5	92%	0.11	85%	gi|395851346|XP_003798222.1
☐	PREDICTED: complement factor I [Chrysochloris asiatica]	37.5	37.5	92%	0.11	77%	gi|586477731|XP_006869402.1
☐	PREDICTED: complement factor I [Sarcophilus harrisii]	36.7	36.7	92%	0.21	77%	gi|395542057|XP_003772951.1
☐	complement factor I precursor [Camelus ferus]	35.8	35.8	92%	0.40	77%	gi|528758403|EPY78062.1
☐	PREDICTED: complement factor I-like [Maylandia zebra]	35.8	35.8	92%	0.40	77%	gi|499048737|XP_004574910.1
☐	PREDICTED: complement factor I-like [Pundamilia nyererei]	35.8	35.8	92%	0.40	77%	gi|548538438|XP_005752638.1
☐	PREDICTED: complement factor I-like [Haplochromis burtoni]	35.8	35.8	92%	0.40	77%	gi|554881320|XP_005950423.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Cam	35.8	35.8	92%	0.41	77%	gi|560925633|XP_006188998.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Vicu	35.8	35.8	92%	0.41	77%	gi|560979761|XP_006212132.1
☐	PREDICTED: complement factor I-like [Equus przewalskii]	35.4	35.4	92%	0.52	77%	gi|664780387|XP_008509513.1
☐	PREDICTED: complement factor I [Jaculus jaculus]	35.4	35.4	92%	0.55	77%	gi|507549735|XP_004658680.1
☐	PREDICTED: complement factor I isoform X2 [Equus caballus]	35.4	35.4	92%	0.56	77%	gi|545210264|XP_005607952.1
☐	PREDICTED: complement factor I isoform X1 [Equus caballus]	35.4	35.4	92%	0.56	77%	gi|545210262|XP_005607951.1
☐	PREDICTED: complement factor I-like [Neolamprologus brichardi]	35.0	35.0	92%	0.76	69%	gi|584028791|XP_006808922.1
☐	PREDICTED: complement factor I [Trichechus manatus latirostris]	35.0	35.0	100%	0.76	71%	gi|471391575|XP_004380312.1
☐	PREDICTED: complement factor I [Ornithorhynchus anatinus]	34.1	34.1	92%	1.4	69%	gi|620978285|XP_007668373.1
☐	PREDICTED: complement factor I isoform X2 [Ictidomys tridecemli	34.1	34.1	92%	1.4	77%	gi|532088899|XP_005330149.1
☐	PREDICTED: complement factor I isoform X1 [Ictidomys tridecemli	34.1	34.1	92%	1.4	77%	gi|532088897|XP_005330148.1
☐	Complement factor I [Fukomys damarensis]	33.7	33.7	92%	1.9	77%	gi|676270629|KFO25832.1
☐	Complement factor I [Heterocephalus glaber]	33.7	33.7	92%	1.9	77%	gi|351696416|EHA99334.1

☐	complement factor I-like protein [Cricetulus griseus]	33.7	33.7	100%	2.0	71%	gi|537261801|ERE90152.1
☐	PREDICTED: complement factor I isoform X2 [Fukomys damarensi	33.7	33.7	92%	2.0	77%	gi|731254237|XP_010639824.1
☐	PREDICTED: complement factor I isoform X2 [Heterocephalus glab	33.7	33.7	92%	2.0	77%	gi|512818622|XP_004878889.1
☐	PREDICTED: complement factor I isoform X1 [Fukomys damarensi	33.7	33.7	92%	2.0	77%	gi|731254235|XP_010639823.1
☐	PREDICTED: complement factor I isoform X2 [Cavia porcellus]	33.7	33.7	92%	2.0	77%	gi|514457647|XP_005002957.1
☐	PREDICTED: complement factor I isoform X1 [Heterocephalus glab	33.7	33.7	92%	2.0	77%	gi|512818618|XP_004878888.1
☐	PREDICTED: complement factor I isoform X1 [Cavia porcellus]	33.7	33.7	92%	2.0	77%	gi|514457649|XP_003468099.2
☐	PREDICTED: complement factor I [Cricetulus griseus]	33.7	33.7	100%	2.0	71%	gi|625241505|XP_007611983.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	33.7	33.7	100%	2.0	71%	gi|625222421|XP_007651009.1
☐	PREDICTED: complement factor I [Tursiops truncatus]	33.3	33.3	92%	2.7	69%	gi|470636247|XP_004323514.1
☐	PREDICTED: complement factor I [Ochotona princeps]	33.3	33.3	92%	2.7	69%	gi|504169976|XP_004594584.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Chin	33.3	33.3	92%	2.7	77%	gi|533186455|XP_005406244.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Orci	33.3	33.3	92%	2.7	69%	gi|466008566|XP_004269732.1
☐	PREDICTED: complement factor I-like [Oreochromis niloticus]	33.3	33.3	92%	2.7	69%	gi|542244580|XP_005459189.1
☐	PREDICTED: complement factor I isoform X5 [Canis lupus familiari	32.5	32.5	100%	5.0	71%	gi|545552244|XP_005639326.1
☐	PREDICTED: complement factor I isoformX3 [Canis lupus familiaris	32.5	32.5	100%	5.0	71%	gi|74002140|XP_863506.1
☐	PREDICTED: complement factor I isoform X4 [Canis lupus familiari	32.5	32.5	100%	5.0	71%	gi|545552242|XP_005639325.1
☐	exopolyphosphatase [Nocardia sp. BMG111209]	31.6	31.6	85%	9.3	75%	gi|518775104|WP_019932393.1
☐	exopolyphosphatase [Nocardia seriolae]	31.6	31.6	85%	9.3	75%	gi|696554125|WP_033086320.1
☐	exopolyphosphatase [Nocardia brasiliensis]	31.6	31.6	85%	9.3	75%	gi|659845710|WP_029893267.1
☐	hypothetical protein NBRGN_070_00400 [Nocardia brasiliensis NBI	31.6	31.6	85%	9.3	75%	gi|635329373|GAJ84235.1
☐	exopolyphosphatase [Nocardia brasiliensis]	31.6	31.6	85%	9.3	75%	gi|504801689|WP_014988791.1
☐	exopolyphosphatase [Nocardia rhamnosiphila]	31.6	31.6	85%	9.3	75%	gi|663748912|WP_030524745.1
☐	hypothetical protein [Nocardioidaceae bacterium Broad-1]	31.6	31.6	85%	9.3	75%	gi|495631501|WP_008356080.1
☐	exopolyphosphatase [Mycobacterium sp. UM_RHS]	31.6	31.6	85%	9.3	75%	gi|639002452|WP_024453128.1
☐	hypothetical protein BN977_01842 [Mycobacterium cosmeticum]	31.6	31.6	85%	9.3	75%	gi|597305418|CDO07043.1
☐	hypothetical protein [Rhodococcus rhodnii]	31.6	31.6	85%	9.3	75%	gi|498798498|WP_010839056.1

⊟ Alignments

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complement factor I light chain

Sequence ID: gi|224798|prf||1202205A **Length:** 200 **Number of Matches:** 1

Related Information

Range 1: 108 to 121 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KLISNCSKFYGNRF  14
            KLISNCSKFYGNRF
Sbjct  108  KLISNCSKFYGNRF  121
```

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PREDICTED: complement factor I-like, partial [Macaca mulatta]

Sequence ID: gi|297293864|ref|XP_002804336.1| **Length:** 214 **Number of Matches:** 1

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic

Range 1: 121 to 134 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KLISNCSKFYGNRF  14
```

```
            KLISNCSKFYGNRF
Sbjct  121  KLISNCSKFYGNRF  134
```

context

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unnamed protein product [Homo sapiens]

Sequence ID: gi|1335056|emb|CAA68418.1| **Length:** 244 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 151 to 164 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KLISNCSKFYGNRF  14
            KLISNCSKFYGNRF
Sbjct  151  KLISNCSKFYGNRF  164
```

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PREDICTED: complement factor I-like, partial [Gorilla gorilla gorilla]

Sequence ID: gi|426345227|ref|XP_004040322.1| **Length:** 281 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 188 to 201 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KLISNCSKFYGNRF  14
            KLISNCSKFYGNRF
Sbjct  188  KLISNCSKFYGNRF  201
```

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PREDICTED: complement factor I-like, partial [Macaca fascicularis]

Sequence ID: gi|544524397|ref|XP_005595214.1| **Length:** 314 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 221 to 234 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KLISNCSKFYGNRF  14
            KLISNCSKFYGNRF
Sbjct  221  KLISNCSKFYGNRF  234
```

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - BTG89JV9016

Your search parameters were adjusted to search for a short input sequence.

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CFI_KLPYQCPKDGTAVCATNRR_Mod

RID BTG89JV9016 (Expires on 01-20 15:32 pm)

Query ID lcl|16661
Description None
Molecule type amino acid
Query Length 19

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

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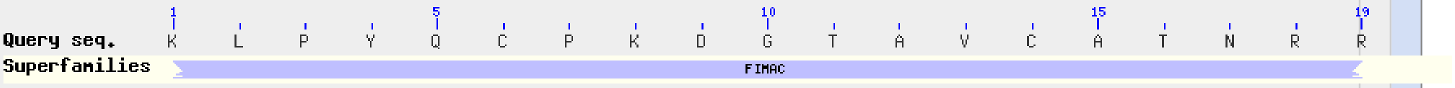
Graphic Summary

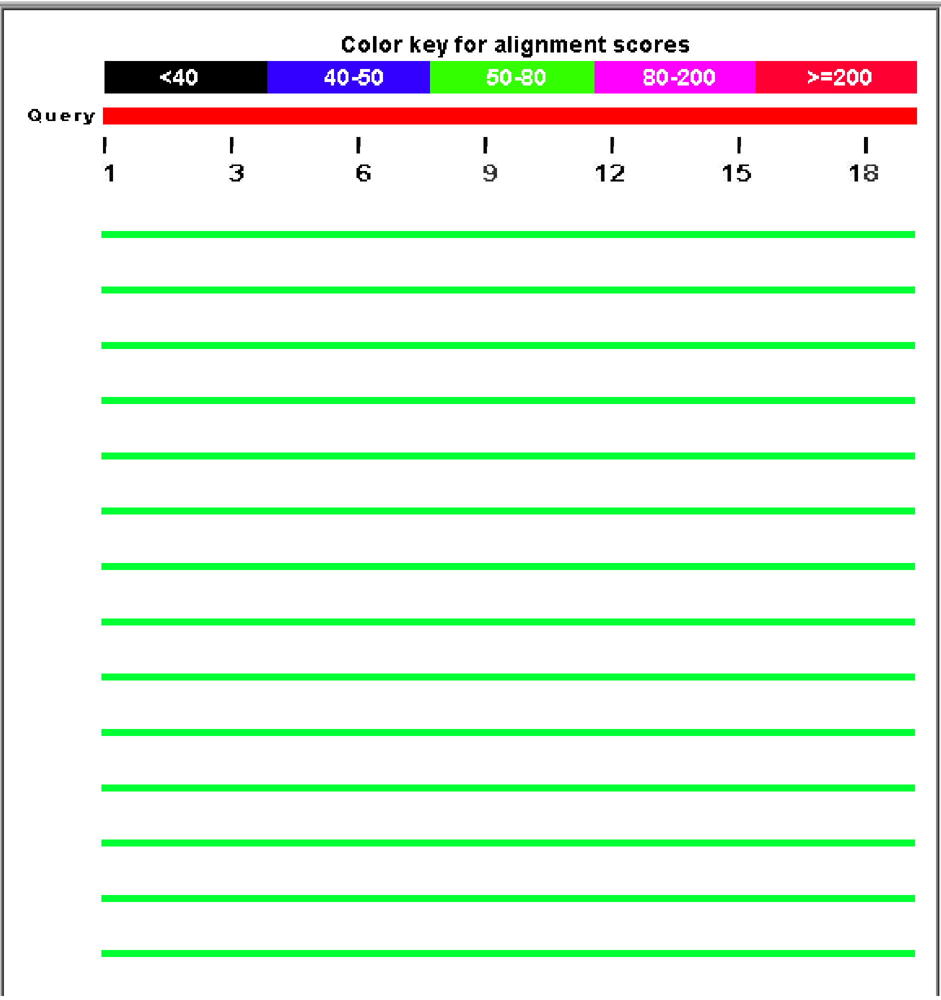
Show Conserved Domains

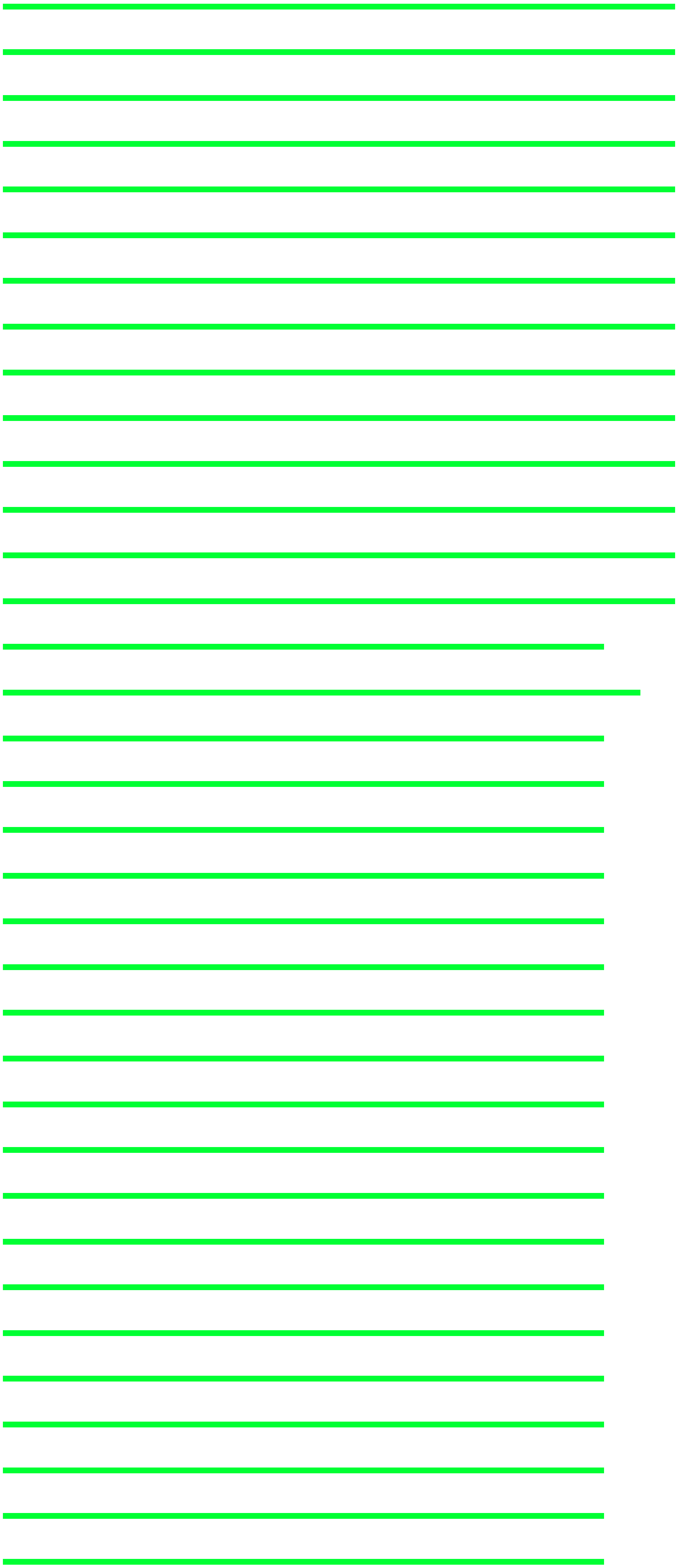
Putative conserved domains have been detected, click on the image below for detailed results.

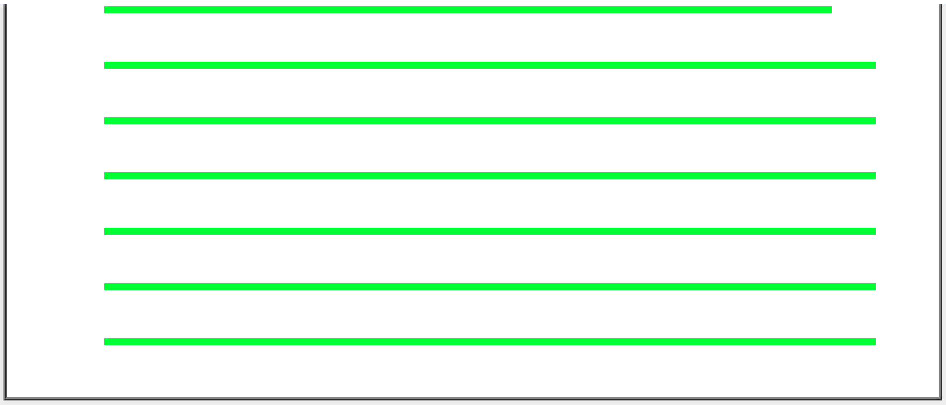


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: complement factor I-like [Gorilla gorilla gorilla]	62.6	62.6	100%	8e-10	95%	gi|426345243|XP_004040330.1
☐	unnamed protein product [Homo sapiens]	62.6	62.6	100%	8e-10	95%	gi|1335055|CAA68417.1
☐	CFI protein [Homo sapiens]	62.6	62.6	100%	8e-10	95%	gi|18089117|AAH20718.1
☐	complement factor I, isoform CRA_a [Homo sapiens]	62.6	62.6	100%	8e-10	95%	gi|119626655|EAX06250.1
☐	PREDICTED: complement factor I isoform X6 [Pan troglodytes]	62.6	62.6	100%	9e-10	95%	gi|694908492|XP_009446407.1
☐	PREDICTED: complement factor I isoform X6 [Pan paniscus]	62.6	62.6	100%	9e-10	95%	gi|675793799|XP_008953634.1
☐	PREDICTED: complement factor I isoform X5 [Pan troglodytes]	62.6	62.6	100%	9e-10	95%	gi|694908490|XP_009446406.1
☐	PREDICTED: complement factor I isoform X5 [Pan paniscus]	62.6	62.6	100%	9e-10	95%	gi|675793797|XP_008953633.1
☐	PREDICTED: complement factor I isoform X4 [Homo sapiens]	62.6	62.6	100%	9e-10	95%	gi|578809103|XP_006714273.1
☐	Chain A, Human Complement Factor I [Homo sapiens]	62.6	62.6	100%	9e-10	95%	gi|339961198|2XRC_A
☐	PREDICTED: complement factor I isoform X4 [Pan troglodytes]	62.6	62.6	100%	9e-10	95%	gi|694908488|XP_009446405.1
☐	PREDICTED: complement factor I isoform X4 [Pan paniscus]	62.6	62.6	100%	9e-10	95%	gi|675793795|XP_008953632.1
☐	PREDICTED: complement factor I isoform X2 [Homo sapiens]	62.6	62.6	100%	9e-10	95%	gi|530377647|XP_005263033.1
☐	PREDICTED: complement factor I isoform X2 [Saimiri boliviens	62.6	62.6	100%	9e-10	95%	gi|725571753|XP_010338379.1
☐	prepro-C3b/C4B inactivator [Homo sapiens]	62.6	62.6	100%	9e-10	95%	gi|182607|AAA52455.1
☐	complement factor I preproprotein [Homo sapiens]	62.6	62.6	100%	9e-10	95%	gi|119392081|NP_000195.2
☐	PREDICTED: complement factor I isoform X3 [Pan paniscus]	62.6	62.6	100%	9e-10	95%	gi|397519838|XP_003830060.1
☐	RecName: Full=Complement factor I; AltName: Full=C3B/C4B i	62.6	62.6	100%	9e-10	95%	gi|317373341|P05156.2
☐	unnamed protein product [Homo sapiens]	62.6	62.6	100%	9e-10	95%	gi|158254682|BAF83314.1
☐	PREDICTED: complement factor I isoform X3 [Pan troglodytes]	62.6	62.6	100%	9e-10	95%	gi|114595644|XP_526653.2
☐	PREDICTED: complement factor I isoform X2 [Pan troglodytes]	62.6	62.6	100%	9e-10	95%	gi|694908485|XP_009446404.1
☐	PREDICTED: complement factor I isoform X2 [Pan paniscus]	62.6	62.6	100%	9e-10	95%	gi|675793792|XP_008953631.1
☐	PREDICTED: complement factor I isoform X3 [Homo sapiens]	62.6	62.6	100%	9e-10	95%	gi|578809101|XP_006714272.1
☐	unnamed protein product [Homo sapiens]	62.6	62.6	100%	9e-10	95%	gi|194387702|BAG61264.1
☐	PREDICTED: complement factor I isoform X1 [Homo sapiens]	62.6	62.6	100%	9e-10	95%	gi|530377645|XP_005263032.1
☐	PREDICTED: complement factor I isoform X1 [Pan paniscus]	62.6	62.6	100%	9e-10	95%	gi|397519840|XP_003830061.1
☐	PREDICTED: complement factor I isoform X1 [Pan troglodytes]	62.6	62.6	100%	9e-10	95%	gi|332820084|XP_003310493.1
☐	PREDICTED: complement factor I isoform X1 [Saimiri boliviens	62.6	62.6	100%	9e-10	95%	gi|725571751|XP_010338378.1

☐	PREDICTED: complement factor I [Nomascus leucogenys]	55.8	55.8	89%	2e-07	94%	gi|332240463|XP_003269405.1
☐	PREDICTED: complement factor I [Ficedula albicollis]	53.7	53.7	94%	9e-07	83%	gi|524994367|XP_005044998.1
☐	Complement factor I [Fukomys damarensis]	53.2	53.2	89%	1e-06	88%	gi|676270629|KFO25832.1
☐	PREDICTED: complement factor I [Condylura cristata]	53.2	53.2	89%	1e-06	88%	gi|507959121|XP_004686530.1
☐	PREDICTED: complement factor I [Echinops telfairi]	53.2	53.2	89%	1e-06	88%	gi|507649004|XP_004703515.1
☐	PREDICTED: complement factor I [Tinamus guttatus]	53.2	53.2	89%	1e-06	88%	gi|719780359|XP_010222070.1
☐	PREDICTED: complement factor I isoform X5 [Canis lupus fam	53.2	53.2	89%	1e-06	88%	gi|545552244|XP_005639326.1
☐	PREDICTED: complement factor I isoformX3 [Canis lupus famil	53.2	53.2	89%	1e-06	88%	gi|74002140|XP_863506.1
☐	PREDICTED: complement factor I isoform X4 [Canis lupus fam	53.2	53.2	89%	1e-06	88%	gi|545552242|XP_005639325.1
☐	PREDICTED: complement factor I isoform X2 [Oryctolagus cun	53.2	53.2	89%	1e-06	88%	gi|655856777|XP_008265709.1
☐	PREDICTED: complement factor I isoform X2 [Fukomys damar	53.2	53.2	89%	1e-06	88%	gi|731254237|XP_010639824.1
☐	PREDICTED: complement factor I isoform X1 [Oryctolagus cun	53.2	53.2	89%	1e-06	88%	gi|655856775|XP_002717177.2
☐	PREDICTED: complement factor I isoform X1 [Fukomys damar	53.2	53.2	89%	1e-06	88%	gi|731254235|XP_010639823.1
☐	complement factor I precursor [Pongo abelii]	52.8	52.8	89%	2e-06	88%	gi|197098986|NP_001127624.1
☐	PREDICTED: complement factor I-like [Macaca mulatta]	52.4	52.4	89%	2e-06	88%	gi|297293220|XP_001087512.2
☐	uncharacterized protein LOC101866929 precursor [Macaca fas	52.4	52.4	89%	2e-06	88%	gi|548961885|NP_001271714.1
☐	PREDICTED: complement factor I isoform X2 [Chlorocebus sa	52.4	52.4	89%	2e-06	88%	gi|635044269|XP_007997719.1
☐	PREDICTED: complement factor I [Rhinopithecus roxellana]	52.4	52.4	89%	2e-06	88%	gi|724946291|XP_010387365.1
☐	PREDICTED: complement factor I isoform X1 [Chlorocebus sa	52.4	52.4	89%	2e-06	88%	gi|635044267|XP_007997718.1
☐	hypothetical protein EGK_16010 [Macaca mulatta]	52.4	52.4	89%	2e-06	88%	gi|355687535|EHH26119.1
☐	PREDICTED: complement factor I [Peromyscus maniculatus ba	52.4	52.4	89%	2e-06	88%	gi|589914217|XP_006970447.1
☐	PREDICTED: complement factor I [Papio anubis]	52.4	52.4	89%	2e-06	88%	gi|685542561|XP_009205631.1
☐	PREDICTED: complement factor I [Jaculus jaculus]	51.5	51.5	94%	5e-06	78%	gi|507549735|XP_004658680.1
☐	Complement factor I [Mesitornis unicolor]	51.1	51.1	94%	7e-06	78%	gi|677422619|KFQ25952.1
☐	Complement factor I [Pelecanus crispus]	51.1	51.1	94%	7e-06	78%	gi|677463622|KFQ53036.1
☐	PREDICTED: complement factor I [Mesitornis unicolor]	51.1	51.1	94%	7e-06	78%	gi|704589946|XP_010191226.1
☐	PREDICTED: complement factor I [Apaloderma vittatum]	51.1	51.1	94%	7e-06	78%	gi|699601233|XP_009870076.1
☐	PREDICTED: complement factor I [Pelecanus crispus]	51.1	51.1	94%	7e-06	78%	gi|694656827|XP_009484259.1
☐	PREDICTED: complement factor I-like [Galeopterus variegatus	50.7	50.7	89%	7e-06	82%	gi|667263801|XP_008568412.1
☐	Complement factor I [Tyto alba]	50.7	50.7	89%	9e-06	82%	gi|678173194|KFV41190.1
☐	Complement factor I [Egretta garzetta]	50.7	50.7	89%	9e-06	82%	gi|676815514|KFP11425.1
☐	Complement factor I [Struthio camelus australis]	50.7	50.7	89%	9e-06	82%	gi|678208918|KFV75898.1
☐	Complement factor I [Heterocephalus glaber]	50.7	50.7	89%	9e-06	82%	gi|351696416|EHA99334.1
☐	PREDICTED: complement factor I isoform X2 [Ictidomys tridec	50.7	50.7	89%	9e-06	82%	gi|532088899|XP_005330149.1
☐	PREDICTED: complement factor I isoform X1 [Ictidomys tridec	50.7	50.7	89%	9e-06	82%	gi|532088897|XP_005330148.1
☐	PREDICTED: complement factor I [Struthio camelus australis]	50.7	50.7	89%	9e-06	82%	gi|697440491|XP_009663701.1
☐	PREDICTED: complement factor I [Tyto alba]	50.7	50.7	89%	9e-06	82%	gi|701416164|XP_009972365.1
☐	PREDICTED: complement factor I [Orycteropus afer afer]	50.7	50.7	89%	9e-06	82%	gi|634848033|XP_007938975.1
☐	PREDICTED: complement factor I [Egretta garzetta]	50.7	50.7	89%	9e-06	82%	gi|697822212|XP_009647488.1
☐	PREDICTED: complement factor I isoform X2 [Heterocephalus	50.7	50.7	89%	9e-06	82%	gi|512818622|XP_004878889.1
☐	PREDICTED: complement factor I [Loxodonta africana]	50.7	50.7	89%	9e-06	82%	gi|731479219|XP_010588889.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	50.7	50.7	89%	9e-06	82%	gi|586984171|XP_006930977.1
☐	PREDICTED: complement factor I [Sus scrofa]	50.7	50.7	89%	9e-06	82%	gi|545846437|XP_005656603.1
☐	PREDICTED: complement factor I isoform X1 [Heterocephalus	50.7	50.7	89%	9e-06	82%	gi|512818618|XP_004878888.1
☐	PREDICTED: complement factor I [Trichechus manatus latirost	50.7	50.7	89%	9e-06	82%	gi|471391575|XP_004380312.1
☐	PREDICTED: complement factor I isoform X2 [Equus przewals	50.3	50.3	89%	1e-05	82%	gi|664769275|XP_008542181.1

☐	PREDICTED: complement factor I isoform X1 [Equus przewalsl	50.3	50.3	89%	1e-05	82%	gi|664769273|XP_008542180.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	50.3	50.3	89%	1e-05	82%	gi|511847748|XP_004748251.1
☐	PREDICTED: complement factor I [Myotis davidii]	50.3	50.3	89%	1e-05	82%	gi|584046382|XP_006767995.1
☐	PREDICTED: complement factor I [Pteropus alecto]	50.3	50.3	89%	1e-05	82%	gi|586528110|XP_006918978.1
☐	PREDICTED: complement factor I isoform X2 [Nannospalax ga	50.3	50.3	89%	1e-05	82%	gi|674034950|XP_008841698.1
☐	PREDICTED: complement factor I isoform X1 [Nannospalax ga	50.3	50.3	89%	1e-05	82%	gi|674034948|XP_008841690.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	50.3	50.3	89%	1e-05	82%	gi|511991360|XP_004813365.1
☐	complement factor I precursor [Rattus norvegicus]	50.3	50.3	89%	1e-05	88%	gi|13162353|NP_077071.1
☐	PREDICTED: complement factor I isoform X2 [Myotis brandtii]	50.3	50.3	89%	1e-05	82%	gi|554556058|XP_005872468.1
☐	PREDICTED: complement factor I [Myotis lucifugus]	50.3	50.3	89%	1e-05	82%	gi|558181756|XP_006101433.1
☐	PREDICTED: complement factor I isoform X1 [Myotis brandtii]	50.3	50.3	89%	1e-05	82%	gi|554556056|XP_005872467.1
☐	PREDICTED: complement factor I isoform X2 [Equus caballus]	50.3	50.3	89%	1e-05	82%	gi|545210264|XP_005607952.1
☐	Complement factor I [Pteropus alecto]	50.3	50.3	89%	1e-05	82%	gi|431897147|ELK06409.1
☐	PREDICTED: complement factor I isoform X1 [Equus caballus]	50.3	50.3	89%	1e-05	82%	gi|545210262|XP_005607951.1
☐	Complement factor I [Myotis brandtii]	50.3	50.3	89%	1e-05	82%	gi|521029771|EPQ11558.1
☐	PREDICTED: complement factor I isoform X1 [Rattus norvegicu	50.3	50.3	89%	1e-05	88%	gi|672044321|XP_008759748.1
☐	PREDICTED: complement factor I-like [Python bivittatus]	49.8	49.8	89%	2e-05	82%	gi|602663653|XP_007437454.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [(	49.8	49.8	89%	2e-05	82%	gi|472383864|XP_004411307.1
☐	PREDICTED: complement factor I [Ochotona princeps]	49.8	49.8	89%	2e-05	82%	gi|504169976|XP_004594584.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [(	49.8	49.8	89%	2e-05	82%	gi|533186455|XP_005406244.1
☐	PREDICTED: complement factor I [Otolemur garnettii]	49.4	49.4	89%	2e-05	82%	gi|395851346|XP_003798222.1
☐	PREDICTED: complement factor I [Callithrix jacchus]	49.4	49.4	89%	2e-05	82%	gi|675648222|XP_002745538.3
☐	PREDICTED: complement factor I [Callithrix jacchus]	49.4	49.4	89%	2e-05	82%	gi|675752511|XP_008984405.1
☐	PREDICTED: complement factor I [Tarsius syrichta]	49.0	49.0	84%	3e-05	88%	gi|640813983|XP_008063707.1
☐	PREDICTED: complement factor I [Eptesicus fuscus]	48.6	48.6	89%	5e-05	82%	gi|641717977|XP_008148531.1
☐	PREDICTED: complement factor I [Ceratotherium simum simur	48.6	48.6	89%	5e-05	82%	gi|478504685|XP_004426641.1

⊟ Alignments

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PREDICTED: complement factor I-like, partial [Gorilla gorilla gorilla]

Sequence ID: gi|426345243|ref|XP_004040330.1| **Length:** 309 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 62 to 80 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	8e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1   KLPYQCPKDGTAVCATNRR  19
           KLPYQCPK+GTAVCATNRR
Sbjct  62  KLPYQCPKNGTAVCATNRR  80
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|1335055|emb|CAA68417.1| **Length:** 321 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 44 to 62 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	8e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1   KLPYQCPKDGTAVCATNRR  19
           KLPYQCPK+GTAVCATNRR
Sbjct  44  KLPYQCPKNGTAVCATNRR  62
```

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CFI protein [Homo sapiens]

Sequence ID: gi|18089117|gb|AAH20718.1| **Length:** 377 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 62 to 80 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	8e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1   KLPYQCPKDGTAVCATNRR  19
           KLPYQCPK+GTAVCATNRR
Sbjct  62  KLPYQCPKNGTAVCATNRR  80
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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complement factor I, isoform CRA_a, partial [Homo sapiens]

Sequence ID: gi|119626655|gb|EAX06250.1| **Length:** 378 **Number of Matches:** 1

Range 1: 62 to 80 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	8e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1   KLPYQCPKDGTAVCATNRR  19
           KLPYQCPK+GTAVCATNRR
Sbjct  62  KLPYQCPKNGTAVCATNRR  80
```

Related Information

Gene - associated gene details

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PREDICTED: complement factor I isoform X6 [Pan troglodytes]

Sequence ID: gi|694908492|ref|XP_009446407.1| **Length:** 516 **Number of Matches:** 1

Range 1: 62 to 80 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	9e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1   KLPYQCPKDGTAVCATNRR  19
           KLPYQCPK+GTAVCATNRR
Sbjct  62  KLPYQCPKNGTAVCATNRR  80
```

Related Information

Gene - associated gene details

NCBI/ BLAST/ blastp suite/ Formatting Results - B93SHEYN01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

CFI_KLPYQCPKNGTAVCATNRR_NonMod

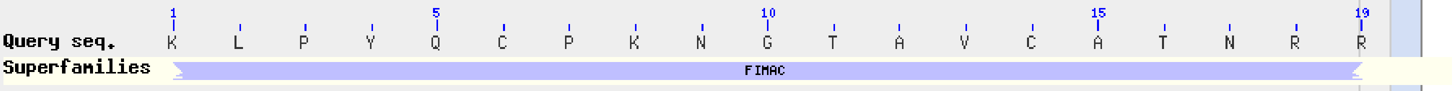
RID	B93SHEYN01R (Expires on 01-14 10:20 am)		
Query ID	lcl|313553	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	19	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

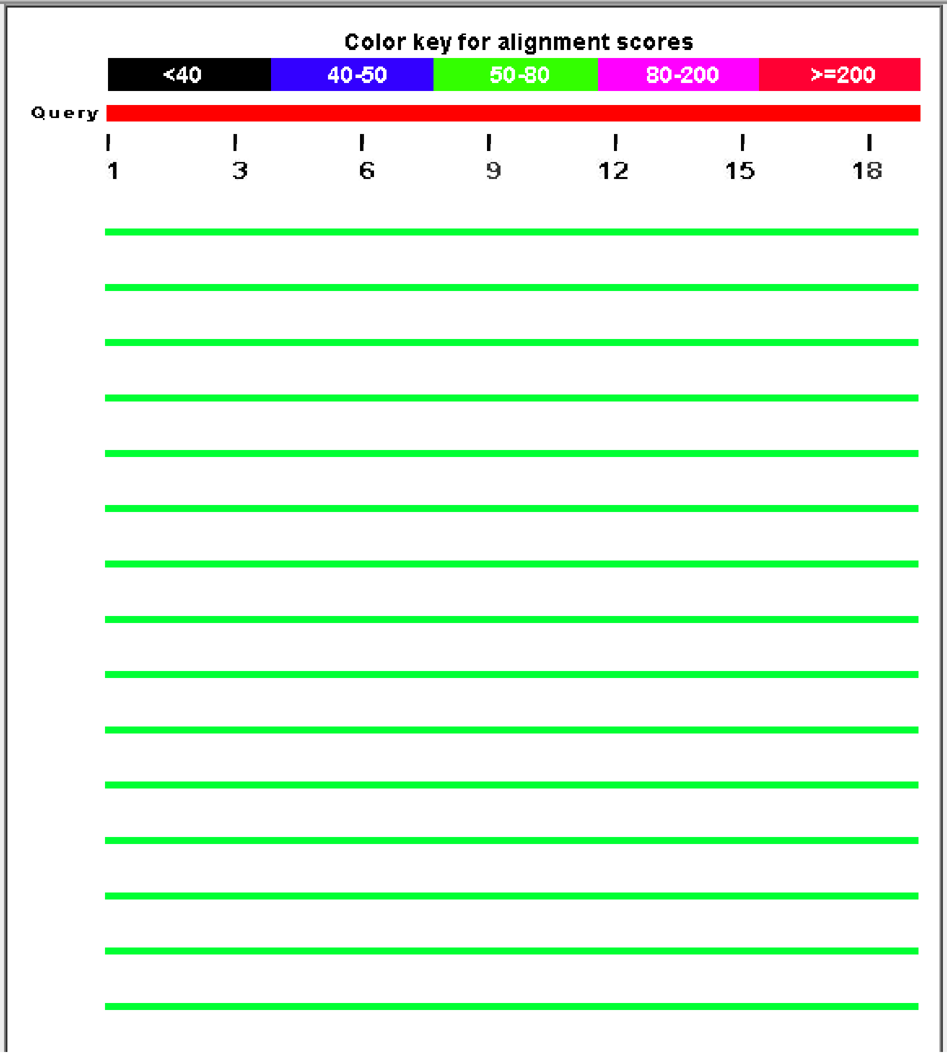
Show Conserved Domains

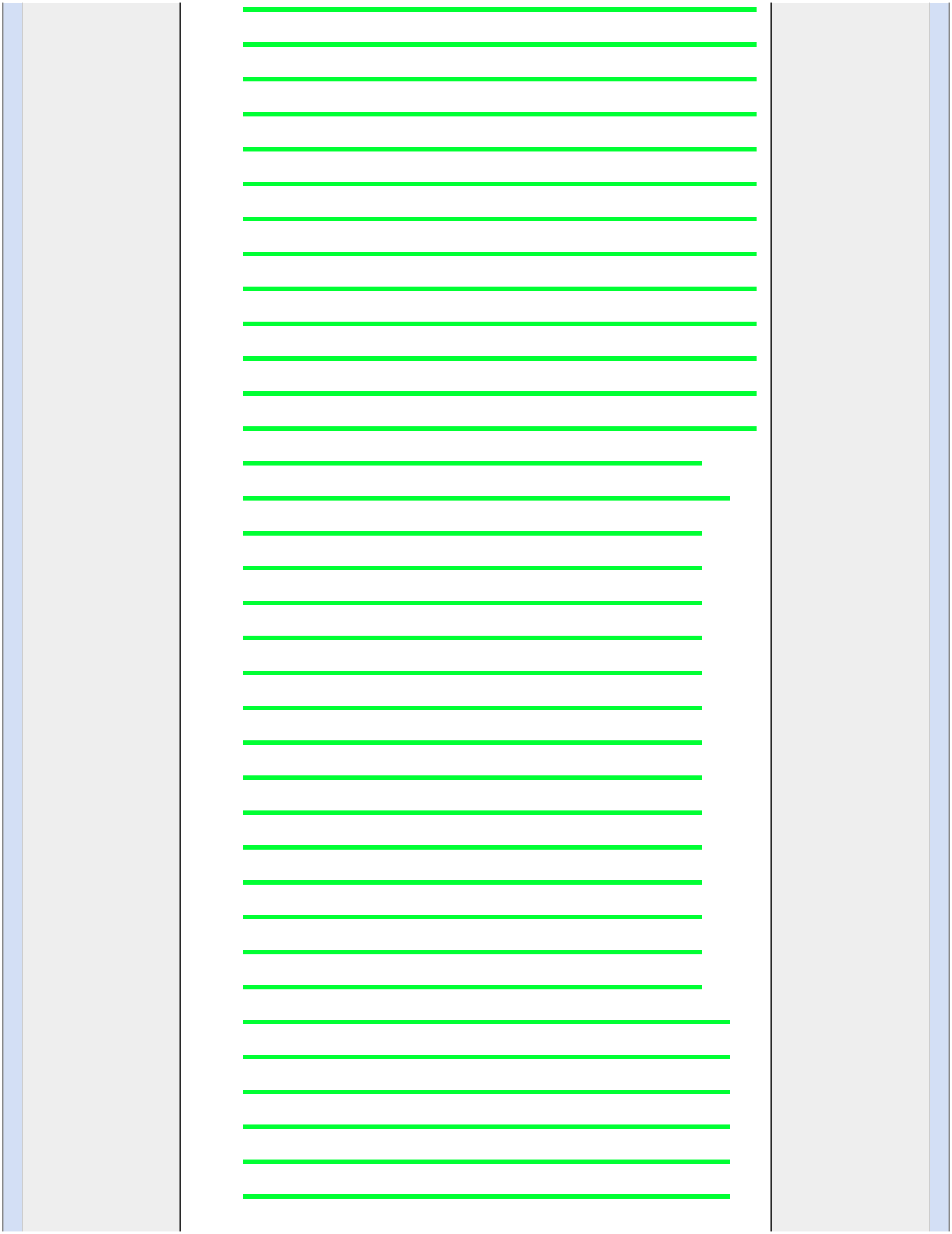
Putative conserved domains have been detected, click on the image below for detailed results.

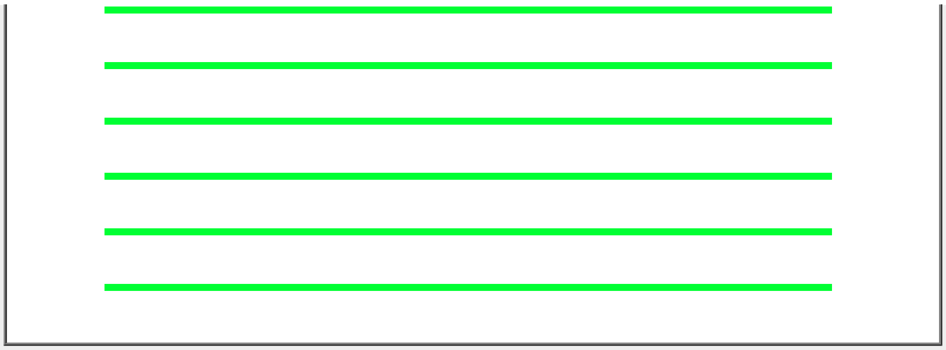


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: complement factor I-like [Gorilla gorilla gorilla]	65.1	65.1	100%	1e-10	100%	gi|426345243|XP_004040330.1
☐	unnamed protein product [Homo sapiens]	65.1	65.1	100%	1e-10	100%	gi|1335055|CAA68417.1
☐	CFI protein [Homo sapiens]	65.1	65.1	100%	1e-10	100%	gi|18089117|AAH20718.1
☐	complement factor I, isoform CRA_a [Homo sapiens]	65.1	65.1	100%	1e-10	100%	gi|119626655|EAX06250.1
☐	PREDICTED: complement factor I isoform X6 [Pan troglodytes]	65.1	65.1	100%	1e-10	100%	gi|694908492|XP_009446407.1
☐	PREDICTED: complement factor I isoform X6 [Pan paniscus]	65.1	65.1	100%	1e-10	100%	gi|675793799|XP_008953634.1
☐	PREDICTED: complement factor I isoform X5 [Pan troglodytes]	65.1	65.1	100%	1e-10	100%	gi|694908490|XP_009446406.1
☐	PREDICTED: complement factor I isoform X5 [Pan paniscus]	65.1	65.1	100%	1e-10	100%	gi|675793797|XP_008953633.1
☐	PREDICTED: complement factor I isoform X4 [Homo sapiens]	65.1	65.1	100%	1e-10	100%	gi|578809103|XP_006714273.1
☐	Chain A, Human Complement Factor I [Homo sapiens]	65.1	65.1	100%	1e-10	100%	gi|339961198|2XRC_A
☐	PREDICTED: complement factor I isoform X4 [Pan troglodytes]	65.1	65.1	100%	1e-10	100%	gi|694908488|XP_009446405.1
☐	PREDICTED: complement factor I isoform X4 [Pan paniscus]	65.1	65.1	100%	1e-10	100%	gi|675793795|XP_008953632.1
☐	PREDICTED: complement factor I isoform X2 [Homo sapiens]	65.1	65.1	100%	1e-10	100%	gi|530377647|XP_005263033.1
☐	PREDICTED: complement factor I isoform X2 [Saimiri boliviensis bo	65.1	65.1	100%	1e-10	100%	gi|725571753|XP_010338379.1
☐	prepro-C3b/C4B inactivator [Homo sapiens]	65.1	65.1	100%	1e-10	100%	gi|182607|AAA52455.1
☐	complement factor I preproprotein [Homo sapiens]	65.1	65.1	100%	1e-10	100%	gi|119392081|NP_000195.2
☐	PREDICTED: complement factor I isoform X3 [Pan paniscus]	65.1	65.1	100%	1e-10	100%	gi|397519838|XP_003830060.1
☐	RecName: Full=Complement factor I; AltName: Full=C3B/C4B inact	65.1	65.1	100%	1e-10	100%	gi|317373341|P05156.2
☐	unnamed protein product [Homo sapiens]	65.1	65.1	100%	1e-10	100%	gi|158254682|BAF83314.1
☐	PREDICTED: complement factor I isoform X3 [Pan troglodytes]	65.1	65.1	100%	1e-10	100%	gi|114595644|XP_526653.2
☐	PREDICTED: complement factor I isoform X2 [Pan troglodytes]	65.1	65.1	100%	1e-10	100%	gi|694908485|XP_009446404.1
☐	PREDICTED: complement factor I isoform X2 [Pan paniscus]	65.1	65.1	100%	1e-10	100%	gi|675793792|XP_008953631.1
☐	PREDICTED: complement factor I isoform X3 [Homo sapiens]	65.1	65.1	100%	1e-10	100%	gi|578809101|XP_006714272.1
☐	unnamed protein product [Homo sapiens]	65.1	65.1	100%	1e-10	100%	gi|194387702|BAG61264.1
☐	PREDICTED: complement factor I isoform X1 [Homo sapiens]	65.1	65.1	100%	1e-10	100%	gi|530377645|XP_005263032.1
☐	PREDICTED: complement factor I isoform X1 [Pan paniscus]	65.1	65.1	100%	1e-10	100%	gi|397519840|XP_003830061.1
☐	PREDICTED: complement factor I isoform X1 [Pan troglodytes]	65.1	65.1	100%	1e-10	100%	gi|332820084|XP_003310493.1
☐	PREDICTED: complement factor I isoform X1 [Saimiri boliviensis bo	65.1	65.1	100%	1e-10	100%	gi|725571751|XP_010338378.1
☐	PREDICTED: complement factor I [Nomascus leucogenys]	58.3	58.3	89%	2e-08	100%	gi|332240463|XP_003269405.1

☐	PREDICTED: complement factor I [Ficedula albicollis]	56.2	56.2	94%	1e-07	89%	gi|524994367|XP_005044998.1
☐	PREDICTED: complement factor I [Condylura cristata]	55.8	55.8	89%	2e-07	94%	gi|507959121|XP_004686530.1
☐	PREDICTED: complement factor I [Echinops telfairi]	55.8	55.8	89%	2e-07	94%	gi|507649004|XP_004703515.1
☐	PREDICTED: complement factor I [Tinamus guttatus]	55.8	55.8	89%	2e-07	94%	gi|719780359|XP_010222070.1
☐	PREDICTED: complement factor I isoform X2 [Oryctolagus cuniculu	55.8	55.8	89%	2e-07	94%	gi|655856777|XP_008265709.1
☐	PREDICTED: complement factor I isoform X1 [Oryctolagus cuniculu	55.8	55.8	89%	2e-07	94%	gi|655856775|XP_002717177.2
☐	complement factor I precursor [Pongo abelii]	55.4	55.4	89%	2e-07	94%	gi|197098986|NP_001127624.1
☐	PREDICTED: complement factor I-like [Macaca mulatta]	54.9	54.9	89%	3e-07	94%	gi|297293220|XP_001087512.2
☐	uncharacterized protein LOC101866929 precursor [Macaca fascicul	54.9	54.9	89%	3e-07	94%	gi|548961885|NP_001271714.1
☐	PREDICTED: complement factor I isoform X2 [Chlorocebus sabaeu	54.9	54.9	89%	3e-07	94%	gi|635044269|XP_007997719.1
☐	PREDICTED: complement factor I [Rhinopithecus roxellana]	54.9	54.9	89%	3e-07	94%	gi|724946291|XP_010387365.1
☐	PREDICTED: complement factor I isoform X1 [Chlorocebus sabaeu	54.9	54.9	89%	3e-07	94%	gi|635044267|XP_007997718.1
☐	hypothetical protein EGK_16010 [Macaca mulatta]	54.9	54.9	89%	3e-07	94%	gi|355687535|EHH26119.1
☐	PREDICTED: complement factor I [Peromyscus maniculatus bairdii	54.9	54.9	89%	3e-07	94%	gi|589914217|XP_006970447.1
☐	PREDICTED: complement factor I [Papio anubis]	54.9	54.9	89%	3e-07	94%	gi|685542561|XP_009205631.1
☐	PREDICTED: complement factor I [Jaculus jaculus]	54.1	54.1	94%	6e-07	83%	gi|507549735|XP_004658680.1
☐	Complement factor I [Mesitornis unicolor]	53.7	53.7	94%	9e-07	83%	gi|677422619|KFQ25952.1
☐	Complement factor I [Pelecanus crispus]	53.7	53.7	94%	9e-07	83%	gi|677463622|KFQ53036.1
☐	PREDICTED: complement factor I [Mesitornis unicolor]	53.7	53.7	94%	9e-07	83%	gi|704589946|XP_010191226.1
☐	PREDICTED: complement factor I [Apaloderma vittatum]	53.7	53.7	94%	9e-07	83%	gi|699601233|XP_009870076.1
☐	PREDICTED: complement factor I [Pelecanus crispus]	53.7	53.7	94%	9e-07	83%	gi|694656827|XP_009484259.1
☐	PREDICTED: complement factor I-like [Galeopterus variegatus]	53.2	53.2	89%	9e-07	88%	gi|667263801|XP_008568412.1
☐	Complement factor I [Tyto alba]	53.2	53.2	89%	1e-06	88%	gi|678173194|KFV41190.1
☐	Complement factor I [Egretta garzetta]	53.2	53.2	89%	1e-06	88%	gi|676815514|KFP11425.1
☐	Complement factor I [Struthio camelus australis]	53.2	53.2	89%	1e-06	88%	gi|678208918|KFV75898.1
☐	Complement factor I [Heterocephalus glaber]	53.2	53.2	89%	1e-06	88%	gi|351696416|EHA99334.1
☐	PREDICTED: complement factor I isoform X2 [Ictidomys tridecemlir	53.2	53.2	89%	1e-06	88%	gi|532088899|XP_005330149.1
☐	PREDICTED: complement factor I isoform X1 [Ictidomys tridecemlir	53.2	53.2	89%	1e-06	88%	gi|532088897|XP_005330148.1
☐	PREDICTED: complement factor I [Struthio camelus australis]	53.2	53.2	89%	1e-06	88%	gi|697440491|XP_009663701.1
☐	PREDICTED: complement factor I [Tyto alba]	53.2	53.2	89%	1e-06	88%	gi|701416164|XP_009972365.1
☐	PREDICTED: complement factor I [Orycteropus afer afer]	53.2	53.2	89%	1e-06	88%	gi|634848033|XP_007938975.1
☐	PREDICTED: complement factor I [Egretta garzetta]	53.2	53.2	89%	1e-06	88%	gi|697822212|XP_009647488.1
☐	PREDICTED: complement factor I isoform X2 [Heterocephalus glab	53.2	53.2	89%	1e-06	88%	gi|512818622|XP_004878889.1
☐	PREDICTED: complement factor I [Loxodonta africana]	53.2	53.2	89%	1e-06	88%	gi|731479219|XP_010588889.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Felis	53.2	53.2	89%	1e-06	88%	gi|586984171|XP_006930977.1
☐	PREDICTED: complement factor I [Sus scrofa]	53.2	53.2	89%	1e-06	88%	gi|545846437|XP_005656603.1
☐	PREDICTED: complement factor I isoform X1 [Heterocephalus glab	53.2	53.2	89%	1e-06	88%	gi|512818618|XP_004878888.1
☐	PREDICTED: complement factor I [Trichechus manatus latirostris]	53.2	53.2	89%	1e-06	88%	gi|471391575|XP_004380312.1
☐	PREDICTED: complement factor I isoform X2 [Equus przewalskii]	52.8	52.8	89%	2e-06	88%	gi|664769275|XP_008542181.1
☐	PREDICTED: complement factor I isoform X1 [Equus przewalskii]	52.8	52.8	89%	2e-06	88%	gi|664769273|XP_008542180.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	52.8	52.8	89%	2e-06	88%	gi|511847748|XP_004748251.1
☐	PREDICTED: complement factor I [Myotis davidii]	52.8	52.8	89%	2e-06	88%	gi|584046382|XP_006767995.1
☐	PREDICTED: complement factor I [Pteropus alecto]	52.8	52.8	89%	2e-06	88%	gi|586528110|XP_006918978.1
☐	PREDICTED: complement factor I isoform X2 [Nannospalax galili]	52.8	52.8	89%	2e-06	88%	gi|674034950|XP_008841698.1
☐	PREDICTED: complement factor I isoform X1 [Nannospalax galili]	52.8	52.8	89%	2e-06	88%	gi|674034948|XP_008841690.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	52.8	52.8	89%	2e-06	88%	gi|511991360|XP_004813365.1

☐ PREDICTED: complement factor I isoform X2 [Myotis brandtii]	52.8	52.8	89%	2e-06	88%	gi|554556058|XP_005872468.1
☐ PREDICTED: complement factor I [Myotis lucifugus]	52.8	52.8	89%	2e-06	88%	gi|558181756|XP_006101433.1
☐ PREDICTED: complement factor I isoform X1 [Myotis brandtii]	52.8	52.8	89%	2e-06	88%	gi|554556056|XP_005872467.1
☐ PREDICTED: complement factor I isoform X2 [Equus caballus]	52.8	52.8	89%	2e-06	88%	gi|545210264|XP_005607952.1
☐ Complement factor I [Pteropus alecto]	52.8	52.8	89%	2e-06	88%	gi|431897147|ELK06409.1
☐ PREDICTED: complement factor I isoform X1 [Equus caballus]	52.8	52.8	89%	2e-06	88%	gi|545210262|XP_005607951.1
☐ Complement factor I [Myotis brandtii]	52.8	52.8	89%	2e-06	88%	gi|521029771|EPQ11558.1
☐ PREDICTED: complement factor I-like [Python bivittatus]	52.4	52.4	89%	2e-06	88%	gi|602663653|XP_007437454.1
☐ PREDICTED: LOW QUALITY PROTEIN: complement factor I [Odo	52.4	52.4	89%	2e-06	88%	gi|472383864|XP_004411307.1
☐ PREDICTED: complement factor I [Ochotona princeps]	52.4	52.4	89%	2e-06	88%	gi|504169976|XP_004594584.1
☐ PREDICTED: LOW QUALITY PROTEIN: complement factor I [Chin	52.4	52.4	89%	2e-06	88%	gi|533186455|XP_005406244.1
☐ PREDICTED: complement factor I [Otolemur garnettii]	52.0	52.0	89%	3e-06	88%	gi|395851346|XP_003798222.1
☐ PREDICTED: complement factor I [Callithrix jacchus]	52.0	52.0	89%	3e-06	88%	gi|675648222|XP_002745538.3
☐ PREDICTED: complement factor I [Callithrix jacchus]	52.0	52.0	89%	3e-06	88%	gi|675752511|XP_008984405.1
☐ PREDICTED: complement factor I [Tarsius syrichta]	51.5	51.5	84%	4e-06	94%	gi|640813983|XP_008063707.1
☐ PREDICTED: complement factor I [Eptesicus fuscus]	51.1	51.1	89%	6e-06	88%	gi|641717977|XP_008148531.1
☐ PREDICTED: complement factor I [Ceratotherium simum simum]	51.1	51.1	89%	6e-06	88%	gi|478504685|XP_004426641.1
☐ PREDICTED: complement factor I [Erinaceus europaeus]	51.1	51.1	100%	6e-06	80%	gi|617652869|XP_007534556.1
☐ Complement factor I [Fukomys damarensis]	50.7	50.7	89%	9e-06	82%	gi|676270629|KFO25832.1
☐ hypothetical protein PANDA_019552 [Ailuropoda melanoleuca]	50.7	50.7	89%	9e-06	88%	gi|281338891|EFB14475.1
☐ PREDICTED: complement factor I [Octodon degus]	50.7	50.7	89%	9e-06	82%	gi|507626946|XP_004626817.1
☐ PREDICTED: complement factor I isoform X5 [Canis lupus familiari	50.7	50.7	89%	9e-06	82%	gi|545552244|XP_005639326.1
☐ PREDICTED: complement factor I isoformX3 [Canis lupus familiaris	50.7	50.7	89%	9e-06	82%	gi|74002140|XP_863506.1
☐ PREDICTED: complement factor I isoform X4 [Canis lupus familiari	50.7	50.7	89%	9e-06	82%	gi|545552242|XP_005639325.1
☐ PREDICTED: complement factor I isoform X2 [Fukomys damarensi	50.7	50.7	89%	9e-06	82%	gi|731254237|XP_010639824.1

⊟ Alignments

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PREDICTED: complement factor I-like, partial [Gorilla gorilla gorilla]

Sequence ID: gi|426345243|ref|XP_004040330.1| **Length:** 309 **Number of Matches:** 1

Range 1: 62 to 80 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.1 bits(146)	1e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLPYQCPKNGTAVCATNRR  19
            KLPYQCPKNGTAVCATNRR
Sbjct  62   KLPYQCPKNGTAVCATNRR  80
```

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

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unnamed protein product [Homo sapiens]

Sequence ID: gi|1335055|emb|CAA68417.1| **Length:** 321 **Number of Matches:** 1

Range 1: 44 to 62 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.1 bits(146)	1e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLPYQCPKNGTAVCATNRR  19
            KLPYQCPKNGTAVCATNRR
Sbjct  44   KLPYQCPKNGTAVCATNRR  62
```

Related Information

Gene - associated gene details

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CFI protein [Homo sapiens]

Sequence ID: gi|18089117|gb|AAH20718.1| **Length:** 377 **Number of Matches:** 1

▹ See 1 more title(s)

Range 1: 62 to 80 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.1 bits(146)	1e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1   KLPYQCPKNGTAVCATNRR  19
           KLPYQCPKNGTAVCATNRR
Sbjct  62  KLPYQCPKNGTAVCATNRR  80
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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complement factor I, isoform CRA_a, partial [Homo sapiens]

Sequence ID: gi|119626655|gb|EAX06250.1| **Length:** 378 **Number of Matches:** 1

Range 1: 62 to 80 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.1 bits(146)	1e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1   KLPYQCPKNGTAVCATNRR  19
           KLPYQCPKNGTAVCATNRR
Sbjct  62  KLPYQCPKNGTAVCATNRR  80
```

Related Information

Gene - associated gene details

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PREDICTED: complement factor I isoform X6 [Pan troglodytes]

Sequence ID: gi|694908492|ref|XP_009446407.1| **Length:** 516 **Number of Matches:** 1

Range 1: 62 to 80 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.1 bits(146)	1e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1   KLPYQCPKNGTAVCATNRR  19
           KLPYQCPKNGTAVCATNRR
Sbjct  62  KLPYQCPKNGTAVCATNRR  80
```

Related Information

Gene - associated gene details

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NCBI/ BLAST/ blastp suite/ Formatting Results - BTG8KRX5013

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CFI_KLSDLSIDSTECLHVHCRG_Mod

RID	BTG8KRX5013 (Expires on 01-20 15:32 pm)		
Query ID	lcl|41510	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	19	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

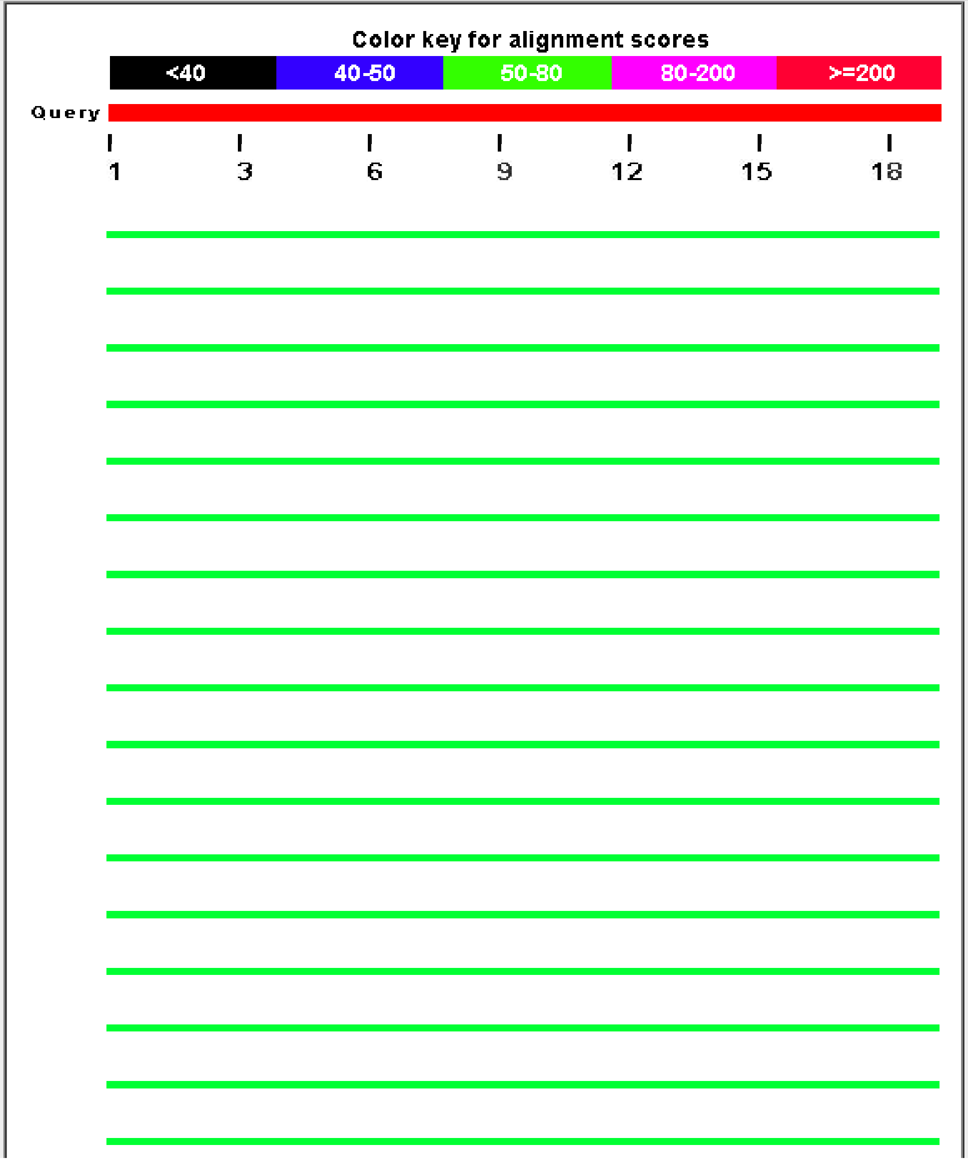
Graphic Summary

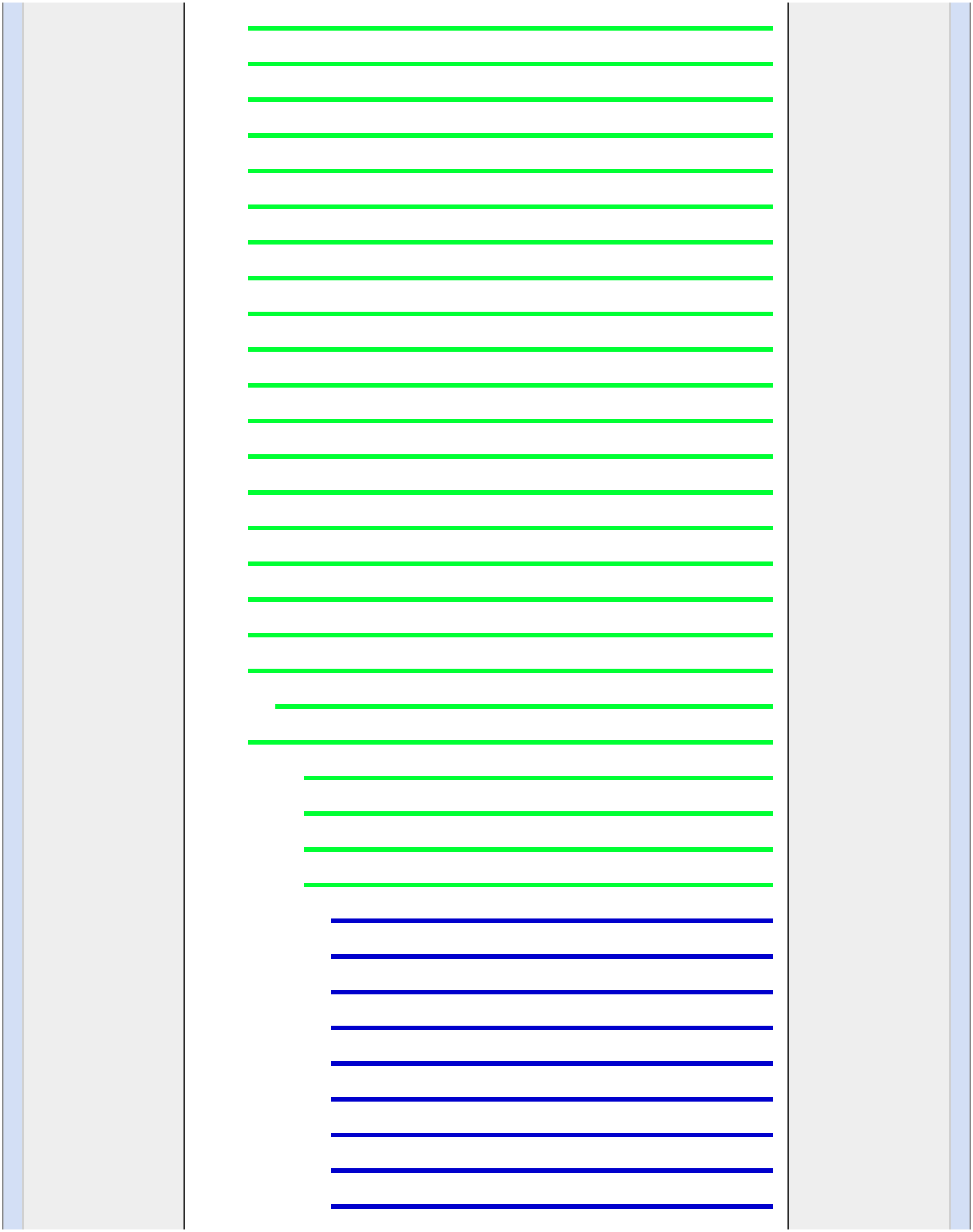
Show Conserved Domains

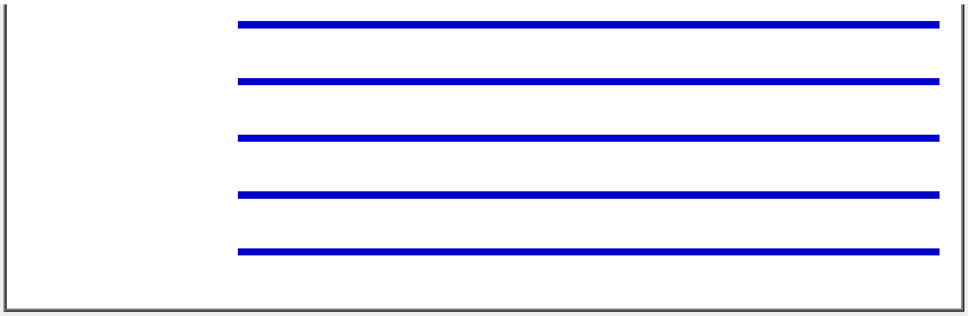
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: complement factor I-like [Gorilla gorilla gorilla]	61.7	61.7	100%	2e-09	95%	gi|426345243|XP_004040330.1
☐	unnamed protein product [Homo sapiens]	61.7	61.7	100%	2e-09	95%	gi|1335055|CAA68417.1
☐	CFI protein [Homo sapiens]	61.7	61.7	100%	2e-09	95%	gi|18089117|AAH20718.1
☐	complement factor I, isoform CRA_a [Homo sapiens]	61.7	61.7	100%	2e-09	95%	gi|119626655|EAX06250.1
☐	PREDICTED: complement factor I-like [Macaca mulatta]	61.7	61.7	100%	2e-09	95%	gi|297293220|XP_001087512.2
☐	PREDICTED: complement factor I isoform X3 [Chlorocebus sal	61.7	61.7	100%	2e-09	95%	gi|635044271|XP_007997720.1
☐	PREDICTED: complement factor I isoform X6 [Pan troglodytes]	61.7	61.7	100%	2e-09	95%	gi|694908492|XP_009446407.1
☐	PREDICTED: complement factor I isoform X6 [Pan paniscus]	61.7	61.7	100%	2e-09	95%	gi|675793799|XP_008953634.1
☐	uncharacterized protein LOC101866929 precursor [Macaca fas	61.7	61.7	100%	2e-09	95%	gi|548961885|NP_001271714.1
☐	PREDICTED: complement factor I isoform X5 [Pan troglodytes]	61.7	61.7	100%	2e-09	95%	gi|694908490|XP_009446406.1
☐	PREDICTED: complement factor I isoform X5 [Pan paniscus]	61.7	61.7	100%	2e-09	95%	gi|675793797|XP_008953633.1
☐	PREDICTED: complement factor I isoform X4 [Homo sapiens]	61.7	61.7	100%	2e-09	95%	gi|578809103|XP_006714273.1
☐	Chain A, Human Complement Factor I [Homo sapiens]	61.7	61.7	100%	2e-09	95%	gi|339961198|2XRC_A
☐	PREDICTED: complement factor I isoform X4 [Pan troglodytes]	61.7	61.7	100%	2e-09	95%	gi|694908488|XP_009446405.1
☐	PREDICTED: complement factor I isoform X4 [Pan paniscus]	61.7	61.7	100%	2e-09	95%	gi|675793795|XP_008953632.1
☐	PREDICTED: complement factor I isoform X2 [Chlorocebus sal	61.7	61.7	100%	2e-09	95%	gi|635044269|XP_007997719.1
☐	PREDICTED: complement factor I isoform X2 [Homo sapiens]	61.7	61.7	100%	2e-09	95%	gi|530377647|XP_005263033.1
☐	PREDICTED: complement factor I [Nomascus leucogenys]	61.7	61.7	100%	2e-09	95%	gi|332240463|XP_003269405.1
☐	PREDICTED: complement factor I isoform X1 [Chlorocebus sal	61.7	61.7	100%	2e-09	95%	gi|635044267|XP_007997718.1
☐	prepro-C3b/C4B inactivator [Homo sapiens]	61.7	61.7	100%	2e-09	95%	gi|182607|AAA52455.1
☐	complement factor I preproprotein [Homo sapiens]	61.7	61.7	100%	2e-09	95%	gi|119392081|NP_000195.2
☐	PREDICTED: complement factor I isoform X3 [Pan paniscus]	61.7	61.7	100%	2e-09	95%	gi|397519838|XP_003830060.1
☐	RecName: Full=Complement factor I; AltName: Full=C3B/C4B i	61.7	61.7	100%	2e-09	95%	gi|317373341|P05156.2
☐	unnamed protein product [Homo sapiens]	61.7	61.7	100%	2e-09	95%	gi|158254682|BAF83314.1
☐	PREDICTED: complement factor I isoform X3 [Pan troglodytes]	61.7	61.7	100%	2e-09	95%	gi|114595644|XP_526653.2
☐	PREDICTED: complement factor I isoform X2 [Pan troglodytes]	61.7	61.7	100%	2e-09	95%	gi|694908485|XP_009446404.1
☐	PREDICTED: complement factor I isoform X2 [Pan paniscus]	61.7	61.7	100%	2e-09	95%	gi|675793792|XP_008953631.1
☐	PREDICTED: complement factor I isoform X3 [Homo sapiens]	61.7	61.7	100%	2e-09	95%	gi|578809101|XP_006714272.1
☐	unnamed protein product [Homo sapiens]	61.7	61.7	100%	2e-09	95%	gi|194387702|BAG61264.1

☐	PREDICTED: complement factor I isoform X1 [Homo sapiens]	61.7	61.7	100%	2e-09	95%	gi|530377645|XP_005263032.1
☐	PREDICTED: complement factor I isoform X1 [Pan paniscus]	61.7	61.7	100%	2e-09	95%	gi|397519840|XP_003830061.1
☐	hypothetical protein EGK_16010 [Macaca mulatta]	61.7	61.7	100%	2e-09	95%	gi|355687535|EHH26119.1
☐	PREDICTED: complement factor I isoform X1 [Pan troglodytes]	61.7	61.7	100%	2e-09	95%	gi|332820084|XP_003310493.1
☐	PREDICTED: complement factor I isoform X1 [Pongo abelii]	59.2	59.2	100%	1e-08	89%	gi|686716760|XP_009238531.1
☐	complement factor I [Pongo abelii]	59.2	59.2	100%	1e-08	89%	gi|207080120|NP_001128776.1
☐	complement factor I precursor [Pongo abelii]	59.2	59.2	100%	1e-08	89%	gi|197098986|NP_001127624.1
☐	PREDICTED: complement factor I [Rhinopithecus roxellana]	56.2	56.2	94%	1e-07	94%	gi|724946291|XP_010387365.1
☐	PREDICTED: complement factor I [Papio anubis]	54.1	54.1	100%	7e-07	89%	gi|685542561|XP_009205631.1
☐	PREDICTED: complement factor I isoform X2 [Saimiri boliviens	50.7	50.7	89%	9e-06	82%	gi|725571753|XP_010338379.1
☐	PREDICTED: complement factor I [Callithrix jacchus]	50.7	50.7	89%	9e-06	82%	gi|675648222|XP_002745538.3
☐	PREDICTED: complement factor I [Callithrix jacchus]	50.7	50.7	89%	9e-06	82%	gi|675752511|XP_008984405.1
☐	PREDICTED: complement factor I isoform X1 [Saimiri boliviens	50.7	50.7	89%	9e-06	82%	gi|725571751|XP_010338378.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	48.1	48.1	84%	6e-05	88%	gi|586984171|XP_006930977.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	48.1	48.1	84%	6e-05	88%	gi|602703733|XP_007463290.1
☐	PREDICTED: complement factor I isoform X2 [Camelus drome	46.0	46.0	84%	3e-04	81%	gi|744567503|XP_010979382.1
☐	PREDICTED: complement factor I isoform X1 [Camelus drome	46.0	46.0	84%	3e-04	81%	gi|744567500|XP_010979381.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	46.0	46.0	84%	3e-04	81%	gi|560979761|XP_006212132.1
☐	PREDICTED: complement factor I isoform X6 [Panthera tigris a	45.6	45.6	84%	4e-04	81%	gi|591346160|XP_007098330.1
☐	PREDICTED: complement factor I isoform X5 [Panthera tigris a	45.6	45.6	84%	4e-04	81%	gi|591346158|XP_007098329.1
☐	PREDICTED: complement factor I isoform X4 [Panthera tigris a	45.6	45.6	84%	4e-04	81%	gi|591346156|XP_007098328.1
☐	PREDICTED: complement factor I isoform X2 [Panthera tigris a	45.6	45.6	84%	4e-04	81%	gi|591346152|XP_007098326.1
☐	PREDICTED: complement factor I isoform X1 [Panthera tigris a	45.6	45.6	84%	4e-04	81%	gi|591346150|XP_007098325.1
☐	complement factor I precursor [Camelus ferus]	45.2	45.2	84%	6e-04	81%	gi|528758403|EPY78062.1
☐	PREDICTED: complement factor I isoform X2 [Camelus bactria	45.2	45.2	84%	6e-04	81%	gi|743716645|XP_010951976.1
☐	PREDICTED: complement factor I isoform X1 [Camelus bactria	45.2	45.2	84%	6e-04	81%	gi|743716643|XP_010951975.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	45.2	45.2	84%	6e-04	81%	gi|560925633|XP_006188998.1
☐	PREDICTED: complement factor I [Mesocricetus auratus]	44.8	44.8	84%	8e-04	81%	gi|524965961|XP_005082885.1
☐	PREDICTED: complement factor I [Tursiops truncatus]	44.3	44.3	68%	0.001	92%	gi|470636247|XP_004323514.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	44.3	44.3	68%	0.001	92%	gi|466008566|XP_004269732.1
☐	PREDICTED: complement factor I [Physeter catodon]	44.3	44.3	68%	0.001	92%	gi|593719134|XP_007105924.1
☐	PREDICTED: complement factor I [Loxodonta africana]	43.9	43.9	78%	0.002	80%	gi|731479219|XP_010588889.1
☐	hypothetical protein PANDA_019552 [Ailuropoda melanoleuca]	43.5	43.5	84%	0.002	75%	gi|281338891|EFB14475.1
☐	PREDICTED: complement factor I-like [Ailuropoda melanoleuc	43.5	43.5	84%	0.002	75%	gi|301787939|XP_002929384.1
☐	PREDICTED: complement factor I [Ursus maritimus]	43.5	43.5	84%	0.002	75%	gi|670993394|XP_008687645.1
☐	complement factor I-like protein [Cricetulus griseus]	42.6	42.6	84%	0.004	81%	gi|537261801|ERE90152.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	42.6	42.6	84%	0.004	81%	gi|625241505|XP_007611983.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	42.6	42.6	84%	0.004	81%	gi|625222421|XP_007651009.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	42.2	42.2	84%	0.006	75%	gi|533186455|XP_005406244.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	41.8	41.8	84%	0.008	75%	gi|585149528|XP_006727262.1
☐	Complement factor I [Tupaia chinensis]	41.8	41.8	78%	0.008	80%	gi|444524072|ELV13709.1
☐	PREDICTED: complement factor I [Tupaia chinensis]	41.8	41.8	78%	0.008	80%	gi|562868474|XP_006162305.1
☐	complement factor I [Mus musculus]	41.4	41.4	84%	0.010	75%	gi|4926957|AAD32965.1
☐	complement component factor i [Mus musculus]	41.4	41.4	84%	0.011	75%	gi|148680281|EDL12228.1
☐	PREDICTED: complement factor I [Ochotona princeps]	41.4	41.4	84%	0.011	75%	gi|504169976|XP_004594584.1

☐	PREDICTED: complement factor I isoform X4 [Mus musculus]	41.4	41.4	84%	0.011	75%	gi|568921717|XP_006501026.1
☐	PREDICTED: complement factor I isoform X3 [Mus musculus]	41.4	41.4	84%	0.011	75%	gi|568921715|XP_006501025.1
☐	PREDICTED: complement factor I isoform X2 [Mus musculus]	41.4	41.4	84%	0.011	75%	gi|568921713|XP_006501024.1
☐	complement factor I [Mus musculus]	41.4	41.4	84%	0.011	75%	gi|1322034|AAB00438.1
☐	complement factor I precursor [Mus musculus]	41.4	41.4	84%	0.011	75%	gi|110347406|NP_031712.2
☐	PREDICTED: complement factor I isoform X2 [Ictidomys tridece	40.9	40.9	84%	0.015	75%	gi|532088899|XP_005330149.1
☐	PREDICTED: complement factor I isoform X1 [Ictidomys tridece	40.9	40.9	84%	0.015	75%	gi|532088897|XP_005330148.1
☐	PREDICTED: complement factor I [Balaenoptera acutorostrata	40.9	40.9	63%	0.015	92%	gi|594687284|XP_007191087.1
☐	PREDICTED: complement factor I [Trichechus manatus latirost	40.5	40.5	78%	0.020	80%	gi|471391575|XP_004380312.1
☐	PREDICTED: complement factor I [Otolemur garnettii]	40.1	40.1	68%	0.027	85%	gi|395851346|XP_003798222.1
☐	PREDICTED: complement factor I [Sus scrofa]	39.7	39.7	68%	0.038	85%	gi|545846437|XP_005656603.1
☐	PREDICTED: complement factor I [Orycteropus afer afer]	39.2	39.2	68%	0.051	77%	gi|634848033|XP_007938975.1
☐	PREDICTED: complement factor I [Erinaceus europaeus]	38.0	38.0	73%	0.13	79%	gi|617652869|XP_007534556.1
☐	PREDICTED: complement factor I [Peromyscus maniculatus ba	37.1	37.1	84%	0.24	69%	gi|589914217|XP_006970447.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	36.7	36.7	73%	0.33	71%	gi|511847748|XP_004748251.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	36.7	36.7	73%	0.33	71%	gi|511991360|XP_004813365.1
☐	Complement factor I [Fukomys damarensis]	36.3	36.3	84%	0.45	69%	gi|676270629|KFO25832.1
☐	Complement factor I [Heterocephalus glaber]	36.3	36.3	84%	0.45	69%	gi|351696416|EHA99334.1
☐	PREDICTED: complement factor I [Tarsius syrichta]	36.3	36.3	63%	0.45	83%	gi|640813983|XP_008063707.1
☐	PREDICTED: complement factor I isoform X2 [Fukomys damar	36.3	36.3	84%	0.45	69%	gi|731254237|XP_010639824.1
☐	PREDICTED: complement factor I isoform X2 [Heterocephalus	36.3	36.3	84%	0.45	69%	gi|512818622|XP_004878889.1
☐	PREDICTED: complement factor I isoform X1 [Fukomys damar	36.3	36.3	84%	0.45	69%	gi|731254235|XP_010639823.1
☐	PREDICTED: complement factor I isoform X1 [Heterocephalus	36.3	36.3	84%	0.45	69%	gi|512818618|XP_004878888.1
☐	PREDICTED: complement factor I [Echinops telfairi]	35.8	35.8	68%	0.62	69%	gi|507649004|XP_004703515.1
☐	complement factor I precursor [Rattus norvegicus]	35.4	35.4	68%	0.84	77%	gi|13162353|NP_077071.1
☐	PREDICTED: complement factor I isoform X1 [Rattus norvegicu	35.4	35.4	68%	0.85	77%	gi|672044321|XP_008759748.1

⊟ Alignments

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PREDICTED: complement factor I-like, partial [Gorilla gorilla gorilla]

Sequence ID: gi|426345243|ref|XP_004040330.1| **Length:** 309 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 170 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.7 bits(138)	2e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLSDLSIDSTECLHVHCRG  19
            KLSDLSI+STECLHVHCRG
Sbjct  170  KLSDLSINSTECLHVHCRG  188
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|1335055|emb|CAA68417.1| **Length:** 321 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 152 to 170 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.7 bits(138)	2e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLSDLSIDSTECLHVHCRG  19
            KLSDLSI+STECLHVHCRG
Sbjct  152  KLSDLSINSTECLHVHCRG  170
```

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CFI protein [Homo sapiens]

Sequence ID: gi|18089117|gb|AAH20718.1| **Length:** 377 **Number of Matches:** 1

See 1 more title(s)

Range 1: 170 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.7 bits(138)	2e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLSDLSIDSTECLHVHCRG  19
            KLSDLSI+STECLHVHCRG
Sbjct  170  KLSDLSINSTECLHVHCRG  188
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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complement factor I, isoform CRA_a, partial [Homo sapiens]

Sequence ID: gi|119626655|gb|EAX06250.1| **Length:** 378 **Number of Matches:** 1

Range 1: 170 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.7 bits(138)	2e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLSDLSIDSTECLHVHCRG  19
            KLSDLSI+STECLHVHCRG
Sbjct  170  KLSDLSINSTECLHVHCRG  188
```

Related Information

Gene - associated gene details

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PREDICTED: complement factor I-like [Macaca mulatta]

Sequence ID: gi|297293220|ref|XP_001087512.2| **Length:** 428 **Number of Matches:** 1

Range 1: 169 to 187 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.7 bits(138)	2e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLSDLSIDSTECLHVHCRG  19
            KLSDLSI+STECLHVHCRG
Sbjct  169  KLSDLSINSTECLHVHCRG  187
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

CFI_KLSDLSINSTECLHVHCRG_NonMod

RID B93SX4T901R (Expires on 01-14 10:21 am)

Query ID	lcl|317045	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	19		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

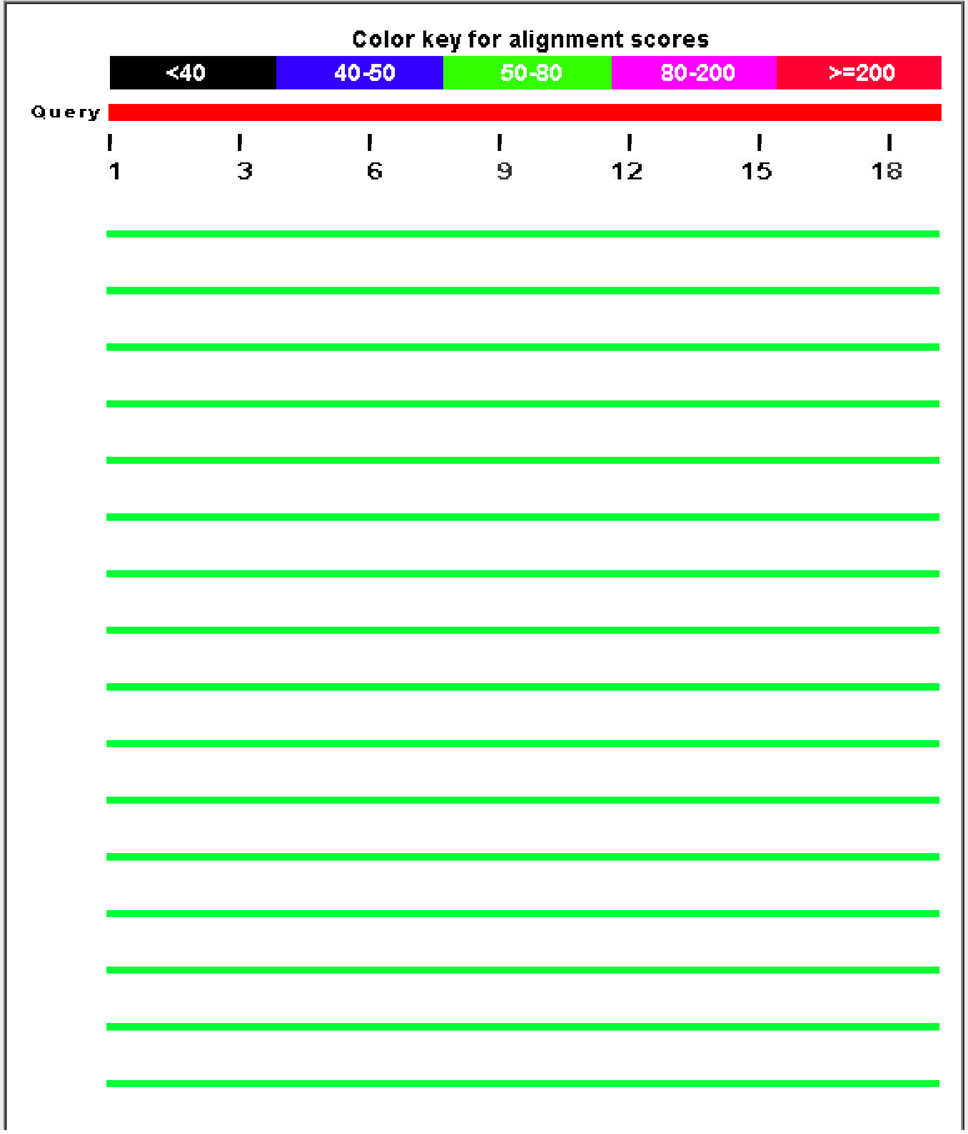
Graphic Summary

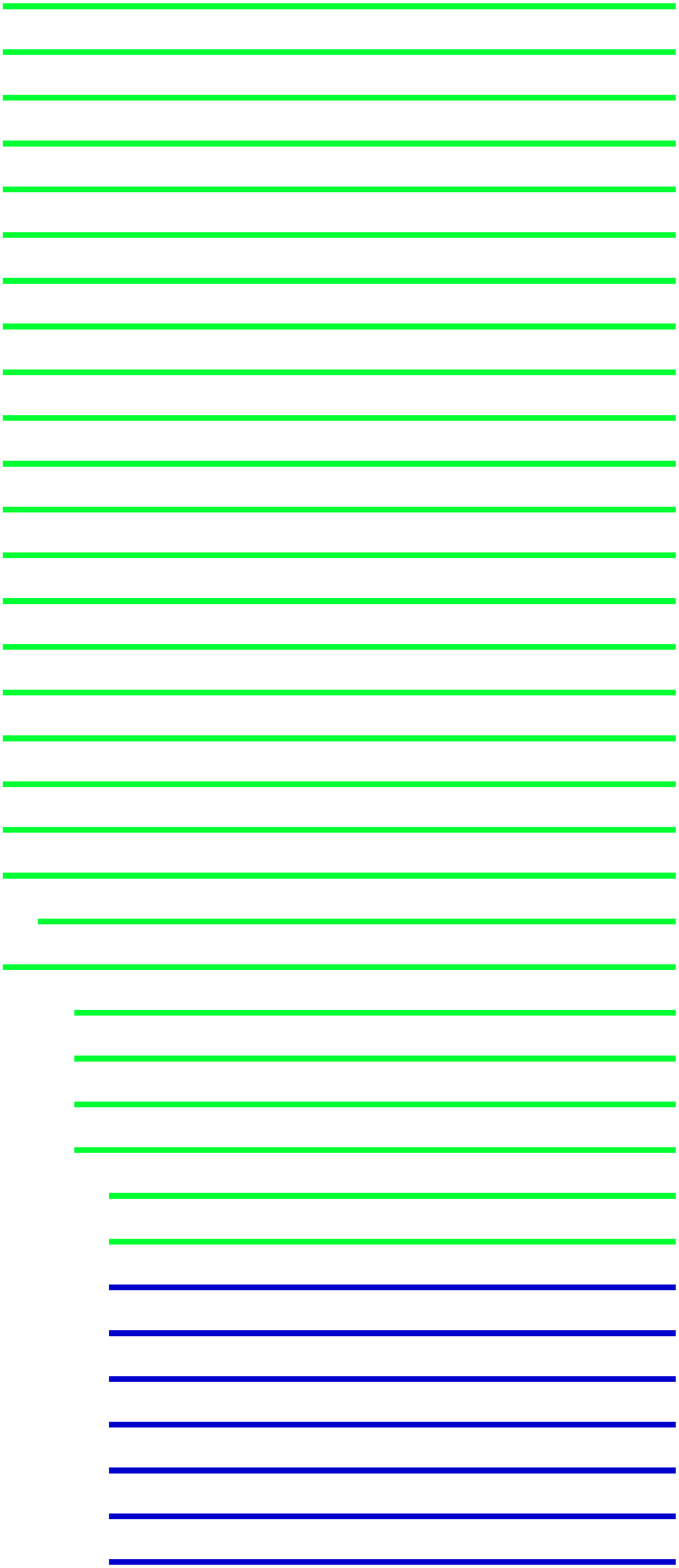
Show Conserved Domains

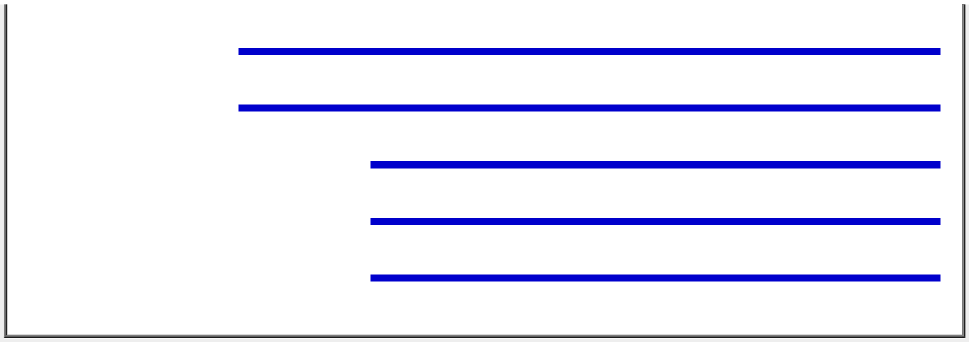
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: complement factor I-like [Gorilla gorilla gorilla]	64.3	64.3	100%	2e-10	100%	gi|426345243|XP_004040330.1
☐	unnamed protein product [Homo sapiens]	64.3	64.3	100%	2e-10	100%	gi|1335055|CAA68417.1
☐	CFI protein [Homo sapiens]	64.3	64.3	100%	2e-10	100%	gi|18089117|AAH20718.1
☐	complement factor I, isoform CRA_a [Homo sapiens]	64.3	64.3	100%	2e-10	100%	gi|119626655|EAX06250.1
☐	PREDICTED: complement factor I-like [Macaca mulatta]	64.3	64.3	100%	2e-10	100%	gi|297293220|XP_001087512.2
☐	PREDICTED: complement factor I isoform X3 [Chlorocebus sabaeu	64.3	64.3	100%	2e-10	100%	gi|635044271|XP_007997720.1
☐	PREDICTED: complement factor I isoform X6 [Pan troglodytes]	64.3	64.3	100%	2e-10	100%	gi|694908492|XP_009446407.1
☐	PREDICTED: complement factor I isoform X6 [Pan paniscus]	64.3	64.3	100%	2e-10	100%	gi|675793799|XP_008953634.1
☐	uncharacterized protein LOC101866929 precursor [Macaca fascicul	64.3	64.3	100%	2e-10	100%	gi|548961885|NP_001271714.1
☐	PREDICTED: complement factor I isoform X5 [Pan troglodytes]	64.3	64.3	100%	2e-10	100%	gi|694908490|XP_009446406.1
☐	PREDICTED: complement factor I isoform X5 [Pan paniscus]	64.3	64.3	100%	2e-10	100%	gi|675793797|XP_008953633.1
☐	PREDICTED: complement factor I isoform X4 [Homo sapiens]	64.3	64.3	100%	2e-10	100%	gi|578809103|XP_006714273.1
☐	Chain A, Human Complement Factor I [Homo sapiens]	64.3	64.3	100%	2e-10	100%	gi|339961198|2XRC_A
☐	PREDICTED: complement factor I isoform X4 [Pan troglodytes]	64.3	64.3	100%	2e-10	100%	gi|694908488|XP_009446405.1
☐	PREDICTED: complement factor I isoform X4 [Pan paniscus]	64.3	64.3	100%	2e-10	100%	gi|675793795|XP_008953632.1
☐	PREDICTED: complement factor I isoform X2 [Chlorocebus sabaeu	64.3	64.3	100%	2e-10	100%	gi|635044269|XP_007997719.1
☐	PREDICTED: complement factor I isoform X2 [Homo sapiens]	64.3	64.3	100%	2e-10	100%	gi|530377647|XP_005263033.1
☐	PREDICTED: complement factor I [Nomascus leucogenys]	64.3	64.3	100%	2e-10	100%	gi|332240463|XP_003269405.1
☐	PREDICTED: complement factor I isoform X1 [Chlorocebus sabaeu	64.3	64.3	100%	2e-10	100%	gi|635044267|XP_007997718.1
☐	prepro-C3b/C4B inactivator [Homo sapiens]	64.3	64.3	100%	2e-10	100%	gi|182607|AAA52455.1
☐	complement factor I preproprotein [Homo sapiens]	64.3	64.3	100%	2e-10	100%	gi|119392081|NP_000195.2
☐	PREDICTED: complement factor I isoform X3 [Pan paniscus]	64.3	64.3	100%	2e-10	100%	gi|397519838|XP_003830060.1
☐	RecName: Full=Complement factor I; AltName: Full=C3B/C4B inact	64.3	64.3	100%	2e-10	100%	gi|317373341|P05156.2
☐	unnamed protein product [Homo sapiens]	64.3	64.3	100%	2e-10	100%	gi|158254682|BAF83314.1
☐	PREDICTED: complement factor I isoform X3 [Pan troglodytes]	64.3	64.3	100%	2e-10	100%	gi|114595644|XP_526653.2
☐	PREDICTED: complement factor I isoform X2 [Pan troglodytes]	64.3	64.3	100%	2e-10	100%	gi|694908485|XP_009446404.1
☐	PREDICTED: complement factor I isoform X2 [Pan paniscus]	64.3	64.3	100%	2e-10	100%	gi|675793792|XP_008953631.1
☐	PREDICTED: complement factor I isoform X3 [Homo sapiens]	64.3	64.3	100%	2e-10	100%	gi|578809101|XP_006714272.1
☐							

	unnamed protein product [Homo sapiens]	64.3	64.3	100%	2e-10	100%	gi|194387702|BAG61264.1
☐	PREDICTED: complement factor I isoform X1 [Homo sapiens]	64.3	64.3	100%	2e-10	100%	gi|530377645|XP_005263032.1
☐	PREDICTED: complement factor I isoform X1 [Pan paniscus]	64.3	64.3	100%	2e-10	100%	gi|397519840|XP_003830061.1
☐	hypothetical protein EGK_16010 [Macaca mulatta]	64.3	64.3	100%	2e-10	100%	gi|355687535|EHH26119.1
☐	PREDICTED: complement factor I isoform X1 [Pan troglodytes]	64.3	64.3	100%	2e-10	100%	gi|332820084|XP_003310493.1
☐	PREDICTED: complement factor I isoform X1 [Pongo abelii]	61.7	61.7	100%	2e-09	95%	gi|686716760|XP_009238531.1
☐	complement factor I [Pongo abelii]	61.7	61.7	100%	2e-09	95%	gi|207080120|NP_001128776.1
☐	complement factor I precursor [Pongo abelii]	61.7	61.7	100%	2e-09	95%	gi|197098986|NP_001127624.1
☐	PREDICTED: complement factor I [Rhinopithecus roxellana]	57.9	57.9	94%	3e-08	94%	gi|724946291|XP_010387365.1
☐	PREDICTED: complement factor I [Papio anubis]	55.4	55.4	100%	2e-07	89%	gi|685542561|XP_009205631.1
☐	PREDICTED: complement factor I isoform X2 [Saimiri boliviensis bo	53.2	53.2	89%	1e-06	88%	gi|725571753|XP_010338379.1
☐	PREDICTED: complement factor I [Callithrix jacchus]	53.2	53.2	89%	1e-06	88%	gi|675648222|XP_002745538.3
☐	PREDICTED: complement factor I [Callithrix jacchus]	53.2	53.2	89%	1e-06	88%	gi|675752511|XP_008984405.1
☐	PREDICTED: complement factor I isoform X1 [Saimiri boliviensis bo	53.2	53.2	89%	1e-06	88%	gi|725571751|XP_010338378.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Felis	50.7	50.7	84%	9e-06	94%	gi|586984171|XP_006930977.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Lipo	50.7	50.7	84%	9e-06	94%	gi|602703733|XP_007463290.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Vicu	48.6	48.6	84%	4e-05	88%	gi|560979761|XP_006212132.1
☐	PREDICTED: complement factor I isoform X6 [Panthera tigris altaic	48.1	48.1	84%	6e-05	88%	gi|591346160|XP_007098330.1
☐	PREDICTED: complement factor I isoform X5 [Panthera tigris altaic	48.1	48.1	84%	6e-05	88%	gi|591346158|XP_007098329.1
☐	PREDICTED: complement factor I isoform X4 [Panthera tigris altaic	48.1	48.1	84%	6e-05	88%	gi|591346156|XP_007098328.1
☐	PREDICTED: complement factor I isoform X2 [Panthera tigris altaic	48.1	48.1	84%	6e-05	88%	gi|591346152|XP_007098326.1
☐	PREDICTED: complement factor I isoform X1 [Panthera tigris altaic	48.1	48.1	84%	6e-05	88%	gi|591346150|XP_007098325.1
☐	complement factor I precursor [Camelus ferus]	47.7	47.7	84%	8e-05	88%	gi|528758403|EPY78062.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Cam	47.7	47.7	84%	8e-05	88%	gi|560925633|XP_006188998.1
☐	PREDICTED: complement factor I [Mesocricetus auratus]	47.3	47.3	84%	1e-04	88%	gi|524965961|XP_005082885.1
☐	PREDICTED: complement factor I [Tursiops truncatus]	46.9	46.9	68%	2e-04	100%	gi|470636247|XP_004323514.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Orci	46.9	46.9	68%	2e-04	100%	gi|466008566|XP_004269732.1
☐	PREDICTED: complement factor I [Physeter catodon]	46.9	46.9	68%	2e-04	100%	gi|593719134|XP_007105924.1
☐	PREDICTED: complement factor I [Loxodonta africana]	46.4	46.4	78%	2e-04	87%	gi|731479219|XP_010588889.1
☐	hypothetical protein PANDA_019552 [Ailuropoda melanoleuca]	46.0	46.0	84%	3e-04	81%	gi|281338891|EFB14475.1
☐	PREDICTED: complement factor I-like [Ailuropoda melanoleuca]	46.0	46.0	84%	3e-04	81%	gi|301787939|XP_002929384.1
☐	PREDICTED: complement factor I [Ursus maritimus]	46.0	46.0	84%	3e-04	81%	gi|670993394|XP_008687645.1
☐	complement factor I-like protein [Cricetulus griseus]	45.2	45.2	84%	6e-04	88%	gi|537261801|ERE90152.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	45.2	45.2	84%	6e-04	88%	gi|625241505|XP_007611983.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	45.2	45.2	84%	6e-04	88%	gi|625222421|XP_007651009.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Chin	44.8	44.8	84%	8e-04	81%	gi|533186455|XP_005406244.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Lept	44.3	44.3	84%	0.001	81%	gi|585149528|XP_006727262.1
☐	Complement factor I [Tupaia chinensis]	44.3	44.3	78%	0.001	87%	gi|444524072|ELV13709.1
☐	PREDICTED: complement factor I [Tupaia chinensis]	44.3	44.3	78%	0.001	87%	gi|562868474|XP_006162305.1
☐	complement factor I [Mus musculus]	43.9	43.9	84%	0.001	81%	gi|4926957|AAD32965.1
☐	complement component factor i [Mus musculus]	43.9	43.9	84%	0.002	81%	gi|148680281|EDL12228.1
☐	PREDICTED: complement factor I [Ochotona princeps]	43.9	43.9	84%	0.002	81%	gi|504169976|XP_004594584.1
☐	PREDICTED: complement factor I isoform X4 [Mus musculus]	43.9	43.9	84%	0.002	81%	gi|568921717|XP_006501026.1
☐	PREDICTED: complement factor I isoform X3 [Mus musculus]	43.9	43.9	84%	0.002	81%	gi|568921715|XP_006501025.1
☐	PREDICTED: complement factor I isoform X2 [Mus musculus]	43.9	43.9	84%	0.002	81%	gi|568921713|XP_006501024.1

☐	complement factor I [Mus musculus]	43.9	43.9	84%	0.002	81%	gi|1322034|AAB00438.1
☐	complement factor I precursor [Mus musculus]	43.9	43.9	84%	0.002	81%	gi|110347406|NP_031712.2
☐	PREDICTED: complement factor I isoform X2 [Ictidomys tridecemlir	43.5	43.5	84%	0.002	81%	gi|532088899|XP_005330149.1
☐	PREDICTED: complement factor I isoform X1 [Ictidomys tridecemlir	43.5	43.5	84%	0.002	81%	gi|532088897|XP_005330148.1
☐	PREDICTED: complement factor I [Balaenoptera acutorostrata scar	43.5	43.5	63%	0.002	100%	gi|594687284|XP_007191087.1
☐	PREDICTED: complement factor I [Trichechus manatus latirostris]	43.1	43.1	78%	0.003	87%	gi|471391575|XP_004380312.1
☐	PREDICTED: complement factor I [Otolemur garnettii]	42.6	42.6	68%	0.004	92%	gi|395851346|XP_003798222.1
☐	PREDICTED: complement factor I [Sus scrofa]	42.2	42.2	68%	0.005	92%	gi|545846437|XP_005656603.1
☐	PREDICTED: complement factor I [Orycteropus afer afer]	41.8	41.8	68%	0.007	85%	gi|634848033|XP_007938975.1
☐	PREDICTED: complement factor I [Peromyscus maniculatus bairdii	39.7	39.7	84%	0.036	75%	gi|589914217|XP_006970447.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	39.2	39.2	73%	0.048	79%	gi|511847748|XP_004748251.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	39.2	39.2	73%	0.049	79%	gi|511991360|XP_004813365.1
☐	Complement factor I [Fukomys damarensis]	38.8	38.8	84%	0.066	75%	gi|676270629|KFO25832.1
☐	Complement factor I [Heterocephalus glaber]	38.8	38.8	84%	0.067	75%	gi|351696416|EHA99334.1
☐	PREDICTED: complement factor I [Tarsius syrichta]	38.8	38.8	63%	0.067	92%	gi|640813983|XP_008063707.1
☐	PREDICTED: complement factor I isoform X2 [Fukomys damarensi	38.8	38.8	84%	0.067	75%	gi|731254237|XP_010639824.1
☐	PREDICTED: complement factor I isoform X2 [Heterocephalus glab	38.8	38.8	84%	0.067	75%	gi|512818622|XP_004878889.1
☐	PREDICTED: complement factor I isoform X1 [Fukomys damarensi	38.8	38.8	84%	0.067	75%	gi|731254235|XP_010639823.1
☐	PREDICTED: complement factor I isoform X1 [Heterocephalus glab	38.8	38.8	84%	0.067	75%	gi|512818618|XP_004878888.1
☐	PREDICTED: complement factor I [Echinops telfairi]	38.4	38.4	68%	0.091	77%	gi|507649004|XP_004703515.1
☐	complement factor I precursor [Rattus norvegicus]	38.0	38.0	68%	0.12	85%	gi|13162353|NP_077071.1
☐	PREDICTED: complement factor I isoform X1 [Rattus norvegicus]	38.0	38.0	68%	0.13	85%	gi|672044321|XP_008759748.1
☐	PREDICTED: complement factor I [Dasypus novemcinctus]	37.5	37.5	84%	0.17	69%	gi|488581726|XP_004476284.1
☐	PREDICTED: complement factor I [Chrysochloris asiatica]	37.5	37.5	68%	0.17	77%	gi|586477731|XP_006869402.1
☐	PREDICTED: complement factor I [Bubalus bubalis]	37.1	37.1	84%	0.23	75%	gi|594056114|XP_006052270.1
☐	PREDICTED: complement factor I [Pantholops hodgsonii]	37.1	37.1	84%	0.23	75%	gi|556750321|XP_005970578.1
☐	PREDICTED: complement factor I isoform X2 [Capra hircus]	37.1	37.1	84%	0.23	75%	gi|548469406|XP_005681373.1

⊟ Alignments

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PREDICTED: complement factor I-like, partial [Gorilla gorilla gorilla]

Sequence ID: gi|426345243|ref|XP_004040330.1| **Length:** 309 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 170 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
64.3 bits(144)	2e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLSDLSINSTECLHVHCRG  19
            KLSDLSINSTECLHVHCRG
Sbjct  170  KLSDLSINSTECLHVHCRG  188
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|1335055|emb|CAA68417.1| **Length:** 321 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 152 to 170 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
64.3 bits(144)	2e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLSDLSINSTECLHVHCRG  19
```

```
                KLSDLSINSTECLHVHCRG
Sbjct  152  KLSDLSINSTECLHVHCRG  170
```

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CFI protein [Homo sapiens]

Sequence ID: gi|18089117|gb|AAH20718.1| **Length:** 377 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 170 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
64.3 bits(144)	2e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLSDLSINSTECLHVHCRG  19
            KLSDLSINSTECLHVHCRG
Sbjct  170  KLSDLSINSTECLHVHCRG  188
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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complement factor I, isoform CRA_a, partial [Homo sapiens]

Sequence ID: gi|119626655|gb|EAX06250.1| **Length:** 378 **Number of Matches:** 1

Range 1: 170 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
64.3 bits(144)	2e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLSDLSINSTECLHVHCRG  19
            KLSDLSINSTECLHVHCRG
Sbjct  170  KLSDLSINSTECLHVHCRG  188
```

Related Information

Gene - associated gene details

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PREDICTED: complement factor I-like [Macaca mulatta]

Sequence ID: gi|297293220|ref|XP_001087512.2| **Length:** 428 **Number of Matches:** 1

Range 1: 169 to 187 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
64.3 bits(144)	2e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLSDLSINSTECLHVHCRG  19
            KLSDLSINSTECLHVHCRG
Sbjct  169  KLSDLSINSTECLHVHCRG  187
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

CFI_RSIPACVPWSPYLFQPDDTCIVSGWGRE_Mod

RID BTG9AZV9013 (Expires on 01-20 15:32 pm)

Query ID lcl|73802
Description None
Molecule type amino acid
Query Length 28

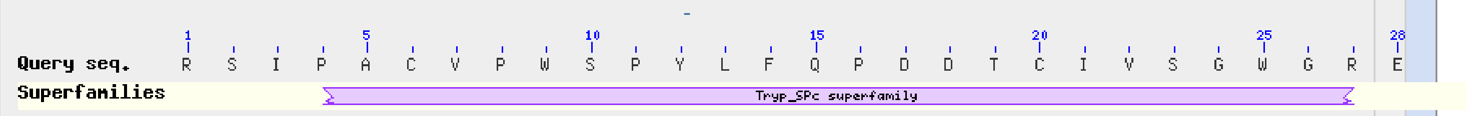
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

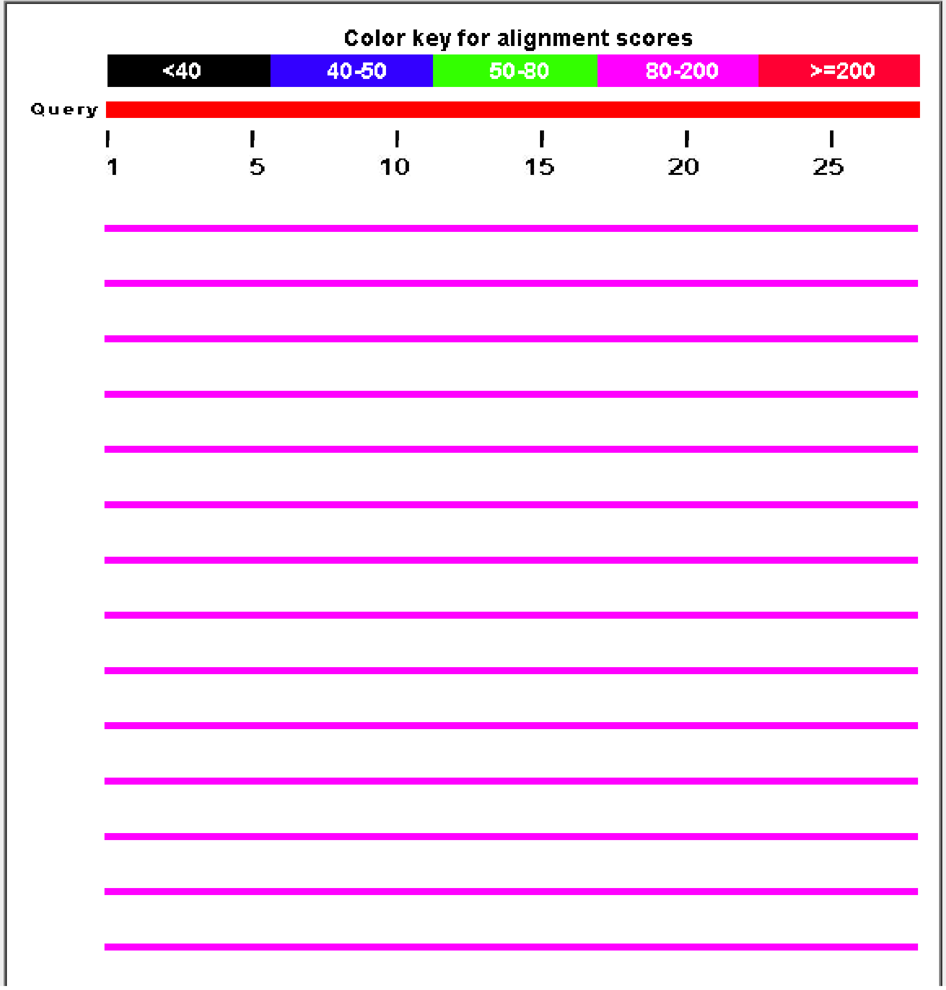
Show Conserved Domains

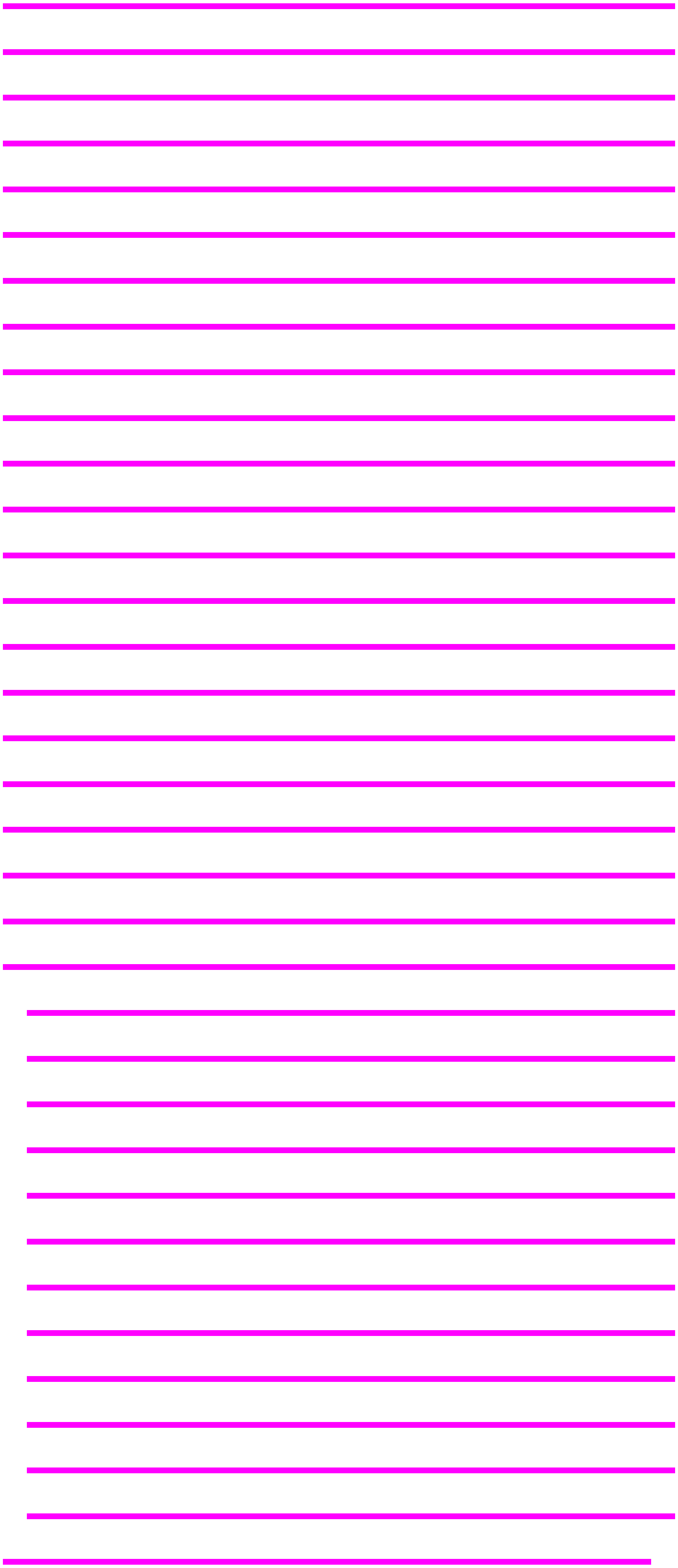
Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: complement factor I-like [Macaca fascicularis]	96.5	96.5	100%	6e-21	96%	gi|544524397|XP_005595214.1
☐	complement factor I light chain [Homo sapiens]	96.1	96.1	100%	6e-21	96%	gi|224798|1202205A
☐	PREDICTED: complement factor I isoform X3 [Chlorocebus sal	96.5	96.5	100%	7e-21	96%	gi|635044271|XP_007997720.1
☐	uncharacterized protein LOC101866929 precursor [Macaca fas	96.5	96.5	100%	7e-21	96%	gi|548961885|NP_001271714.1
☐	PREDICTED: complement factor I isoform X2 [Chlorocebus sal	96.5	96.5	100%	7e-21	96%	gi|635044269|XP_007997719.1
☐	unnamed protein product [Homo sapiens]	96.1	96.1	100%	7e-21	96%	gi|1335056|CAA68418.1
☐	PREDICTED: complement factor I isoform X1 [Chlorocebus sal	96.5	96.5	100%	7e-21	96%	gi|635044267|XP_007997718.1
☐	hypothetical protein EGK_16010 [Macaca mulatta]	96.5	96.5	100%	7e-21	96%	gi|355687535|EHH26119.1
☐	PREDICTED: complement factor I [Papio anubis]	96.5	96.5	100%	7e-21	96%	gi|685542561|XP_009205631.1
☐	PREDICTED: complement factor I isoform X1 [Pongo abelii]	96.1	96.1	100%	1e-20	96%	gi|686716760|XP_009238531.1
☐	complement factor I [Pongo abelii]	96.1	96.1	100%	1e-20	96%	gi|207080120|NP_001128776.1
☐	PREDICTED: complement factor I isoform X4 [Homo sapiens]	96.1	96.1	100%	1e-20	96%	gi|578809103|XP_006714273.1
☐	Chain A, Human Complement Factor I [Homo sapiens]	96.1	96.1	100%	1e-20	96%	gi|339961198|2XRC_A
☐	PREDICTED: complement factor I isoform X2 [Homo sapiens]	96.1	96.1	100%	1e-20	96%	gi|530377647|XP_005263033.1
☐	PREDICTED: complement factor I [Nomascus leucogenys]	96.1	96.1	100%	1e-20	96%	gi|332240463|XP_003269405.1
☐	prepro-C3b/C4B inactivator [Homo sapiens]	96.1	96.1	100%	1e-20	96%	gi|182607|AAA52455.1
☐	complement factor I preproprotein [Homo sapiens]	96.1	96.1	100%	1e-20	96%	gi|119392081|NP_000195.2
☐	complement factor I precursor [Pongo abelii]	96.1	96.1	100%	1e-20	96%	gi|197098986|NP_001127624.1
☐	RecName: Full=Complement factor I; AltName: Full=C3B/C4B i	96.1	96.1	100%	1e-20	96%	gi|317373341|P05156.2
☐	unnamed protein product [Homo sapiens]	96.1	96.1	100%	1e-20	96%	gi|158254682|BAF83314.1
☐	PREDICTED: complement factor I isoform X3 [Homo sapiens]	96.1	96.1	100%	1e-20	96%	gi|578809101|XP_006714272.1
☐	unnamed protein product [Homo sapiens]	96.1	96.1	100%	1e-20	96%	gi|194387702|BAG61264.1
☐	PREDICTED: complement factor I isoform X1 [Homo sapiens]	96.1	96.1	100%	1e-20	96%	gi|530377645|XP_005263032.1
☐	PREDICTED: complement factor I-like [Gorilla gorilla gorilla]	94.0	94.0	100%	4e-20	93%	gi|426345227|XP_004040322.1
☐	PREDICTED: complement factor I isoform X6 [Pan troglodytes]	94.0	94.0	100%	5e-20	93%	gi|694908492|XP_009446407.1
☐	PREDICTED: complement factor I isoform X6 [Pan paniscus]	94.0	94.0	100%	5e-20	93%	gi|675793799|XP_008953634.1
☐	PREDICTED: complement factor I isoform X5 [Pan troglodytes]	94.0	94.0	100%	5e-20	93%	gi|694908490|XP_009446406.1
☐	PREDICTED: complement factor I isoform X5 [Pan paniscus]	94.0	94.0	100%	5e-20	93%	gi|675793797|XP_008953633.1

☐	PREDICTED: complement factor I isoform X4 [Pan troglodytes]	94.0	94.0	100%	6e-20	93%	gi|694908488|XP_009446405.1
☐	PREDICTED: complement factor I isoform X4 [Pan paniscus]	94.0	94.0	100%	6e-20	93%	gi|675793795|XP_008953632.1
☐	PREDICTED: complement factor I isoform X3 [Pan paniscus]	94.0	94.0	100%	6e-20	93%	gi|397519838|XP_003830060.1
☐	PREDICTED: complement factor I isoform X3 [Pan troglodytes]	94.0	94.0	100%	6e-20	93%	gi|114595644|XP_526653.2
☐	PREDICTED: complement factor I isoform X2 [Pan troglodytes]	94.0	94.0	100%	6e-20	93%	gi|694908485|XP_009446404.1
☐	PREDICTED: complement factor I isoform X2 [Pan paniscus]	94.0	94.0	100%	6e-20	93%	gi|675793792|XP_008953631.1
☐	PREDICTED: complement factor I isoform X1 [Pan paniscus]	94.0	94.0	100%	6e-20	93%	gi|397519840|XP_003830061.1
☐	PREDICTED: complement factor I isoform X1 [Pan troglodytes]	94.0	94.0	100%	6e-20	93%	gi|332820084|XP_003310493.1
☐	PREDICTED: complement factor I [Dasypus novemcinctus]	90.6	90.6	96%	8e-19	96%	gi|488581726|XP_004476284.1
☐	PREDICTED: complement factor I isoform X2 [Saimiri boliviens	90.1	90.1	96%	1e-18	93%	gi|725571753|XP_010338379.1
☐	PREDICTED: complement factor I [Callithrix jacchus]	90.1	90.1	96%	1e-18	93%	gi|675648222|XP_002745538.3
☐	PREDICTED: complement factor I [Callithrix jacchus]	90.1	90.1	96%	1e-18	93%	gi|675752511|XP_008984405.1
☐	PREDICTED: complement factor I isoform X1 [Saimiri boliviens	90.1	90.1	96%	1e-18	93%	gi|725571751|XP_010338378.1
☐	PREDICTED: complement factor I [Chrysochloris asiatica]	90.1	90.1	96%	1e-18	93%	gi|586477731|XP_006869402.1
☐	PREDICTED: complement factor I-like [Galeopterus variegatus	88.4	88.4	96%	4e-18	93%	gi|667268997|XP_008570201.1
☐	PREDICTED: complement factor I [Loxodonta africana]	88.4	88.4	96%	4e-18	93%	gi|731479219|XP_010588889.1
☐	complement factor I precursor [Bos taurus]	88.4	88.4	96%	4e-18	93%	gi|84000165|NP_001033185.1
☐	PREDICTED: complement factor I [Bos mutus]	88.4	88.4	96%	4e-18	93%	gi|555968512|XP_005896291.1
☐	TPA: complement factor I [Bos taurus]	88.4	88.4	96%	4e-18	93%	gi|296486756|DAA28869.1
☐	PREDICTED: complement factor I [Physeter catodon]	88.4	88.4	96%	4e-18	93%	gi|593719134|XP_007105924.1
☐	PREDICTED: complement factor I [Rhinopithecus roxellana]	87.6	87.6	96%	8e-18	93%	gi|724946291|XP_010387365.1
☐	PREDICTED: complement factor I [Pteropus alecto]	87.2	87.2	96%	1e-17	89%	gi|586528110|XP_006918978.1
☐	Complement factor I [Pteropus alecto]	87.2	87.2	96%	1e-17	89%	gi|431897147|ELK06409.1
☐	PREDICTED: complement factor I [Elephantulus edwardii]	85.9	85.9	96%	3e-17	89%	gi|585642072|XP_006881212.1
☐	PREDICTED: complement factor I [Tursiops truncatus]	85.9	85.9	96%	3e-17	89%	gi|470636247|XP_004323514.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	85.9	85.9	96%	3e-17	89%	gi|602703733|XP_007463290.1
☐	PREDICTED: complement factor I [Balaenoptera acutorostrata	85.9	85.9	96%	3e-17	89%	gi|594687284|XP_007191087.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	85.9	85.9	96%	3e-17	89%	gi|466008566|XP_004269732.1
☐	PREDICTED: complement factor I [Trichechus manatus latirost	85.9	85.9	96%	3e-17	89%	gi|471391575|XP_004380312.1
☐	Complement factor I [Fukomys damarensis]	85.0	85.0	96%	6e-17	89%	gi|676270629|KFO25832.1
☐	Complement factor I [Heterocephalus glaber]	85.0	85.0	96%	6e-17	89%	gi|351696416|EHA99334.1
☐	PREDICTED: complement factor I [Octodon degus]	85.0	85.0	96%	6e-17	89%	gi|507626946|XP_004626817.1
☐	PREDICTED: complement factor I isoform X2 [Fukomys damar	85.0	85.0	96%	6e-17	89%	gi|731254237|XP_010639824.1
☐	PREDICTED: complement factor I isoform X2 [Heterocephalus	85.0	85.0	96%	6e-17	89%	gi|512818622|XP_004878889.1
☐	PREDICTED: complement factor I isoform X1 [Fukomys damar	85.0	85.0	96%	6e-17	89%	gi|731254235|XP_010639823.1
☐	PREDICTED: complement factor I isoform X1 [Heterocephalus	85.0	85.0	96%	6e-17	89%	gi|512818618|XP_004878888.1
☐	PREDICTED: complement factor I isoform X2 [Ictidomys tridec	84.6	84.6	96%	9e-17	93%	gi|532088899|XP_005330149.1
☐	PREDICTED: complement factor I isoform X1 [Ictidomys tridec	84.6	84.6	96%	9e-17	93%	gi|532088897|XP_005330148.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	84.6	84.6	96%	9e-17	89%	gi|533186455|XP_005406244.1
☐	PREDICTED: complement factor I [Erinaceus europaeus]	84.6	84.6	96%	9e-17	89%	gi|617652869|XP_007534556.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	84.2	84.2	96%	1e-16	89%	gi|585149528|XP_006727262.1
☐	PREDICTED: complement factor I [Orycteropus afer afer]	84.2	84.2	96%	1e-16	89%	gi|634848033|XP_007938975.1
☐	PREDICTED: complement factor I isoform X2 [Camelus drome	83.8	83.8	96%	2e-16	85%	gi|744567503|XP_010979382.1
☐	PREDICTED: complement factor I isoform X2 [Camelus bactria	83.8	83.8	96%	2e-16	85%	gi|743716645|XP_010951976.1
☐	PREDICTED: complement factor I isoform X1 [Camelus drome	83.8	83.8	96%	2e-16	85%	gi|744567500|XP_010979381.1
☐	PREDICTED: complement factor I isoform X1 [Camelus bactria	83.8	83.8	96%	2e-16	85%	gi|743716643|XP_010951975.1

☐	complement factor I-like protein [Cricetulus griseus]	83.8	83.8	96%	2e-16	85%	gi|537261801|ERE90152.1
☐	PREDICTED: complement factor I [Bubalus bubalis]	83.8	83.8	96%	2e-16	85%	gi|594056114|XP_006052270.1
☐	PREDICTED: complement factor I [Pantholops hodgsonii]	83.8	83.8	96%	2e-16	85%	gi|556750321|XP_005970578.1
☐	PREDICTED: complement factor I isoform X2 [Capra hircus]	83.8	83.8	96%	2e-16	85%	gi|548469406|XP_005681373.1
☐	PREDICTED: complement factor I isoform X1 [Capra hircus]	83.8	83.8	96%	2e-16	85%	gi|548469399|XP_005681372.1
☐	PREDICTED: complement factor I [Ovis aries]	83.8	83.8	96%	2e-16	85%	gi|426231287|XP_004009671.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	83.8	83.8	96%	2e-16	85%	gi|625241505|XP_007611983.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	83.8	83.8	96%	2e-16	85%	gi|625222421|XP_007651009.1
☐	PREDICTED: complement factor I [Mesocricetus auratus]	83.8	83.8	96%	2e-16	85%	gi|524965961|XP_005082885.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	83.8	83.8	96%	2e-16	85%	gi|560925633|XP_006188998.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	83.8	83.8	96%	2e-16	85%	gi|560979761|XP_006212132.1
☐	PREDICTED: complement factor I [Jaculus jaculus]	83.3	83.3	96%	2e-16	89%	gi|507549735|XP_004658680.1
☐	complement factor I [Rattus norvegicus]	82.5	82.5	96%	4e-16	85%	gi|149025945|EDL82188.1
☐	PREDICTED: complement factor I isoform X6 [Panthera tigris a	82.5	82.5	96%	5e-16	85%	gi|591346160|XP_007098330.1
☐	PREDICTED: complement factor I isoform X5 [Panthera tigris a	82.5	82.5	96%	5e-16	85%	gi|591346158|XP_007098329.1
☐	PREDICTED: complement factor I isoform X4 [Panthera tigris a	82.5	82.5	96%	5e-16	85%	gi|591346156|XP_007098328.1
☐	complement factor I precursor [Rattus norvegicus]	82.5	82.5	96%	5e-16	85%	gi|13162353|NP_077071.1
☐	PREDICTED: complement factor I isoform X2 [Panthera tigris a	82.5	82.5	96%	5e-16	85%	gi|591346152|XP_007098326.1
☐	PREDICTED: complement factor I isoform X1 [Panthera tigris a	82.5	82.5	96%	5e-16	85%	gi|591346150|XP_007098325.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [	82.5	82.5	96%	5e-16	85%	gi|586984171|XP_006930977.1
☐	PREDICTED: complement factor I isoform X2 [Cavia porcellus]	82.5	82.5	96%	5e-16	89%	gi|514457647|XP_005002957.1
☐	PREDICTED: complement factor I isoform X1 [Cavia porcellus]	82.5	82.5	96%	5e-16	89%	gi|514457649|XP_003468099.2
☐	PREDICTED: complement factor I isoform X1 [Rattus norvegicu	82.5	82.5	96%	5e-16	85%	gi|672044321|XP_008759748.1
☐	PREDICTED: complement factor I-like [Equus przewalskii]	82.1	82.1	96%	5e-16	85%	gi|664780387|XP_008509513.1
☐	PREDICTED: complement factor I isoform X2 [Equus caballus]	82.1	82.1	96%	7e-16	85%	gi|545210264|XP_005607952.1
☐	PREDICTED: complement factor I isoform X1 [Equus caballus]	82.1	82.1	96%	7e-16	85%	gi|545210262|XP_005607951.1

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - B93T8V5W01R

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How to read this page | Blast report description

CFI_RSIPACVPWSPYLFQPNDTCIVSGWGRE_NonMod

RID B93T8V5W01R (Expires on 01-14 10:21 am)

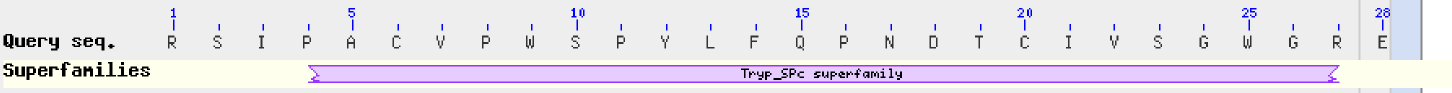
Query ID	lcl|319133	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	28		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

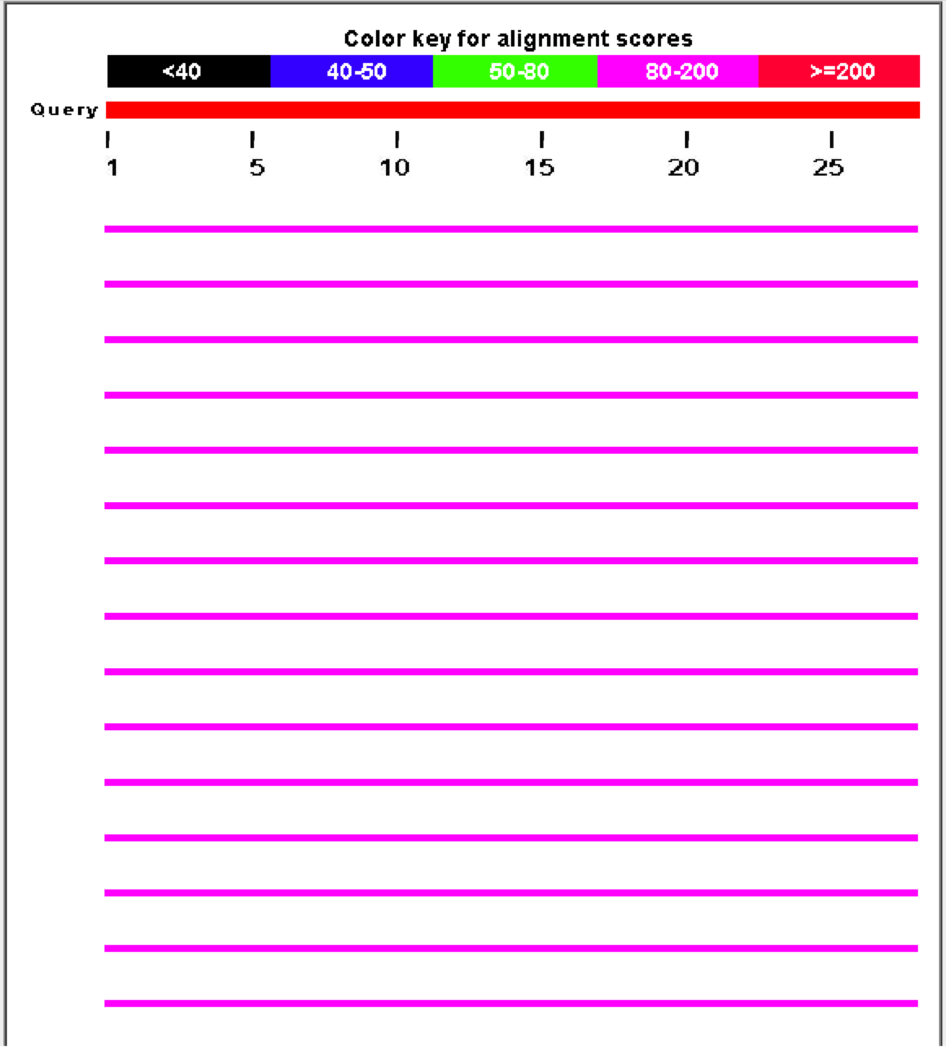
Show Conserved Domains

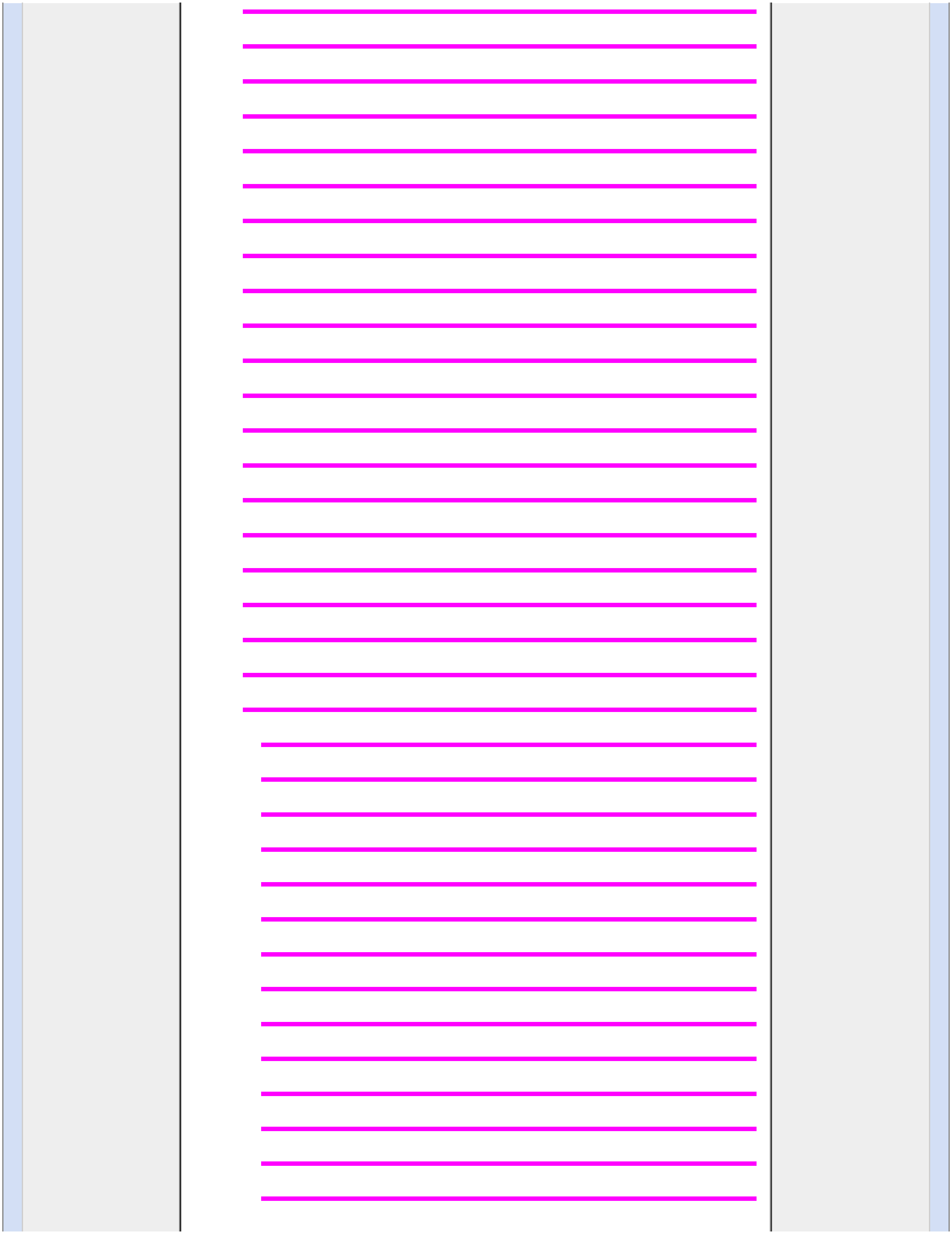
Putative conserved domains have been detected, click on the image below for detailed results.

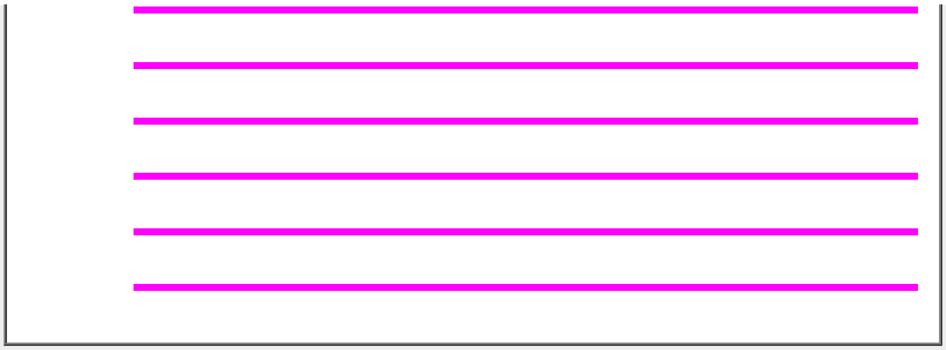


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	complement factor I light chain [Homo sapiens]	98.6	98.6	100%	8e-22	100%	gi|224798|1202205A
☐	unnamed protein product [Homo sapiens]	98.6	98.6	100%	9e-22	100%	gi|1335056|CAA68418.1
☐	PREDICTED: complement factor I isoform X1 [Pongo abelii]	98.6	98.6	100%	1e-21	100%	gi|686716760|XP_009238531.1
☐	complement factor I [Pongo abelii]	98.6	98.6	100%	1e-21	100%	gi|207080120|NP_001128776.1
☐	PREDICTED: complement factor I isoform X4 [Homo sapiens]	98.6	98.6	100%	1e-21	100%	gi|578809103|XP_006714273.1
☐	Chain A, Human Complement Factor I [Homo sapiens]	98.6	98.6	100%	1e-21	100%	gi|339961198|2XRC_A
☐	PREDICTED: complement factor I isoform X2 [Homo sapiens]	98.6	98.6	100%	1e-21	100%	gi|530377647|XP_005263033.1
☐	PREDICTED: complement factor I [Nomascus leucogenys]	98.6	98.6	100%	1e-21	100%	gi|332240463|XP_003269405.1
☐	prepro-C3b/C4B inactivator [Homo sapiens]	98.6	98.6	100%	1e-21	100%	gi|182607|AAA52455.1
☐	complement factor I preproprotein [Homo sapiens]	98.6	98.6	100%	1e-21	100%	gi|119392081|NP_000195.2
☐	complement factor I precursor [Pongo abelii]	98.6	98.6	100%	1e-21	100%	gi|197098986|NP_001127624.1
☐	RecName: Full=Complement factor I; AltName: Full=C3B/C4B inact	98.6	98.6	100%	1e-21	100%	gi|317373341|P05156.2
☐	unnamed protein product [Homo sapiens]	98.6	98.6	100%	1e-21	100%	gi|158254682|BAF83314.1
☐	PREDICTED: complement factor I isoform X3 [Homo sapiens]	98.6	98.6	100%	1e-21	100%	gi|578809101|XP_006714272.1
☐	unnamed protein product [Homo sapiens]	98.6	98.6	100%	1e-21	100%	gi|194387702|BAG61264.1
☐	PREDICTED: complement factor I isoform X1 [Homo sapiens]	98.6	98.6	100%	1e-21	100%	gi|530377645|XP_005263032.1
☐	PREDICTED: complement factor I-like [Gorilla gorilla gorilla]	96.5	96.5	100%	5e-21	96%	gi|426345227|XP_004040322.1
☐	PREDICTED: complement factor I isoform X6 [Pan troglodytes]	96.5	96.5	100%	7e-21	96%	gi|694908492|XP_009446407.1
☐	PREDICTED: complement factor I isoform X6 [Pan paniscus]	96.5	96.5	100%	7e-21	96%	gi|675793799|XP_008953634.1
☐	PREDICTED: complement factor I isoform X5 [Pan troglodytes]	96.5	96.5	100%	7e-21	96%	gi|694908490|XP_009446406.1
☐	PREDICTED: complement factor I isoform X5 [Pan paniscus]	96.5	96.5	100%	7e-21	96%	gi|675793797|XP_008953633.1
☐	PREDICTED: complement factor I isoform X4 [Pan troglodytes]	96.5	96.5	100%	7e-21	96%	gi|694908488|XP_009446405.1
☐	PREDICTED: complement factor I isoform X4 [Pan paniscus]	96.5	96.5	100%	7e-21	96%	gi|675793795|XP_008953632.1
☐	PREDICTED: complement factor I isoform X3 [Pan paniscus]	96.5	96.5	100%	7e-21	96%	gi|397519838|XP_003830060.1
☐	PREDICTED: complement factor I isoform X3 [Pan troglodytes]	96.5	96.5	100%	7e-21	96%	gi|114595644|XP_526653.2
☐	PREDICTED: complement factor I isoform X2 [Pan troglodytes]	96.5	96.5	100%	7e-21	96%	gi|694908485|XP_009446404.1
☐	PREDICTED: complement factor I isoform X2 [Pan paniscus]	96.5	96.5	100%	7e-21	96%	gi|675793792|XP_008953631.1
☐	PREDICTED: complement factor I isoform X1 [Pan paniscus]	96.5	96.5	100%	7e-21	96%	gi|397519840|XP_003830061.1
☐	PREDICTED: complement factor I isoform X1 [Pan troglodytes]	96.5	96.5	100%	7e-21	96%	gi|332820084|XP_003310493.1

☐	PREDICTED: complement factor I-like [Macaca fascicularis]	94.0	94.0	100%	4e-20	93%	gi|544524397|XP_005595214.1
☐	PREDICTED: complement factor I isoform X3 [Chlorocebus sabaeu	94.0	94.0	100%	5e-20	93%	gi|635044271|XP_007997720.1
☐	uncharacterized protein LOC101866929 precursor [Macaca fascicul	94.0	94.0	100%	5e-20	93%	gi|548961885|NP_001271714.1
☐	PREDICTED: complement factor I isoform X2 [Chlorocebus sabaeu	94.0	94.0	100%	5e-20	93%	gi|635044269|XP_007997719.1
☐	PREDICTED: complement factor I isoform X1 [Chlorocebus sabaeu	94.0	94.0	100%	5e-20	93%	gi|635044267|XP_007997718.1
☐	hypothetical protein EGK_16010 [Macaca mulatta]	94.0	94.0	100%	5e-20	93%	gi|355687535|EHH26119.1
☐	PREDICTED: complement factor I [Papio anubis]	94.0	94.0	100%	5e-20	93%	gi|685542561|XP_009205631.1
☐	PREDICTED: complement factor I isoform X2 [Saimiri boliviensis bo	92.7	92.7	96%	1e-19	96%	gi|725571753|XP_010338379.1
☐	PREDICTED: complement factor I [Callithrix jacchus]	92.7	92.7	96%	1e-19	96%	gi|675648222|XP_002745538.3
☐	PREDICTED: complement factor I [Callithrix jacchus]	92.7	92.7	96%	1e-19	96%	gi|675752511|XP_008984405.1
☐	PREDICTED: complement factor I isoform X1 [Saimiri boliviensis bo	92.7	92.7	96%	1e-19	96%	gi|725571751|XP_010338378.1
☐	PREDICTED: complement factor I [Chrysochloris asiatica]	92.7	92.7	96%	1e-19	96%	gi|586477731|XP_006869402.1
☐	PREDICTED: complement factor I-like [Galeopterus variegatus]	91.0	91.0	96%	5e-19	96%	gi|667268997|XP_008570201.1
☐	PREDICTED: complement factor I [Loxodonta africana]	91.0	91.0	96%	6e-19	96%	gi|731479219|XP_010588889.1
☐	complement factor I precursor [Bos taurus]	91.0	91.0	96%	6e-19	96%	gi|84000165|NP_001033185.1
☐	PREDICTED: complement factor I [Bos mutus]	91.0	91.0	96%	6e-19	96%	gi|555968512|XP_005896291.1
☐	TPA: complement factor I [Bos taurus]	91.0	91.0	96%	6e-19	96%	gi|296486756|DAA28869.1
☐	PREDICTED: complement factor I [Physeter catodon]	91.0	91.0	96%	6e-19	96%	gi|593719134|XP_007105924.1
☐	PREDICTED: complement factor I [Dasypus novemcinctus]	90.6	90.6	96%	8e-19	96%	gi|488581726|XP_004476284.1
☐	PREDICTED: complement factor I [Pteropus alecto]	89.7	89.7	96%	2e-18	93%	gi|586528110|XP_006918978.1
☐	Complement factor I [Pteropus alecto]	89.7	89.7	96%	2e-18	93%	gi|431897147|ELK06409.1
☐	PREDICTED: complement factor I [Elephantulus edwardii]	88.4	88.4	96%	4e-18	93%	gi|585642072|XP_006881212.1
☐	PREDICTED: complement factor I [Tursiops truncatus]	88.4	88.4	96%	4e-18	93%	gi|470636247|XP_004323514.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Lipo	88.4	88.4	96%	4e-18	93%	gi|602703733|XP_007463290.1
☐	PREDICTED: complement factor I [Balaenoptera acutorostrata scar	88.4	88.4	96%	4e-18	93%	gi|594687284|XP_007191087.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Orcir	88.4	88.4	96%	4e-18	93%	gi|466008566|XP_004269732.1
☐	PREDICTED: complement factor I [Trichechus manatus latirostris]	88.4	88.4	96%	4e-18	93%	gi|471391575|XP_004380312.1
☐	PREDICTED: complement factor I [Erinaceus europaeus]	87.2	87.2	96%	1e-17	93%	gi|617652869|XP_007534556.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Lept	86.7	86.7	96%	2e-17	93%	gi|585149528|XP_006727262.1
☐	PREDICTED: complement factor I [Orycteropus afer afer]	86.7	86.7	96%	2e-17	93%	gi|634848033|XP_007938975.1
☐	Complement factor I [Fukomys damarensis]	86.3	86.3	96%	2e-17	89%	gi|676270629|KFO25832.1
☐	Complement factor I [Heterocephalus glaber]	86.3	86.3	96%	2e-17	89%	gi|351696416|EHA99334.1
☐	PREDICTED: complement factor I [Octodon degus]	86.3	86.3	96%	2e-17	89%	gi|507626946|XP_004626817.1
☐	complement factor I-like protein [Cricetulus griseus]	86.3	86.3	96%	2e-17	89%	gi|537261801|ERE90152.1
☐	PREDICTED: complement factor I isoform X2 [Fukomys damarensi	86.3	86.3	96%	2e-17	89%	gi|731254237|XP_010639824.1
☐	PREDICTED: complement factor I isoform X2 [Heterocephalus glab	86.3	86.3	96%	2e-17	89%	gi|512818622|XP_004878889.1
☐	PREDICTED: complement factor I [Bubalus bubalis]	86.3	86.3	96%	2e-17	89%	gi|594056114|XP_006052270.1
☐	PREDICTED: complement factor I [Pantholops hodgsonii]	86.3	86.3	96%	2e-17	89%	gi|556750321|XP_005970578.1
☐	PREDICTED: complement factor I isoform X2 [Capra hircus]	86.3	86.3	96%	2e-17	89%	gi|548469406|XP_005681373.1
☐	PREDICTED: complement factor I isoform X1 [Capra hircus]	86.3	86.3	96%	2e-17	89%	gi|548469399|XP_005681372.1
☐	PREDICTED: complement factor I [Ovis aries]	86.3	86.3	96%	2e-17	89%	gi|426231287|XP_004009671.1
☐	PREDICTED: complement factor I isoform X1 [Fukomys damarensi	86.3	86.3	96%	2e-17	89%	gi|731254235|XP_010639823.1
☐	PREDICTED: complement factor I isoform X1 [Heterocephalus glab	86.3	86.3	96%	2e-17	89%	gi|512818618|XP_004878888.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	86.3	86.3	96%	2e-17	89%	gi|625241505|XP_007611983.1
☐	PREDICTED: complement factor I [Cricetulus griseus]	86.3	86.3	96%	2e-17	89%	gi|625222421|XP_007651009.1
☐	PREDICTED: complement factor I [Mesocricetus auratus]	86.3	86.3	96%	2e-17	89%	gi|524965961|XP_005082885.1

☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Cam	86.3	86.3	96%	2e-17	89%	gi|560925633|XP_006188998.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Vicu	86.3	86.3	96%	2e-17	89%	gi|560979761|XP_006212132.1
☐	PREDICTED: complement factor I isoform X2 [Ictidomys tridecemlir	85.9	85.9	96%	3e-17	93%	gi|532088899|XP_005330149.1
☐	PREDICTED: complement factor I isoform X1 [Ictidomys tridecemlir	85.9	85.9	96%	3e-17	93%	gi|532088897|XP_005330148.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Chin	85.9	85.9	96%	3e-17	89%	gi|533186455|XP_005406244.1
☐	complement factor I [Rattus norvegicus]	85.0	85.0	96%	5e-17	89%	gi|149025945|EDL82188.1
☐	PREDICTED: complement factor I isoform X6 [Panthera tigris altaic	85.0	85.0	96%	6e-17	89%	gi|591346160|XP_007098330.1
☐	PREDICTED: complement factor I [Rhinopithecus roxellana]	85.0	85.0	96%	6e-17	89%	gi|724946291|XP_010387365.1
☐	PREDICTED: complement factor I isoform X5 [Panthera tigris altaic	85.0	85.0	96%	6e-17	89%	gi|591346158|XP_007098329.1
☐	PREDICTED: complement factor I isoform X4 [Panthera tigris altaic	85.0	85.0	96%	6e-17	89%	gi|591346156|XP_007098328.1
☐	complement factor I precursor [Rattus norvegicus]	85.0	85.0	96%	6e-17	89%	gi|13162353|NP_077071.1
☐	PREDICTED: complement factor I isoform X2 [Panthera tigris altaic	85.0	85.0	96%	6e-17	89%	gi|591346152|XP_007098326.1
☐	PREDICTED: complement factor I isoform X1 [Panthera tigris altaic	85.0	85.0	96%	6e-17	89%	gi|591346150|XP_007098325.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Felis	85.0	85.0	96%	6e-17	89%	gi|586984171|XP_006930977.1
☐	PREDICTED: complement factor I isoform X1 [Rattus norvegicus]	85.0	85.0	96%	6e-17	89%	gi|672044321|XP_008759748.1
☐	PREDICTED: complement factor I-like [Equus przewalskii]	84.6	84.6	96%	7e-17	89%	gi|664780387|XP_008509513.1
☐	PREDICTED: complement factor I [Jaculus jaculus]	84.6	84.6	96%	8e-17	89%	gi|507549735|XP_004658680.1
☐	PREDICTED: complement factor I isoform X2 [Equus caballus]	84.6	84.6	96%	8e-17	89%	gi|545210264|XP_005607952.1
☐	PREDICTED: complement factor I isoform X1 [Equus caballus]	84.6	84.6	96%	9e-17	89%	gi|545210262|XP_005607951.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	84.2	84.2	96%	1e-16	89%	gi|511847748|XP_004748251.1
☐	PREDICTED: LOW QUALITY PROTEIN: complement factor I [Odo	84.2	84.2	96%	1e-16	89%	gi|472383864|XP_004411307.1
☐	PREDICTED: complement factor I [Mustela putorius furo]	84.2	84.2	96%	1e-16	89%	gi|511991360|XP_004813365.1
☐	PREDICTED: complement factor I [Peromyscus maniculatus bairdii	83.8	83.8	96%	2e-16	85%	gi|589914217|XP_006970447.1
☐	PREDICTED: complement factor I [Ceratotherium simum simum]	83.8	83.8	96%	2e-16	93%	gi|478504685|XP_004426641.1
☐	PREDICTED: complement factor I isoform X2 [Cavia porcellus]	83.8	83.8	96%	2e-16	89%	gi|514457647|XP_005002957.1

⊟ Alignments

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complement factor I light chain

Sequence ID: gi|224798|prf||1202205A **Length:** 200 **Number of Matches:** 1

Related Information

Range 1: 66 to 93 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
98.6 bits(225)	8e-22	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    RSIPACVPWSPYLFQPNDTCIVSGWGRE  28
            RSIPACVPWSPYLFQPNDTCIVSGWGRE
Sbjct  66   RSIPACVPWSPYLFQPNDTCIVSGWGRE  93
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|1335056|emb|CAA68418.1| **Length:** 244 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 109 to 136 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
98.6 bits(225)	9e-22	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1     RSIPACVPWSPYLFQPNDTCIVSGWGRE  28
             RSIPACVPWSPYLFQPNDTCIVSGWGRE
Sbjct  109   RSIPACVPWSPYLFQPNDTCIVSGWGRE  136
```

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PREDICTED: complement factor I isoform X1 [Pongo abelii]

Sequence ID: gi|686716760|ref|XP_009238531.1| **Length:** 446 **Number of Matches:** 1

Range 1: 311 to 338 GenPept Graphics

Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
98.6 bits(225)	1e-21	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    RSIPACVPWSPYLFQPNDTCIVSGWGRE  28
            RSIPACVPWSPYLFQPNDTCIVSGWGRE
Sbjct  311  RSIPACVPWSPYLFQPNDTCIVSGWGRE  338
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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complement factor I [Pongo abelii]

Sequence ID: gi|207080120|ref|NP_001128776.1| **Length:** 446 **Number of Matches:** 1

See 1 more title(s)

Range 1: 311 to 338 GenPept Graphics

Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
98.6 bits(225)	1e-21	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    RSIPACVPWSPYLFQPNDTCIVSGWGRE  28
            RSIPACVPWSPYLFQPNDTCIVSGWGRE
Sbjct  311  RSIPACVPWSPYLFQPNDTCIVSGWGRE  338
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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PREDICTED: complement factor I isoform X4 [Homo sapiens]

Sequence ID: gi|578809103|ref|XP_006714273.1| **Length:** 531 **Number of Matches:** 1

Range 1: 456 to 483 GenPept Graphics

Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
98.6 bits(225)	1e-21	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    RSIPACVPWSPYLFQPNDTCIVSGWGRE  28
            RSIPACVPWSPYLFQPNDTCIVSGWGRE
Sbjct  456  RSIPACVPWSPYLFQPNDTCIVSGWGRE  483
```

Related Information

Gene - associated gene details

Your search parameters were adjusted to search for a short input sequence.

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CNDP1_RLVPHMDVSAVEKQ_Mod

RID BTGBDV8F016 (Expires on 01-20 15:33 pm)

Query ID lcl|29627
Description None
Molecule type amino acid
Query Length 14

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

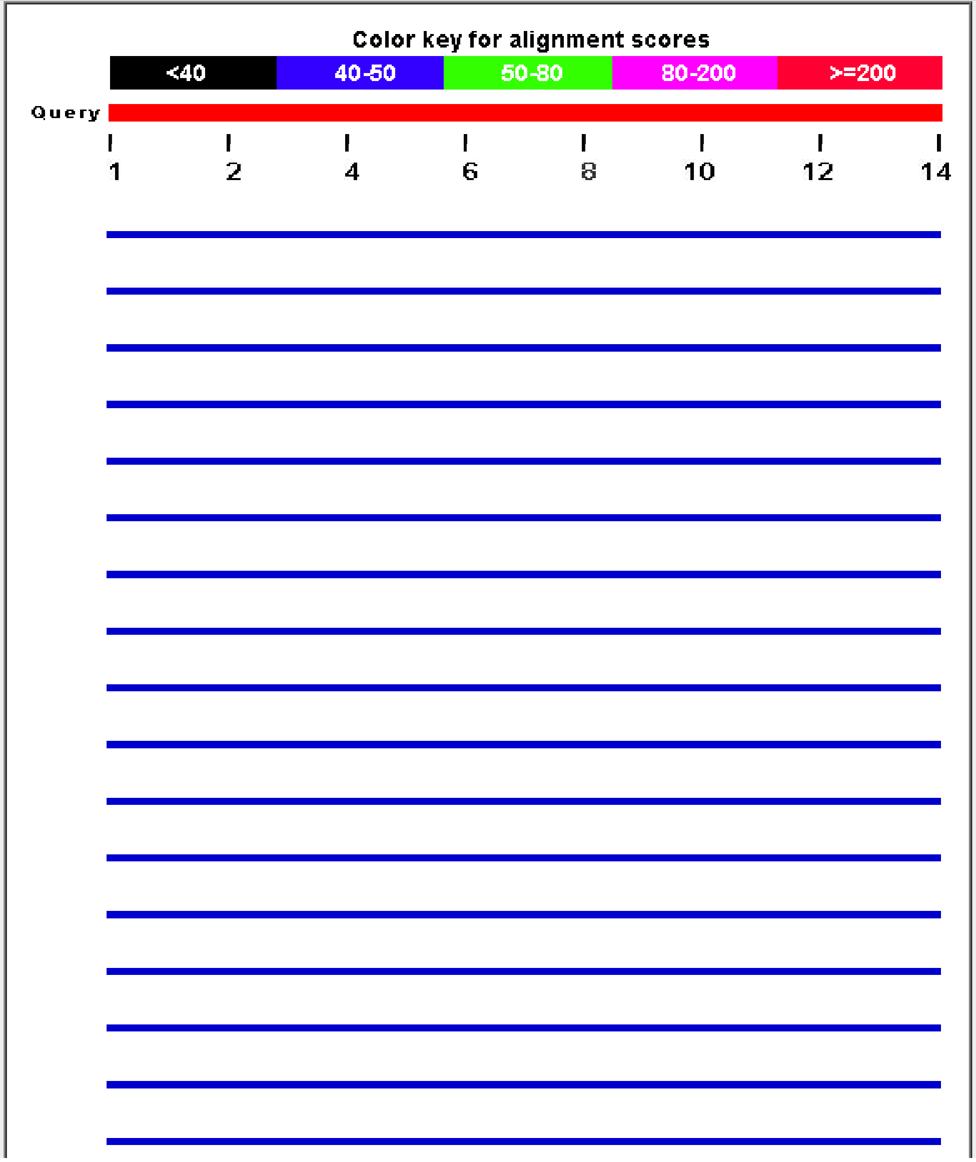
Graphic Summary

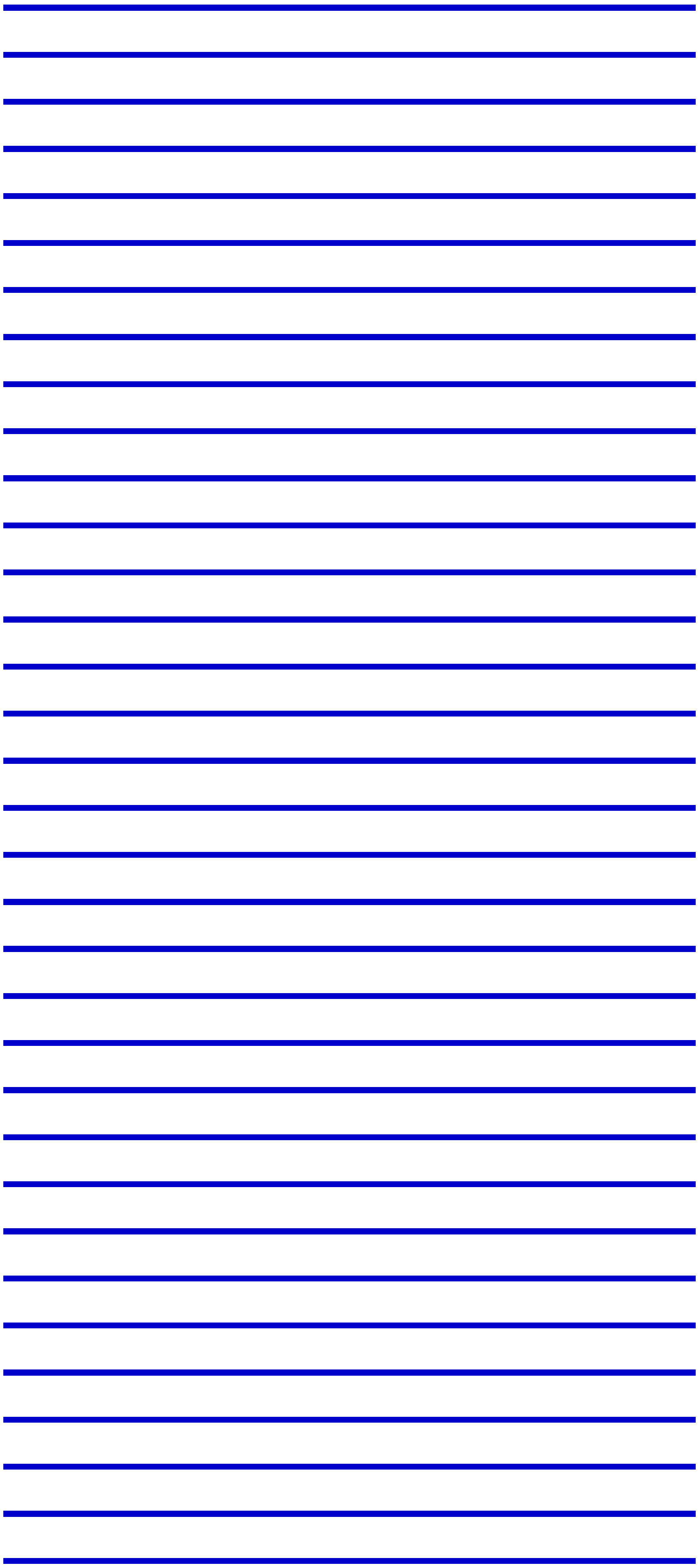
Show Conserved Domains

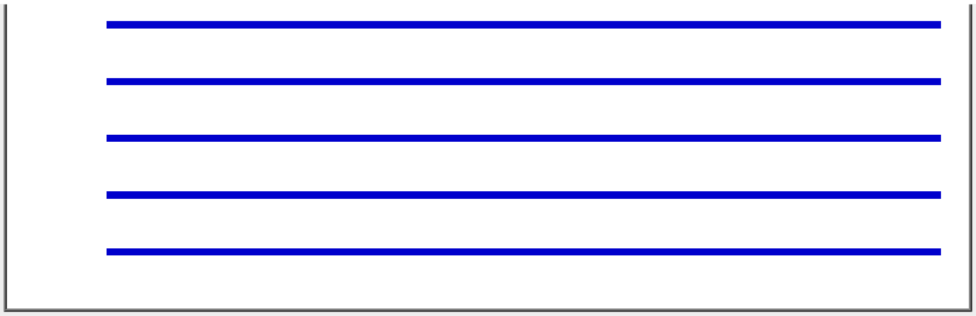
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	carnosine dipeptidase 1 (metallopeptidase M20 family), isoform	46.0	46.0	100%	2e-04	93%	gi|119586964|EAW66560.1
☐	carnosine dipeptidase 1 (metallopeptidase M20 family), isoform	46.0	46.0	100%	2e-04	93%	gi|119586963|EAW66559.1
☐	Chain A, Crystal Structure Of Human Carnosine Dipeptidase 1	46.0	46.0	100%	2e-04	93%	gi|197107410|3DLJ_A
☐	unnamed protein product [Homo sapiens]	46.0	46.0	100%	2e-04	93%	gi|194383442|BAG64692.1
☐	beta-Ala-His dipeptidase precursor [Homo sapiens]	46.0	46.0	100%	2e-04	93%	gi|21071039|NP_116038.4
☐	RecName: Full=Beta-Ala-His dipeptidase; AltName: Full=CNDF	46.0	46.0	100%	2e-04	93%	gi|317373563|Q96KN2.4
☐	unnamed protein product [Homo sapiens]	46.0	46.0	100%	2e-04	93%	gi|158260855|BAF82605.1
☐	Carnosine dipeptidase 1 (metallopeptidase M20 family) [Homo	46.0	46.0	100%	2e-04	93%	gi|83759081|AAI10296.1
☐	Carnosine dipeptidase 1 (metallopeptidase M20 family) [Homo	46.0	46.0	100%	2e-04	93%	gi|109658940|AAI17123.1
☐	glutamate carboxypeptidase-like protein 2 [Homo sapiens]	46.0	46.0	100%	2e-04	93%	gi|16555792|CAD10388.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X4 [Mustela put	44.3	44.3	100%	7e-04	93%	gi|511959771|XP_004798117.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Mustela put	44.3	44.3	100%	7e-04	93%	gi|511842482|XP_004745710.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X3 [Mustela put	44.3	44.3	100%	7e-04	93%	gi|511959769|XP_004798116.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Mustela put	44.3	44.3	100%	7e-04	93%	gi|511842480|XP_004745709.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Mustela put	44.3	44.3	100%	7e-04	93%	gi|511959765|XP_004798114.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Fukomys da	43.1	43.1	100%	0.002	86%	gi|731191032|XP_010608870.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Fukomys da	43.1	43.1	100%	0.002	86%	gi|731191030|XP_010608813.1
☐	Beta-Ala-His dipeptidase [Fukomys damarensis]	43.1	43.1	100%	0.002	86%	gi|676287801|KFO38436.1
☐	PREDICTED: beta-Ala-His dipeptidase-like [Gorilla gorilla gorill	42.6	42.6	100%	0.002	86%	gi|426386236|XP_004059596.1
☐	beta-Ala-His dipeptidase [Pongo abelii]	42.6	42.6	100%	0.002	86%	gi|197100618|NP_001125793.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X4 [Callithrix ja	42.6	42.6	100%	0.002	86%	gi|675718012|XP_008978248.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Oryctolagus	42.6	42.6	100%	0.002	86%	gi|655836920|XP_008259692.1
☐	PREDICTED: LOW QUALITY PROTEIN: beta-Ala-His dipeptida	42.6	42.6	100%	0.002	86%	gi|507684395|XP_004640269.1
☐	PREDICTED: cytosolic non-specific dipeptidase isoform X4 [Pa	42.6	42.6	100%	0.002	86%	gi|675787003|XP_008950931.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X6 [Pan troglod	42.6	42.6	100%	0.002	86%	gi|694971841|XP_009432466.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X3 [Callithrix ja	42.6	42.6	100%	0.002	86%	gi|390474059|XP_002757384.2
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Callithrix ja	42.6	42.6	100%	0.002	86%	gi|675718001|XP_008978246.1
☐	PREDICTED: beta-Ala-His dipeptidase [Rhinopithecus roxellan	42.6	42.6	100%	0.002	86%	gi|724961646|XP_010355009.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Oryctolagus	42.6	42.6	100%	0.002	86%	gi|655836917|XP_008259691.1

☐ PREDICTED: beta-Ala-His dipeptidase isoform X2 [Macaca fas	42.6	42.6	100%	0.002	86%	gi|544505241|XP_005586497.1
☐ PREDICTED: beta-Ala-His dipeptidase [Papio anubis]	42.6	42.6	100%	0.002	86%	gi|402903362|XP_003914537.1
☐ Beta-Ala-His dipeptidase [Macaca mulatta]	42.6	42.6	100%	0.002	86%	gi|355702017|EHH29370.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform 1 [Nomascus le	42.6	42.6	100%	0.002	86%	gi|332230419|XP_003264388.1
☐ PREDICTED: hypothetical protein LOC695195 isoform 2 [Maca	42.6	42.6	100%	0.002	86%	gi|109122502|XP_001085457.1
☐ PREDICTED: hypothetical protein LOC695195 isoform 1 [Maca	42.6	42.6	100%	0.002	86%	gi|297275497|XP_001085348.2
☐ PREDICTED: cytosolic non-specific dipeptidase isoform X3 [Pa	42.6	42.6	100%	0.002	86%	gi|397514119|XP_003827346.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X5 [Pan troglod	42.6	42.6	100%	0.002	86%	gi|114673583|XP_001136945.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X4 [Pan troglod	42.6	42.6	100%	0.002	86%	gi|694971838|XP_009432465.1
☐ PREDICTED: beta-Ala-His dipeptidase [Chlorocebus sabaeus]	42.6	42.6	100%	0.002	86%	gi|635098010|XP_008011959.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X1 [Macaca fas	42.6	42.6	100%	0.002	86%	gi|544505239|XP_005586496.1
☐ PREDICTED: beta-Ala-His dipeptidase [Saimiri boliviensis boliv	42.6	42.6	100%	0.002	86%	gi|725563408|XP_010335022.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X1 [Callithrix jac	42.6	42.6	100%	0.002	86%	gi|675717997|XP_008978245.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X3 [Pan troglod	42.6	42.6	100%	0.002	86%	gi|694971836|XP_009432464.1
☐ PREDICTED: cytosolic non-specific dipeptidase isoform X2 [Pa	42.6	42.6	100%	0.002	86%	gi|675787000|XP_008950929.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X2 [Pan troglod	42.6	42.6	100%	0.002	86%	gi|694971834|XP_009432463.1
☐ PREDICTED: cytosolic non-specific dipeptidase isoform X1 [Pa	42.6	42.6	100%	0.002	86%	gi|675786998|XP_008950928.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X1 [Pan troglod	42.6	42.6	100%	0.002	86%	gi|694971832|XP_009432462.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform 2 [Dasypus nov	41.8	41.8	100%	0.005	86%	gi|488587738|XP_004479187.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform 1 [Dasypus nov	41.8	41.8	100%	0.005	86%	gi|488587736|XP_004479186.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X7 [Heteroceph	41.4	41.4	100%	0.006	86%	gi|513000966|XP_004862006.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X6 [Heteroceph	41.4	41.4	100%	0.006	86%	gi|512861920|XP_004890014.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X4 [Heteroceph	41.4	41.4	100%	0.006	86%	gi|513000960|XP_004862003.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X4 [Heteroceph	41.4	41.4	100%	0.006	86%	gi|512861913|XP_004890012.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X3 [Heteroceph	41.4	41.4	100%	0.006	86%	gi|513000958|XP_004862002.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X3 [Heteroceph	41.4	41.4	100%	0.006	86%	gi|512861909|XP_004890011.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X2 [Heteroceph	41.4	41.4	100%	0.007	86%	gi|513000956|XP_004862001.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X1 [Heteroceph	41.4	41.4	100%	0.007	86%	gi|513000954|XP_004862000.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X2 [Heteroceph	41.4	41.4	100%	0.007	86%	gi|512861905|XP_004890010.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X1 [Heteroceph	41.4	41.4	100%	0.007	86%	gi|512861902|XP_004890009.1
☐ PREDICTED: beta-Ala-His dipeptidase [Ochotona princeps]	41.4	41.4	100%	0.007	86%	gi|504134362|XP_004579710.1
☐ Beta-Ala-His dipeptidase [Heterocephalus glaber]	41.4	41.4	100%	0.007	86%	gi|351703454|EHB06373.1
☐ PREDICTED: beta-Ala-His dipeptidase [Condylura cristata]	40.5	40.5	100%	0.013	79%	gi|507952033|XP_004684097.1
☐ PREDICTED: beta-Ala-His dipeptidase [Orycteropus afer afer]	39.7	39.7	100%	0.023	79%	gi|634881439|XP_007950930.1
☐ PREDICTED: beta-Ala-His dipeptidase [Ornithorhynchus anatir	39.7	39.7	100%	0.024	79%	gi|620952581|XP_007671072.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X3 [Sus scrofa]	39.2	39.2	100%	0.032	79%	gi|545801834|XP_005659878.1
☐ PREDICTED: beta-Ala-His dipeptidase [Physeter catodon]	39.2	39.2	100%	0.033	79%	gi|593754813|XP_007116282.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X4 [Chinchilla la	39.2	39.2	100%	0.033	79%	gi|533114973|XP_005373141.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X4 [Balaenopte	39.2	39.2	100%	0.033	79%	gi|594639072|XP_007172817.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X2 [Balaenopte	39.2	39.2	100%	0.033	79%	gi|594639068|XP_007172815.1
☐ carnosine dipeptidase 1 (metallopeptidase M20 family) [Sus scr	39.2	39.2	100%	0.033	79%	gi|594140552|NP_001277253.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X3 [Chinchilla la	39.2	39.2	100%	0.033	79%	gi|533114971|XP_005373140.1
☐ PREDICTED: beta-Ala-His dipeptidase [Orcinus orca]	39.2	39.2	100%	0.033	79%	gi|466059455|XP_004280059.1
☐ PREDICTED: beta-Ala-His dipeptidase [Tupaia chinensis]	39.2	39.2	100%	0.033	79%	gi|562881153|XP_006168179.1
☐ PREDICTED: beta-Ala-His dipeptidase isoform X2 [Chinchilla la	39.2	39.2	100%	0.033	79%	gi|533114969|XP_005373139.1

☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Chinchilla la	39.2	39.2	100%	0.033	79%	gi|533114967|XP_005373138.1
☐	PREDICTED: LOW QUALITY PROTEIN: beta-Ala-His dipeptida	39.2	39.2	100%	0.033	79%	gi|602728599|XP_007449731.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Balaenopte	39.2	39.2	100%	0.033	79%	gi|594639066|XP_007172814.1
☐	PREDICTED: beta-Ala-His dipeptidase [Otolemur garnettii]	39.2	39.2	100%	0.033	79%	gi|395830795|XP_003788502.1
☐	PREDICTED: beta-Ala-His dipeptidase [Erinaceus europaeus]	39.2	39.2	100%	0.033	79%	gi|617592053|XP_007520644.1
☐	Zinc finger protein 407 [Tupaia chinensis]	39.2	39.2	100%	0.034	79%	gi|444515465|ELV10904.1
☐	beta-Ala-His dipeptidase-like protein [Cricetulus griseus]	38.8	38.8	100%	0.044	79%	gi|537229377|ERE83812.1
☐	Beta-Ala-His dipeptidase [Cricetulus griseus]	38.8	38.8	100%	0.045	79%	gi|344256459|EGW12563.1
☐	PREDICTED: beta-Ala-His dipeptidase [Loxodonta africana]	38.8	38.8	100%	0.045	79%	gi|731460034|XP_010584989.1
☐	PREDICTED: beta-Ala-His dipeptidase [Nannospalax galili]	38.8	38.8	100%	0.045	79%	gi|674082518|XP_008848916.1
☐	PREDICTED: beta-Ala-His dipeptidase [Eptesicus fuscus]	38.8	38.8	100%	0.045	79%	gi|641694915|XP_008158650.1
☐	PREDICTED: beta-Ala-His dipeptidase [Elephantulus edwardii]	38.8	38.8	100%	0.045	79%	gi|585700922|XP_006897297.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Cricetulus g	38.8	38.8	100%	0.045	79%	gi|625218554|XP_003510704.2
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Cricetulus g	38.8	38.8	100%	0.045	79%	gi|625242672|XP_007612561.1
☐	PREDICTED: beta-Ala-His dipeptidase [Tarsius syrichta]	38.8	38.8	100%	0.045	79%	gi|640832941|XP_008072129.1
☐	PREDICTED: LOW QUALITY PROTEIN: beta-Ala-His dipeptida	38.8	38.8	100%	0.045	79%	gi|524922064|XP_005065294.1
☐	PREDICTED: LOW QUALITY PROTEIN: beta-Ala-His dipeptida	38.8	38.8	100%	0.045	79%	gi|532026811|XP_005356384.1
☐	PREDICTED: beta-Ala-His dipeptidase [Trichechus manatus la	38.8	38.8	100%	0.045	79%	gi|471411632|XP_004387369.1
☐	hypothetical protein PANDA_013728 [Ailuropoda melanoleuca]	38.4	38.4	100%	0.062	79%	gi|281349002|EFB24586.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Canis lupus	38.4	38.4	100%	0.062	79%	gi|545485033|XP_005615365.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform 2 [Ceratotheriur	38.4	38.4	100%	0.062	79%	gi|478496719|XP_004422698.1
☐	PREDICTED: beta-Ala-His dipeptidase [Felis catus]	38.4	38.4	100%	0.062	79%	gi|587007722|XP_006939039.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Myotis bran	38.4	38.4	100%	0.062	79%	gi|554533774|XP_005861635.1
☐	PREDICTED: beta-Ala-His dipeptidase [Odobenus rosmarus di	38.4	38.4	100%	0.062	79%	gi|472393864|XP_004416194.1
☐	PREDICTED: beta-Ala-His dipeptidase [Panthera tigris altaica]	38.4	38.4	100%	0.062	79%	gi|591316978|XP_007084799.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Camelus ba	38.4	38.4	100%	0.062	79%	gi|743700606|XP_010970079.1

⊟ Alignments

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carnosine dipeptidase 1 (metallopeptidase M20 family), isoform CRA_b [Homo sapiens]

Sequence ID: gi|119586964|gb|EAW66560.1| **Length:** 310 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 179 to 192 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.0 bits(101)	2e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    RLVPHMDVSAVEKQ  14
            RLVPHM+VSAVEKQ
Sbjct  179  RLVPHMNVSAVEKQ  192
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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carnosine dipeptidase 1 (metallopeptidase M20 family), isoform CRA_a [Homo sapiens]

Sequence ID: gi|119586963|gb|EAW66559.1| **Length:** 423 **Number of Matches:** 1

Range 1: 292 to 305 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.0 bits(101)	2e-04	13/14(93%)	14/14(100%)	0/14(0%)

Related Information

Gene - associated gene details

```
Query  1    RLVPHMDVSAVEKQ  14
            RLVPHM+VSAVEKQ
Sbjct  292  RLVPHMNVSAVEKQ  305
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of Human Carnosine Dipeptidase 1

Sequence ID: gi|197107410|pdb|3DLJ|A **Length:** 485 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 354 to 367 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.0 bits(101)	2e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    RLVPHMDVSAVEKQ  14
            RLVPHM+VSAVEKQ
Sbjct  354  RLVPHMNVSAVEKQ  367
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194383442|dbj|BAG64692.1| **Length:** 493 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 362 to 375 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.0 bits(101)	2e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    RLVPHMDVSAVEKQ  14
            RLVPHM+VSAVEKQ
Sbjct  362  RLVPHMNVSAVEKQ  375
```

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beta-Ala-His dipeptidase precursor [Homo sapiens]

Sequence ID: gi|21071039|ref|NP_116038.4| **Length:** 507 **Number of Matches:** 1

▷ See 4 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 376 to 389 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.0 bits(101)	2e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    RLVPHMDVSAVEKQ  14
            RLVPHM+VSAVEKQ
Sbjct  376  RLVPHMNVSAVEKQ  389
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

CNDP1_RLVPHMNVSAVEKQ_NonMod

RID	B94FHW7801R (Expires on 01-14 10:33 am)
Query ID	lcl|221108
Description	None
Molecule type	amino acid
Query Length	14
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

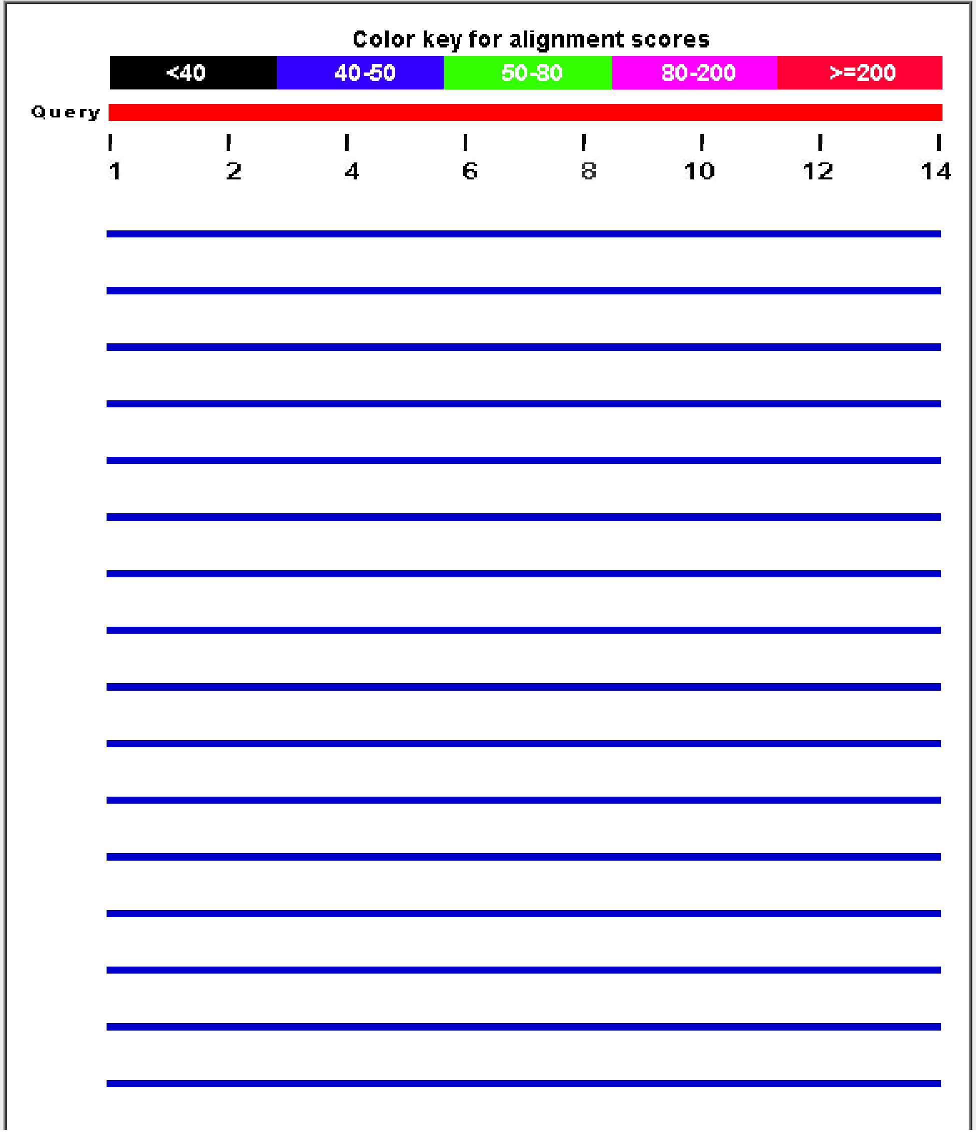
Graphic Summary

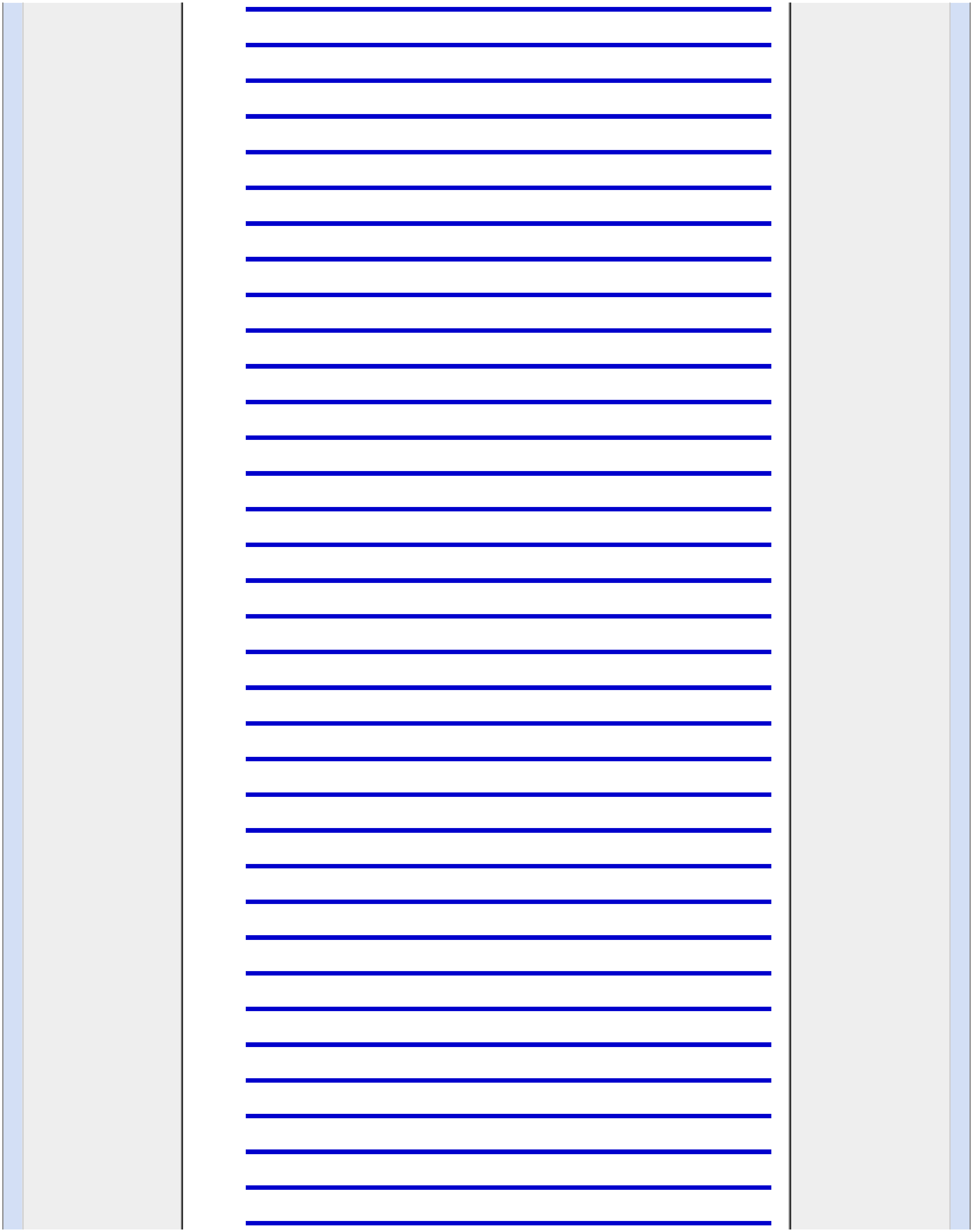
Show Conserved Domains

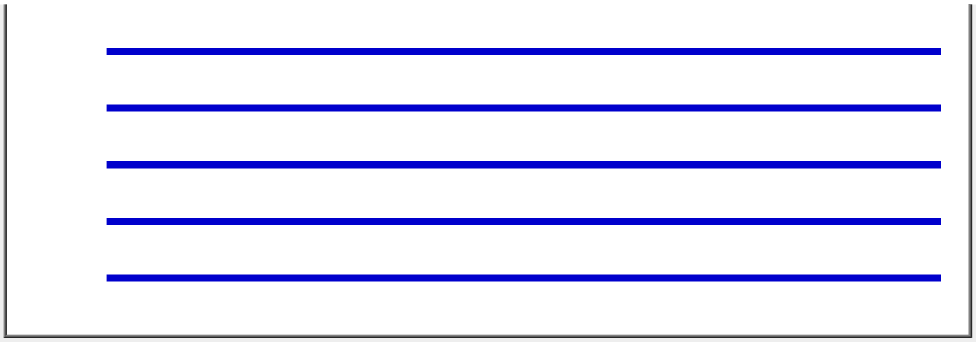
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	carnosine dipeptidase 1 (metallopeptidase M20 family), isoform CR	48.6	48.6	100%	2e-05	100%	gi|119586964|EAW66560.1
☐	carnosine dipeptidase 1 (metallopeptidase M20 family), isoform CR	48.6	48.6	100%	2e-05	100%	gi|119586963|EAW66559.1
☐	Chain A, Crystal Structure Of Human Carnosine Dipeptidase 1 [Hor	48.6	48.6	100%	2e-05	100%	gi|197107410|3DLJ_A
☐	unnamed protein product [Homo sapiens]	48.6	48.6	100%	2e-05	100%	gi|194383442|BAG64692.1
☐	beta-Ala-His dipeptidase precursor [Homo sapiens]	48.6	48.6	100%	2e-05	100%	gi|21071039|NP_116038.4
☐	RecName: Full=Beta-Ala-His dipeptidase; AltName: Full=CNDP dip	48.6	48.6	100%	2e-05	100%	gi|317373563|Q96KN2.4
☐	unnamed protein product [Homo sapiens]	48.6	48.6	100%	2e-05	100%	gi|158260855|BAF82605.1
☐	Carnosine dipeptidase 1 (metallopeptidase M20 family) [Homo sapi	48.6	48.6	100%	2e-05	100%	gi|83759081|AAI10296.1
☐	Carnosine dipeptidase 1 (metallopeptidase M20 family) [Homo sapi	48.6	48.6	100%	2e-05	100%	gi|109658940|AAI17123.1
☐	glutamate carboxypeptidase-like protein 2 [Homo sapiens]	48.6	48.6	100%	2e-05	100%	gi|16555792|CAD10388.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Fukomys dama	45.6	45.6	100%	2e-04	93%	gi|731191032|XP_010608870.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Fukomys dama	45.6	45.6	100%	2e-04	93%	gi|731191030|XP_010608813.1
☐	Beta-Ala-His dipeptidase [Fukomys damarensis]	45.6	45.6	100%	2e-04	93%	gi|676287801|KFO38436.1
☐	PREDICTED: beta-Ala-His dipeptidase-like [Gorilla gorilla gorilla]	45.2	45.2	100%	3e-04	93%	gi|426386236|XP_004059596.1
☐	beta-Ala-His dipeptidase [Pongo abelii]	45.2	45.2	100%	3e-04	93%	gi|197100618|NP_001125793.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X4 [Callithrix jacchu	45.2	45.2	100%	3e-04	93%	gi|675718012|XP_008978248.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Oryctolagus cur	45.2	45.2	100%	3e-04	93%	gi|655836920|XP_008259692.1
☐	PREDICTED: LOW QUALITY PROTEIN: beta-Ala-His dipeptidase	45.2	45.2	100%	3e-04	93%	gi|507684395|XP_004640269.1
☐	PREDICTED: cytosolic non-specific dipeptidase isoform X4 [Pan pa	45.2	45.2	100%	3e-04	93%	gi|675787003|XP_008950931.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X6 [Pan troglodytes	45.2	45.2	100%	3e-04	93%	gi|694971841|XP_009432466.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X3 [Callithrix jacchu	45.2	45.2	100%	3e-04	93%	gi|390474059|XP_002757384.2
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Callithrix jacchu	45.2	45.2	100%	3e-04	93%	gi|675718001|XP_008978246.1
☐	PREDICTED: beta-Ala-His dipeptidase [Rhinopithecus roxellana]	45.2	45.2	100%	3e-04	93%	gi|724961646|XP_010355009.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Oryctolagus cur	45.2	45.2	100%	3e-04	93%	gi|655836917|XP_008259691.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Macaca fascicu	45.2	45.2	100%	3e-04	93%	gi|544505241|XP_005586497.1
☐	PREDICTED: beta-Ala-His dipeptidase [Papio anubis]	45.2	45.2	100%	3e-04	93%	gi|402903362|XP_003914537.1
☐	Beta-Ala-His dipeptidase [Macaca mulatta]	45.2	45.2	100%	3e-04	93%	gi|355702017|EHH29370.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform 1 [Nomascus leuco	45.2	45.2	100%	3e-04	93%	gi|332230419|XP_003264388.1
☐							

	PREDICTED: hypothetical protein LOC695195 isoform 2 [Macaca n	45.2	45.2	100%	3e-04	93%	gi|109122502|XP_001085457.1
☐	PREDICTED: hypothetical protein LOC695195 isoform 1 [Macaca n	45.2	45.2	100%	3e-04	93%	gi|297275497|XP_001085348.2
☐	PREDICTED: cytosolic non-specific dipeptidase isoform X3 [Pan pa	45.2	45.2	100%	3e-04	93%	gi|397514119|XP_003827346.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X5 [Pan troglodytes	45.2	45.2	100%	3e-04	93%	gi|114673583|XP_001136945.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X4 [Pan troglodytes	45.2	45.2	100%	3e-04	93%	gi|694971838|XP_009432465.1
☐	PREDICTED: beta-Ala-His dipeptidase [Chlorocebus sabaeus]	45.2	45.2	100%	3e-04	93%	gi|635098010|XP_008011959.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Macaca fascicu	45.2	45.2	100%	3e-04	93%	gi|544505239|XP_005586496.1
☐	PREDICTED: beta-Ala-His dipeptidase [Saimiri boliviensis boliviens	45.2	45.2	100%	3e-04	93%	gi|725563408|XP_010335022.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Callithrix jacchu	45.2	45.2	100%	3e-04	93%	gi|675717997|XP_008978245.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X3 [Pan troglodytes	45.2	45.2	100%	3e-04	93%	gi|694971836|XP_009432464.1
☐	PREDICTED: cytosolic non-specific dipeptidase isoform X2 [Pan pa	45.2	45.2	100%	3e-04	93%	gi|675787000|XP_008950929.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Pan troglodytes	45.2	45.2	100%	3e-04	93%	gi|694971834|XP_009432463.1
☐	PREDICTED: cytosolic non-specific dipeptidase isoform X1 [Pan pa	45.2	45.2	100%	3e-04	93%	gi|675786998|XP_008950928.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Pan troglodytes	45.2	45.2	100%	3e-04	93%	gi|694971832|XP_009432462.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X7 [Heterocephalus	43.9	43.9	100%	9e-04	93%	gi|513000966|XP_004862006.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X6 [Heterocephalus	43.9	43.9	100%	9e-04	93%	gi|512861920|XP_004890014.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X4 [Heterocephalus	43.9	43.9	100%	9e-04	93%	gi|513000960|XP_004862003.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X4 [Heterocephalus	43.9	43.9	100%	9e-04	93%	gi|512861913|XP_004890012.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X3 [Heterocephalus	43.9	43.9	100%	9e-04	93%	gi|513000958|XP_004862002.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X3 [Heterocephalus	43.9	43.9	100%	9e-04	93%	gi|512861909|XP_004890011.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Heterocephalus	43.9	43.9	100%	9e-04	93%	gi|513000956|XP_004862001.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Heterocephalus	43.9	43.9	100%	9e-04	93%	gi|513000954|XP_004862000.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Heterocephalus	43.9	43.9	100%	9e-04	93%	gi|512861905|XP_004890010.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Heterocephalus	43.9	43.9	100%	9e-04	93%	gi|512861902|XP_004890009.1
☐	PREDICTED: beta-Ala-His dipeptidase [Ochotona princeps]	43.9	43.9	100%	9e-04	93%	gi|504134362|XP_004579710.1
☐	Beta-Ala-His dipeptidase [Heterocephalus glaber]	43.9	43.9	100%	9e-04	93%	gi|351703454|EHB06373.1
☐	PREDICTED: beta-Ala-His dipeptidase [Condylura cristata]	43.1	43.1	100%	0.002	86%	gi|507952033|XP_004684097.1
☐	PREDICTED: beta-Ala-His dipeptidase [Orycteropus afer afer]	42.2	42.2	100%	0.003	86%	gi|634881439|XP_007950930.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X3 [Sus scrofa]	41.8	41.8	100%	0.004	86%	gi|545801834|XP_005659878.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X4 [Mustela putoriu	41.8	41.8	100%	0.004	86%	gi|511959771|XP_004798117.1
☐	PREDICTED: beta-Ala-His dipeptidase [Physeter catodon]	41.8	41.8	100%	0.004	86%	gi|593754813|XP_007116282.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X4 [Chinchilla lanig	41.8	41.8	100%	0.004	86%	gi|533114973|XP_005373141.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X4 [Balaenoptera a	41.8	41.8	100%	0.004	86%	gi|594639072|XP_007172817.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Balaenoptera a	41.8	41.8	100%	0.004	86%	gi|594639068|XP_007172815.1
☐	carnosine dipeptidase 1 (metallopeptidase M20 family) [Sus scrofa]	41.8	41.8	100%	0.004	86%	gi|594140552|NP_001277253.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X3 [Chinchilla lanig	41.8	41.8	100%	0.004	86%	gi|533114971|XP_005373140.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Mustela putoriu	41.8	41.8	100%	0.004	86%	gi|511842482|XP_004745710.1
☐	PREDICTED: beta-Ala-His dipeptidase [Orcinus orca]	41.8	41.8	100%	0.004	86%	gi|466059455|XP_004280059.1
☐	PREDICTED: beta-Ala-His dipeptidase [Tupaia chinensis]	41.8	41.8	100%	0.004	86%	gi|562881153|XP_006168179.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Chinchilla lanig	41.8	41.8	100%	0.004	86%	gi|533114969|XP_005373139.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Chinchilla lanig	41.8	41.8	100%	0.004	86%	gi|533114967|XP_005373138.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X3 [Mustela putoriu	41.8	41.8	100%	0.004	86%	gi|511959769|XP_004798116.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Mustela putoriu	41.8	41.8	100%	0.004	86%	gi|511842480|XP_004745709.1
☐	PREDICTED: LOW QUALITY PROTEIN: beta-Ala-His dipeptidase	41.8	41.8	100%	0.004	86%	gi|602728599|XP_007449731.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Balaenoptera a	41.8	41.8	100%	0.004	86%	gi|594639066|XP_007172814.1

☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Mustela putoriu	41.8	41.8	100%	0.004	86%	gi|511959765|XP_004798114.1
☐	PREDICTED: beta-Ala-His dipeptidase [Otolemur garnettii]	41.8	41.8	100%	0.004	86%	gi|395830795|XP_003788502.1
☐	PREDICTED: beta-Ala-His dipeptidase [Erinaceus europaeus]	41.8	41.8	100%	0.005	86%	gi|617592053|XP_007520644.1
☐	Zinc finger protein 407 [Tupaia chinensis]	41.8	41.8	100%	0.005	86%	gi|444515465|ELV10904.1
☐	beta-Ala-His dipeptidase-like protein [Cricetulus griseus]	41.4	41.4	100%	0.006	86%	gi|537229377|ERE83812.1
☐	Beta-Ala-His dipeptidase [Cricetulus griseus]	41.4	41.4	100%	0.006	86%	gi|344256459|EGW12563.1
☐	PREDICTED: beta-Ala-His dipeptidase [Loxodonta africana]	41.4	41.4	100%	0.006	86%	gi|731460034|XP_010584989.1
☐	PREDICTED: beta-Ala-His dipeptidase [Nannospalax galili]	41.4	41.4	100%	0.006	86%	gi|674082518|XP_008848916.1
☐	PREDICTED: beta-Ala-His dipeptidase [Eptesicus fuscus]	41.4	41.4	100%	0.006	86%	gi|641694915|XP_008158650.1
☐	PREDICTED: beta-Ala-His dipeptidase [Elephantulus edwardii]	41.4	41.4	100%	0.006	86%	gi|585700922|XP_006897297.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Cricetulus grise	41.4	41.4	100%	0.006	86%	gi|625218554|XP_003510704.2
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Cricetulus grise	41.4	41.4	100%	0.006	86%	gi|625242672|XP_007612561.1
☐	PREDICTED: beta-Ala-His dipeptidase [Tarsius syrichta]	41.4	41.4	100%	0.006	86%	gi|640832941|XP_008072129.1
☐	PREDICTED: LOW QUALITY PROTEIN: beta-Ala-His dipeptidase	41.4	41.4	100%	0.006	86%	gi|524922064|XP_005065294.1
☐	PREDICTED: LOW QUALITY PROTEIN: beta-Ala-His dipeptidase	41.4	41.4	100%	0.006	86%	gi|532026811|XP_005356384.1
☐	PREDICTED: beta-Ala-His dipeptidase [Trichechus manatus latiros	41.4	41.4	100%	0.006	86%	gi|471411632|XP_004387369.1
☐	hypothetical protein PANDA_013728 [Ailuropoda melanoleuca]	40.9	40.9	100%	0.008	86%	gi|281349002|EFB24586.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Canis lupus fan	40.9	40.9	100%	0.008	86%	gi|545485033|XP_005615365.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform 2 [Ceratotherium sir	40.9	40.9	100%	0.008	86%	gi|478496719|XP_004422698.1
☐	PREDICTED: beta-Ala-His dipeptidase [Felis catus]	40.9	40.9	100%	0.009	86%	gi|587007722|XP_006939039.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X2 [Myotis brandtii]	40.9	40.9	100%	0.009	86%	gi|554533774|XP_005861635.1
☐	PREDICTED: beta-Ala-His dipeptidase [Odobenus rosmarus diverg	40.9	40.9	100%	0.009	86%	gi|472393864|XP_004416194.1
☐	PREDICTED: beta-Ala-His dipeptidase [Panthera tigris altaica]	40.9	40.9	100%	0.009	86%	gi|591316978|XP_007084799.1
☐	PREDICTED: beta-Ala-His dipeptidase [Vicugna pacos]	40.9	40.9	100%	0.009	86%	gi|560982102|XP_006213282.1
☐	PREDICTED: beta-Ala-His dipeptidase [Camelus ferus]	40.9	40.9	100%	0.009	86%	gi|560923439|XP_006187914.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform X1 [Canis lupus fan	40.9	40.9	100%	0.009	86%	gi|545485031|XP_005615364.1
☐	PREDICTED: beta-Ala-His dipeptidase isoform 1 [Ceratotherium sir	40.9	40.9	100%	0.009	86%	gi|478496717|XP_004422697.1

⊟ Alignments

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carnosine dipeptidase 1 (metallopeptidase M20 family), isoform CRA_b [Homo sapiens]

Sequence ID: gi|119586964|gb|EAW66560.1| **Length:** 310 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 179 to 192 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.6 bits(107)	2e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    RLVPHMNVSAVEKQ  14
            RLVPHMNVSAVEKQ
Sbjct  179  RLVPHMNVSAVEKQ  192
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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carnosine dipeptidase 1 (metallopeptidase M20 family), isoform CRA_a [Homo sapiens]

Sequence ID: gi|119586963|gb|EAW66559.1| **Length:** 423 **Number of Matches:** 1

Range 1: 292 to 305 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.6 bits(107)	2e-05	14/14(100%)	14/14(100%)	0/14(0%)

Related Information

Gene - associated gene details

```
Query  1    RLVPHMNVSAVEKQ  14
            RLVPHMNVSAVEKQ
Sbjct  292  RLVPHMNVSAVEKQ  305
```

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Chain A, Crystal Structure Of Human Carnosine Dipeptidase 1

Sequence ID: gi|197107410|pdb|3DLJ|A **Length:** 485 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 354 to 367 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.6 bits(107)	2e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    RLVPHMNVSAVEKQ  14
            RLVPHMNVSAVEKQ
Sbjct  354  RLVPHMNVSAVEKQ  367
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194383442|dbj|BAG64692.1| **Length:** 493 **Number of Matches:** 1

Range 1: 362 to 375 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.6 bits(107)	2e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    RLVPHMNVSAVEKQ  14
            RLVPHMNVSAVEKQ
Sbjct  362  RLVPHMNVSAVEKQ  375
```

Related Information

Gene - associated gene details

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

beta-Ala-His dipeptidase precursor [Homo sapiens]

Sequence ID: gi|21071039|ref|NP_116038.4| **Length:** 507 **Number of Matches:** 1

▷ See 4 more title(s)

Range 1: 376 to 389 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.6 bits(107)	2e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    RLVPHMNVSAVEKQ  14
            RLVPHMNVSAVEKQ
Sbjct  376  RLVPHMNVSAVEKQ  389
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

BLAST ®

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BTGCJ3C8016**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download   How to read this page   Blast report description

CPB2_KKKQVHFFVDASDVDNVKA_Mod

RID BTGCJ3C8016 (Expires on 01-20 15:34 pm)

Query ID lcl|22070
Description None
Molecule type amino acid
Query Length 19

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

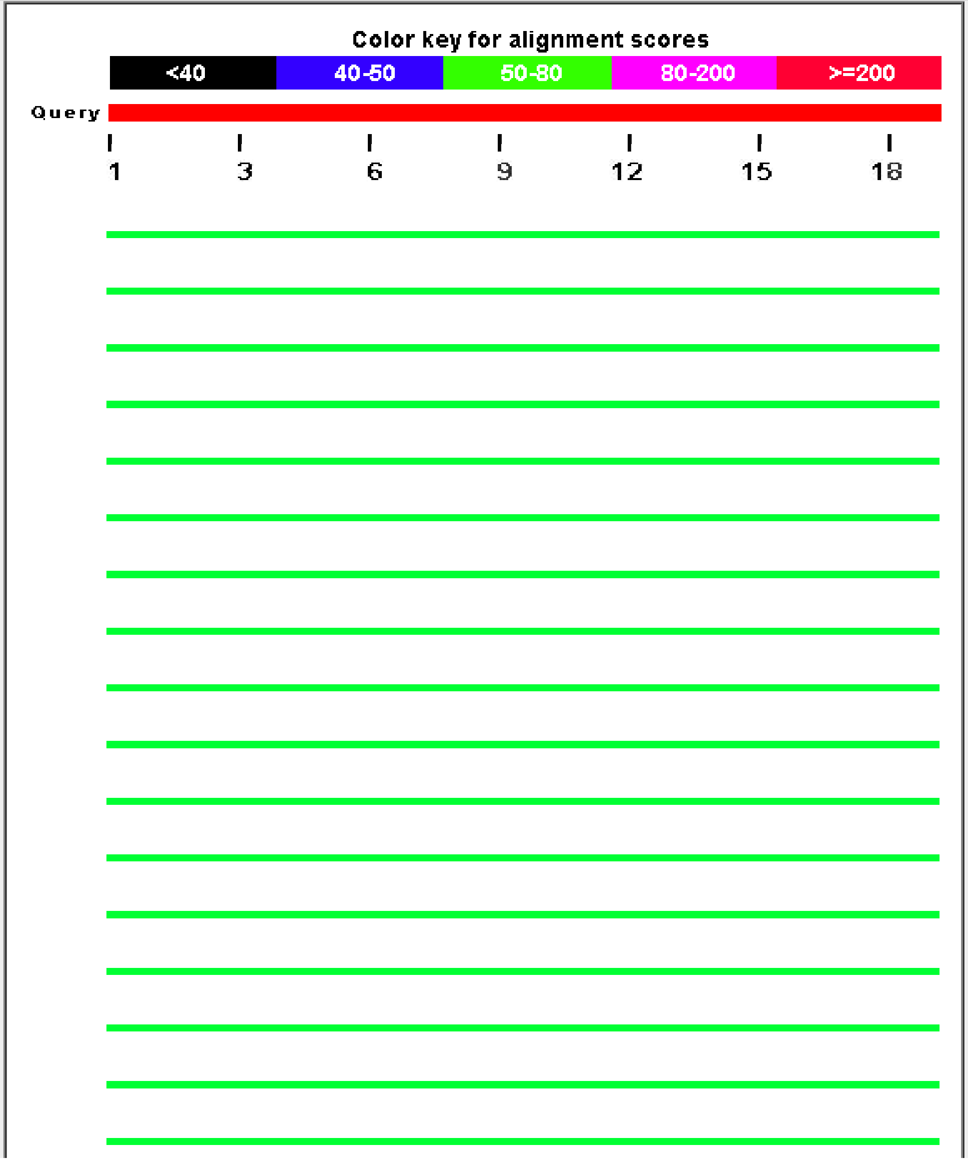
Graphic Summary

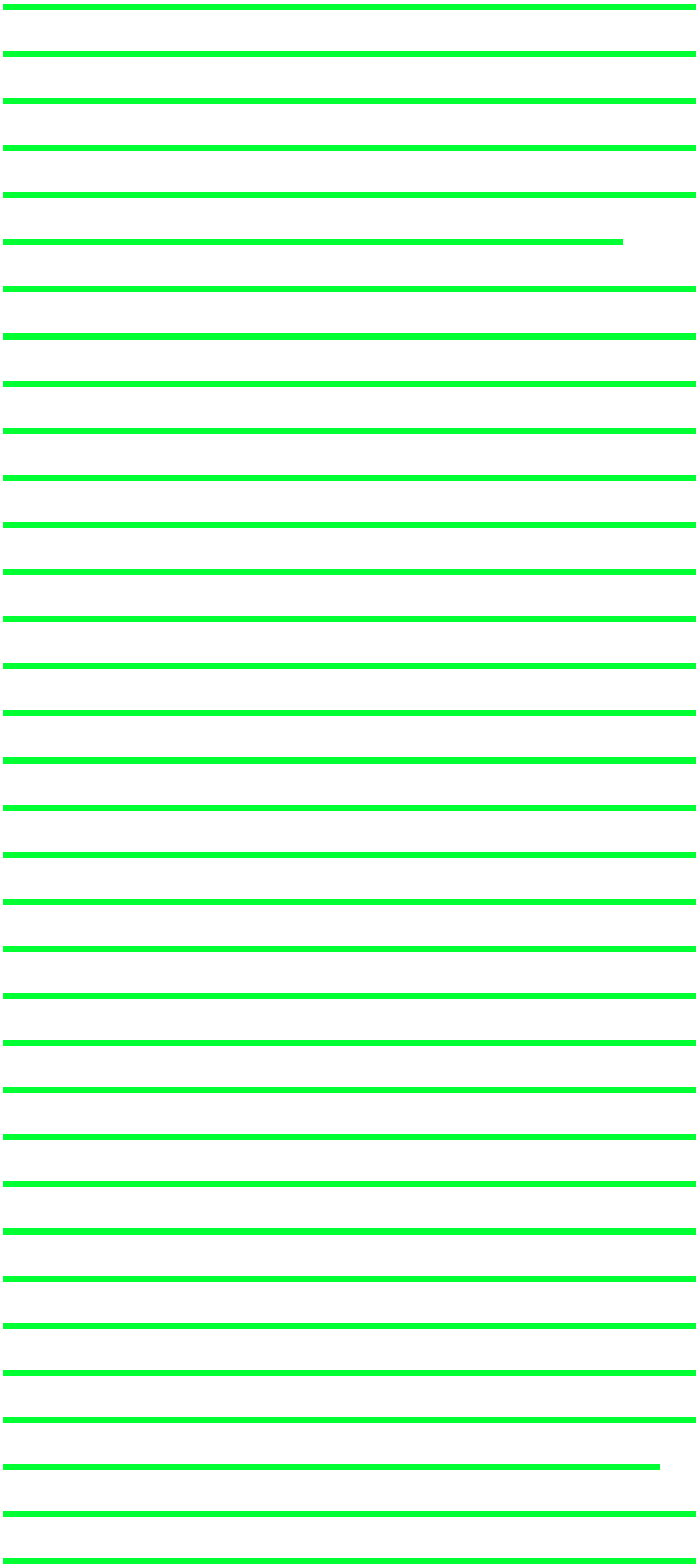
Show Conserved Domains

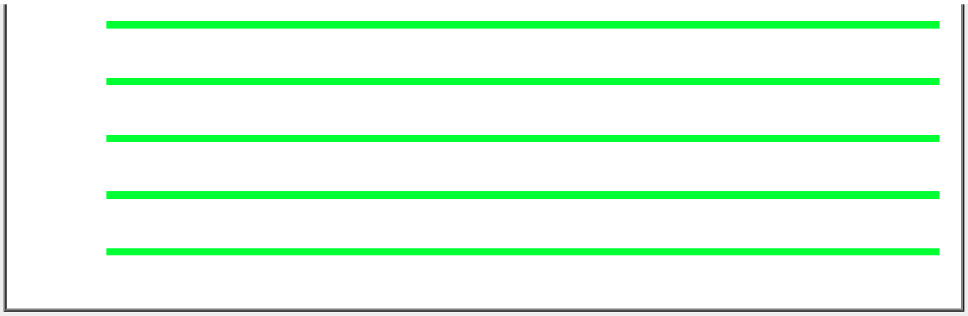
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Homo sapiens]	60.4	60.4	100%	4e-09	95%	gi|530402101|XP_005266316.1
☐	carboxypeptidase B-like protein [Homo sapiens]	60.4	60.4	100%	4e-09	95%	gi|6855464|BAA90475.1
☐	carboxypeptidase B2 (plasma, carboxypeptidase U), isoform CI	60.4	60.4	100%	4e-09	95%	gi|119629159|EAX08754.1
☐	carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]	60.4	60.4	100%	4e-09	95%	gi|513126877|NP_001265470.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Pongo abelii]	60.4	60.4	100%	4e-09	95%	gi|686743701|XP_009246910.1
☐	Chain A, Pro-carboxypeptidase U In Complex With 5-(3-aminop	60.4	60.4	100%	4e-09	95%	gi|672886543|4P10_A
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Homo sapiens]	60.4	60.4	100%	4e-09	95%	gi|530402099|XP_005266315.1
☐	prepro-plasma carboxypeptidase B [Homo sapiens]	60.4	60.4	100%	4e-09	95%	gi|189687|AAA60042.1
☐	PREDICTED: carboxypeptidase B2 [Gorilla gorilla gorilla]	60.4	60.4	100%	4e-09	95%	gi|426375394|XP_004054526.1
☐	Carboxypeptidase B2 (plasma) [Homo sapiens]	60.4	60.4	100%	4e-09	95%	gi|13937897|AAH07057.1
☐	carboxypeptidase B2 isoform 1 preproprotein [Homo sapiens]	60.4	60.4	100%	4e-09	95%	gi|513126885|NP_001863.3
☐	carboxypeptidase B2 (plasma) [synthetic construct]	60.4	60.4	100%	4e-09	95%	gi|157927966|ABW03279.1
☐	carboxypeptidase B2 (plasma, carboxypeptidase U) [synthetic c	60.4	60.4	100%	4e-09	95%	gi|124126823|ABM92184.1
☐	PREDICTED: carboxypeptidase B2 [Pan troglodytes]	60.4	60.4	100%	4e-09	95%	gi|114651557|XP_509667.2
☐	Chain A, Crystal Structure Of Thrombin-Activatable Fibrinolysis	60.4	60.4	100%	4e-09	95%	gi|193506809|3D66_A
☐	Homo sapiens carboxypeptidase B2 (plasma, carboxypeptidase	60.4	60.4	100%	4e-09	95%	gi|30584819|AAP36662.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Pongo abelii]	60.4	60.4	100%	4e-09	95%	gi|297694016|XP_002824293.1
☐	Chain A, Crystal Structure Of A T325i/t329i/h333y/h335q Mutar	60.4	60.4	100%	4e-09	95%	gi|253722661|3D68_A
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Homo sapiens]	60.4	60.4	100%	4e-09	95%	gi|530402097|XP_005266314.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Rhinopithecus	57.9	57.9	100%	3e-08	89%	gi|724966280|XP_010356389.1
☐	PREDICTED: carboxypeptidase B2 [Papio anubis]	57.9	57.9	100%	3e-08	89%	gi|402901940|XP_003913891.1
☐	PREDICTED: carboxypeptidase B2 [Nomascus leucogenys]	57.1	57.1	100%	6e-08	89%	gi|332241864|XP_003270104.1
☐	PREDICTED: carboxypeptidase B2 [Callithrix jacchus]	54.9	54.9	89%	3e-07	94%	gi|390457680|XP_002742737.2
☐	PREDICTED: carboxypeptidase B2 [Chlorocebus sabaeus]	54.5	54.5	100%	5e-07	84%	gi|635025444|XP_007958527.1
☐	PREDICTED: carboxypeptidase B2-like [Peromyscus manicula	54.1	54.1	100%	5e-07	84%	gi|589996660|XP_006998803.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Cricetulus grise	54.1	54.1	100%	6e-07	84%	gi|625193824|XP_007639419.1
☐	PREDICTED: carboxypeptidase B2 isoform X4 [Cricetulus grise	54.1	54.1	100%	6e-07	84%	gi|625271974|XP_007627553.1
☐	PREDICTED: carboxypeptidase B2 [Peromyscus maniculatus b	54.1	54.1	100%	6e-07	84%	gi|589957698|XP_006991448.1
☐	Carboxypeptidase B2 (plasma) [Mus musculus]	54.1	54.1	100%	6e-07	84%	gi|59808067|AAH89577.1

☐	carboxypeptidase U [Mus musculus]	54.1	54.1	100%	6e-07	84%	gi|6003652|AAF00528.1
☐	PREDICTED: carboxypeptidase B2 [Mesocricetus auratus]	54.1	54.1	100%	6e-07	84%	gi|524935646|XP_005071018.1
☐	carboxypeptidase B2 precursor [Mus musculus]	54.1	54.1	100%	6e-07	84%	gi|31982712|NP_062749.2
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Cricetulus grise	54.1	54.1	100%	6e-07	84%	gi|354476626|XP_003500525.1
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Cricetulus grise	54.1	54.1	100%	6e-07	84%	gi|625271972|XP_007627552.1
☐	zinc finger CCCH domain-containing protein 13 [Cricetulus gris	54.1	54.1	100%	7e-07	84%	gi|537241932|ERE87338.1
☐	Carboxypeptidase B2 [Fukomys damarensis]	52.4	52.4	100%	2e-06	84%	gi|676273139|KFO27861.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Camelus drom	52.4	52.4	100%	2e-06	84%	gi|744566815|XP_010979147.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Camelus bactri	52.4	52.4	100%	2e-06	84%	gi|743712317|XP_010949694.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Macaca fascicu	52.4	52.4	100%	2e-06	84%	gi|544503644|XP_005585858.1
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Chinchilla lanig	52.4	52.4	100%	2e-06	84%	gi|533192699|XP_005409155.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Chinchilla lanig	52.4	52.4	100%	2e-06	84%	gi|533192697|XP_005409154.1
☐	PREDICTED: carboxypeptidase B2 [Otolemur garnettii]	52.4	52.4	100%	2e-06	84%	gi|395835377|XP_003790657.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Camelus drom	52.4	52.4	100%	2e-06	84%	gi|744566812|XP_010979146.1
☐	PREDICTED: carboxypeptidase B2 [Canis lupus familiaris]	52.4	52.4	100%	2e-06	84%	gi|73989292|XP_851154.1
☐	PREDICTED: carboxypeptidase B2 [Vicugna pacos]	52.4	52.4	100%	2e-06	84%	gi|560974364|XP_006209502.1
☐	PREDICTED: carboxypeptidase B2 [Camelus ferus]	52.4	52.4	100%	2e-06	84%	gi|560922422|XP_006187410.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Macaca fascicu	52.4	52.4	100%	2e-06	84%	gi|544503642|XP_005585857.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Chinchilla lanig	52.4	52.4	100%	2e-06	84%	gi|533192695|XP_005409153.1
☐	PREDICTED: carboxypeptidase B2 [Saimiri boliviensis bolivien	52.4	52.4	94%	2e-06	89%	gi|403286234|XP_003934405.1
☐	Carboxypeptidase B2 [Macaca mulatta]	52.4	52.4	100%	2e-06	84%	gi|355700980|EHH29001.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Fukomys dama	52.4	52.4	100%	2e-06	84%	gi|731244313|XP_010635336.1
☐	PREDICTED: carboxypeptidase B2 [Felis catus]	52.4	52.4	100%	2e-06	84%	gi|586973570|XP_006927367.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Fukomys dama	52.4	52.4	100%	2e-06	84%	gi|731244311|XP_010635335.1
☐	PREDICTED: carboxypeptidase B2 [Panthera tigris altaica]	52.4	52.4	100%	2e-06	84%	gi|591318467|XP_007085493.1
☐	plastin-2 isoform 16 [Camelus ferus]	52.4	52.4	100%	3e-06	84%	gi|528759255|EPY78914.1
☐	carboxypeptidase B2 (plasma), isoform CRA_b [Rattus norvegi	51.5	51.5	100%	4e-06	79%	gi|149049966|EDM02290.1
☐	carboxypeptidase B2 (plasma), isoform CRA_a [Rattus norvegi	51.5	51.5	100%	5e-06	79%	gi|149049965|EDM02289.1
☐	Cpb2 protein [Rattus norvegicus]	51.5	51.5	100%	5e-06	79%	gi|60688161|AAH91133.1
☐	carboxypeptidase B2 precursor [Rattus norvegicus]	51.5	51.5	100%	5e-06	79%	gi|16758414|NP_446069.1
☐	PREDICTED: carboxypeptidase B2 [Tupaia chinensis]	51.5	51.5	100%	5e-06	79%	gi|562871068|XP_006163508.1
☐	PREDICTED: carboxypeptidase B2 [Equus caballus]	51.1	51.1	100%	6e-06	84%	gi|545190694|XP_005601424.1
☐	PREDICTED: carboxypeptidase B2 [Microtus ochrogaster]	50.3	50.3	100%	1e-05	79%	gi|532025304|XP_005355675.1
☐	PREDICTED: carboxypeptidase B2 isoform 1 [Macaca mulatta]	49.8	49.8	94%	2e-05	83%	gi|109120669|XP_001097310.1
☐	Carboxypeptidase B2 [Macaca fascicularis]	49.8	49.8	94%	2e-05	83%	gi|355754683|EHH58584.1
☐	PREDICTED: carboxypeptidase B2 isoform 3 [Macaca mulatta]	49.8	49.8	94%	2e-05	83%	gi|109120665|XP_001097608.1
☐	PREDICTED: carboxypeptidase B2 [Cavia porcellus]	49.8	49.8	100%	2e-05	79%	gi|348583190|XP_003477356.1
☐	PREDICTED: carboxypeptidase B2 [Balaenoptera acutorostrata	49.4	49.4	100%	2e-05	79%	gi|594678268|XP_007186896.1
☐	PREDICTED: carboxypeptidase B2 [Octodon degus]	49.0	49.0	100%	3e-05	79%	gi|507684606|XP_004640321.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Heterocephalus	48.6	48.6	100%	4e-05	79%	gi|512921202|XP_004904434.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Heterocephalus	48.6	48.6	100%	4e-05	79%	gi|512964055|XP_004844264.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Heterocephalus	48.6	48.6	100%	4e-05	79%	gi|512921198|XP_004904433.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Heterocephalus	48.6	48.6	100%	4e-05	79%	gi|512964053|XP_004844263.1
☐	PREDICTED: carboxypeptidase B2 [Tursiops truncatus]	47.7	47.7	100%	8e-05	79%	gi|470653285|XP_004329533.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Lipotes vexillife	47.7	47.7	100%	8e-05	79%	gi|602712571|XP_007466515.1

☐	PREDICTED: carboxypeptidase B2 [Physeter catodon]	47.7	47.7	100%	8e-05	79%	gi|593749228|XP_007129852.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Lipotes vexillife	47.7	47.7	100%	9e-05	79%	gi|602712569|XP_007466514.1
☐	PREDICTED: carboxypeptidase B2 [Orcinus orca]	47.7	47.7	100%	9e-05	79%	gi|466032575|XP_004274629.1
☐	PREDICTED: carboxypeptidase B2 [Ochotona princeps]	46.9	46.9	100%	2e-04	79%	gi|504128560|XP_004577530.1
☐	PREDICTED: carboxypeptidase B2 [Nannospalax galili]	46.4	46.4	100%	2e-04	74%	gi|674098370|XP_008822615.1
☐	PREDICTED: carboxypeptidase B2 [Ceratotherium simum simu	46.4	46.4	94%	2e-04	78%	gi|478518956|XP_004433702.1
☐	PREDICTED: carboxypeptidase B2 [Ictidomys tridecemlineatus	46.4	46.4	94%	2e-04	78%	gi|532113245|XP_005341304.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Pteropus alecto	46.0	46.0	100%	3e-04	74%	gi|586560565|XP_006913553.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Pteropus alecto	46.0	46.0	100%	3e-04	74%	gi|586560563|XP_006913552.1
☐	PREDICTED: carboxypeptidase B2 [Odobenus rosmarus diverg	45.2	45.2	100%	6e-04	74%	gi|472378433|XP_004408637.1
☐	PREDICTED: carboxypeptidase B2 [Sus scrofa]	44.8	44.8	94%	8e-04	78%	gi|194040626|XP_001929181.1
☐	PREDICTED: carboxypeptidase B2 [Leptonychotes weddellii]	44.8	44.8	100%	8e-04	74%	gi|585191930|XP_006747204.1
☐	PREDICTED: carboxypeptidase B2 [Elephantulus edwardii]	44.3	44.3	100%	0.001	74%	gi|585654497|XP_006884668.1
☐	PREDICTED: carboxypeptidase B2 [Erinaceus europaeus]	43.9	43.9	100%	0.002	74%	gi|617593818|XP_007521293.1
☐	PREDICTED: carboxypeptidase B2 [Anolis carolinensis]	43.9	43.9	100%	0.002	68%	gi|327260978|XP_003215309.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Bos mutus]	43.5	43.5	84%	0.002	81%	gi|555969567|XP_005896807.1
☐	Chain A, Crystal Structure Of Thrombin Activatable Fibrinolysis	43.5	43.5	84%	0.002	81%	gi|194368809|3DGV_A
☐	hypothetical protein PANDA_002961 [Ailuropoda melanoleuca]	43.5	43.5	100%	0.002	68%	gi|281349951|EFB25535.1
☐	PREDICTED: carboxypeptidase B2 [Jaculus jaculus]	43.5	43.5	89%	0.002	76%	gi|507564474|XP_004665908.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Bison bison bis	43.5	43.5	84%	0.002	81%	gi|742181236|XP_010852934.1
☐	carboxypeptidase B2 precursor [Bos taurus]	43.5	43.5	84%	0.002	81%	gi|114050845|NP_001039462.1
☐	PREDICTED: carboxypeptidase B2 [Capra hircus]	43.5	43.5	84%	0.002	81%	gi|548487919|XP_005687494.1
☐	PREDICTED: carboxypeptidase B2 [Ovis aries]	43.5	43.5	84%	0.002	81%	gi|426236307|XP_004012111.1
☐	PREDICTED: carboxypeptidase B2-like [Ailuropoda melanoleuc	43.5	43.5	100%	0.002	68%	gi|301758334|XP_002915018.1
☐	PREDICTED: carboxypeptidase B2 [Ursus maritimus]	43.5	43.5	100%	0.002	68%	gi|671028730|XP_008705148.1
☐	PREDICTED: carboxypeptidase B2 [Chrysemys picta bellii]	43.1	43.1	100%	0.003	63%	gi|641751137|XP_008166719.1

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NCBI/ BLAST/ blastp suite/ Formatting Results - B94MHV3301R

Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

CPB2_KKKQVHFFVNASDVDNVKA_NonMod

RID B94MHV3301R (Expires on 01-14 10:35 am)

Query ID lcl|131897
Description None
Molecule type amino acid
Query Length 19

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

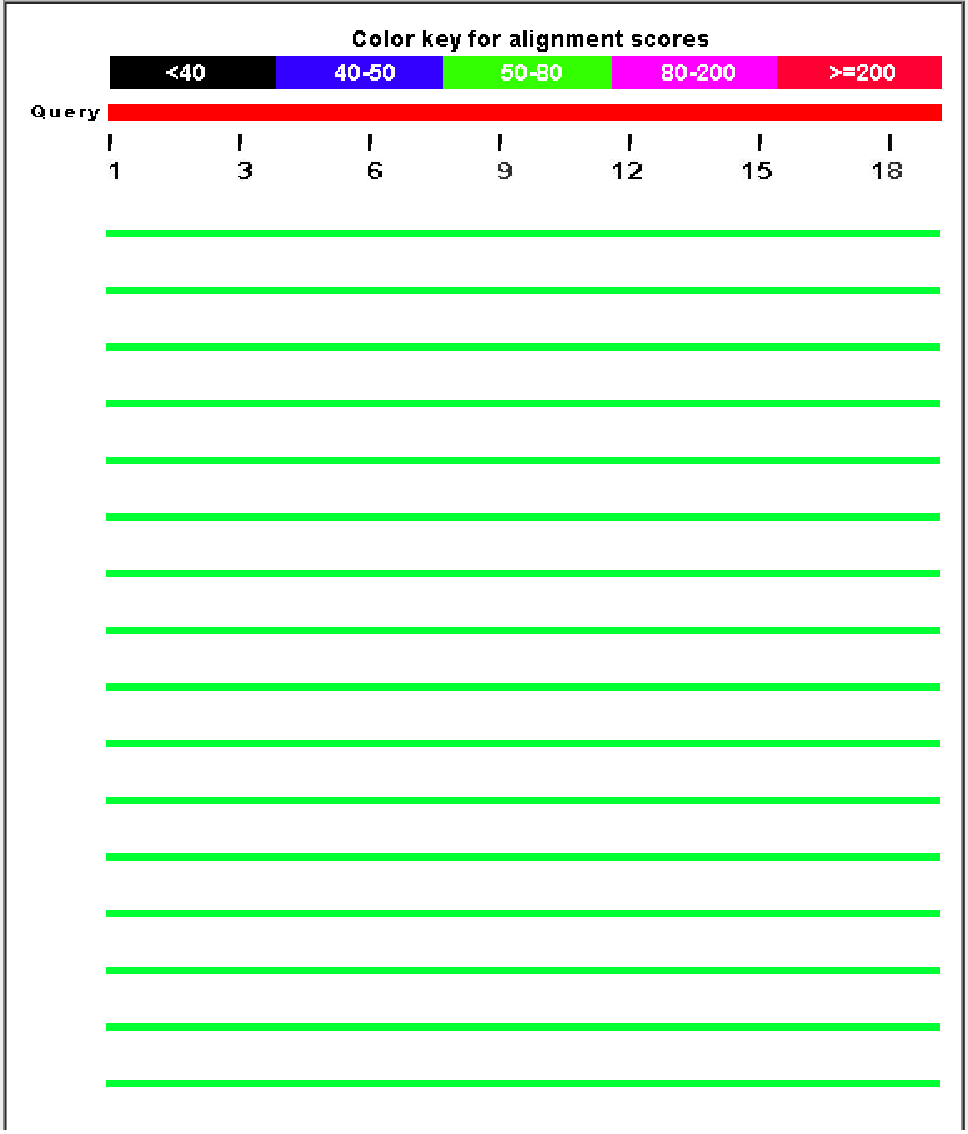
Graphic Summary

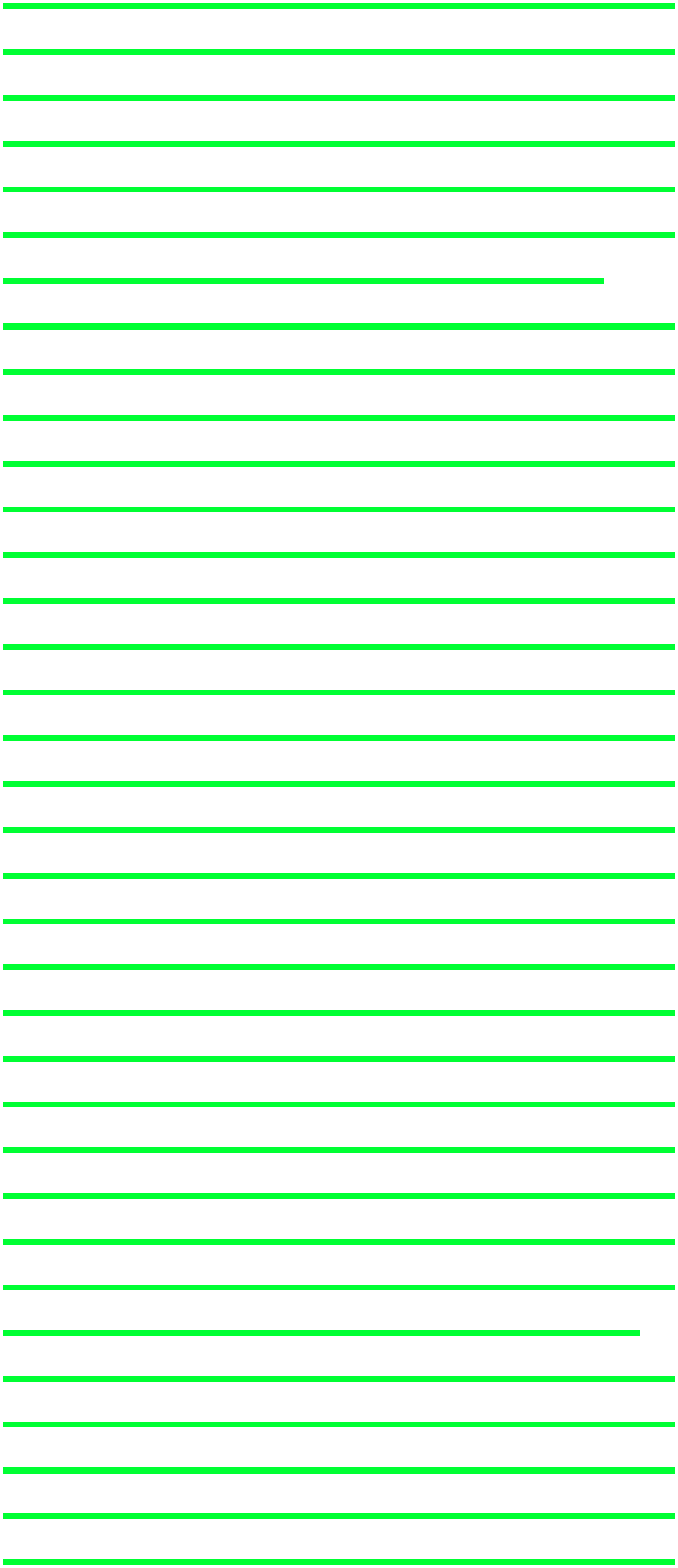
Show Conserved Domains

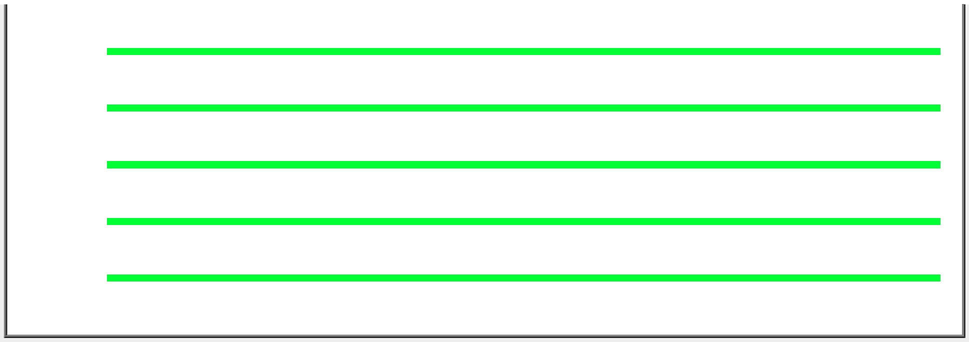
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Homo sapiens]	63.0	63.0	100%	5e-10	100%	gi|530402101|XP_005266316.1
☐	carboxypeptidase B-like protein [Homo sapiens]	63.0	63.0	100%	6e-10	100%	gi|6855464|BAA90475.1
☐	carboxypeptidase B2 (plasma, carboxypeptidase U), isoform CRA_	63.0	63.0	100%	6e-10	100%	gi|119629159|EAX08754.1
☐	carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]	63.0	63.0	100%	6e-10	100%	gi|513126877|NP_001265470.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Pongo abelii]	63.0	63.0	100%	6e-10	100%	gi|686743701|XP_009246910.1
☐	Chain A, Pro-carboxypeptidase U In Complex With 5-(3-aminopropy	63.0	63.0	100%	6e-10	100%	gi|672886543|4P10_A
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Homo sapiens]	63.0	63.0	100%	6e-10	100%	gi|530402099|XP_005266315.1
☐	prepro-plasma carboxypeptidase B [Homo sapiens]	63.0	63.0	100%	6e-10	100%	gi|189687|AAA60042.1
☐	PREDICTED: carboxypeptidase B2 [Gorilla gorilla gorilla]	63.0	63.0	100%	6e-10	100%	gi|426375394|XP_004054526.1
☐	Carboxypeptidase B2 (plasma) [Homo sapiens]	63.0	63.0	100%	6e-10	100%	gi|13937897|AAH07057.1
☐	carboxypeptidase B2 isoform 1 preproprotein [Homo sapiens]	63.0	63.0	100%	6e-10	100%	gi|513126885|NP_001863.3
☐	carboxypeptidase B2 (plasma) [synthetic construct]	63.0	63.0	100%	6e-10	100%	gi|157927966|ABW03279.1
☐	carboxypeptidase B2 (plasma, carboxypeptidase U) [synthetic cons	63.0	63.0	100%	6e-10	100%	gi|124126823|ABM92184.1
☐	PREDICTED: carboxypeptidase B2 [Pan troglodytes]	63.0	63.0	100%	6e-10	100%	gi|114651557|XP_509667.2
☐	Chain A, Crystal Structure Of Thrombin-Activatable Fibrinolysis Inhi	63.0	63.0	100%	6e-10	100%	gi|193506809|3D66_A
☐	Homo sapiens carboxypeptidase B2 (plasma, carboxypeptidase U)	63.0	63.0	100%	6e-10	100%	gi|30584819|AAP36662.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Pongo abelii]	63.0	63.0	100%	6e-10	100%	gi|297694016|XP_002824293.1
☐	Chain A, Crystal Structure Of A T325i/t329i/h333y/h335q Mutant Of	63.0	63.0	100%	6e-10	100%	gi|253722661|3D68_A
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Homo sapiens]	63.0	63.0	100%	6e-10	100%	gi|530402097|XP_005266314.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Rhinopithecus roxe	60.4	60.4	100%	4e-09	95%	gi|724966280|XP_010356389.1
☐	PREDICTED: carboxypeptidase B2 [Papio anubis]	60.4	60.4	100%	4e-09	95%	gi|402901940|XP_003913891.1
☐	PREDICTED: carboxypeptidase B2 [Nomascus leucogenys]	59.6	59.6	100%	8e-09	95%	gi|332241864|XP_003270104.1
☐	PREDICTED: carboxypeptidase B2 [Callithrix jacchus]	57.5	57.5	89%	4e-08	100%	gi|390457680|XP_002742737.2
☐	PREDICTED: carboxypeptidase B2 [Chlorocebus sabaeus]	57.1	57.1	100%	6e-08	89%	gi|635025444|XP_007958527.1
☐	PREDICTED: carboxypeptidase B2-like [Peromyscus maniculatus b	56.6	56.6	100%	7e-08	89%	gi|589996660|XP_006998803.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Cricetulus griseus]	56.6	56.6	100%	8e-08	89%	gi|625193824|XP_007639419.1
☐	PREDICTED: carboxypeptidase B2 isoform X4 [Cricetulus griseus]	56.6	56.6	100%	8e-08	89%	gi|625271974|XP_007627553.1
☐	PREDICTED: carboxypeptidase B2 [Peromyscus maniculatus baird	56.6	56.6	100%	8e-08	89%	gi|589957698|XP_006991448.1
☐							

	Carboxypeptidase B2 (plasma) [Mus musculus]	56.6	56.6	100%	8e-08	89%	gi|59808067|AAH89577.1
☐	carboxypeptidase U [Mus musculus]	56.6	56.6	100%	8e-08	89%	gi|6003652|AAF00528.1
☐	PREDICTED: carboxypeptidase B2 [Mesocricetus auratus]	56.6	56.6	100%	8e-08	89%	gi|524935646|XP_005071018.1
☐	carboxypeptidase B2 precursor [Mus musculus]	56.6	56.6	100%	8e-08	89%	gi|31982712|NP_062749.2
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Cricetulus griseus]	56.6	56.6	100%	8e-08	89%	gi|354476626|XP_003500525.1
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Cricetulus griseus]	56.6	56.6	100%	8e-08	89%	gi|625271972|XP_007627552.1
☐	zinc finger CCCH domain-containing protein 13 [Cricetulus griseus]	56.6	56.6	100%	9e-08	89%	gi|537241932|ERE87338.1
☐	Carboxypeptidase B2 [Fukomys damarensis]	54.9	54.9	100%	3e-07	89%	gi|676273139|KFO27861.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Macaca fascicularis	54.9	54.9	100%	3e-07	89%	gi|544503644|XP_005585858.1
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Chinchilla lanigera]	54.9	54.9	100%	3e-07	89%	gi|533192699|XP_005409155.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Chinchilla lanigera]	54.9	54.9	100%	3e-07	89%	gi|533192697|XP_005409154.1
☐	PREDICTED: carboxypeptidase B2 [Otolemur garnettii]	54.9	54.9	100%	3e-07	89%	gi|395835377|XP_003790657.1
☐	PREDICTED: carboxypeptidase B2 [Canis lupus familiaris]	54.9	54.9	100%	3e-07	89%	gi|73989292|XP_851154.1
☐	PREDICTED: carboxypeptidase B2 [Vicugna pacos]	54.9	54.9	100%	3e-07	89%	gi|560974364|XP_006209502.1
☐	PREDICTED: carboxypeptidase B2 [Camelus ferus]	54.9	54.9	100%	3e-07	89%	gi|560922422|XP_006187410.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Macaca fascicularis	54.9	54.9	100%	3e-07	89%	gi|544503642|XP_005585857.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Chinchilla lanigera]	54.9	54.9	100%	3e-07	89%	gi|533192695|XP_005409153.1
☐	PREDICTED: carboxypeptidase B2 [Saimiri boliviensis boliviensis]	54.9	54.9	94%	3e-07	94%	gi|403286234|XP_003934405.1
☐	Carboxypeptidase B2 [Macaca mulatta]	54.9	54.9	100%	3e-07	89%	gi|355700980|EHH29001.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Fukomys damarens	54.9	54.9	100%	3e-07	89%	gi|731244313|XP_010635336.1
☐	PREDICTED: carboxypeptidase B2 [Felis catus]	54.9	54.9	100%	3e-07	89%	gi|586973570|XP_006927367.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Fukomys damarens	54.9	54.9	100%	3e-07	89%	gi|731244311|XP_010635335.1
☐	PREDICTED: carboxypeptidase B2 [Panthera tigris altaica]	54.9	54.9	100%	3e-07	89%	gi|591318467|XP_007085493.1
☐	plastin-2 isoform 16 [Camelus ferus]	54.9	54.9	100%	3e-07	89%	gi|528759255|EPY78914.1
☐	carboxypeptidase B2 (plasma), isoform CRA_b [Rattus norvegicus]	54.1	54.1	100%	6e-07	84%	gi|149049966|EDM02290.1
☐	carboxypeptidase B2 (plasma), isoform CRA_a [Rattus norvegicus]	54.1	54.1	100%	6e-07	84%	gi|149049965|EDM02289.1
☐	Cpb2 protein [Rattus norvegicus]	54.1	54.1	100%	6e-07	84%	gi|60688161|AAH91133.1
☐	carboxypeptidase B2 precursor [Rattus norvegicus]	54.1	54.1	100%	6e-07	84%	gi|16758414|NP_446069.1
☐	PREDICTED: carboxypeptidase B2 [Tupaia chinensis]	54.1	54.1	100%	6e-07	84%	gi|562871068|XP_006163508.1
☐	PREDICTED: carboxypeptidase B2 [Equus caballus]	53.7	53.7	100%	8e-07	89%	gi|545190694|XP_005601424.1
☐	PREDICTED: carboxypeptidase B2 [Microtus ochrogaster]	52.8	52.8	100%	2e-06	84%	gi|532025304|XP_005355675.1
☐	PREDICTED: carboxypeptidase B2 isoform 1 [Macaca mulatta]	52.4	52.4	94%	2e-06	89%	gi|109120669|XP_001097310.1
☐	Carboxypeptidase B2 [Macaca fascicularis]	52.4	52.4	94%	2e-06	89%	gi|355754683|EHH58584.1
☐	PREDICTED: carboxypeptidase B2 isoform 3 [Macaca mulatta]	52.4	52.4	94%	2e-06	89%	gi|109120665|XP_001097608.1
☐	PREDICTED: carboxypeptidase B2 [Cavia porcellus]	52.4	52.4	100%	2e-06	84%	gi|348583190|XP_003477356.1
☐	PREDICTED: carboxypeptidase B2 [Balaenoptera acutorostrata sca	52.0	52.0	100%	3e-06	84%	gi|594678268|XP_007186896.1
☐	PREDICTED: carboxypeptidase B2 [Octodon degus]	51.5	51.5	100%	4e-06	84%	gi|507684606|XP_004640321.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Heterocephalus gla	51.1	51.1	100%	6e-06	84%	gi|512921202|XP_004904434.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Heterocephalus gla	51.1	51.1	100%	6e-06	84%	gi|512964055|XP_004844264.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Heterocephalus gla	51.1	51.1	100%	6e-06	84%	gi|512921198|XP_004904433.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Heterocephalus gla	51.1	51.1	100%	6e-06	84%	gi|512964053|XP_004844263.1
☐	PREDICTED: carboxypeptidase B2 [Tursiops truncatus]	50.3	50.3	100%	1e-05	84%	gi|470653285|XP_004329533.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Lipotes vexillifer]	50.3	50.3	100%	1e-05	84%	gi|602712571|XP_007466515.1
☐	PREDICTED: carboxypeptidase B2 [Physeter catodon]	50.3	50.3	100%	1e-05	84%	gi|593749228|XP_007129852.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Lipotes vexillifer]	50.3	50.3	100%	1e-05	84%	gi|602712569|XP_007466514.1

☐	PREDICTED: carboxypeptidase B2 [Orcinus orca]	50.3	50.3	100%	1e-05	84%	gi|466032575|XP_004274629.1
☐	PREDICTED: carboxypeptidase B2 [Ochotona princeps]	49.4	49.4	100%	2e-05	84%	gi|504128560|XP_004577530.1
☐	PREDICTED: carboxypeptidase B2 [Nannospalax galili]	49.0	49.0	100%	3e-05	79%	gi|674098370|XP_008822615.1
☐	PREDICTED: carboxypeptidase B2 [Ceratotherium simum simum]	49.0	49.0	94%	3e-05	83%	gi|478518956|XP_004433702.1
☐	PREDICTED: carboxypeptidase B2 [Ictidomys tridecemlineatus]	49.0	49.0	94%	3e-05	83%	gi|532113245|XP_005341304.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Pteropus alecto]	48.6	48.6	100%	4e-05	79%	gi|586560565|XP_006913553.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Pteropus alecto]	48.6	48.6	100%	4e-05	79%	gi|586560563|XP_006913552.1
☐	PREDICTED: carboxypeptidase B2 [Odobenus rosmarus divergens	47.7	47.7	100%	8e-05	79%	gi|472378433|XP_004408637.1
☐	PREDICTED: carboxypeptidase B2 [Sus scrofa]	47.3	47.3	94%	1e-04	83%	gi|194040626|XP_001929181.1
☐	PREDICTED: carboxypeptidase B2 [Elephantulus edwardii]	46.9	46.9	100%	2e-04	79%	gi|585654497|XP_006884668.1
☐	PREDICTED: carboxypeptidase B2 [Erinaceus europaeus]	46.4	46.4	100%	2e-04	79%	gi|617593818|XP_007521293.1
☐	PREDICTED: carboxypeptidase B2 [Leptonychotes weddellii]	46.4	46.4	100%	2e-04	74%	gi|585191930|XP_006747204.1
☐	PREDICTED: carboxypeptidase B2 [Anolis carolinensis]	46.4	46.4	100%	2e-04	74%	gi|327260978|XP_003215309.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Bos mutus]	46.0	46.0	84%	3e-04	88%	gi|555969567|XP_005896807.1
☐	Chain A, Crystal Structure Of Thrombin Activatable Fibrinolysis Inhi	46.0	46.0	84%	3e-04	88%	gi|194368809|3DGV_A
☐	hypothetical protein PANDA_002961 [Ailuropoda melanoleuca]	46.0	46.0	100%	3e-04	74%	gi|281349951|EFB25535.1
☐	PREDICTED: carboxypeptidase B2 [Jaculus jaculus]	46.0	46.0	89%	3e-04	82%	gi|507564474|XP_004665908.1
☐	carboxypeptidase B2 precursor [Bos taurus]	46.0	46.0	84%	3e-04	88%	gi|114050845|NP_001039462.1
☐	PREDICTED: carboxypeptidase B2 [Capra hircus]	46.0	46.0	84%	3e-04	88%	gi|548487919|XP_005687494.1
☐	PREDICTED: carboxypeptidase B2 [Ovis aries]	46.0	46.0	84%	3e-04	88%	gi|426236307|XP_004012111.1
☐	PREDICTED: carboxypeptidase B2-like [Ailuropoda melanoleuca]	46.0	46.0	100%	3e-04	74%	gi|301758334|XP_002915018.1
☐	PREDICTED: carboxypeptidase B2 [Ursus maritimus]	46.0	46.0	100%	3e-04	74%	gi|671028730|XP_008705148.1
☐	PREDICTED: carboxypeptidase B2 [Chrysemys picta bellii]	45.6	45.6	100%	4e-04	68%	gi|641751137|XP_008166719.1
☐	PREDICTED: carboxypeptidase B2 [Pelodiscus sinensis]	45.6	45.6	100%	4e-04	68%	gi|558138783|XP_006118064.1
☐	PREDICTED: carboxypeptidase B2-like [Trichechus manatus latiros	44.8	44.8	100%	8e-04	79%	gi|471377782|XP_004376698.1
☐	PREDICTED: carboxypeptidase B2-like [Trichechus manatus latiros	44.8	44.8	100%	8e-04	79%	gi|471377780|XP_004376697.1
☐	PREDICTED: carboxypeptidase B2 [Condylura cristata]	44.8	44.8	84%	8e-04	83%	gi|507939327|XP_004680202.1

⊟ Alignments

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PREDICTED: carboxypeptidase B2 isoform X3 [Homo sapiens]

Sequence ID: gi|530402101|ref|XP_005266316.1| **Length:** 226 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 83 to 101 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	5e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KKKQVHFFVNASDVDNVKA  19
            KKKQVHFFVNASDVDNVKA
Sbjct  83   KKKQVHFFVNASDVDNVKA  101
```

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carboxypeptidase B-like protein [Homo sapiens]

Sequence ID: gi|6855464|dbj|BAA90475.1| **Length:** 360 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 64 to 82 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	6e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1   KKKQVHFFVNASDVDNVKA  19
```

```
                 KKKQVHFFVNASDVDNVKA
Sbjct  64  KKKQVHFFVNASDVDNVKA  82
```

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carboxypeptidase B2 (plasma, carboxypeptidase U), isoform CRA_a [Homo sapiens]

Sequence ID: gi|119629159|gb|EAX08754.1| **Length:** 360 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 64 to 82 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	6e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KKKQVHFFVNASDVDNVKA  19
            KKKQVHFFVNASDVDNVKA
Sbjct  64   KKKQVHFFVNASDVDNVKA  82
```

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carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]

Sequence ID: gi|513126877|ref|NP_001265470.1| **Length:** 386 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 64 to 82 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	6e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KKKQVHFFVNASDVDNVKA  19
            KKKQVHFFVNASDVDNVKA
Sbjct  64   KKKQVHFFVNASDVDNVKA  82
```

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PREDICTED: carboxypeptidase B2 isoform X2 [Pongo abelii]

Sequence ID: gi|686743701|ref|XP_009246910.1| **Length:** 387 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 64 to 82 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	6e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KKKQVHFFVNASDVDNVKA  19
            KKKQVHFFVNASDVDNVKA
Sbjct  64   KKKQVHFFVNASDVDNVKA  82
```

BLAST ®

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NCBI/ BLAST/ blastp suite/ Formatting Results - BTGDXY3F016

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CPB2_KKQVHFFVDASDVDNVKA_Mod

RID	BTGDXY3F016 (Expires on 01-20 15:35 pm)		
Query ID	lcl|47924	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	18	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

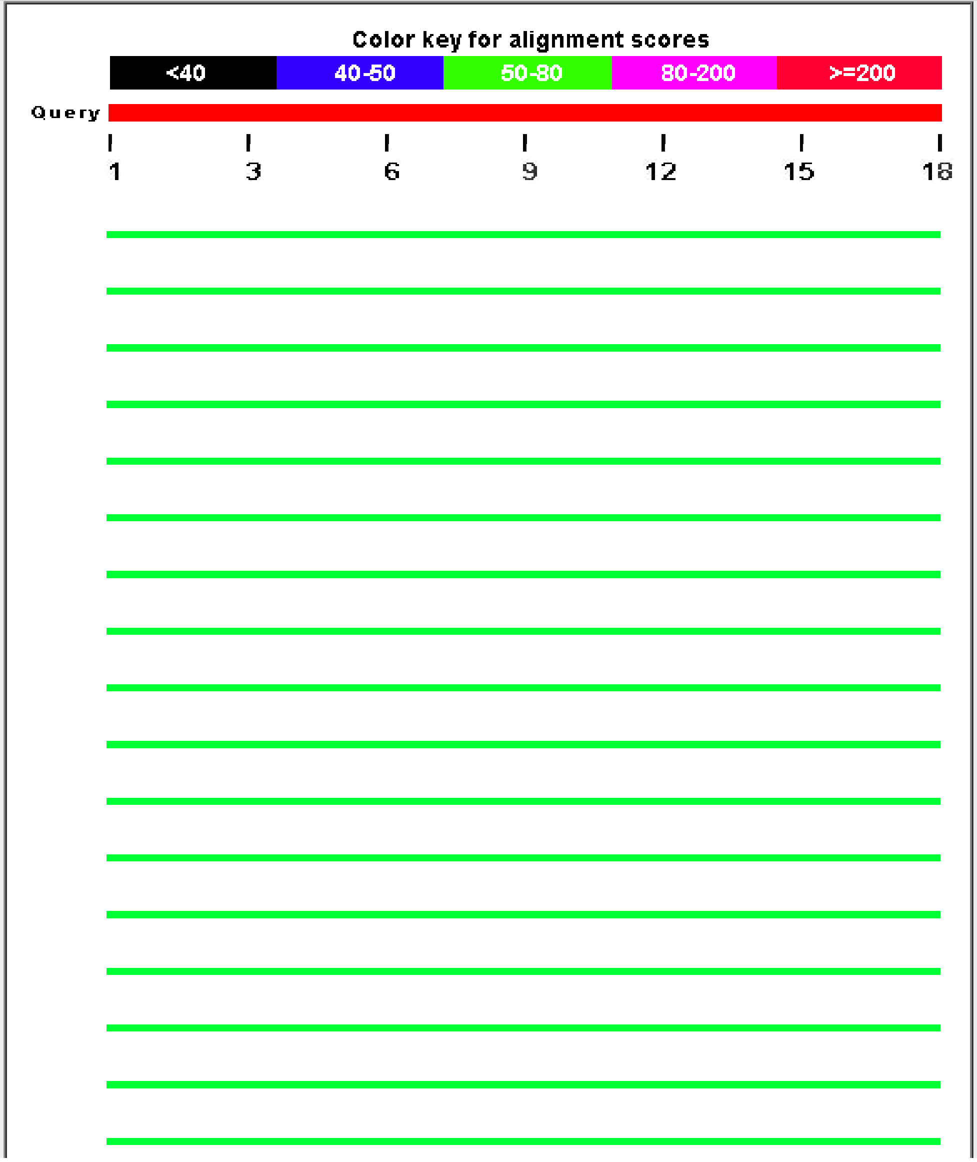
Graphic Summary

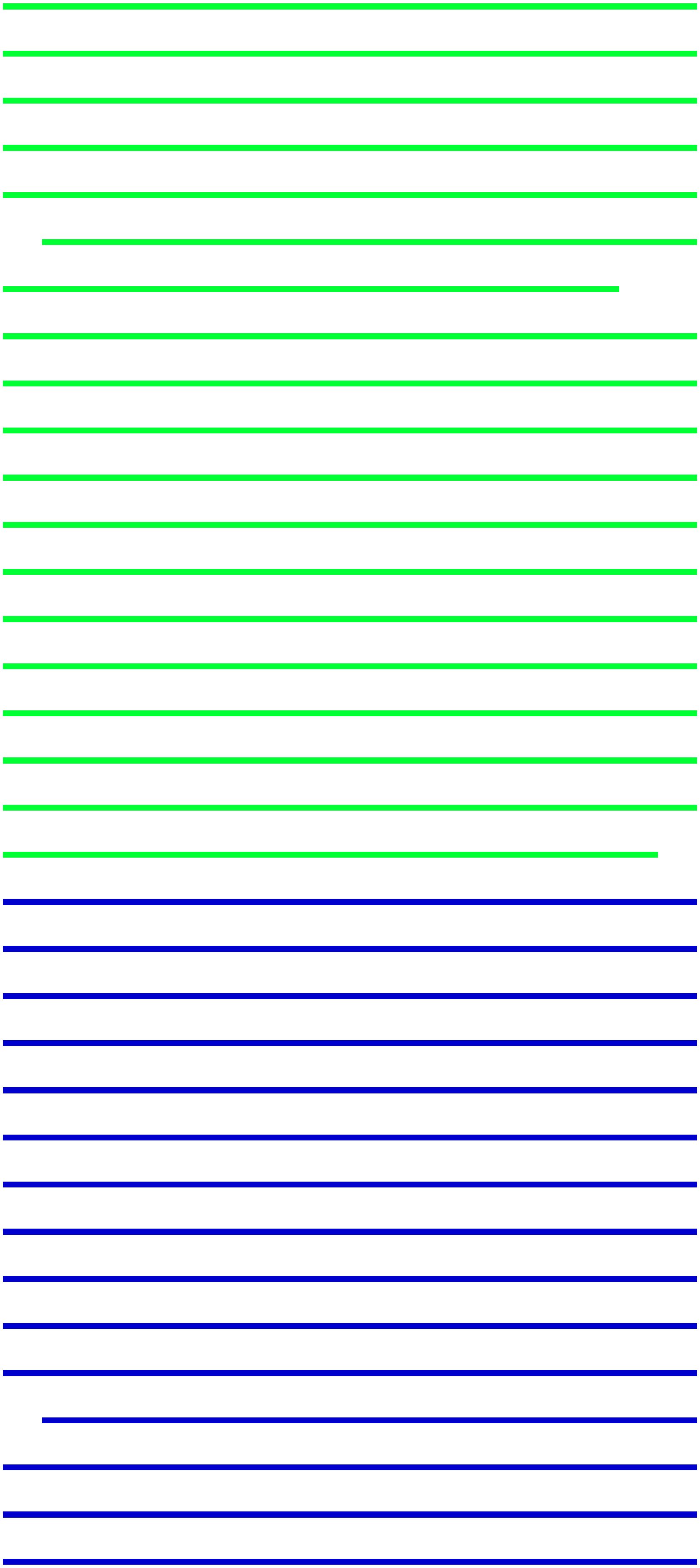
Show Conserved Domains

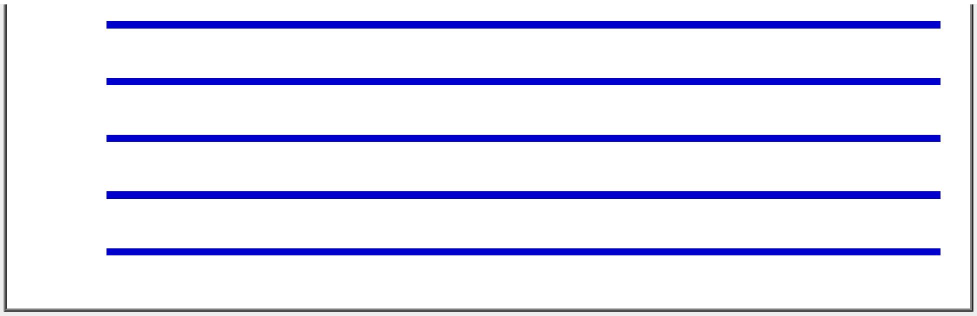
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Homo sapiens]	57.5	57.5	100%	3e-08	94%	gi|530402101|XP_005266316.1
☐	carboxypeptidase B-like protein [Homo sapiens]	57.5	57.5	100%	4e-08	94%	gi|6855464|BAA90475.1
☐	carboxypeptidase B2 (plasma, carboxypeptidase U), isoform CI	57.5	57.5	100%	4e-08	94%	gi|119629159|EAX08754.1
☐	carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]	57.5	57.5	100%	4e-08	94%	gi|513126877|NP_001265470.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Pongo abelii]	57.5	57.5	100%	4e-08	94%	gi|686743701|XP_009246910.1
☐	Chain A, Pro-carboxypeptidase U In Complex With 5-(3-aminop	57.5	57.5	100%	4e-08	94%	gi|672886543|4P10_A
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Homo sapiens]	57.5	57.5	100%	4e-08	94%	gi|530402099|XP_005266315.1
☐	prepro-plasma carboxypeptidase B [Homo sapiens]	57.5	57.5	100%	4e-08	94%	gi|189687|AAA60042.1
☐	PREDICTED: carboxypeptidase B2 [Gorilla gorilla gorilla]	57.5	57.5	100%	4e-08	94%	gi|426375394|XP_004054526.1
☐	Carboxypeptidase B2 (plasma) [Homo sapiens]	57.5	57.5	100%	4e-08	94%	gi|13937897|AAH07057.1
☐	carboxypeptidase B2 isoform 1 preproprotein [Homo sapiens]	57.5	57.5	100%	4e-08	94%	gi|513126885|NP_001863.3
☐	carboxypeptidase B2 (plasma) [synthetic construct]	57.5	57.5	100%	4e-08	94%	gi|157927966|ABW03279.1
☐	carboxypeptidase B2 (plasma, carboxypeptidase U) [synthetic c	57.5	57.5	100%	4e-08	94%	gi|124126823|ABM92184.1
☐	PREDICTED: carboxypeptidase B2 [Pan troglodytes]	57.5	57.5	100%	4e-08	94%	gi|114651557|XP_509667.2
☐	Chain A, Crystal Structure Of Thrombin-Activatable Fibrinolysis	57.5	57.5	100%	4e-08	94%	gi|193506809|3D66_A
☐	Homo sapiens carboxypeptidase B2 (plasma, carboxypeptidase	57.5	57.5	100%	4e-08	94%	gi|30584819|AAP36662.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Pongo abelii]	57.5	57.5	100%	4e-08	94%	gi|297694016|XP_002824293.1
☐	Chain A, Crystal Structure Of A T325i/t329i/h333y/h335q Mutar	57.5	57.5	100%	4e-08	94%	gi|253722661|3D68_A
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Homo sapiens]	57.5	57.5	100%	4e-08	94%	gi|530402097|XP_005266314.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Rhinopithecus	54.9	54.9	100%	3e-07	89%	gi|724966280|XP_010356389.1
☐	PREDICTED: carboxypeptidase B2 [Papio anubis]	54.9	54.9	100%	3e-07	89%	gi|402901940|XP_003913891.1
☐	PREDICTED: carboxypeptidase B2 [Nomascus leucogenys]	54.1	54.1	100%	6e-07	89%	gi|332241864|XP_003270104.1
☐	PREDICTED: carboxypeptidase B2 [Chlorocebus sabaeus]	52.0	52.0	94%	3e-06	88%	gi|635025444|XP_007958527.1
☐	PREDICTED: carboxypeptidase B2 [Callithrix jacchus]	52.0	52.0	88%	3e-06	94%	gi|390457680|XP_002742737.2
☐	PREDICTED: carboxypeptidase B2-like [Peromyscus manicula	51.1	51.1	100%	5e-06	83%	gi|589996660|XP_006998803.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Cricetulus grise	51.1	51.1	100%	6e-06	83%	gi|625193824|XP_007639419.1
☐	PREDICTED: carboxypeptidase B2 isoform X4 [Cricetulus grise	51.1	51.1	100%	6e-06	83%	gi|625271974|XP_007627553.1
☐	PREDICTED: carboxypeptidase B2 [Peromyscus maniculatus b	51.1	51.1	100%	6e-06	83%	gi|589957698|XP_006991448.1
☐	Carboxypeptidase B2 (plasma) [Mus musculus]	51.1	51.1	100%	6e-06	83%	gi|59808067|AAH89577.1

☐	carboxypeptidase U [Mus musculus]	51.1	51.1	100%	6e-06	83%	gi|6003652|AAF00528.1
☐	PREDICTED: carboxypeptidase B2 [Mesocricetus auratus]	51.1	51.1	100%	6e-06	83%	gi|524935646|XP_005071018.1
☐	carboxypeptidase B2 precursor [Mus musculus]	51.1	51.1	100%	6e-06	83%	gi|31982712|NP_062749.2
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Cricetulus grise	51.1	51.1	100%	6e-06	83%	gi|354476626|XP_003500525.1
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Cricetulus grise	51.1	51.1	100%	6e-06	83%	gi|625271972|XP_007627552.1
☐	zinc finger CCCH domain-containing protein 13 [Cricetulus gris	51.1	51.1	100%	6e-06	83%	gi|537241932|ERE87338.1
☐	PREDICTED: carboxypeptidase B2 [Saimiri boliviensis bolivien	50.7	50.7	94%	8e-06	89%	gi|403286234|XP_003934405.1
☐	Carboxypeptidase B2 [Fukomys damarensis]	49.4	49.4	100%	2e-05	83%	gi|676273139|KFO27861.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Camelus drom	49.4	49.4	100%	2e-05	83%	gi|744566815|XP_010979147.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Camelus bactri	49.4	49.4	100%	2e-05	83%	gi|743712317|XP_010949694.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Macaca fascicu	49.4	49.4	100%	2e-05	83%	gi|544503644|XP_005585858.1
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Chinchilla lanig	49.4	49.4	100%	2e-05	83%	gi|533192699|XP_005409155.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Chinchilla lanig	49.4	49.4	100%	2e-05	83%	gi|533192697|XP_005409154.1
☐	PREDICTED: carboxypeptidase B2 [Otolemur garnettii]	49.4	49.4	100%	2e-05	83%	gi|395835377|XP_003790657.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Camelus drom	49.4	49.4	100%	2e-05	83%	gi|744566812|XP_010979146.1
☐	PREDICTED: carboxypeptidase B2 [Canis lupus familiaris]	49.4	49.4	100%	2e-05	83%	gi|73989292|XP_851154.1
☐	PREDICTED: carboxypeptidase B2 [Vicugna pacos]	49.4	49.4	100%	2e-05	83%	gi|560974364|XP_006209502.1
☐	PREDICTED: carboxypeptidase B2 [Camelus ferus]	49.4	49.4	100%	2e-05	83%	gi|560922422|XP_006187410.1
☐	PREDICTED: carboxypeptidase B2 [Equus caballus]	49.4	49.4	94%	2e-05	88%	gi|545190694|XP_005601424.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Macaca fascicu	49.4	49.4	100%	2e-05	83%	gi|544503642|XP_005585857.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Chinchilla lanig	49.4	49.4	100%	2e-05	83%	gi|533192695|XP_005409153.1
☐	Carboxypeptidase B2 [Macaca mulatta]	49.4	49.4	100%	2e-05	83%	gi|355700980|EHH29001.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Fukomys dama	49.4	49.4	100%	2e-05	83%	gi|731244313|XP_010635336.1
☐	PREDICTED: carboxypeptidase B2 [Felis catus]	49.4	49.4	100%	2e-05	83%	gi|586973570|XP_006927367.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Fukomys dama	49.4	49.4	100%	2e-05	83%	gi|731244311|XP_010635335.1
☐	PREDICTED: carboxypeptidase B2 [Panthera tigris altaica]	49.4	49.4	100%	2e-05	83%	gi|591318467|XP_007085493.1
☐	plastin-2 isoform 16 [Camelus ferus]	49.4	49.4	100%	2e-05	83%	gi|528759255|EPY78914.1
☐	carboxypeptidase B2 (plasma), isoform CRA_b [Rattus norvegi	48.6	48.6	100%	4e-05	78%	gi|149049966|EDM02290.1
☐	carboxypeptidase B2 (plasma), isoform CRA_a [Rattus norvegi	48.6	48.6	100%	4e-05	78%	gi|149049965|EDM02289.1
☐	Cpb2 protein [Rattus norvegicus]	48.6	48.6	100%	4e-05	78%	gi|60688161|AAH91133.1
☐	carboxypeptidase B2 precursor [Rattus norvegicus]	48.6	48.6	100%	4e-05	78%	gi|16758414|NP_446069.1
☐	PREDICTED: carboxypeptidase B2 [Tupaia chinensis]	48.6	48.6	100%	4e-05	78%	gi|562871068|XP_006163508.1
☐	PREDICTED: carboxypeptidase B2 [Microtus ochrogaster]	47.3	47.3	100%	1e-04	78%	gi|532025304|XP_005355675.1
☐	PREDICTED: carboxypeptidase B2 isoform 1 [Macaca mulatta]	46.9	46.9	94%	1e-04	82%	gi|109120669|XP_001097310.1
☐	Carboxypeptidase B2 [Macaca fascicularis]	46.9	46.9	94%	1e-04	82%	gi|355754683|EHH58584.1
☐	PREDICTED: carboxypeptidase B2 isoform 3 [Macaca mulatta]	46.9	46.9	94%	1e-04	82%	gi|109120665|XP_001097608.1
☐	PREDICTED: carboxypeptidase B2 [Cavia porcellus]	46.9	46.9	100%	1e-04	78%	gi|348583190|XP_003477356.1
☐	PREDICTED: carboxypeptidase B2 [Tursiops truncatus]	46.4	46.4	94%	2e-04	82%	gi|470653285|XP_004329533.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Lipotes vexillife	46.4	46.4	94%	2e-04	82%	gi|602712571|XP_007466515.1
☐	PREDICTED: carboxypeptidase B2 [Physeter catodon]	46.4	46.4	94%	2e-04	82%	gi|593749228|XP_007129852.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Lipotes vexillife	46.4	46.4	94%	2e-04	82%	gi|602712569|XP_007466514.1
☐	PREDICTED: carboxypeptidase B2 [Balaenoptera acutorostrata	46.4	46.4	94%	2e-04	82%	gi|594678268|XP_007186896.1
☐	PREDICTED: carboxypeptidase B2 [Ochotona princeps]	46.4	46.4	94%	2e-04	82%	gi|504128560|XP_004577530.1
☐	PREDICTED: carboxypeptidase B2 [Orcinus orca]	46.4	46.4	94%	2e-04	82%	gi|466032575|XP_004274629.1
☐	PREDICTED: carboxypeptidase B2 [Octodon degus]	46.0	46.0	100%	3e-04	78%	gi|507684606|XP_004640321.1

☐	PREDICTED: carboxypeptidase B2 isoform X2 [Heterocephalu	45.6	45.6	100%	4e-04	78%	gi|512921202|XP_004904434.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Heterocephalu	45.6	45.6	100%	4e-04	78%	gi|512964055|XP_004844264.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Heterocephalu	45.6	45.6	100%	4e-04	78%	gi|512921198|XP_004904433.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Heterocephalu	45.6	45.6	100%	4e-04	78%	gi|512964053|XP_004844263.1
☐	PREDICTED: carboxypeptidase B2 [Odobenus rosmarus diver	44.8	44.8	100%	7e-04	75%	gi|472378433|XP_004408637.1
☐	PREDICTED: carboxypeptidase B2 [Leptonychotes weddellii]	44.3	44.3	100%	0.001	75%	gi|585191930|XP_006747204.1
☐	PREDICTED: carboxypeptidase B2 [Ictidomys tridecemlineatus	43.9	43.9	88%	0.001	81%	gi|532113245|XP_005341304.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Bos mutus]	43.5	43.5	88%	0.002	81%	gi|555969567|XP_005896807.1
☐	Chain A, Crystal Structure Of Thrombin Activatable Fibrinolysis	43.5	43.5	88%	0.002	81%	gi|194368809|3DGV_A
☐	PREDICTED: carboxypeptidase B2 [Nannospalax galili]	43.5	43.5	100%	0.002	72%	gi|674098370|XP_008822615.1
☐	PREDICTED: carboxypeptidase B2 [Ceratotherium simum simu	43.5	43.5	94%	0.002	76%	gi|478518956|XP_004433702.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Bison bison bis	43.5	43.5	88%	0.002	81%	gi|742181236|XP_010852934.1
☐	carboxypeptidase B2 precursor [Bos taurus]	43.5	43.5	88%	0.002	81%	gi|114050845|NP_001039462.1
☐	PREDICTED: carboxypeptidase B2 [Capra hircus]	43.5	43.5	88%	0.002	81%	gi|548487919|XP_005687494.1
☐	PREDICTED: carboxypeptidase B2 [Ovis aries]	43.5	43.5	88%	0.002	81%	gi|426236307|XP_004012111.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Pteropus alect	43.1	43.1	100%	0.003	72%	gi|586560565|XP_006913553.1
☐	hypothetical protein PANDA_002961 [Ailuropoda melanoleuca]	43.1	43.1	100%	0.003	70%	gi|281349951|EFB25535.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Pteropus alect	43.1	43.1	100%	0.003	72%	gi|586560563|XP_006913552.1
☐	PREDICTED: carboxypeptidase B2-like [Ailuropoda melanoleu	43.1	43.1	100%	0.003	70%	gi|301758334|XP_002915018.1
☐	PREDICTED: carboxypeptidase B2 [Ursus maritimus]	43.1	43.1	100%	0.003	70%	gi|671028730|XP_008705148.1
☐	PREDICTED: carboxypeptidase B2 [Condylura cristata]	42.2	42.2	88%	0.005	78%	gi|507939327|XP_004680202.1
☐	PREDICTED: carboxypeptidase B2 [Sus scrofa]	41.8	41.8	94%	0.007	76%	gi|194040626|XP_001929181.1
☐	Carboxypeptidase B2 [Ophiophagus hannah]	41.4	41.4	94%	0.009	71%	gi|565306861|ETE61379.1
☐	PREDICTED: carboxypeptidase B2 [Elephantulus edwardii]	41.4	41.4	100%	0.010	72%	gi|585654497|XP_006884668.1
☐	PREDICTED: carboxypeptidase B2 [Anolis carolinensis]	41.4	41.4	94%	0.010	71%	gi|327260978|XP_003215309.1
☐	PREDICTED: carboxypeptidase B2 [Erinaceus europaeus]	40.9	40.9	94%	0.013	76%	gi|617593818|XP_007521293.1

⊟Alignments

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PREDICTED: carboxypeptidase B2 isoform X3 [Homo sapiens]

Sequence ID: gi|530402101|ref|XP_005266316.1| **Length:** 226 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 84 to 101 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.5 bits(128)	3e-08	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KKQVHFFVDASDVDNVKA  18
            KKQVHFFV+ASDVDNVKA
Sbjct  84   KKQVHFFVNASDVDNVKA  101
```

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carboxypeptidase B-like protein [Homo sapiens]

Sequence ID: gi|6855464|dbj|BAA90475.1| **Length:** 360 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 65 to 82 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.5 bits(128)	4e-08	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1   KKQVHFFVDASDVDNVKA  18
           KKQVHFFV+ASDVDNVKA
Sbjct  65  KKQVHFFVNASDVDNVKA  82
```

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carboxypeptidase B2 (plasma, carboxypeptidase U), isoform CRA_a [Homo sapiens]

Sequence ID: gi|119629159|gb|EAX08754.1| **Length:** 360 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 65 to 82 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.5 bits(128)	4e-08	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1   KKQVHFFVDASDVDNVKA  18
           KKQVHFFV+ASDVDNVKA
Sbjct  65  KKQVHFFVNASDVDNVKA  82
```

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carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]

Sequence ID: gi|513126877|ref|NP_001265470.1| **Length:** 386 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 65 to 82 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.5 bits(128)	4e-08	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1   KKQVHFFVDASDVDNVKA  18
           KKQVHFFV+ASDVDNVKA
Sbjct  65  KKQVHFFVNASDVDNVKA  82
```

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PREDICTED: carboxypeptidase B2 isoform X2 [Pongo abelii]

Sequence ID: gi|686743701|ref|XP_009246910.1| **Length:** 387 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 65 to 82 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.5 bits(128)	4e-08	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1   KKQVHFFVDASDVDNVKA  18
           KKQVHFFV+ASDVDNVKA
Sbjct  65  KKQVHFFVNASDVDNVKA  82
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - B94GRTUF01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

CPB2_KKQVHFFVNASDVDNVKA_NonMod

RID	B94GRTUF01R (Expires on 01-14 10:33 am)
Query ID	lcl|231962
Description	None
Molecule type	amino acid
Query Length	18

Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

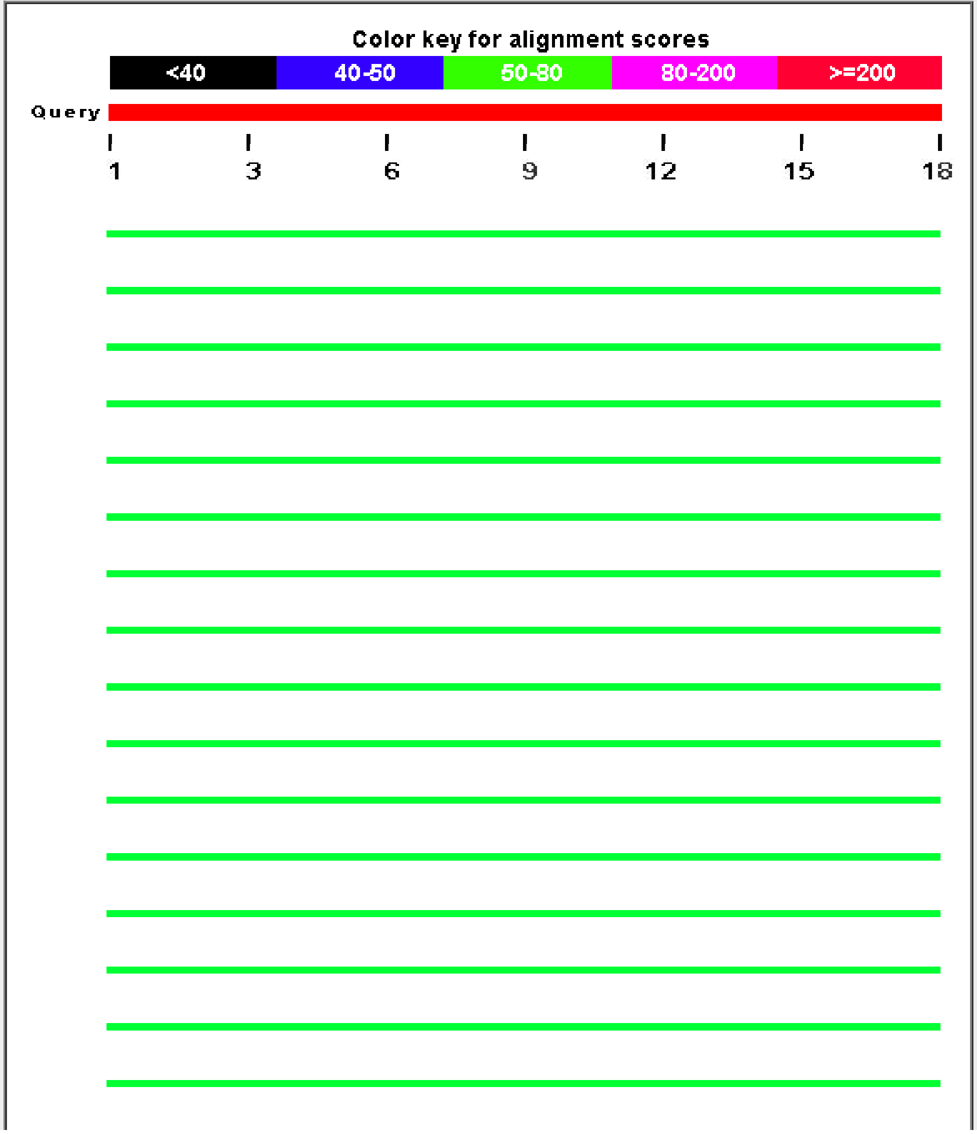
Graphic Summary

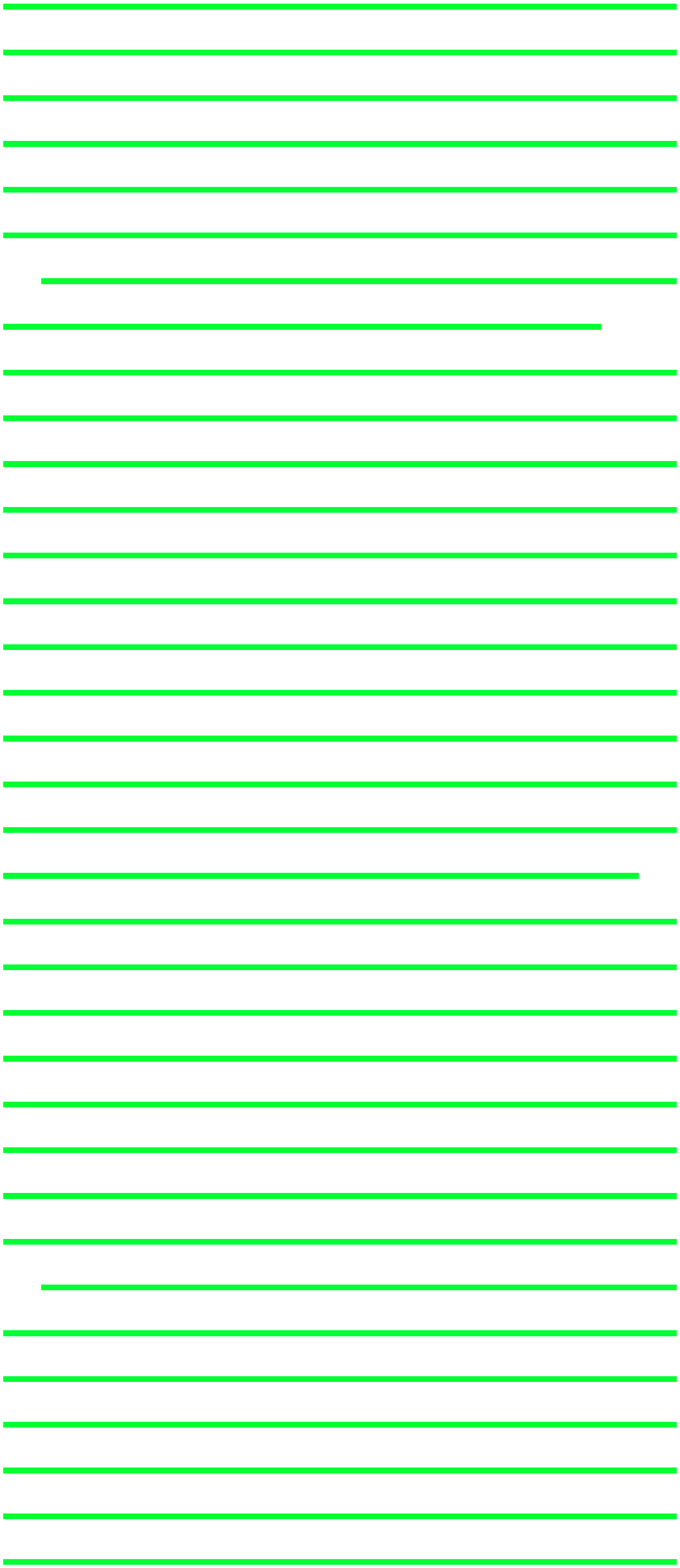
Show Conserved Domains

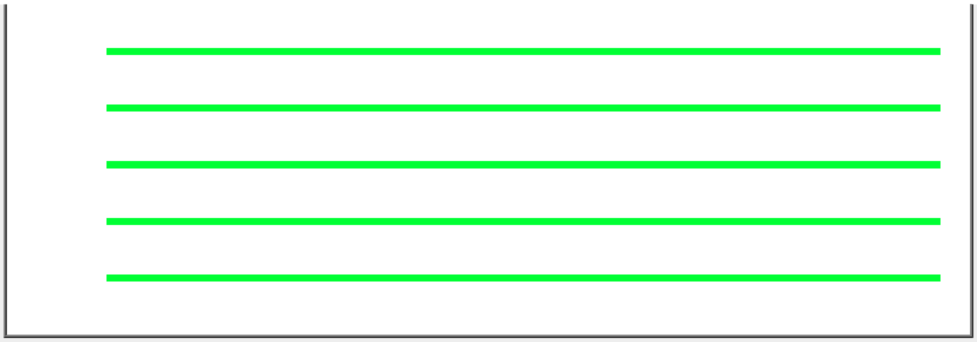
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Homo sapiens]	60.0	60.0	100%	4e-09	100%	gi|530402101|XP_005266316.1
☐	carboxypeptidase B-like protein [Homo sapiens]	60.0	60.0	100%	5e-09	100%	gi|6855464|BAA90475.1
☐	carboxypeptidase B2 (plasma, carboxypeptidase U), isoform CRA_	60.0	60.0	100%	5e-09	100%	gi|119629159|EAX08754.1
☐	carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]	60.0	60.0	100%	5e-09	100%	gi|513126877|NP_001265470.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Pongo abelii]	60.0	60.0	100%	5e-09	100%	gi|686743701|XP_009246910.1
☐	Chain A, Pro-carboxypeptidase U In Complex With 5-(3-aminopropy	60.0	60.0	100%	5e-09	100%	gi|672886543|4P10_A
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Homo sapiens]	60.0	60.0	100%	5e-09	100%	gi|530402099|XP_005266315.1
☐	prepro-plasma carboxypeptidase B [Homo sapiens]	60.0	60.0	100%	5e-09	100%	gi|189687|AAA60042.1
☐	PREDICTED: carboxypeptidase B2 [Gorilla gorilla gorilla]	60.0	60.0	100%	5e-09	100%	gi|426375394|XP_004054526.1
☐	Carboxypeptidase B2 (plasma) [Homo sapiens]	60.0	60.0	100%	5e-09	100%	gi|13937897|AAH07057.1
☐	carboxypeptidase B2 isoform 1 preproprotein [Homo sapiens]	60.0	60.0	100%	5e-09	100%	gi|513126885|NP_001863.3
☐	carboxypeptidase B2 (plasma) [synthetic construct]	60.0	60.0	100%	5e-09	100%	gi|157927966|ABW03279.1
☐	carboxypeptidase B2 (plasma, carboxypeptidase U) [synthetic cons	60.0	60.0	100%	5e-09	100%	gi|124126823|ABM92184.1
☐	PREDICTED: carboxypeptidase B2 [Pan troglodytes]	60.0	60.0	100%	5e-09	100%	gi|114651557|XP_509667.2
☐	Chain A, Crystal Structure Of Thrombin-Activatable Fibrinolysis Inhi	60.0	60.0	100%	5e-09	100%	gi|193506809|3D66_A
☐	Homo sapiens carboxypeptidase B2 (plasma, carboxypeptidase U)	60.0	60.0	100%	5e-09	100%	gi|30584819|AAP36662.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Pongo abelii]	60.0	60.0	100%	5e-09	100%	gi|297694016|XP_002824293.1
☐	Chain A, Crystal Structure Of A T325i/t329i/h333y/h335q Mutant Of	60.0	60.0	100%	5e-09	100%	gi|253722661|3D68_A
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Homo sapiens]	60.0	60.0	100%	5e-09	100%	gi|530402097|XP_005266314.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Rhinopithecus roxe	57.5	57.5	100%	4e-08	94%	gi|724966280|XP_010356389.1
☐	PREDICTED: carboxypeptidase B2 [Papio anubis]	57.5	57.5	100%	4e-08	94%	gi|402901940|XP_003913891.1
☐	PREDICTED: carboxypeptidase B2 [Nomascus leucogenys]	56.6	56.6	100%	7e-08	94%	gi|332241864|XP_003270104.1
☐	PREDICTED: carboxypeptidase B2 [Chlorocebus sabaeus]	54.5	54.5	94%	4e-07	94%	gi|635025444|XP_007958527.1
☐	PREDICTED: carboxypeptidase B2 [Callithrix jacchus]	54.5	54.5	88%	4e-07	100%	gi|390457680|XP_002742737.2
☐	PREDICTED: carboxypeptidase B2-like [Peromyscus maniculatus b	53.7	53.7	100%	6e-07	89%	gi|589996660|XP_006998803.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Cricetulus griseus]	53.7	53.7	100%	7e-07	89%	gi|625193824|XP_007639419.1
☐	PREDICTED: carboxypeptidase B2 isoform X4 [Cricetulus griseus]	53.7	53.7	100%	7e-07	89%	gi|625271974|XP_007627553.1
☐	PREDICTED: carboxypeptidase B2 [Peromyscus maniculatus baird	53.7	53.7	100%	7e-07	89%	gi|589957698|XP_006991448.1
☐							

	Carboxypeptidase B2 (plasma) [Mus musculus]	53.7	53.7	100%	7e-07	89%	gi|59808067|AAH89577.1
☐	carboxypeptidase U [Mus musculus]	53.7	53.7	100%	7e-07	89%	gi|6003652|AAF00528.1
☐	PREDICTED: carboxypeptidase B2 [Mesocricetus auratus]	53.7	53.7	100%	7e-07	89%	gi|524935646|XP_005071018.1
☐	carboxypeptidase B2 precursor [Mus musculus]	53.7	53.7	100%	7e-07	89%	gi|31982712|NP_062749.2
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Cricetulus griseus]	53.7	53.7	100%	7e-07	89%	gi|354476626|XP_003500525.1
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Cricetulus griseus]	53.7	53.7	100%	7e-07	89%	gi|625271972|XP_007627552.1
☐	zinc finger CCCH domain-containing protein 13 [Cricetulus griseus]	53.7	53.7	100%	8e-07	89%	gi|537241932|ERE87338.1
☐	PREDICTED: carboxypeptidase B2 [Saimiri boliviensis boliviensis]	53.2	53.2	94%	1e-06	94%	gi|403286234|XP_003934405.1
☐	Carboxypeptidase B2 [Fukomys damarensis]	52.0	52.0	100%	3e-06	89%	gi|676273139|KFO27861.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Macaca fascicularis	52.0	52.0	100%	3e-06	89%	gi|544503644|XP_005585858.1
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Chinchilla lanigera]	52.0	52.0	100%	3e-06	89%	gi|533192699|XP_005409155.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Chinchilla lanigera]	52.0	52.0	100%	3e-06	89%	gi|533192697|XP_005409154.1
☐	PREDICTED: carboxypeptidase B2 [Otolemur garnettii]	52.0	52.0	100%	3e-06	89%	gi|395835377|XP_003790657.1
☐	PREDICTED: carboxypeptidase B2 [Canis lupus familiaris]	52.0	52.0	100%	3e-06	89%	gi|73989292|XP_851154.1
☐	PREDICTED: carboxypeptidase B2 [Vicugna pacos]	52.0	52.0	100%	3e-06	89%	gi|560974364|XP_006209502.1
☐	PREDICTED: carboxypeptidase B2 [Camelus ferus]	52.0	52.0	100%	3e-06	89%	gi|560922422|XP_006187410.1
☐	PREDICTED: carboxypeptidase B2 [Equus caballus]	52.0	52.0	94%	3e-06	94%	gi|545190694|XP_005601424.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Macaca fascicularis	52.0	52.0	100%	3e-06	89%	gi|544503642|XP_005585857.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Chinchilla lanigera]	52.0	52.0	100%	3e-06	89%	gi|533192695|XP_005409153.1
☐	Carboxypeptidase B2 [Macaca mulatta]	52.0	52.0	100%	3e-06	89%	gi|355700980|EHH29001.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Fukomys damarens	52.0	52.0	100%	3e-06	89%	gi|731244313|XP_010635336.1
☐	PREDICTED: carboxypeptidase B2 [Felis catus]	52.0	52.0	100%	3e-06	89%	gi|586973570|XP_006927367.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Fukomys damarens	52.0	52.0	100%	3e-06	89%	gi|731244311|XP_010635335.1
☐	PREDICTED: carboxypeptidase B2 [Panthera tigris altaica]	52.0	52.0	100%	3e-06	89%	gi|591318467|XP_007085493.1
☐	plastin-2 isoform 16 [Camelus ferus]	52.0	52.0	100%	3e-06	89%	gi|528759255|EPY78914.1
☐	carboxypeptidase B2 (plasma), isoform CRA_b [Rattus norvegicus]	51.1	51.1	100%	5e-06	83%	gi|149049966|EDM02290.1
☐	carboxypeptidase B2 (plasma), isoform CRA_a [Rattus norvegicus]	51.1	51.1	100%	5e-06	83%	gi|149049965|EDM02289.1
☐	Cpb2 protein [Rattus norvegicus]	51.1	51.1	100%	5e-06	83%	gi|60688161|AAH91133.1
☐	carboxypeptidase B2 precursor [Rattus norvegicus]	51.1	51.1	100%	5e-06	83%	gi|16758414|NP_446069.1
☐	PREDICTED: carboxypeptidase B2 [Tupaia chinensis]	51.1	51.1	100%	5e-06	83%	gi|562871068|XP_006163508.1
☐	PREDICTED: carboxypeptidase B2 [Microtus ochrogaster]	49.8	49.8	100%	1e-05	83%	gi|532025304|XP_005355675.1
☐	PREDICTED: carboxypeptidase B2 isoform 1 [Macaca mulatta]	49.4	49.4	94%	2e-05	88%	gi|109120669|XP_001097310.1
☐	Carboxypeptidase B2 [Macaca fascicularis]	49.4	49.4	94%	2e-05	88%	gi|355754683|EHH58584.1
☐	PREDICTED: carboxypeptidase B2 isoform 3 [Macaca mulatta]	49.4	49.4	94%	2e-05	88%	gi|109120665|XP_001097608.1
☐	PREDICTED: carboxypeptidase B2 [Cavia porcellus]	49.4	49.4	100%	2e-05	83%	gi|348583190|XP_003477356.1
☐	PREDICTED: carboxypeptidase B2 [Tursiops truncatus]	49.0	49.0	94%	3e-05	88%	gi|470653285|XP_004329533.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Lipotes vexillifer]	49.0	49.0	94%	3e-05	88%	gi|602712571|XP_007466515.1
☐	PREDICTED: carboxypeptidase B2 [Physeter catodon]	49.0	49.0	94%	3e-05	88%	gi|593749228|XP_007129852.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Lipotes vexillifer]	49.0	49.0	94%	3e-05	88%	gi|602712569|XP_007466514.1
☐	PREDICTED: carboxypeptidase B2 [Balaenoptera acutorostrata sca	49.0	49.0	94%	3e-05	88%	gi|594678268|XP_007186896.1
☐	PREDICTED: carboxypeptidase B2 [Ochotona princeps]	49.0	49.0	94%	3e-05	88%	gi|504128560|XP_004577530.1
☐	PREDICTED: carboxypeptidase B2 [Orcinus orca]	49.0	49.0	94%	3e-05	88%	gi|466032575|XP_004274629.1
☐	PREDICTED: carboxypeptidase B2 [Octodon degus]	48.6	48.6	100%	4e-05	83%	gi|507684606|XP_004640321.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Heterocephalus gla	48.1	48.1	100%	5e-05	83%	gi|512921202|XP_004904434.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Heterocephalus gla	48.1	48.1	100%	5e-05	83%	gi|512964055|XP_004844264.1

☐	PREDICTED: carboxypeptidase B2 isoform X1 [Heterocephalus gla	48.1	48.1	100%	5e-05	83%	gi|512921198|XP_004904433.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Heterocephalus gla	48.1	48.1	100%	5e-05	83%	gi|512964053|XP_004844263.1
☐	PREDICTED: carboxypeptidase B2 [Odobenus rosmarus divergens	47.3	47.3	100%	1e-04	80%	gi|472378433|XP_004408637.1
☐	PREDICTED: carboxypeptidase B2 [Ictidomys tridecemlineatus]	46.4	46.4	88%	2e-04	88%	gi|532113245|XP_005341304.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Bos mutus]	46.0	46.0	88%	3e-04	88%	gi|555969567|XP_005896807.1
☐	Chain A, Crystal Structure Of Thrombin Activatable Fibrinolysis Inhi	46.0	46.0	88%	3e-04	88%	gi|194368809|3DGV_A
☐	PREDICTED: carboxypeptidase B2 [Nannospalax galili]	46.0	46.0	100%	3e-04	78%	gi|674098370|XP_008822615.1
☐	PREDICTED: carboxypeptidase B2 [Ceratotherium simum simum]	46.0	46.0	94%	3e-04	82%	gi|478518956|XP_004433702.1
☐	carboxypeptidase B2 precursor [Bos taurus]	46.0	46.0	88%	3e-04	88%	gi|114050845|NP_001039462.1
☐	PREDICTED: carboxypeptidase B2 [Leptonychotes weddellii]	46.0	46.0	100%	3e-04	75%	gi|585191930|XP_006747204.1
☐	PREDICTED: carboxypeptidase B2 [Capra hircus]	46.0	46.0	88%	3e-04	88%	gi|548487919|XP_005687494.1
☐	PREDICTED: carboxypeptidase B2 [Ovis aries]	46.0	46.0	88%	3e-04	88%	gi|426236307|XP_004012111.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Pteropus alecto]	45.6	45.6	100%	4e-04	78%	gi|586560565|XP_006913553.1
☐	hypothetical protein PANDA_002961 [Ailuropoda melanoleuca]	45.6	45.6	100%	4e-04	75%	gi|281349951|EFB25535.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Pteropus alecto]	45.6	45.6	100%	4e-04	78%	gi|586560563|XP_006913552.1
☐	PREDICTED: carboxypeptidase B2-like [Ailuropoda melanoleuca]	45.6	45.6	100%	4e-04	75%	gi|301758334|XP_002915018.1
☐	PREDICTED: carboxypeptidase B2 [Ursus maritimus]	45.6	45.6	100%	4e-04	75%	gi|671028730|XP_008705148.1
☐	PREDICTED: carboxypeptidase B2 [Condylura cristata]	44.8	44.8	88%	7e-04	83%	gi|507939327|XP_004680202.1
☐	PREDICTED: carboxypeptidase B2 [Sus scrofa]	44.3	44.3	94%	0.001	82%	gi|194040626|XP_001929181.1
☐	Carboxypeptidase B2 [Ophiophagus hannah]	43.9	43.9	94%	0.001	76%	gi|565306861|ETE61379.1
☐	PREDICTED: carboxypeptidase B2 [Elephantulus edwardii]	43.9	43.9	100%	0.001	78%	gi|585654497|XP_006884668.1
☐	PREDICTED: carboxypeptidase B2 [Anolis carolinensis]	43.9	43.9	94%	0.001	76%	gi|327260978|XP_003215309.1
☐	PREDICTED: carboxypeptidase B2 [Erinaceus europaeus]	43.5	43.5	94%	0.002	82%	gi|617593818|XP_007521293.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Galeopterus varieg	43.1	43.1	88%	0.003	81%	gi|667276404|XP_008572661.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Galeopterus varieg	43.1	43.1	88%	0.003	81%	gi|667276401|XP_008572660.1
☐	PREDICTED: carboxypeptidase B2 [Chrysemys picta bellii]	43.1	43.1	94%	0.003	71%	gi|641751137|XP_008166719.1
☐	PREDICTED: carboxypeptidase B2 [Jaculus jaculus]	43.1	43.1	88%	0.003	81%	gi|507564474|XP_004665908.1

⊟ Alignments

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PREDICTED: carboxypeptidase B2 isoform X3 [Homo sapiens]

Sequence ID: gi|530402101|ref|XP_005266316.1| **Length:** 226 **Number of Matches:** 1

Range 1: 84 to 101 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	4e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    KKQVHFFVNASDVDNVKA  18
            KKQVHFFVNASDVDNVKA
Sbjct  84   KKQVHFFVNASDVDNVKA  101
```

Related Information

Gene - associated gene details

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carboxypeptidase B-like protein [Homo sapiens]

Sequence ID: gi|6855464|dbj|BAA90475.1| **Length:** 360 **Number of Matches:** 1

Range 1: 65 to 82 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	5e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1   KKQVHFFVNASDVDNVKA  18
```

Related Information

Gene - associated gene details

```
               KKQVHFFVNASDVDNVKA
Sbjct  65   KKQVHFFVNASDVDNVKA  82
```

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carboxypeptidase B2 (plasma, carboxypeptidase U), isoform CRA_a [Homo sapiens]

Sequence ID: gi|119629159|gb|EAX08754.1| **Length:** 360 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 65 to 82 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	5e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    KKQVHFFVNASDVDNVKA  18
            KKQVHFFVNASDVDNVKA
Sbjct  65   KKQVHFFVNASDVDNVKA  82
```

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carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]

Sequence ID: gi|513126877|ref|NP_001265470.1| **Length:** 386 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 65 to 82 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	5e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    KKQVHFFVNASDVDNVKA  18
            KKQVHFFVNASDVDNVKA
Sbjct  65   KKQVHFFVNASDVDNVKA  82
```

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PREDICTED: carboxypeptidase B2 isoform X2 [Pongo abelii]

Sequence ID: gi|686743701|ref|XP_009246910.1| **Length:** 387 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 65 to 82 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	5e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    KKQVHFFVNASDVDNVKA  18
            KKQVHFFVNASDVDNVKA
Sbjct  65   KKQVHFFVNASDVDNVKA  82
```

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Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

CPB2_KQVHFFVDASDVDNVKA_Mod

RID BTGWP217016 (Expires on 01-20 15:43 pm)

Query ID lcl|20348

Description None

Molecule type amino acid

Query Length 17

Database Name nr

Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

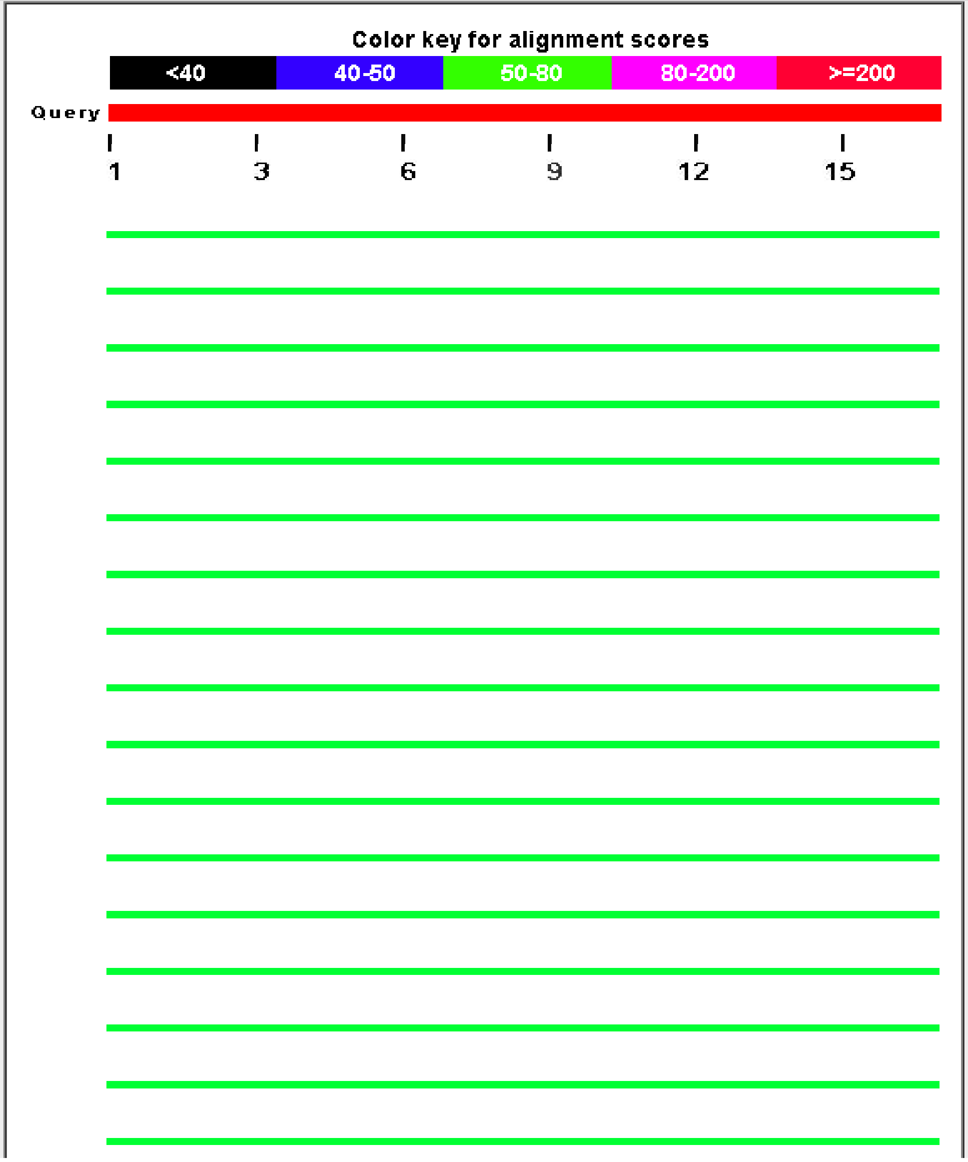
Graphic Summary

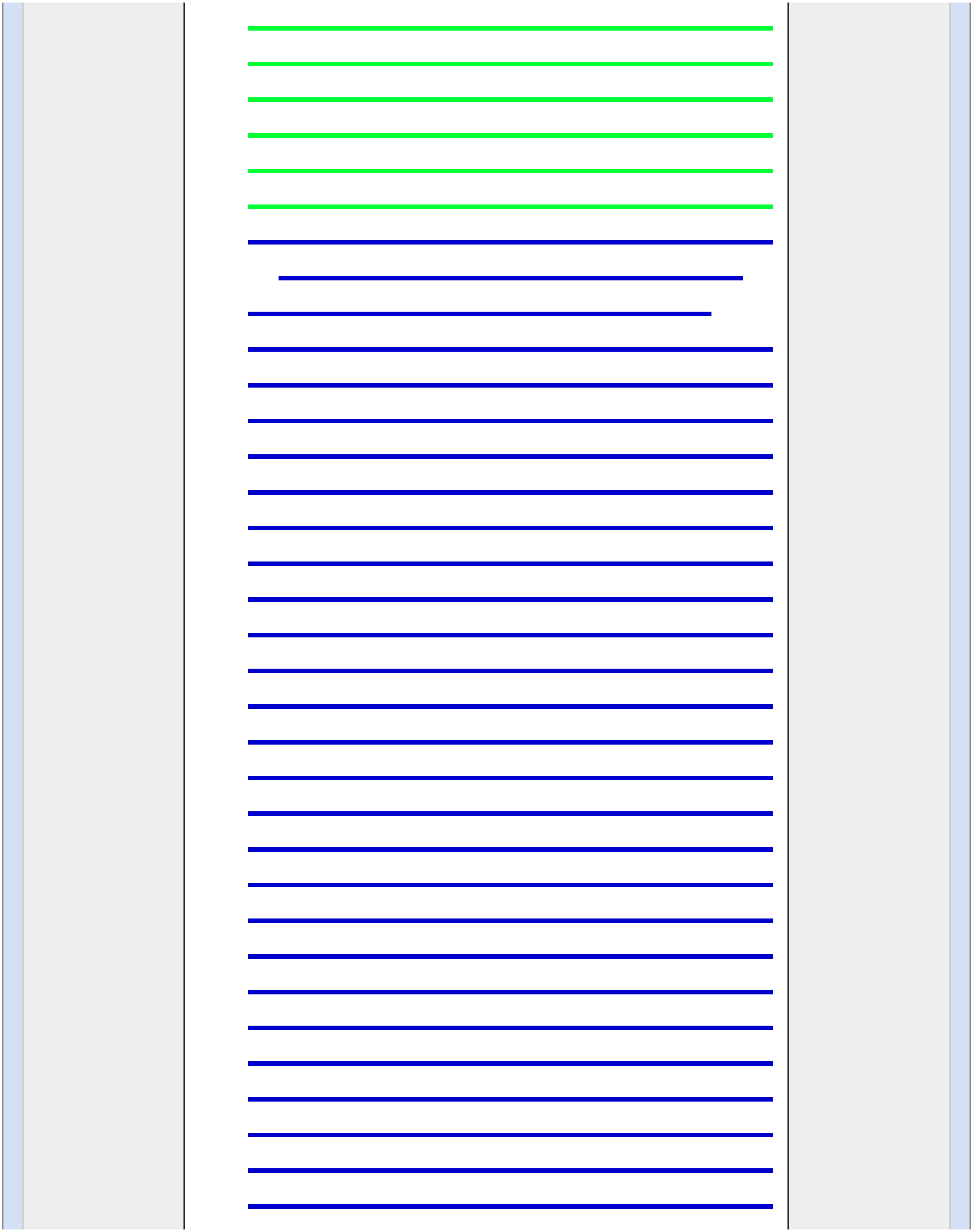
Show Conserved Domains

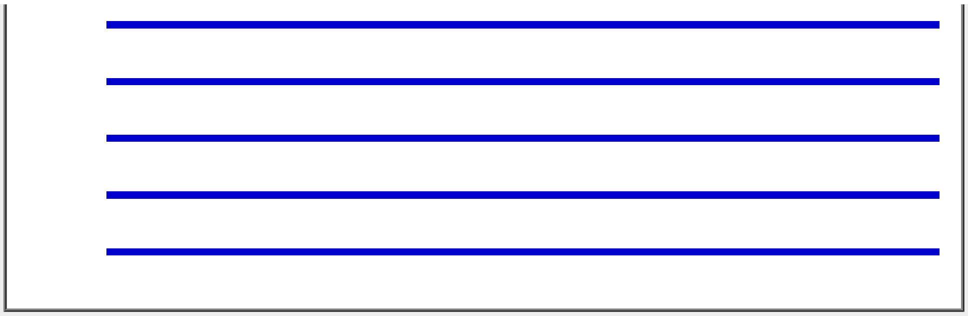
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Homo sapiens]	54.5	54.5	100%	3e-07	94%	gi|530402101|XP_005266316.1
☐	carboxypeptidase B-like protein [Homo sapiens]	54.5	54.5	100%	3e-07	94%	gi|6855464|BAA90475.1
☐	carboxypeptidase B2 (plasma, carboxypeptidase U), isoform CI	54.5	54.5	100%	3e-07	94%	gi|119629159|EAX08754.1
☐	carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]	54.5	54.5	100%	3e-07	94%	gi|513126877|NP_001265470.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Pongo abelii]	54.5	54.5	100%	3e-07	94%	gi|686743701|XP_009246910.1
☐	Chain A, Pro-carboxypeptidase U In Complex With 5-(3-aminor	54.5	54.5	100%	4e-07	94%	gi|672886543|4P10_A
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Homo sapiens]	54.5	54.5	100%	4e-07	94%	gi|530402099|XP_005266315.1
☐	prepro-plasma carboxypeptidase B [Homo sapiens]	54.5	54.5	100%	4e-07	94%	gi|189687|AAA60042.1
☐	PREDICTED: carboxypeptidase B2 [Gorilla gorilla gorilla]	54.5	54.5	100%	4e-07	94%	gi|426375394|XP_004054526.1
☐	Carboxypeptidase B2 (plasma) [Homo sapiens]	54.5	54.5	100%	4e-07	94%	gi|13937897|AAH07057.1
☐	carboxypeptidase B2 isoform 1 preproprotein [Homo sapiens]	54.5	54.5	100%	4e-07	94%	gi|513126885|NP_001863.3
☐	carboxypeptidase B2 (plasma) [synthetic construct]	54.5	54.5	100%	4e-07	94%	gi|157927966|ABW03279.1
☐	carboxypeptidase B2 (plasma, carboxypeptidase U) [synthetic c	54.5	54.5	100%	4e-07	94%	gi|124126823|ABM92184.1
☐	PREDICTED: carboxypeptidase B2 [Pan troglodytes]	54.5	54.5	100%	4e-07	94%	gi|114651557|XP_509667.2
☐	Chain A, Crystal Structure Of Thrombin-Activatable Fibrinolysis	54.5	54.5	100%	4e-07	94%	gi|193506809|3D66_A
☐	Homo sapiens carboxypeptidase B2 (plasma, carboxypeptidase	54.5	54.5	100%	4e-07	94%	gi|30584819|AAP36662.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Pongo abelii]	54.5	54.5	100%	4e-07	94%	gi|297694016|XP_002824293.1
☐	Chain A, Crystal Structure Of A T325i/t329i/h333y/h335q Mutar	54.5	54.5	100%	4e-07	94%	gi|253722661|3D68_A
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Homo sapiens]	54.5	54.5	100%	4e-07	94%	gi|530402097|XP_005266314.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Rhinopithecus	52.0	52.0	100%	3e-06	88%	gi|724966280|XP_010356389.1
☐	PREDICTED: carboxypeptidase B2 [Chlorocebus sabaeus]	52.0	52.0	100%	3e-06	88%	gi|635025444|XP_007958527.1
☐	PREDICTED: carboxypeptidase B2 [Papio anubis]	52.0	52.0	100%	3e-06	88%	gi|402901940|XP_003913891.1
☐	PREDICTED: carboxypeptidase B2 [Nomascus leucogenys]	51.1	51.1	100%	5e-06	88%	gi|332241864|XP_003270104.1
☐	PREDICTED: carboxypeptidase B2 [Equus caballus]	49.4	49.4	100%	2e-05	88%	gi|545190694|XP_005601424.1
☐	PREDICTED: carboxypeptidase B2 [Saimiri boliviensis bolivien	49.0	49.0	88%	3e-05	93%	gi|403286234|XP_003934405.1
☐	PREDICTED: carboxypeptidase B2 [Callithrix jacchus]	49.0	49.0	88%	3e-05	93%	gi|390457680|XP_002742737.2
☐	PREDICTED: carboxypeptidase B2-like [Peromyscus manicula	48.1	48.1	100%	4e-05	82%	gi|589996660|XP_006998803.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Cricetulus grise	48.1	48.1	100%	5e-05	82%	gi|625193824|XP_007639419.1
☐	PREDICTED: carboxypeptidase B2 isoform X4 [Cricetulus grise	48.1	48.1	100%	5e-05	82%	gi|625271974|XP_007627553.1

☐	PREDICTED: carboxypeptidase B2 [Peromyscus maniculatus b	48.1	48.1	100%	5e-05	82%	gi|589957698|XP_006991448.1
☐	Carboxypeptidase B2 (plasma) [Mus musculus]	48.1	48.1	100%	5e-05	82%	gi|59808067|AAH89577.1
☐	carboxypeptidase U [Mus musculus]	48.1	48.1	100%	5e-05	82%	gi|6003652|AAF00528.1
☐	PREDICTED: carboxypeptidase B2 [Mesocricetus auratus]	48.1	48.1	100%	5e-05	82%	gi|524935646|XP_005071018.1
☐	carboxypeptidase B2 precursor [Mus musculus]	48.1	48.1	100%	5e-05	82%	gi|31982712|NP_062749.2
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Cricetulus grise	48.1	48.1	100%	5e-05	82%	gi|354476626|XP_003500525.1
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Cricetulus grise	48.1	48.1	100%	5e-05	82%	gi|625271972|XP_007627552.1
☐	zinc finger CCCH domain-containing protein 13 [Cricetulus gris	48.1	48.1	100%	5e-05	82%	gi|537241932|ERE87338.1
☐	PREDICTED: carboxypeptidase B2 [Tursiops truncatus]	46.4	46.4	100%	2e-04	82%	gi|470653285|XP_004329533.1
☐	Carboxypeptidase B2 [Fukomys damarensis]	46.4	46.4	100%	2e-04	82%	gi|676273139|KFO27861.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Camelus drom	46.4	46.4	100%	2e-04	82%	gi|744566815|XP_010979147.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Camelus bactri	46.4	46.4	100%	2e-04	82%	gi|743712317|XP_010949694.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Lipotes vexillife	46.4	46.4	100%	2e-04	82%	gi|602712571|XP_007466515.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Macaca fascicu	46.4	46.4	100%	2e-04	82%	gi|544503644|XP_005585858.1
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Chinchilla lanig	46.4	46.4	100%	2e-04	82%	gi|533192699|XP_005409155.1
☐	PREDICTED: carboxypeptidase B2 [Physeter catodon]	46.4	46.4	100%	2e-04	82%	gi|593749228|XP_007129852.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Chinchilla lanig	46.4	46.4	100%	2e-04	82%	gi|533192697|XP_005409154.1
☐	PREDICTED: carboxypeptidase B2 [Otolemur garnettii]	46.4	46.4	100%	2e-04	82%	gi|395835377|XP_003790657.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Camelus drom	46.4	46.4	100%	2e-04	82%	gi|744566812|XP_010979146.1
☐	PREDICTED: carboxypeptidase B2 [Canis lupus familiaris]	46.4	46.4	100%	2e-04	82%	gi|73989292|XP_851154.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Lipotes vexillife	46.4	46.4	100%	2e-04	82%	gi|602712569|XP_007466514.1
☐	PREDICTED: carboxypeptidase B2 [Balaenoptera acutorostrat	46.4	46.4	100%	2e-04	82%	gi|594678268|XP_007186896.1
☐	PREDICTED: carboxypeptidase B2 [Vicugna pacos]	46.4	46.4	100%	2e-04	82%	gi|560974364|XP_006209502.1
☐	PREDICTED: carboxypeptidase B2 [Camelus ferus]	46.4	46.4	100%	2e-04	82%	gi|560922422|XP_006187410.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Macaca fascicu	46.4	46.4	100%	2e-04	82%	gi|544503642|XP_005585857.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Chinchilla lanig	46.4	46.4	100%	2e-04	82%	gi|533192695|XP_005409153.1
☐	PREDICTED: carboxypeptidase B2 [Ochotona princeps]	46.4	46.4	100%	2e-04	82%	gi|504128560|XP_004577530.1
☐	PREDICTED: carboxypeptidase B2 [Orcinus orca]	46.4	46.4	100%	2e-04	82%	gi|466032575|XP_004274629.1
☐	Carboxypeptidase B2 [Macaca mulatta]	46.4	46.4	100%	2e-04	82%	gi|355700980|EHH29001.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Fukomys dama	46.4	46.4	100%	2e-04	82%	gi|731244313|XP_010635336.1
☐	PREDICTED: carboxypeptidase B2 [Felis catus]	46.4	46.4	100%	2e-04	82%	gi|586973570|XP_006927367.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Fukomys dama	46.4	46.4	100%	2e-04	82%	gi|731244311|XP_010635335.1
☐	PREDICTED: carboxypeptidase B2 [Panthera tigris altaica]	46.4	46.4	100%	2e-04	82%	gi|591318467|XP_007085493.1
☐	plastin-2 isoform 16 [Camelus ferus]	46.4	46.4	100%	2e-04	82%	gi|528759255|EPY78914.1
☐	PREDICTED: carboxypeptidase B2 [Tupaia chinensis]	46.0	46.0	94%	3e-04	81%	gi|562871068|XP_006163508.1
☐	carboxypeptidase B2 (plasma), isoform CRA_b [Rattus norvegi	45.6	45.6	100%	3e-04	76%	gi|149049966|EDM02290.1
☐	carboxypeptidase B2 (plasma), isoform CRA_a [Rattus norvegi	45.6	45.6	100%	3e-04	76%	gi|149049965|EDM02289.1
☐	Cpb2 protein [Rattus norvegicus]	45.6	45.6	100%	3e-04	76%	gi|60688161|AAH91133.1
☐	carboxypeptidase B2 precursor [Rattus norvegicus]	45.6	45.6	100%	3e-04	76%	gi|16758414|NP_446069.1
☐	PREDICTED: carboxypeptidase B2 [Microtus ochrogaster]	44.3	44.3	100%	0.001	76%	gi|532025304|XP_005355675.1
☐	PREDICTED: carboxypeptidase B2 isoform 1 [Macaca mulatta]	43.9	43.9	94%	0.001	81%	gi|109120669|XP_001097310.1
☐	PREDICTED: carboxypeptidase B2 [Ictidomys tridecemlineatus	43.9	43.9	94%	0.001	81%	gi|532113245|XP_005341304.1
☐	Carboxypeptidase B2 [Macaca fascicularis]	43.9	43.9	94%	0.001	81%	gi|355754683|EHH58584.1
☐	PREDICTED: carboxypeptidase B2 isoform 3 [Macaca mulatta]	43.9	43.9	94%	0.001	81%	gi|109120665|XP_001097608.1
☐	PREDICTED: carboxypeptidase B2 [Cavia porcellus]	43.9	43.9	100%	0.001	76%	gi|348583190|XP_003477356.1

☐ PREDICTED: carboxypeptidase B2 isoform X2 [Bos mutus]	43.5	43.5	94%	0.002	81%	gi|555969567|XP_005896807.1
☐ Chain A, Crystal Structure Of Thrombin Activatable Fibrinolysis	43.5	43.5	94%	0.002	81%	gi|194368809|3DGV_A
☐ PREDICTED: carboxypeptidase B2 isoform X1 [Bison bison bis	43.5	43.5	94%	0.002	81%	gi|742181236|XP_010852934.1
☐ carboxypeptidase B2 precursor [Bos taurus]	43.5	43.5	94%	0.002	81%	gi|114050845|NP_001039462.1
☐ PREDICTED: carboxypeptidase B2 [Capra hircus]	43.5	43.5	94%	0.002	81%	gi|548487919|XP_005687494.1
☐ PREDICTED: carboxypeptidase B2 [Odobenus rosmarus diverg	43.5	43.5	100%	0.002	76%	gi|472378433|XP_004408637.1
☐ PREDICTED: carboxypeptidase B2 [Ovis aries]	43.5	43.5	94%	0.002	81%	gi|426236307|XP_004012111.1
☐ PREDICTED: carboxypeptidase B2 [Leptonychotes weddellii]	43.1	43.1	100%	0.002	76%	gi|585191930|XP_006747204.1
☐ PREDICTED: carboxypeptidase B2 [Octodon degus]	43.1	43.1	100%	0.002	76%	gi|507684606|XP_004640321.1
☐ PREDICTED: carboxypeptidase B2 isoform X2 [Heterocephalus	42.6	42.6	100%	0.003	76%	gi|512921202|XP_004904434.1
☐ PREDICTED: carboxypeptidase B2 isoform X2 [Heterocephalus	42.6	42.6	100%	0.003	76%	gi|512964055|XP_004844264.1
☐ PREDICTED: carboxypeptidase B2 isoform X1 [Heterocephalus	42.6	42.6	100%	0.003	76%	gi|512921198|XP_004904433.1
☐ PREDICTED: carboxypeptidase B2 isoform X1 [Heterocephalus	42.6	42.6	100%	0.003	76%	gi|512964053|XP_004844263.1
☐ PREDICTED: carboxypeptidase B2 [Condylura cristata]	42.2	42.2	94%	0.005	78%	gi|507939327|XP_004680202.1
☐ hypothetical protein PANDA_002961 [Ailuropoda melanoleuca]	41.8	41.8	100%	0.006	71%	gi|281349951|EFB25535.1
☐ PREDICTED: carboxypeptidase B2-like [Ailuropoda melanoleuc	41.8	41.8	100%	0.006	71%	gi|301758334|XP_002915018.1
☐ PREDICTED: carboxypeptidase B2 [Ursus maritimus]	41.8	41.8	100%	0.006	71%	gi|671028730|XP_008705148.1
☐ Carboxypeptidase B2 [Ophiophagus hannah]	41.4	41.4	100%	0.008	71%	gi|565306861|ETE61379.1
☐ PREDICTED: carboxypeptidase B2 [Anolis carolinensis]	41.4	41.4	100%	0.009	71%	gi|327260978|XP_003215309.1
☐ PREDICTED: carboxypeptidase B2 [Erinaceus europaeus]	40.9	40.9	100%	0.012	76%	gi|617593818|XP_007521293.1
☐ PREDICTED: carboxypeptidase B2 [Ceratotherium simum simu	40.9	40.9	88%	0.012	80%	gi|478518956|XP_004433702.1
☐ PREDICTED: carboxypeptidase B2 isoform X2 [Galeopterus va	40.5	40.5	94%	0.016	75%	gi|667276404|XP_008572661.1
☐ PREDICTED: carboxypeptidase B2 [Nannospalax galili]	40.5	40.5	100%	0.017	71%	gi|674098370|XP_008822615.1
☐ PREDICTED: carboxypeptidase B2 isoform X1 [Galeopterus va	40.5	40.5	94%	0.017	75%	gi|667276401|XP_008572660.1
☐ PREDICTED: carboxypeptidase B2 [Chrysemys picta bellii]	40.5	40.5	100%	0.017	65%	gi|641751137|XP_008166719.1
☐ PREDICTED: carboxypeptidase B2 [Oryctolagus cuniculus]	40.5	40.5	100%	0.017	74%	gi|655832146|XP_008258213.1

⊟ Alignments

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PREDICTED: carboxypeptidase B2 isoform X3 [Homo sapiens]

Sequence ID: gi|530402101|ref|XP_005266316.1| **Length:** 226 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 85 to 101 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.5 bits(121)	3e-07	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1    KQVHFFVDASDVDNVKA  17
            KQVHFFV+ASDVDNVKA
Sbjct  85   KQVHFFVNASDVDNVKA  101
```

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carboxypeptidase B-like protein [Homo sapiens]

Sequence ID: gi|6855464|dbj|BAA90475.1| **Length:** 360 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 66 to 82 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.5 bits(121)	3e-07	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   KQVHFFVDASDVDNVKA  17
           KQVHFFV+ASDVDNVKA
Sbjct  66  KQVHFFVNASDVDNVKA  82
```

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carboxypeptidase B2 (plasma, carboxypeptidase U), isoform CRA_a [Homo sapiens]

Sequence ID: gi|119629159|gb|EAX08754.1| **Length:** 360 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 66 to 82 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.5 bits(121)	3e-07	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   KQVHFFVDASDVDNVKA  17
           KQVHFFV+ASDVDNVKA
Sbjct  66  KQVHFFVNASDVDNVKA  82
```

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carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]

Sequence ID: gi|513126877|ref|NP_001265470.1| **Length:** 386 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 66 to 82 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.5 bits(121)	3e-07	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   KQVHFFVDASDVDNVKA  17
           KQVHFFV+ASDVDNVKA
Sbjct  66  KQVHFFVNASDVDNVKA  82
```

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PREDICTED: carboxypeptidase B2 isoform X2 [Pongo abelii]

Sequence ID: gi|686743701|ref|XP_009246910.1| **Length:** 387 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 66 to 82 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.5 bits(121)	3e-07	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   KQVHFFVDASDVDNVKA  17
           KQVHFFV+ASDVDNVKA
Sbjct  66  KQVHFFVNASDVDNVKA  82
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - B94HAJG001R

Your search parameters were adjusted to search for a short input sequence.

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How to read this page | Blast report description

CPB2_KQVHFFVNASDVDNVKA_NonMod

RID B94HAJG001R (Expires on 01-14 10:34 am)

Query ID	lcl|239111	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	17		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

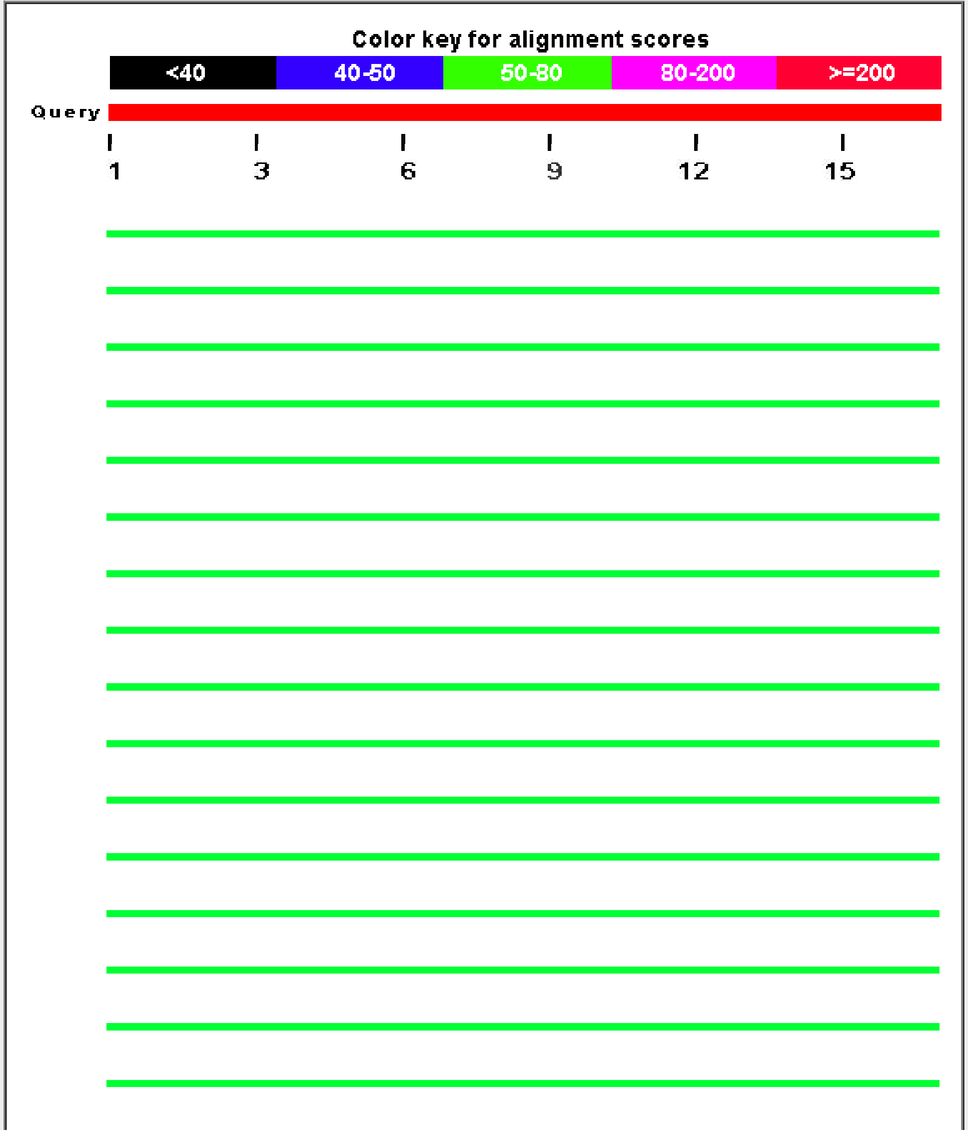
Graphic Summary

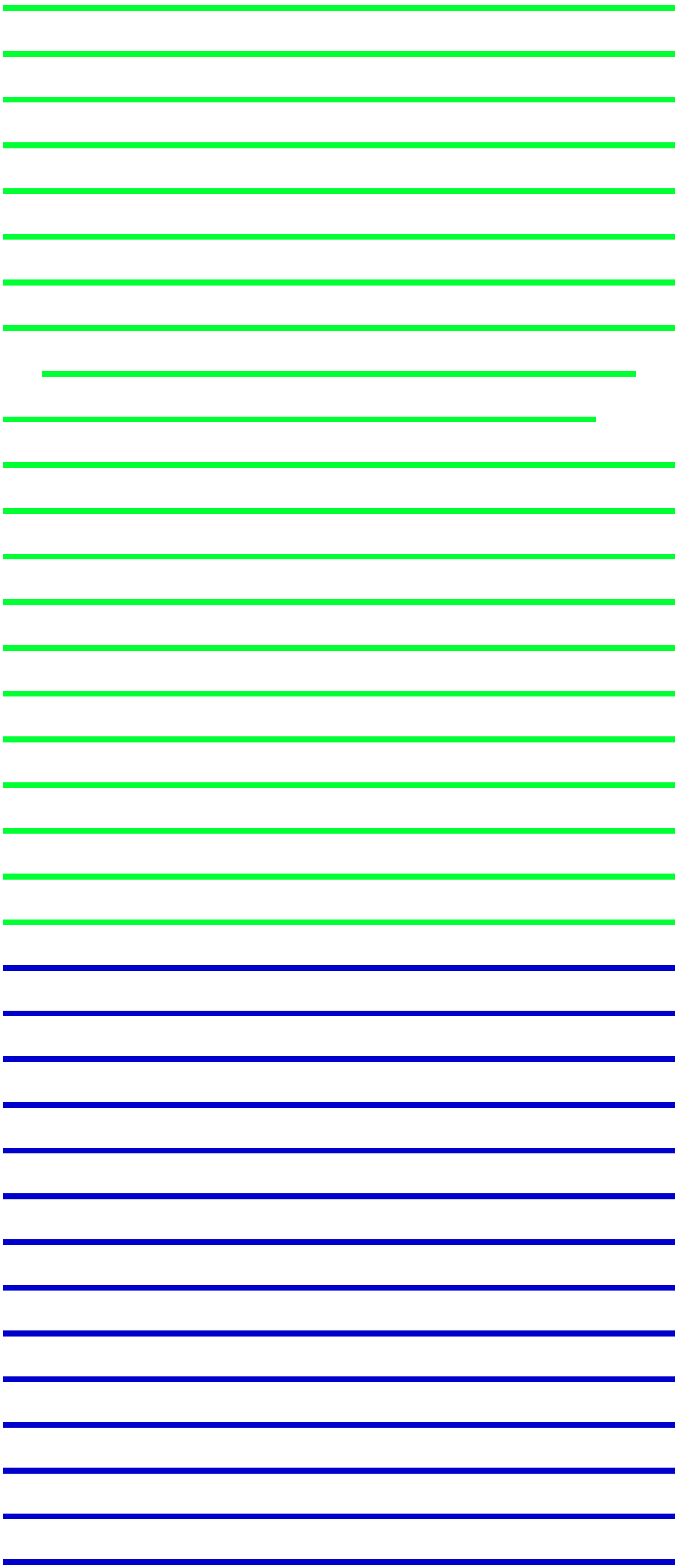
Show Conserved Domains

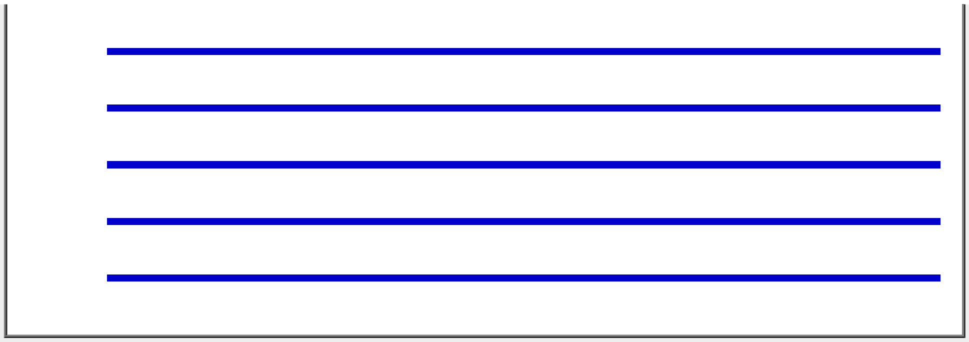
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Homo sapiens]	57.1	57.1	100%	4e-08	100%	gi|530402101|XP_005266316.1
☐	carboxypeptidase B-like protein [Homo sapiens]	57.1	57.1	100%	4e-08	100%	gi|6855464|BAA90475.1
☐	carboxypeptidase B2 (plasma, carboxypeptidase U), isoform CRA_	57.1	57.1	100%	4e-08	100%	gi|119629159|EAX08754.1
☐	carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]	57.1	57.1	100%	5e-08	100%	gi|513126877|NP_001265470.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Pongo abelii]	57.1	57.1	100%	5e-08	100%	gi|686743701|XP_009246910.1
☐	Chain A, Pro-carboxypeptidase U In Complex With 5-(3-aminopropy	57.1	57.1	100%	5e-08	100%	gi|672886543|4P10_A
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Homo sapiens]	57.1	57.1	100%	5e-08	100%	gi|530402099|XP_005266315.1
☐	prepro-plasma carboxypeptidase B [Homo sapiens]	57.1	57.1	100%	5e-08	100%	gi|189687|AAA60042.1
☐	PREDICTED: carboxypeptidase B2 [Gorilla gorilla gorilla]	57.1	57.1	100%	5e-08	100%	gi|426375394|XP_004054526.1
☐	Carboxypeptidase B2 (plasma) [Homo sapiens]	57.1	57.1	100%	5e-08	100%	gi|13937897|AAH07057.1
☐	carboxypeptidase B2 isoform 1 preproprotein [Homo sapiens]	57.1	57.1	100%	5e-08	100%	gi|513126885|NP_001863.3
☐	carboxypeptidase B2 (plasma) [synthetic construct]	57.1	57.1	100%	5e-08	100%	gi|157927966|ABW03279.1
☐	carboxypeptidase B2 (plasma, carboxypeptidase U) [synthetic cons	57.1	57.1	100%	5e-08	100%	gi|124126823|ABM92184.1
☐	PREDICTED: carboxypeptidase B2 [Pan troglodytes]	57.1	57.1	100%	5e-08	100%	gi|114651557|XP_509667.2
☐	Chain A, Crystal Structure Of Thrombin-Activatable Fibrinolysis Inhi	57.1	57.1	100%	5e-08	100%	gi|193506809|3D66_A
☐	Homo sapiens carboxypeptidase B2 (plasma, carboxypeptidase U)	57.1	57.1	100%	5e-08	100%	gi|30584819|AAP36662.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Pongo abelii]	57.1	57.1	100%	5e-08	100%	gi|297694016|XP_002824293.1
☐	Chain A, Crystal Structure Of A T325i/t329i/h333y/h335q Mutant Of	57.1	57.1	100%	5e-08	100%	gi|253722661|3D68_A
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Homo sapiens]	57.1	57.1	100%	5e-08	100%	gi|530402097|XP_005266314.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Rhinopithecus roxe	54.5	54.5	100%	3e-07	94%	gi|724966280|XP_010356389.1
☐	PREDICTED: carboxypeptidase B2 [Chlorocebus sabaeus]	54.5	54.5	100%	3e-07	94%	gi|635025444|XP_007958527.1
☐	PREDICTED: carboxypeptidase B2 [Papio anubis]	54.5	54.5	100%	3e-07	94%	gi|402901940|XP_003913891.1
☐	PREDICTED: carboxypeptidase B2 [Nomascus leucogenys]	53.7	53.7	100%	7e-07	94%	gi|332241864|XP_003270104.1
☐	PREDICTED: carboxypeptidase B2 [Equus caballus]	52.0	52.0	100%	2e-06	94%	gi|545190694|XP_005601424.1
☐	PREDICTED: carboxypeptidase B2 [Saimiri boliviensis boliviensis]	51.5	51.5	88%	3e-06	100%	gi|403286234|XP_003934405.1
☐	PREDICTED: carboxypeptidase B2 [Callithrix jacchus]	51.5	51.5	88%	3e-06	100%	gi|390457680|XP_002742737.2
☐	PREDICTED: carboxypeptidase B2-like [Peromyscus maniculatus b	50.7	50.7	100%	5e-06	88%	gi|589996660|XP_006998803.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Cricetulus griseus]	50.7	50.7	100%	6e-06	88%	gi|625193824|XP_007639419.1
☐							

	PREDICTED: carboxypeptidase B2 isoform X4 [Cricetulus griseus]	50.7	50.7	100%	6e-06	88%	gi|625271974|XP_007627553.1
☐	PREDICTED: carboxypeptidase B2 [Peromyscus maniculatus baird	50.7	50.7	100%	7e-06	88%	gi|589957698|XP_006991448.1
☐	Carboxypeptidase B2 (plasma) [Mus musculus]	50.7	50.7	100%	7e-06	88%	gi|59808067|AAH89577.1
☐	carboxypeptidase U [Mus musculus]	50.7	50.7	100%	7e-06	88%	gi|6003652|AAF00528.1
☐	PREDICTED: carboxypeptidase B2 [Mesocricetus auratus]	50.7	50.7	100%	7e-06	88%	gi|524935646|XP_005071018.1
☐	carboxypeptidase B2 precursor [Mus musculus]	50.7	50.7	100%	7e-06	88%	gi|31982712|NP_062749.2
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Cricetulus griseus]	50.7	50.7	100%	7e-06	88%	gi|354476626|XP_003500525.1
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Cricetulus griseus]	50.7	50.7	100%	7e-06	88%	gi|625271972|XP_007627552.1
☐	zinc finger CCCH domain-containing protein 13 [Cricetulus griseus]	50.7	50.7	100%	7e-06	88%	gi|537241932|ERE87338.1
☐	PREDICTED: carboxypeptidase B2 [Tursiops truncatus]	49.0	49.0	100%	2e-05	88%	gi|470653285|XP_004329533.1
☐	Carboxypeptidase B2 [Fukomys damarensis]	49.0	49.0	100%	2e-05	88%	gi|676273139|KFO27861.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Lipotes vexillifer]	49.0	49.0	100%	2e-05	88%	gi|602712571|XP_007466515.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Macaca fascicularis	49.0	49.0	100%	2e-05	88%	gi|544503644|XP_005585858.1
☐	PREDICTED: carboxypeptidase B2 isoform X3 [Chinchilla lanigera]	49.0	49.0	100%	2e-05	88%	gi|533192699|XP_005409155.1
☐	PREDICTED: carboxypeptidase B2 [Physeter catodon]	49.0	49.0	100%	2e-05	88%	gi|593749228|XP_007129852.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Chinchilla lanigera]	49.0	49.0	100%	2e-05	88%	gi|533192697|XP_005409154.1
☐	PREDICTED: carboxypeptidase B2 [Otolemur garnettii]	49.0	49.0	100%	2e-05	88%	gi|395835377|XP_003790657.1
☐	PREDICTED: carboxypeptidase B2 [Canis lupus familiaris]	49.0	49.0	100%	2e-05	88%	gi|73989292|XP_851154.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Lipotes vexillifer]	49.0	49.0	100%	2e-05	88%	gi|602712569|XP_007466514.1
☐	PREDICTED: carboxypeptidase B2 [Balaenoptera acutorostrata sca	49.0	49.0	100%	2e-05	88%	gi|594678268|XP_007186896.1
☐	PREDICTED: carboxypeptidase B2 [Vicugna pacos]	49.0	49.0	100%	2e-05	88%	gi|560974364|XP_006209502.1
☐	PREDICTED: carboxypeptidase B2 [Camelus ferus]	49.0	49.0	100%	2e-05	88%	gi|560922422|XP_006187410.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Macaca fascicularis	49.0	49.0	100%	2e-05	88%	gi|544503642|XP_005585857.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Chinchilla lanigera]	49.0	49.0	100%	2e-05	88%	gi|533192695|XP_005409153.1
☐	PREDICTED: carboxypeptidase B2 [Ochotona princeps]	49.0	49.0	100%	2e-05	88%	gi|504128560|XP_004577530.1
☐	PREDICTED: carboxypeptidase B2 [Orcinus orca]	49.0	49.0	100%	2e-05	88%	gi|466032575|XP_004274629.1
☐	Carboxypeptidase B2 [Macaca mulatta]	49.0	49.0	100%	2e-05	88%	gi|355700980|EHH29001.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Fukomys damarens	49.0	49.0	100%	2e-05	88%	gi|731244313|XP_010635336.1
☐	PREDICTED: carboxypeptidase B2 [Felis catus]	49.0	49.0	100%	2e-05	88%	gi|586973570|XP_006927367.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Fukomys damarens	49.0	49.0	100%	2e-05	88%	gi|731244311|XP_010635335.1
☐	PREDICTED: carboxypeptidase B2 [Panthera tigris altaica]	49.0	49.0	100%	3e-05	88%	gi|591318467|XP_007085493.1
☐	plastin-2 isoform 16 [Camelus ferus]	49.0	49.0	100%	3e-05	88%	gi|528759255|EPY78914.1
☐	PREDICTED: carboxypeptidase B2 [Tupaia chinensis]	48.6	48.6	94%	3e-05	88%	gi|562871068|XP_006163508.1
☐	carboxypeptidase B2 (plasma), isoform CRA_b [Rattus norvegicus]	48.1	48.1	100%	5e-05	82%	gi|149049966|EDM02290.1
☐	carboxypeptidase B2 (plasma), isoform CRA_a [Rattus norvegicus]	48.1	48.1	100%	5e-05	82%	gi|149049965|EDM02289.1
☐	Cpb2 protein [Rattus norvegicus]	48.1	48.1	100%	5e-05	82%	gi|60688161|AAH91133.1
☐	carboxypeptidase B2 precursor [Rattus norvegicus]	48.1	48.1	100%	5e-05	82%	gi|16758414|NP_446069.1
☐	PREDICTED: carboxypeptidase B2 [Microtus ochrogaster]	46.9	46.9	100%	1e-04	82%	gi|532025304|XP_005355675.1
☐	PREDICTED: carboxypeptidase B2 isoform 1 [Macaca mulatta]	46.4	46.4	94%	2e-04	88%	gi|109120669|XP_001097310.1
☐	PREDICTED: carboxypeptidase B2 [Ictidomys tridecemlineatus]	46.4	46.4	94%	2e-04	88%	gi|532113245|XP_005341304.1
☐	Carboxypeptidase B2 [Macaca fascicularis]	46.4	46.4	94%	2e-04	88%	gi|355754683|EHH58584.1
☐	PREDICTED: carboxypeptidase B2 isoform 3 [Macaca mulatta]	46.4	46.4	94%	2e-04	88%	gi|109120665|XP_001097608.1
☐	PREDICTED: carboxypeptidase B2 [Cavia porcellus]	46.4	46.4	100%	2e-04	82%	gi|348583190|XP_003477356.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Bos mutus]	46.0	46.0	94%	2e-04	88%	gi|555969567|XP_005896807.1
☐	Chain A, Crystal Structure Of Thrombin Activatable Fibrinolysis Inhi	46.0	46.0	94%	2e-04	88%	gi|194368809|3DGV_A

☐	carboxypeptidase B2 precursor [Bos taurus]	46.0	46.0	94%	2e-04	88%	gi|114050845|NP_001039462.1
☐	PREDICTED: carboxypeptidase B2 [Capra hircus]	46.0	46.0	94%	2e-04	88%	gi|548487919|XP_005687494.1
☐	PREDICTED: carboxypeptidase B2 [Odobenus rosmarus divergens	46.0	46.0	100%	2e-04	82%	gi|472378433|XP_004408637.1
☐	PREDICTED: carboxypeptidase B2 [Ovis aries]	46.0	46.0	94%	2e-04	88%	gi|426236307|XP_004012111.1
☐	PREDICTED: carboxypeptidase B2 [Octodon degus]	45.6	45.6	100%	3e-04	82%	gi|507684606|XP_004640321.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Heterocephalus gla	45.2	45.2	100%	5e-04	82%	gi|512921202|XP_004904434.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Heterocephalus gla	45.2	45.2	100%	5e-04	82%	gi|512964055|XP_004844264.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Heterocephalus gla	45.2	45.2	100%	5e-04	82%	gi|512921198|XP_004904433.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Heterocephalus gla	45.2	45.2	100%	5e-04	82%	gi|512964053|XP_004844263.1
☐	PREDICTED: carboxypeptidase B2 [Leptonychotes weddellii]	44.8	44.8	100%	6e-04	76%	gi|585191930|XP_006747204.1
☐	PREDICTED: carboxypeptidase B2 [Condylura cristata]	44.8	44.8	94%	6e-04	83%	gi|507939327|XP_004680202.1
☐	hypothetical protein PANDA_002961 [Ailuropoda melanoleuca]	44.3	44.3	100%	9e-04	76%	gi|281349951|EFB25535.1
☐	PREDICTED: carboxypeptidase B2-like [Ailuropoda melanoleuca]	44.3	44.3	100%	9e-04	76%	gi|301758334|XP_002915018.1
☐	PREDICTED: carboxypeptidase B2 [Ursus maritimus]	44.3	44.3	100%	9e-04	76%	gi|671028730|XP_008705148.1
☐	Carboxypeptidase B2 [Ophiophagus hannah]	43.9	43.9	100%	0.001	76%	gi|565306861|ETE61379.1
☐	PREDICTED: carboxypeptidase B2 [Anolis carolinensis]	43.9	43.9	100%	0.001	76%	gi|327260978|XP_003215309.1
☐	PREDICTED: carboxypeptidase B2 [Erinaceus europaeus]	43.5	43.5	100%	0.002	82%	gi|617593818|XP_007521293.1
☐	PREDICTED: carboxypeptidase B2 [Ceratotherium simum simum]	43.5	43.5	88%	0.002	87%	gi|478518956|XP_004433702.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Galeopterus varieg	43.1	43.1	94%	0.002	81%	gi|667276404|XP_008572661.1
☐	PREDICTED: carboxypeptidase B2 [Nannospalax galili]	43.1	43.1	100%	0.002	76%	gi|674098370|XP_008822615.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Galeopterus varieg	43.1	43.1	94%	0.002	81%	gi|667276401|XP_008572660.1
☐	PREDICTED: carboxypeptidase B2 [Chrysemys picta bellii]	43.1	43.1	100%	0.002	71%	gi|641751137|XP_008166719.1
☐	PREDICTED: carboxypeptidase B2 [Oryctolagus cuniculus]	43.1	43.1	100%	0.002	79%	gi|655832146|XP_008258213.1
☐	PREDICTED: carboxypeptidase B2 [Pelodiscus sinensis]	43.1	43.1	100%	0.002	71%	gi|558138783|XP_006118064.1
☐	PREDICTED: carboxypeptidase B2 isoform X2 [Pteropus alecto]	42.6	42.6	100%	0.003	76%	gi|586560565|XP_006913553.1
☐	PREDICTED: carboxypeptidase B2 isoform X1 [Pteropus alecto]	42.6	42.6	100%	0.003	76%	gi|586560563|XP_006913552.1
☐	PREDICTED: carboxypeptidase B2 [Bubalus bubalis]	42.2	42.2	94%	0.004	81%	gi|594098932|XP_006072612.1

⊟ Alignments

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PREDICTED: carboxypeptidase B2 isoform X3 [Homo sapiens]

Sequence ID: gi|530402101|ref|XP_005266316.1| **Length:** 226 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 85 to 101 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.1 bits(127)	4e-08	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    KQVHFFVNASDVDNVKA  17
            KQVHFFVNASDVDNVKA
Sbjct  85   KQVHFFVNASDVDNVKA  101
```

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carboxypeptidase B-like protein [Homo sapiens]

Sequence ID: gi|6855464|dbj|BAA90475.1| **Length:** 360 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 66 to 82 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.1 bits(127)	4e-08	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1   KQVHFFVNASDVDNVKA  17
```

```
                KQVHFFVNASDVDNVKA
Sbjct  66   KQVHFFVNASDVDNVKA  82
```

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carboxypeptidase B2 (plasma, carboxypeptidase U), isoform CRA_a [Homo sapiens]

Sequence ID: gi|119629159|gb|EAX08754.1| **Length:** 360 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 66 to 82 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.1 bits(127)	4e-08	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    KQVHFFVNASDVDNVKA  17
            KQVHFFVNASDVDNVKA
Sbjct  66   KQVHFFVNASDVDNVKA  82
```

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carboxypeptidase B2 isoform 2 preproprotein [Homo sapiens]

Sequence ID: gi|513126877|ref|NP_001265470.1| **Length:** 386 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 66 to 82 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.1 bits(127)	5e-08	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    KQVHFFVNASDVDNVKA  17
            KQVHFFVNASDVDNVKA
Sbjct  66   KQVHFFVNASDVDNVKA  82
```

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PREDICTED: carboxypeptidase B2 isoform X2 [Pongo abelii]

Sequence ID: gi|686743701|ref|XP_009246910.1| **Length:** 387 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 66 to 82 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.1 bits(127)	5e-08	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    KQVHFFVNASDVDNVKA  17
            KQVHFFVNASDVDNVKA
Sbjct  66   KQVHFFVNASDVDNVKA  82
```

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Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

CRISP3_RDSCKASCDCSNSIY_Mod

RID BTGXY5C6013 (Expires on 01-20 15:43 pm)

Query ID lcl|74444
Description None
Molecule type amino acid
Query Length 15

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

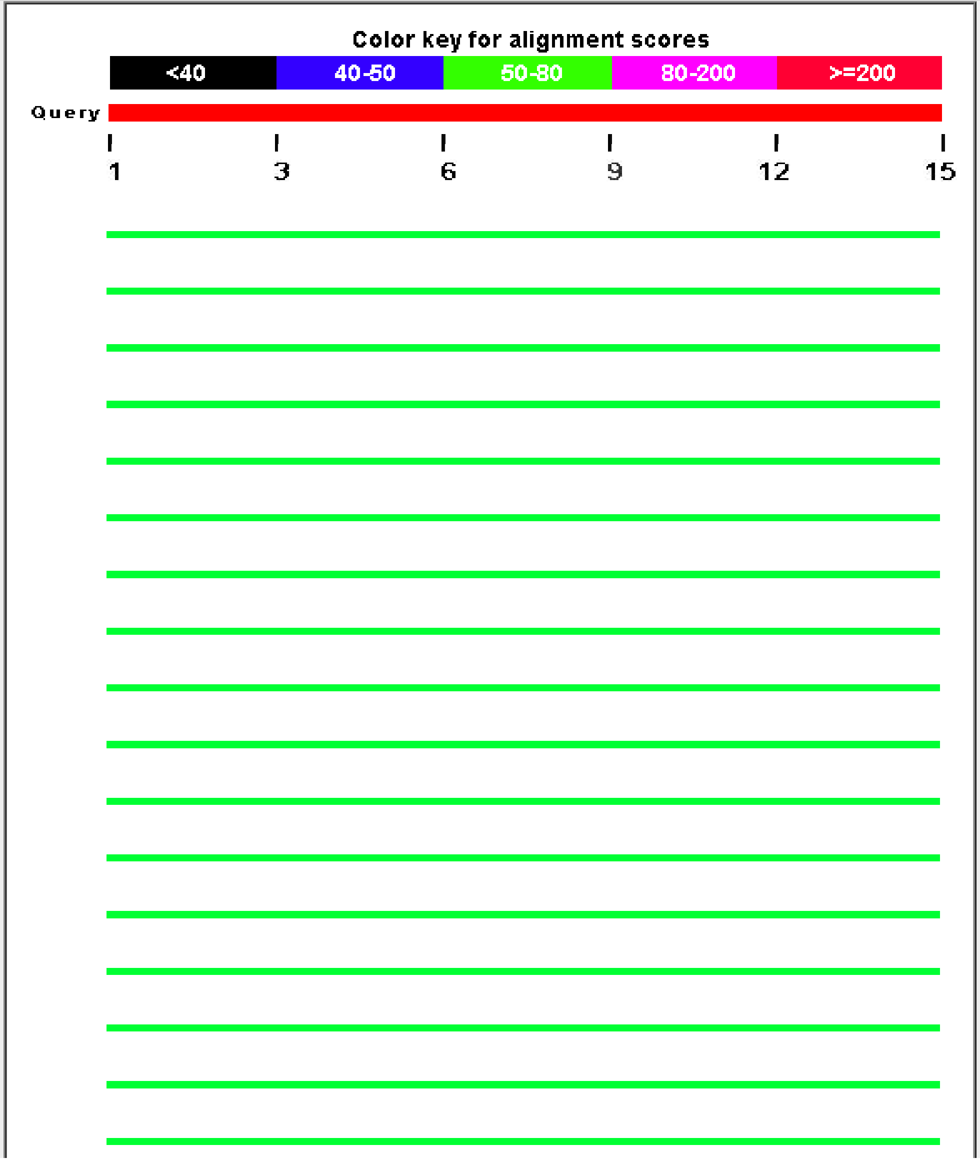
Graphic Summary

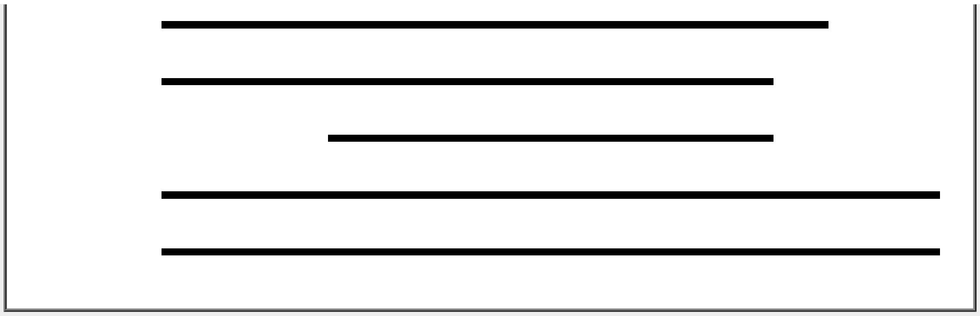
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	50.3	50.3	100%	6e-06	93%	gi|194384234|BAG64890.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X2 [Chlc	50.3	50.3	100%	7e-06	93%	gi|635094563|XP_007970486.1
☐	RecName: Full=Cysteine-rich secretory protein 3; Short=CRISF	50.3	50.3	100%	7e-06	93%	gi|1706135|P54108.1
☐	SGP28 protein [Homo sapiens]	50.3	50.3	100%	7e-06	93%	gi|1213613|CAA63984.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Papio anubis]	50.3	50.3	100%	7e-06	93%	gi|402867229|XP_003897768.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform 1 [Noma	50.3	50.3	100%	7e-06	93%	gi|332210261|XP_003254226.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform 2 [Maca	50.3	50.3	100%	7e-06	93%	gi|109071442|XP_001105287.1
☐	cysteine-rich secretory protein 3 variant [Homo sapiens]	50.3	50.3	100%	7e-06	93%	gi|62898321|BAD97100.1
☐	PREDICTED: LOW QUALITY PROTEIN: cysteine-rich secretor	50.3	50.3	100%	7e-06	93%	gi|544427465|XP_005552824.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform 1 [Gorill	50.3	50.3	100%	7e-06	93%	gi|426353468|XP_004044216.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X2 [Pan	50.3	50.3	100%	7e-06	93%	gi|397526631|XP_003833222.1
☐	cysteine-rich secretory protein 3 isoform 1 precursor [Homo sap	50.3	50.3	100%	7e-06	93%	gi|300244560|NP_006052.2
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X2 [Pon	50.3	50.3	100%	7e-06	93%	gi|297678316|XP_002817022.1
☐	unnamed protein product [Homo sapiens]	50.3	50.3	100%	7e-06	93%	gi|158259033|BAF85475.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X2 [Pan	50.3	50.3	100%	7e-06	93%	gi|114607750|XP_001148602.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform 2 [Gorill	50.3	50.3	100%	7e-06	93%	gi|426353470|XP_004044217.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X1 [Pan	50.3	50.3	100%	7e-06	93%	gi|397526633|XP_003833223.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X1 [Pon	50.3	50.3	100%	7e-06	93%	gi|395737328|XP_003776901.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X1 [Pan	50.3	50.3	100%	7e-06	93%	gi|332824193|XP_001148538.2
☐	cysteine-rich secretory protein 3 isoform 2 precursor [Homo sap	50.3	50.3	100%	7e-06	93%	gi|300244562|NP_001177915.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X1 [Chlc	50.3	50.3	100%	7e-06	93%	gi|635094561|XP_007970484.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Rhinopithecus r	47.7	47.7	100%	5e-05	87%	gi|724882502|XP_010373294.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X2 [Sair	47.7	47.7	100%	5e-05	87%	gi|403261483|XP_003923149.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X1 [Sair	47.7	47.7	100%	5e-05	87%	gi|403261485|XP_003923150.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Pteropus alecto	40.1	40.1	93%	0.018	79%	gi|586556147|XP_006926516.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Galeopterus va	36.7	36.7	80%	0.23	83%	gi|667299696|XP_008580716.1
☐	PREDICTED: cysteine-rich secretory protein 2-like [Sarcophilus	32.5	32.5	80%	5.3	75%	gi|395537432|XP_003770705.1
☐	PREDICTED: cysteine-rich secretory protein 3-like [Tarsius syri	32.5	32.5	80%	5.3	75%	gi|640824360|XP_008069246.1
☐	PREDICTED: cysteine-rich secretory protein 3-like [Fukomys da	32.5	32.5	80%	5.4	75%	gi|731231228|XP_010629409.1

☐	PREDICTED: cysteine-rich secretory protein 3-like [Loxodonta	32.0	32.0	100%	7.3	60%	gi|731453844|XP_003404193.2
☐	PREDICTED: cysteine-rich secretory protein 2-like [Trichechus	31.6	31.6	66%	10.0	80%	gi|471414464|XP_004388770.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Tupaia chinens	31.2	31.2	80%	14	75%	gi|562840038|XP_006149164.1
☐	uncharacterized protein TOT_030000442 [Theileria orientalis st	31.2	31.2	73%	14	82%	gi|697892480|XP_009691480.1
☐	PREDICTED: cysteine-rich secretory protein 2 isoform X2 [Can	30.8	30.8	93%	19	64%	gi|545519430|XP_005627520.1
☐	PREDICTED: cysteine-rich secretory protein 2 isoform X1 [Can	30.8	30.8	93%	19	64%	gi|545519428|XP_005627519.1
☐	Cysteine-rich secretory protein 3 [Myotis brandtii]	30.3	30.3	80%	24	67%	gi|521023357|EPQ05145.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Myotis lucifugus	30.3	30.3	80%	25	67%	gi|558145271|XP_006093280.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Myotis brandtii]	30.3	30.3	80%	25	67%	gi|554534799|XP_005862127.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Myotis davidii]	30.3	30.3	80%	25	67%	gi|584041718|XP_006765775.1
☐	PREDICTED: cysteine-rich secretory protein 2-like [Felis catus]	30.3	30.3	93%	25	71%	gi|586986758|XP_003986274.2
☐	PREDICTED: fatty-acid amide hydrolase 1-like [Pundamilia nye	30.3	30.3	60%	26	89%	gi|548459219|XP_005747619.1
☐	PREDICTED: fatty-acid amide hydrolase 1-like [Haplochromis b	30.3	30.3	60%	26	89%	gi|554885687|XP_005952459.1
☐	PREDICTED: fatty-acid amide hydrolase 1-like isoform X2 [May	30.3	30.3	60%	26	89%	gi|499001912|XP_004555098.1
☐	PREDICTED: fatty-acid amide hydrolase 1-like isoform X1 [May	30.3	30.3	60%	27	89%	gi|499001908|XP_004555097.1
☐	PREDICTED: cysteine-rich secretory protein 3-like [Erinaceus e	29.9	29.9	86%	35	69%	gi|617602602|XP_007523359.1
☐	PREDICTED: cysteine-rich secretory protein 2-like [Leptonycho	29.9	29.9	80%	35	67%	gi|585150326|XP_006727639.1
☐	PREDICTED: cysteine-rich secretory protein 3-like [Camelus dr	29.9	29.9	93%	35	57%	gi|744591208|XP_010987243.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Vicugna pacos]	29.9	29.9	93%	35	57%	gi|560959057|XP_006201984.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Camelus ferus]	29.9	29.9	93%	35	57%	gi|560929288|XP_006190797.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Mustela putoriu	29.9	29.9	80%	35	67%	gi|511904944|XP_004771951.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Ceratotherium s	29.9	29.9	93%	35	57%	gi|478500344|XP_004424494.1
☐	hypothetical protein Moror_2055 [Moniliophthora roreri MCA 29	29.5	29.5	80%	48	75%	gi|630205342|XP_007853192.1
☐	PREDICTED: chorion-specific transcription factor GCMb [Pelod	29.5	29.5	73%	49	44%	gi|558230180|XP_006138838.1
☐	hypothetical protein LOAG_07568 [Loa loa]	29.1	29.1	53%	64	100%	gi|312081727|XP_003143149.1
☐	cysteine-rich secretory protein 3 precursor [Equus caballus]	29.1	29.1	93%	64	57%	gi|126352542|NP_001075343.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Ochotona princ	29.1	29.1	93%	64	64%	gi|504158252|XP_004590597.1
☐	PREDICTED: uncharacterized protein LOC104218494 isoform	29.1	29.1	73%	66	82%	gi|698545175|XP_009767299.1
☐	PREDICTED: uncharacterized protein LOC104218494 isoform	29.1	29.1	73%	66	82%	gi|698545171|XP_009767298.1
☐	PREDICTED: uncharacterized protein LOC104218494 isoform	29.1	29.1	73%	66	82%	gi|698545156|XP_009767295.1
☐	hypothetical protein TTHERM_01169520 [Tetrahymena thermo	29.1	29.1	86%	68	64%	gi|118395393|XP_001030047.1
☐	hypothetical protein TTHERM_01169520 [Tetrahymena thermo	29.1	29.1	86%	68	64%	gi|586737343|EAR82384.2
☐	hypothetical protein [Achromobacter xylosoxidans]	28.6	28.6	66%	80	70%	gi|737214877|WP_035199582.1
☐	GM15650 [Drosophila sechellia]	28.6	28.6	60%	90	89%	gi|195346678|XP_002039884.1
☐	GE18088 [Drosophila yakuba]	28.6	28.6	60%	90	89%	gi|195488632|XP_002092397.1
☐	GG20706 [Drosophila erecta]	28.6	28.6	60%	91	89%	gi|194882155|XP_001975178.1
☐	hypothetical protein H105_06384 [Trichophyton soudanense C	28.6	28.6	60%	92	89%	gi|607938037|EZF71419.1
☐	hypothetical protein H106_06212 [Trichophyton rubrum CBS 73	28.6	28.6	60%	92	89%	gi|607974736|EZG03991.1
☐	hypothetical protein TERG_01735 [Trichophyton rubrum CBS 1	28.6	28.6	60%	92	89%	gi|327304641|XP_003237012.1
☐	tRNA 2' phosphotransferase, putative [Eimeria acervulina]	28.6	28.6	86%	92	63%	gi|557124170|CDI78405.1
☐	hypothetical protein PPL_01971 [Polysphondylium pallidum PN	28.6	28.6	66%	92	80%	gi|281210811|EFA84977.1
☐	Cysteine-rich secretory protein 2 [Pteropus alecto]	28.2	28.2	80%	118	67%	gi|431838288|ELK00220.1
☐	PREDICTED: cysteine-rich secretory protein 2 [Pteropus alecto	28.2	28.2	80%	120	67%	gi|586556149|XP_006926517.1
☐	PREDICTED: cysteine-rich secretory protein 2 [Ictidomys tridec	28.2	28.2	80%	120	67%	gi|532065569|XP_005318643.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Chrysochloris a	28.2	28.2	93%	120	57%	gi|586460042|XP_006860679.1

☐	PREDICTED: cysteine-rich secretory protein 2-like [Galeopteru	28.2	28.2	80%	122	67%	gi|667335258|XP_008592870.1
☐	SAP domain-containing protein [Trichophyton equinum CBS 12	28.2	28.2	60%	125	89%	gi|326477338|EGE01348.1
☐	conserved hypothetical protein [Trichophyton verrucosum HKI	28.2	28.2	60%	125	89%	gi|302667025|XP_003025107.1
☐	hypothetical protein H109_04555 [Trichophyton interdigitale M	28.2	28.2	60%	125	89%	gi|633046989|KDB23552.1
☐	hypothetical protein H101_02809 [Trichophyton interdigitale H6	28.2	28.2	60%	125	89%	gi|607894816|EZF33634.1
☐	hypothetical protein TESG_04396 [Trichophyton tonsurans CB	28.2	28.2	60%	125	89%	gi|326472966|EGD96975.1
☐	conserved hypothetical protein [Arthroderma benhamiae CBS 1	28.2	28.2	60%	125	89%	gi|302501356|XP_003012670.1
☐	PREDICTED: cysteine-rich secretory protein 2-like [Ursus marit	27.8	27.8	80%	163	67%	gi|670998279|XP_008690031.1
☐	PREDICTED: cysteine-rich secretory protein 3-like [Nannospala	27.8	27.8	80%	164	67%	gi|674104542|XP_008823456.1
☐	PREDICTED: cysteine-rich secretory protein 2-like [Panthera ti	27.8	27.8	93%	164	64%	gi|591340164|XP_007095568.1
☐	hypothetical protein CCM_02846 [Cordyceps militaris CM01]	27.8	27.8	60%	165	89%	gi|573980232|XP_006668061.1
☐	PREDICTED: cysteine-rich secretory protein 3-like [Chinchilla l	27.8	27.8	80%	166	67%	gi|533125534|XP_005377985.1
☐	Solute carrier organic anion transporter family member 4A1 [Cr	27.8	27.8	60%	169	89%	gi|405958473|EKC24600.1
☐	hypothetical protein [Plasmodium yoelii yoelii 17XNL]	27.8	27.8	73%	171	73%	gi|82541076|XP_724807.1
☐	hypothetical protein YYC_03031 [Plasmodium yoelii 17X]	27.8	27.8	73%	171	73%	gi|564278173|ETB59592.1
☐	liver specific protein 1 [Plasmodium yoelii]	27.8	27.8	73%	171	73%	gi|675232727|CDU85100.1
☐	hypothetical protein BC1G_16107 [Botryotinia fuckeliana B05.1	27.4	27.4	73%	207	82%	gi|154289331|XP_001545300.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Echinops telfair	27.4	27.4	93%	223	57%	gi|507620678|XP_004696622.1
☐	Tms1p [Rhizophagus irregularis DAOM 197198w]	27.4	27.4	73%	228	73%	gi|595438682|EXX52304.1
☐	hypothetical protein LRAMOSA01456 [Absidia idahoensis var. t	27.4	27.4	73%	229	73%	gi|671692776|CDS07507.1
☐	related to tms1 protein [Lichtheimia corymbifera JMRC:FSU:96	27.4	27.4	73%	229	73%	gi|661183725|CDH53974.1
☐	PREDICTED: uncharacterized protein LOC101258431 [Solanu	27.4	27.4	73%	229	82%	gi|723675971|XP_010316951.1
☐	hypothetical protein [Mucilaginibacter paludis]	26.9	26.9	46%	272	100%	gi|495785995|WP_008510574.1
☐	hypothetical protein GMDG_07051 [Pseudogymnoascus destru	26.9	26.9	46%	294	100%	gi|440634907|ELR04826.1
☐	PREDICTED: tetraspanin-8 [Poecilia reticulata]	26.9	26.9	93%	305	48%	gi|658918509|XP_008399014.1
☐	cysteine-rich secretory protein 2 precursor [Xenopus (Silurana)	26.9	26.9	93%	306	64%	gi|56118480|NP_001008204.1

Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194384234|dbj|BAG64890.1| **Length:** 155 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 141 to 155 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
50.3 bits(111)	6e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    RDSCKASCDCSNSIY  15
            RDSCKASC+CSNSIY
Sbjct  141  RDSCKASCNCSNSIY  155
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: cysteine-rich secretory protein 3 isoform X2 [Chlorocebus sabaeus]

Sequence ID: gi|635094563|ref|XP_007970486.1| **Length:** 245 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic

Range 1: 231 to 245 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
50.3 bits(111)	7e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    RDSCKASCDCSNSIY  15
            RDSCKASC+CSNSIY
Sbjct  231  RDSCKASCNCSNSIY  245
```

context
[Identical Proteins](#) - Proteins identical to the subject

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RecName: Full=Cysteine-rich secretory protein 3; Short=CRISP-3; AltName: Full=Specific granule protein of 28 kDa; Short=SGP28; Flags: Precursor [Homo sapiens]

Sequence ID: gi|1706135|sp|P54108.1|CRIS3_HUMAN **Length:** 245 **Number of Matches:** 1

See 6 more title(s)

Range 1: 231 to 245 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
50.3 bits(111)	7e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    RDSCKASCDCSNSIY  15
            RDSCKASC+CSNSIY
Sbjct  231  RDSCKASCNCSNSIY  245
```

Related Information

Gene - associated gene details
Identical Proteins - Proteins identical to the subject

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SGP28 protein [Homo sapiens]

Sequence ID: gi|1213613|emb|CAA63984.1| **Length:** 245 **Number of Matches:** 1

See 2 more title(s)

Range 1: 231 to 245 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
50.3 bits(111)	7e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    RDSCKASCDCSNSIY  15
            RDSCKASC+CSNSIY
Sbjct  231  RDSCKASCNCSNSIY  245
```

Related Information

Gene - associated gene details
Identical Proteins - Proteins identical to the subject

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PREDICTED: cysteine-rich secretory protein 3 [Papio anubis]

Sequence ID: gi|402867229|ref|XP_003897768.1| **Length:** 245 **Number of Matches:** 1

See 4 more title(s)

Range 1: 231 to 245 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
50.3 bits(111)	7e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    RDSCKASCDCSNSIY  15
            RDSCKASC+CSNSIY
Sbjct  231  RDSCKASCNCSNSIY  245
```

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context
Identical Proteins - Proteins identical to the subject

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

CRISP3_RDSCKASCNCSNSIY_NonMod

RID B94UF42601R (Expires on 01-14 10:38 am)

Query ID	lcl|191300	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	15		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

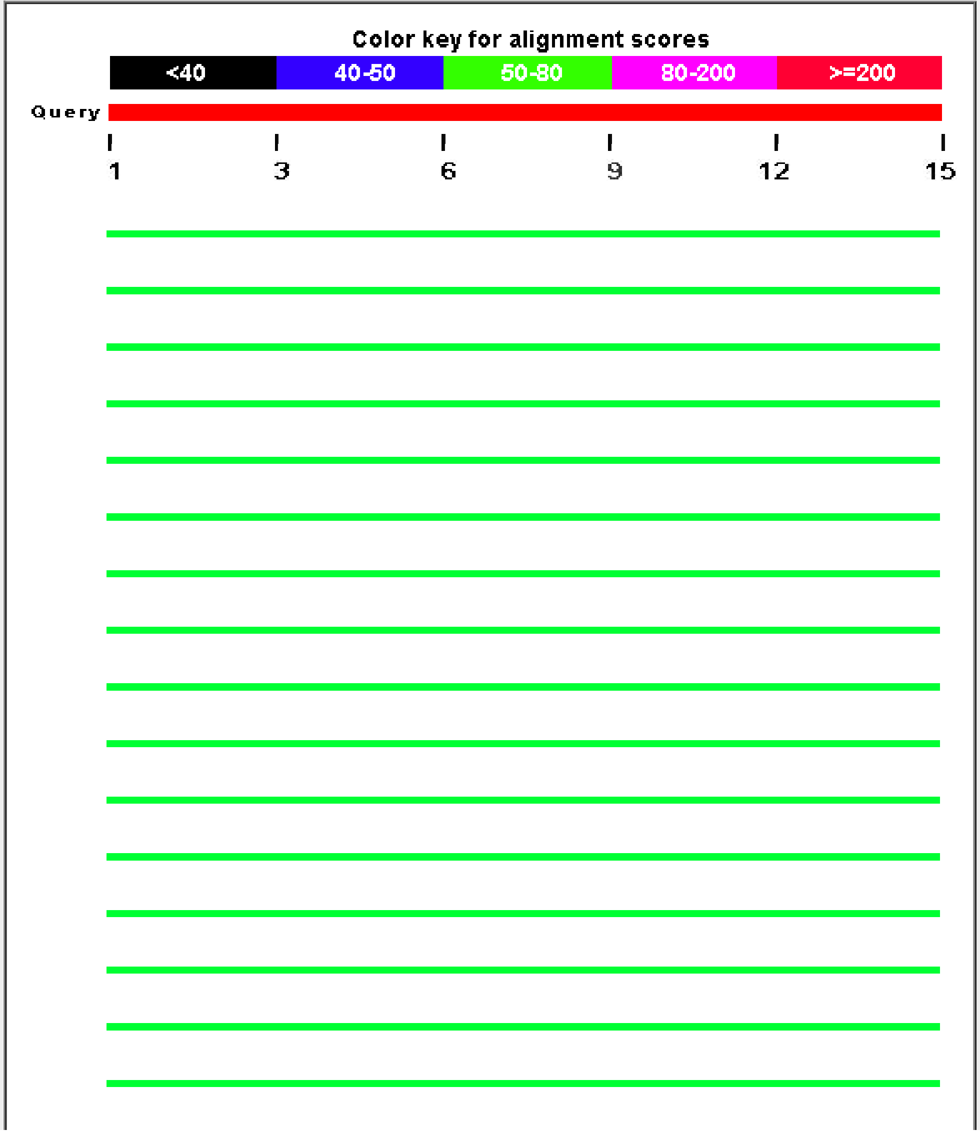
Graphic Summary

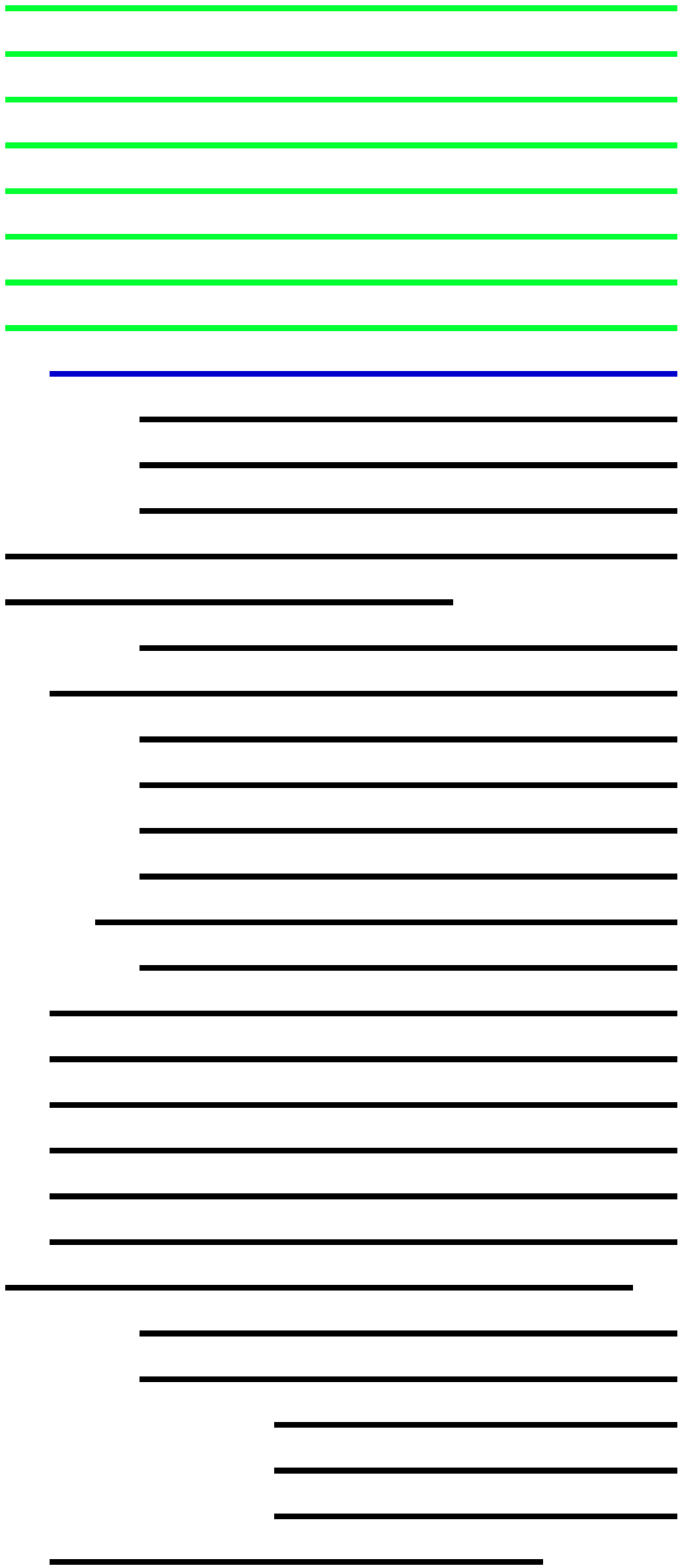
Show Conserved Domains

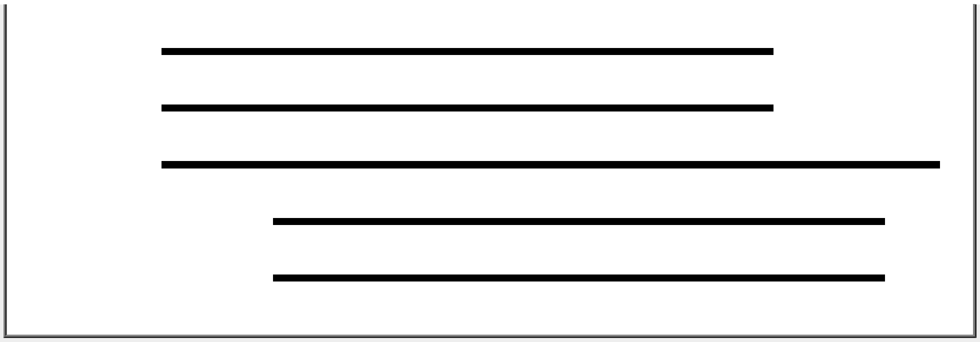
No putative conserved domains have been detected

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	52.8	52.8	100%	7e-07	100%	gi|194384234|BAG64890.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X2 [Chloroce	52.8	52.8	100%	9e-07	100%	gi|635094563|XP_007970486.1
☐	RecName: Full=Cysteine-rich secretory protein 3; Short=CRISP-3;	52.8	52.8	100%	9e-07	100%	gi|1706135|P54108.1
☐	SGP28 protein [Homo sapiens]	52.8	52.8	100%	9e-07	100%	gi|1213613|CAA63984.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Papio anubis]	52.8	52.8	100%	9e-07	100%	gi|402867229|XP_003897768.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform 1 [Nomascu	52.8	52.8	100%	9e-07	100%	gi|332210261|XP_003254226.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform 2 [Macaca m	52.8	52.8	100%	9e-07	100%	gi|109071442|XP_001105287.1
☐	cysteine-rich secretory protein 3 variant [Homo sapiens]	52.8	52.8	100%	9e-07	100%	gi|62898321|BAD97100.1
☐	PREDICTED: LOW QUALITY PROTEIN: cysteine-rich secretory pr	52.8	52.8	100%	9e-07	100%	gi|544427465|XP_005552824.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform 1 [Gorilla go	52.8	52.8	100%	9e-07	100%	gi|426353468|XP_004044216.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X2 [Pan pan	52.8	52.8	100%	9e-07	100%	gi|397526631|XP_003833222.1
☐	cysteine-rich secretory protein 3 isoform 1 precursor [Homo sapiens	52.8	52.8	100%	9e-07	100%	gi|300244560|NP_006052.2
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X2 [Pongo a	52.8	52.8	100%	9e-07	100%	gi|297678316|XP_002817022.1
☐	unnamed protein product [Homo sapiens]	52.8	52.8	100%	9e-07	100%	gi|158259033|BAF85475.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X2 [Pan trog	52.8	52.8	100%	9e-07	100%	gi|114607750|XP_001148602.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform 2 [Gorilla go	52.8	52.8	100%	9e-07	100%	gi|426353470|XP_004044217.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X1 [Pan pan	52.8	52.8	100%	9e-07	100%	gi|397526633|XP_003833223.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X1 [Pongo a	52.8	52.8	100%	9e-07	100%	gi|395737328|XP_003776901.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X1 [Pan trog	52.8	52.8	100%	9e-07	100%	gi|332824193|XP_001148538.2
☐	cysteine-rich secretory protein 3 isoform 2 precursor [Homo sapiens	52.8	52.8	100%	9e-07	100%	gi|300244562|NP_001177915.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X1 [Chloroce	52.8	52.8	100%	9e-07	100%	gi|635094561|XP_007970484.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Rhinopithecus roxel	50.3	50.3	100%	6e-06	93%	gi|724882502|XP_010373294.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X2 [Saimiri b	50.3	50.3	100%	6e-06	93%	gi|403261483|XP_003923149.1
☐	PREDICTED: cysteine-rich secretory protein 3 isoform X1 [Saimiri b	50.3	50.3	100%	7e-06	93%	gi|403261485|XP_003923150.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Pteropus alecto]	42.6	42.6	93%	0.002	86%	gi|586556147|XP_006926516.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Galeopterus variega	39.2	39.2	80%	0.031	92%	gi|667299696|XP_008580716.1
☐	PREDICTED: cysteine-rich secretory protein 3-like [Tarsius syrichta	35.0	35.0	80%	0.77	83%	gi|640824360|XP_008069246.1
☐	PREDICTED: cysteine-rich secretory protein 3-like [Fukomys dama	35.0	35.0	80%	0.77	83%	gi|731231228|XP_010629409.1
☐							

PREDICTED: cysteine-rich secretory protein 3-like [Loxodonta afric	34.6	34.6	100%	1.1	67%	gi|731453844|XP_003404193.2
☐ PREDICTED: cysteine-rich secretory protein 2-like [Trichechus mar	34.1	34.1	66%	1.4	90%	gi|471414464|XP_004388770.1
☐ PREDICTED: cysteine-rich secretory protein 3 [Tupaia chinensis]	33.7	33.7	80%	2.0	83%	gi|562840038|XP_006149164.1
☐ PREDICTED: cysteine-rich secretory protein 2-like [Felis catus]	33.3	33.3	93%	2.7	71%	gi|586986758|XP_003986274.2
☐ Cysteine-rich secretory protein 3 [Myotis brandtii]	32.9	32.9	80%	3.4	75%	gi|521023357|EPQ05145.1
☐ PREDICTED: cysteine-rich secretory protein 3 [Myotis lucifugus]	32.9	32.9	80%	3.7	75%	gi|558145271|XP_006093280.1
☐ PREDICTED: cysteine-rich secretory protein 3 [Myotis brandtii]	32.9	32.9	80%	3.7	75%	gi|554534799|XP_005862127.1
☐ PREDICTED: cysteine-rich secretory protein 3 [Myotis davidii]	32.9	32.9	80%	3.7	75%	gi|584041718|XP_006765775.1
☐ PREDICTED: cysteine-rich secretory protein 3-like [Erinaceus euro	32.5	32.5	86%	5.1	77%	gi|617602602|XP_007523359.1
☐ PREDICTED: cysteine-rich secretory protein 2-like [Sarcophilus ha	32.0	32.0	80%	6.9	75%	gi|395537432|XP_003770705.1
☐ PREDICTED: cysteine-rich secretory protein 2 isoform X2 [Canis lu	32.0	32.0	93%	7.0	64%	gi|545519430|XP_005627520.1
☐ PREDICTED: cysteine-rich secretory protein 2 isoform X1 [Canis lu	32.0	32.0	93%	7.0	64%	gi|545519428|XP_005627519.1
☐ PREDICTED: cysteine-rich secretory protein 3 [Vicugna pacos]	31.2	31.2	93%	13	57%	gi|560959057|XP_006201984.1
☐ PREDICTED: cysteine-rich secretory protein 3 [Camelus ferus]	31.2	31.2	93%	13	57%	gi|560929288|XP_006190797.1
☐ PREDICTED: cysteine-rich secretory protein 3 [Ochotona princeps]	31.2	31.2	93%	13	64%	gi|504158252|XP_004590597.1
☐ PREDICTED: cysteine-rich secretory protein 2-like [Panthera tigris	30.8	30.8	93%	18	64%	gi|591340164|XP_007095568.1
☐ PREDICTED: cysteine-rich secretory protein 3 [Chrysochloris asiati	30.8	30.8	93%	18	64%	gi|586460042|XP_006860679.1
☐ PREDICTED: cysteine-rich secretory protein 3-like [Nannospalax g	30.3	30.3	80%	24	75%	gi|674104542|XP_008823456.1
☐ PREDICTED: cysteine-rich secretory protein 3-like [Chinchilla lanig	30.3	30.3	80%	25	75%	gi|533125534|XP_005377985.1
☐ hypothetical protein H105_06384 [Trichophyton soudanense CBS 4	30.3	30.3	60%	25	89%	gi|607938037|EZF71419.1
☐ hypothetical protein H106_06212 [Trichophyton rubrum CBS 735.8	30.3	30.3	60%	25	89%	gi|607974736|EZG03991.1
☐ hypothetical protein TERG_01735 [Trichophyton rubrum CBS 1188	30.3	30.3	60%	25	89%	gi|327304641|XP_003237012.1
☐ hypothetical protein [Plasmodium yoelii yoelii 17XNL]	30.3	30.3	73%	26	82%	gi|82541076|XP_724807.1
☐ hypothetical protein YYC_03031 [Plasmodium yoelii 17X]	30.3	30.3	73%	26	82%	gi|564278173|ETB59592.1
☐ liver specific protein 1 [Plasmodium yoelii]	30.3	30.3	73%	26	82%	gi|675232727|CDU85100.1
☐ PREDICTED: cysteine-rich secretory protein 3 [Echinops telfairi]	29.9	29.9	93%	33	64%	gi|507620678|XP_004696622.1
☐ Tms1p [Rhizophagus irregularis DAOM 197198w]	29.9	29.9	73%	34	82%	gi|595438682|EXX52304.1
☐ hypothetical protein LRAMOSA01456 [Absidia idahoensis var. ther	29.9	29.9	73%	34	82%	gi|671692776|CDS07507.1
☐ related to tms1 protein [Lichtheimia corymbifera JMRC:FSU:9682]	29.9	29.9	73%	34	82%	gi|661183725|CDH53974.1
☐ PREDICTED: tetraspanin-8 [Poecilia reticulata]	29.5	29.5	93%	44	52%	gi|658918509|XP_008399014.1
☐ PREDICTED: cysteine-rich secretory protein 3 [Ceratotherium simu	29.5	29.5	93%	45	57%	gi|478500344|XP_004424494.1
☐ SAP domain-containing protein [Trichophyton equinum CBS 127.97	29.5	29.5	60%	47	89%	gi|326477338|EGE01348.1
☐ conserved hypothetical protein [Trichophyton verrucosum HKI 0517	29.5	29.5	60%	47	89%	gi|302667025|XP_003025107.1
☐ hypothetical protein H109_04555 [Trichophyton interdigitale MR816	29.5	29.5	60%	47	89%	gi|633046989|KDB23552.1
☐ hypothetical protein H101_02809 [Trichophyton interdigitale H6]	29.5	29.5	60%	47	89%	gi|607894816|EZF33634.1
☐ hypothetical protein TESG_04396 [Trichophyton tonsurans CBS 11	29.5	29.5	60%	47	89%	gi|326472966|EGD96975.1
☐ conserved hypothetical protein [Arthroderma benhamiae CBS 1123	29.5	29.5	60%	47	89%	gi|302501356|XP_003012670.1
☐ hypothetical protein D910_03959 [Dendroctonus ponderosae]	29.5	29.5	86%	47	77%	gi|546675335|ERL86552.1
☐ hypothetical protein YQE_02834 [Dendroctonus ponderosae]	29.5	29.5	86%	47	77%	gi|478261334|ENN80748.1
☐ Laminin subunit beta-1 [Zootermopsis nevadensis]	29.5	53.4	93%	47	75%	gi|646710327|KDR15871.1
☐ hypothetical protein BC1G_16107 [Botryotinia fuckeliana B05.10]	29.1	29.1	73%	55	82%	gi|154289331|XP_001545300.1
☐ cysteine-rich secretory protein 2 precursor [Xenopus (Silurana) trop	29.1	29.1	93%	61	64%	gi|56118480|NP_001008204.1
☐ PREDICTED: cysteine-rich secretory protein 3 [Ictidomys tridecemli	29.1	29.1	80%	61	67%	gi|532065565|XP_005318641.1
☐ PREDICTED: cysteine-rich secretory protein 3 [Jaculus jaculus]	29.1	29.1	86%	61	62%	gi|507530833|XP_004649500.1
☐ hypothetical protein CAEBREN_14933 [Caenorhabditis brenneri]	28.6	28.6	73%	80	64%	gi|341904208|EGT60041.1

☐	hypothetical protein [Atopobium sp. oral taxon 810]	28.2	28.2	60%	83	89%	gi|545384353|WP_021625327.1
☐	PREDICTED: cysteine-rich secretory protein 3-like [Eptesicus fuscu	28.6	28.6	80%	83	67%	gi|641723213|XP_008151421.1
☐	PREDICTED: cysteine-rich secretory protein 3-like [Orycteropus afe	28.6	28.6	86%	83	69%	gi|634835100|XP_007934348.1
☐	cysteine-rich secretory protein 3 precursor [Equus caballus]	28.6	28.6	93%	83	57%	gi|126352542|NP_001075343.1
☐	uncharacterized protein TOT_030000442 [Theileria orientalis strain	28.6	28.6	73%	86	73%	gi|697892480|XP_009691480.1
☐	neuraminidase [Influenza A virus (A/turkey/France/03295/2003(H9N	28.2	28.2	60%	102	89%	gi|319412002|CAM29146.1
☐	PREDICTED: cysteine-rich secretory protein 2-like [Leptonychotes	28.2	28.2	80%	113	67%	gi|585150326|XP_006727639.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Condylura cristata]	28.2	28.2	86%	113	69%	gi|507924694|XP_004673614.1
☐	PREDICTED: cysteine-rich secretory protein 3-like [Oryctolagus cu	28.2	28.2	93%	114	57%	gi|291396349|XP_002714427.1
☐	PREDICTED: cysteine-rich secretory protein 3 [Mustela putorius fur	28.2	28.2	80%	114	67%	gi|511904944|XP_004771951.1
☐	neuraminidase [Influenza A virus (A/duck/Hong Kong/278/1978(H2N	28.2	28.2	60%	117	89%	gi|78097496|ABB20243.1
☐	neuraminidase [Influenza A virus (A/duck/Hong Kong/562/1979(H10	28.2	28.2	60%	117	89%	gi|125995193|BAF47128.1
☐	neuraminidase [Influenza A virus (A/duck/Hong Kong/278/1978(H2N	28.2	28.2	60%	117	89%	gi|125995201|BAF47132.1
☐	neuraminidase [Influenza A virus (A/duck/Hong Kong/562/1979(H10	28.2	28.2	60%	117	89%	gi|115278151|ABI84470.1
☐	PREDICTED: EGF-like module-containing mucin-like hormone rece	28.2	28.2	73%	117	73%	gi|542240884|XP_005457837.1
☐	PREDICTED: EGF-like module-containing mucin-like hormone rece	28.2	28.2	73%	117	73%	gi|499015500|XP_004558563.1
☐	PREDICTED: EGF-like module-containing mucin-like hormone rece	28.2	28.2	73%	118	73%	gi|548382986|XP_005734751.1
☐	PREDICTED: EGF-like module-containing mucin-like hormone rece	28.2	28.2	73%	118	73%	gi|554873208|XP_005946535.1
☐	unnamed protein product [Oikopleura dioica]	28.2	28.2	80%	119	69%	gi|313236333|CBY11653.1
☐	PREDICTED: serotriflin-like [Chinchilla lanigera]	27.8	27.8	86%	152	62%	gi|533125536|XP_005377986.1
☐	Cysteine-rich secretory protein 2 [Pteropus alecto]	27.8	27.8	80%	153	67%	gi|431838288|ELK00220.1
☐	unnamed protein product [Oncorhynchus mykiss]	27.8	27.8	73%	155	64%	gi|642099914|CDQ77198.1
☐	PREDICTED: cysteine-rich venom protein tigrin-like [Xenopus (Silu	27.8	27.8	80%	155	67%	gi|301608117|XP_002933626.1
☐	PREDICTED: cysteine-rich secretory protein 2 [Pteropus alecto]	27.8	27.8	80%	155	67%	gi|586556149|XP_006926517.1
☐	PREDICTED: cysteine-rich secretory protein 2 [Ictidomys tridecemli	27.8	27.8	80%	155	67%	gi|532065569|XP_005318643.1
☐	PREDICTED: furin-1-like [Neolamprologus brichardi]	27.8	27.8	73%	155	64%	gi|584031494|XP_006810189.1
☐	putative uncharacterized protein [Faecalibacterium sp. CAG:74]	27.8	27.8	73%	156	73%	gi|548226737|WP_022445585.1

⊟ Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194384234|dbj|BAG64890.1| **Length:** 155 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 141 to 155 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.8 bits(117)	7e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    RDSCKASCNCSNSIY  15
            RDSCKASCNCSNSIY
Sbjct  141  RDSCKASCNCSNSIY  155
```

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PREDICTED: cysteine-rich secretory protein 3 isoform X2 [Chlorocebus sabaeus]

Sequence ID: gi|635094563|ref|XP_007970486.1| **Length:** 245 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 231 to 245 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.8 bits(117)	9e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    RDSCKASCNCSNSIY  15
            RDSCKASCNCSNSIY
Sbjct  231  RDSCKASCNCSNSIY  245
```

[Identical Proteins](#) - Proteins identical to the subject

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RecName: Full=Cysteine-rich secretory protein 3; Short=CRISP-3; AltName: Full=Specific granule protein of 28 kDa; Short=SGP28; Flags: Precursor [Homo sapiens]

Sequence ID: gi|1706135|sp|P54108.1|CRIS3_HUMAN **Length:** 245 **Number of Matches:** 1

See 6 more title(s)

Range 1: 231 to 245 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.8 bits(117)	9e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    RDSCKASCNCSNSIY  15
            RDSCKASCNCSNSIY
Sbjct  231  RDSCKASCNCSNSIY  245
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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SGP28 protein [Homo sapiens]

Sequence ID: gi|1213613|emb|CAA63984.1| **Length:** 245 **Number of Matches:** 1

See 2 more title(s)

Range 1: 231 to 245 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.8 bits(117)	9e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    RDSCKASCNCSNSIY  15
            RDSCKASCNCSNSIY
Sbjct  231  RDSCKASCNCSNSIY  245
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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PREDICTED: cysteine-rich secretory protein 3 [Papio anubis]

Sequence ID: gi|402867229|ref|XP_003897768.1| **Length:** 245 **Number of Matches:** 1

See 4 more title(s)

Range 1: 231 to 245 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.8 bits(117)	9e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    RDSCKASCNCSNSIY  15
            RDSCKASCNCSNSIY
Sbjct  231  RDSCKASCNCSNSIY  245
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVDCCBR501R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

DBH_RSLEAIDGSGLQMGLQRV_Mod

RID BVDCCBR501R (Expires on 01-21 08:55 am)

Query ID	lcl|391439	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	18		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

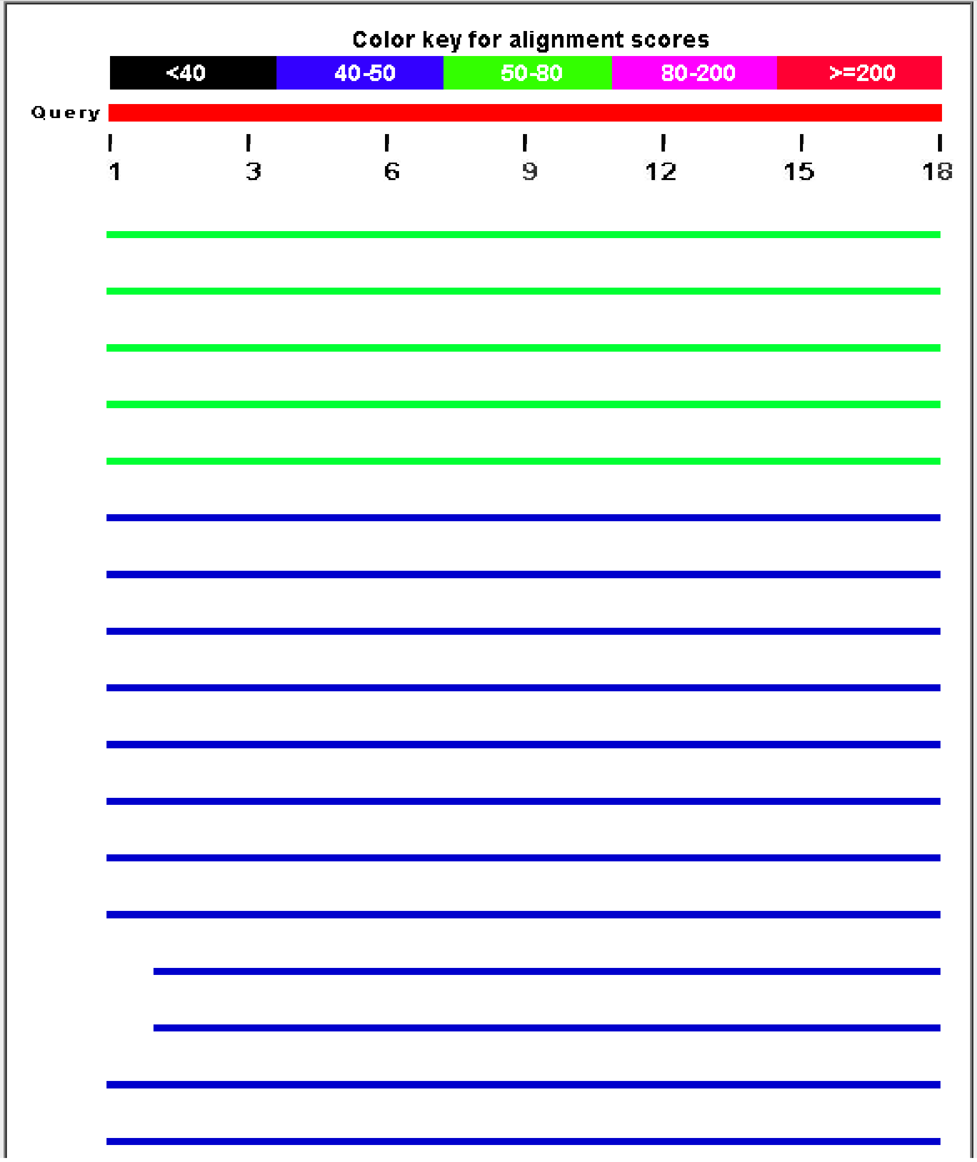
Graphic Summary

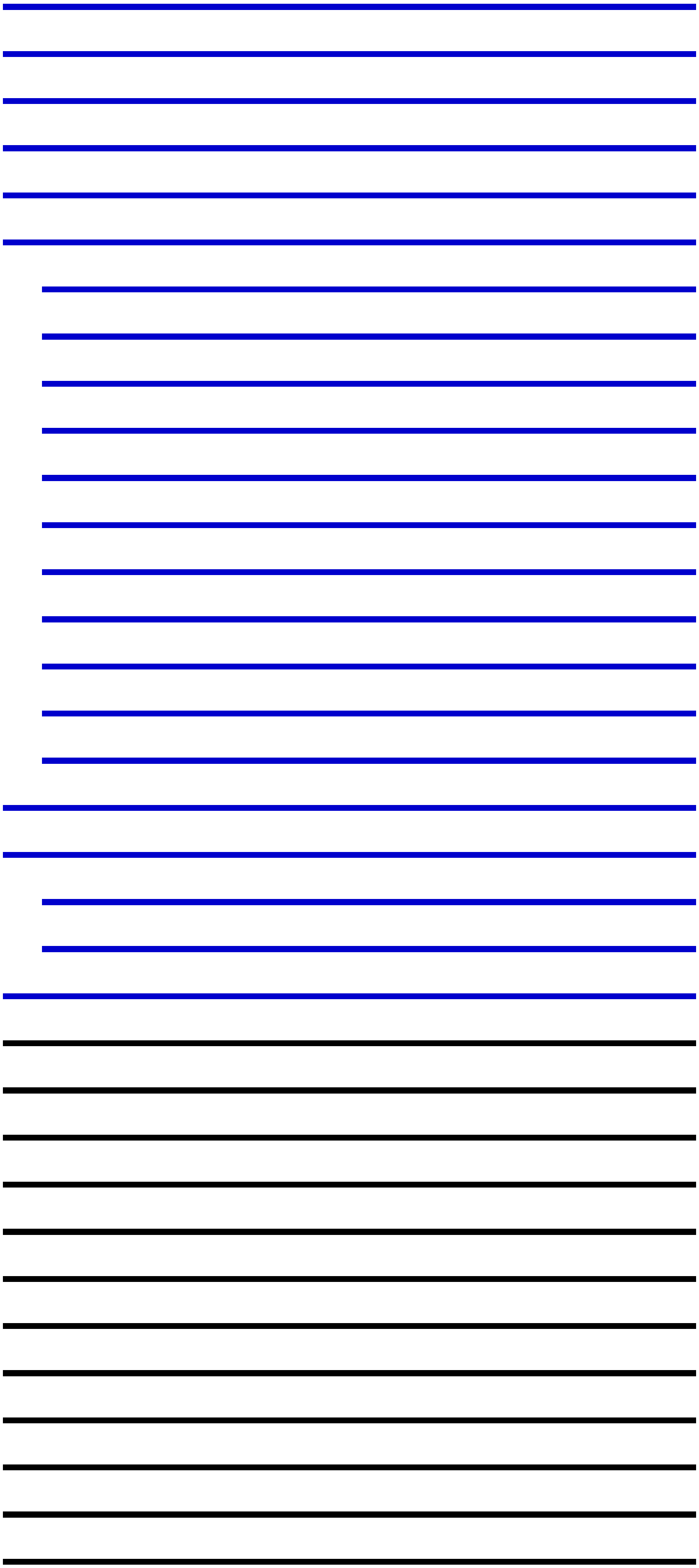
Show Conserved Domains

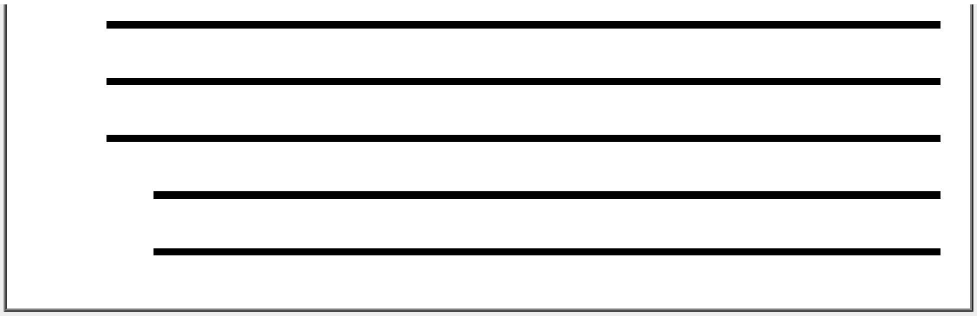
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	dopamine beta-hydroxylase preprotein (AA -25 to 578) [Homo sapiens]	56.2	56.2	100%	1e-07	94%	CAA31631.1
☐	DBH protein [Homo sapiens]	56.2	56.2	100%	1e-07	94%	AAH17174.1
☐	unnamed protein product [Homo sapiens]	56.2	56.2	100%	1e-07	94%	CAA68285.1
☐	Homo sapiens dopamine beta-hydroxylase (dopamine beta-monooxygenase)	56.2	56.2	100%	1e-07	94%	AAP36138.1
☐	dopamine beta-hydroxylase precursor [Homo sapiens]	56.2	56.2	100%	1e-07	94%	NP_000778.3
☐	PREDICTED: dopamine beta-hydroxylase isoform X2 [Pan troglodytes]	49.8	49.8	100%	2e-05	89%	XP_009455932.1
☐	PREDICTED: dopamine beta-hydroxylase [Gorilla gorilla gorilla]	49.8	49.8	100%	2e-05	89%	XP_004048873.1
☐	PREDICTED: dopamine beta-hydroxylase [Pongo abelii]	49.8	49.8	100%	2e-05	89%	XP_002820399.1
☐	PREDICTED: dopamine beta-hydroxylase isoform X1 [Pan troglodytes]	49.8	49.8	100%	2e-05	89%	XP_520341.2
☐	PREDICTED: dopamine beta-hydroxylase isoform 1 [Nomascus leucogenys]	46.4	46.4	100%	2e-04	83%	XP_003276787.1
☐	dopamine beta-hydroxylase [Sus scrofa]	44.8	44.8	100%	8e-04	83%	AAZ30054.1
☐	PREDICTED: dopamine beta-hydroxylase [Sus scrofa]	44.8	44.8	100%	8e-04	83%	XP_001927246.3
☐	PREDICTED: dopamine beta-hydroxylase [Ursus maritimus]	44.8	44.8	100%	8e-04	83%	XP_008707666.1
☐	PREDICTED: dopamine beta-hydroxylase [Saimiri boliviensis boliviensis]	43.5	43.5	94%	0.002	82%	XP_003941430.1
☐	PREDICTED: LOW QUALITY PROTEIN: dopamine beta-hydroxylase [Callithr	43.5	43.5	94%	0.002	82%	XP_003732129.1
☐	PREDICTED: dopamine beta-hydroxylase [Sorex araneus]	43.1	43.1	100%	0.003	78%	XP_004613476.1
☐	PREDICTED: dopamine beta-hydroxylase [Tupaia chinensis]	42.6	42.6	100%	0.004	83%	XP_006164329.1
☐	hypothetical protein EGM_06549 [Macaca fascicularis]	42.2	42.2	100%	0.005	78%	EHH56997.1
☐	hypothetical protein EGK_07229 [Macaca mulatta]	42.2	42.2	100%	0.005	78%	EHH23697.1
☐	PREDICTED: dopamine beta-hydroxylase [Felis catus]	42.2	42.2	100%	0.005	78%	XP_003996085.1
☐	PREDICTED: dopamine beta-hydroxylase [Macaca fascicularis]	42.2	42.2	100%	0.005	78%	XP_005580554.1
☐	PREDICTED: dopamine beta-hydroxylase [Papio anubis]	42.2	42.2	100%	0.005	78%	XP_003911179.1
☐	dopamine beta-hydroxylase [Macaca mulatta]	42.2	42.2	100%	0.005	78%	NP_001265274.1
☐	dopamine beta-hydroxylase [Canis lupus familiaris]	42.2	42.2	94%	0.005	82%	NP_001005263.1
☐	PREDICTED: dopamine beta-hydroxylase [Trichechus manatus latirostris]	41.4	41.4	94%	0.010	82%	XP_004388724.1
☐	PREDICTED: dopamine beta-hydroxylase [Odobenus rosmarus divergens]	41.4	41.4	94%	0.010	82%	XP_004411441.1
☐	PREDICTED: dopamine beta-hydroxylase [Fukomys damarensis]	41.4	41.4	94%	0.010	82%	XP_010607223.1
☐	PREDICTED: dopamine beta-hydroxylase [Orycteropus afer afer]	41.4	41.4	94%	0.010	82%	XP_007952494.1
☐	PREDICTED: dopamine beta-hydroxylase [Heterocephalus glaber]	41.4	41.4	94%	0.010	82%	XP_004849647.1

☐	PREDICTED: dopamine beta-hydroxylase [Heterocephalus glaber]	41.4	41.4	94%	0.010	82%	XP_004888900.1
☐	PREDICTED: dopamine beta-hydroxylase [Otolemur garnettii]	41.4	41.4	94%	0.010	82%	XP_003795019.1
☐	PREDICTED: dopamine beta-hydroxylase [Cavia porcellus]	41.4	41.4	94%	0.010	82%	XP_003473049.1
☐	Dopamine beta-hydroxylase [Fukomys damarensis]	41.4	41.4	94%	0.010	82%	KFO21516.1
☐	Dopamine beta-hydroxylase [Heterocephalus glaber]	41.4	41.4	94%	0.010	82%	EHB05593.1
☐	PREDICTED: dopamine beta-hydroxylase [Pantholops hodgsonii]	40.5	40.5	100%	0.019	78%	XP_005984927.1
☐	PREDICTED: dopamine beta-hydroxylase [Bos mutus]	40.5	40.5	100%	0.019	78%	XP_005897496.1
☐	PREDICTED: dopamine beta-hydroxylase-like [Ailuropoda melanoleuca]	40.5	40.5	94%	0.019	82%	XP_002920753.1
☐	hypothetical protein PANDA_009520 [Ailuropoda melanoleuca]	40.5	40.5	94%	0.019	82%	EFB24902.1
☐	Dopamine beta-hydroxylase [Bos mutus]	40.5	40.5	100%	0.019	78%	ELR55184.1
☐	PREDICTED: LOW QUALITY PROTEIN: dopamine beta-hydroxylase (dopam	39.7	39.7	100%	0.035	72%	XP_007099357.1
☐	PREDICTED: dopamine beta-hydroxylase [Bubalus bubalis]	39.7	39.7	100%	0.035	78%	XP_006062530.1
☐	PREDICTED: dopamine beta-hydroxylase-like [Vicugna pacos]	39.2	39.2	100%	0.046	72%	XP_006219741.1
☐	dopamine beta-hydroxylase [Bos taurus]	39.2	39.2	100%	0.048	72%	AAA30491.1
☐	dopamine beta-hydroxylase [Camelus ferus]	39.2	39.2	100%	0.048	72%	EPY84719.1
☐	PREDICTED: dopamine beta-hydroxylase [Camelus ferus]	39.2	39.2	100%	0.048	72%	XP_006179943.1
☐	PREDICTED: dopamine beta-hydroxylase [Camelus dromedarius]	39.2	39.2	100%	0.048	72%	XP_010998455.1
☐	PREDICTED: dopamine beta-hydroxylase [Camelus bactrianus]	39.2	39.2	100%	0.048	72%	XP_010952799.1
☐	dopamine beta-hydroxylase precursor (EC 1.14.17.1) [Bos taurus]	39.2	39.2	100%	0.048	72%	AAA30490.1
☐	dopamine beta-hydroxylase precursor [Bos taurus]	39.2	39.2	100%	0.048	72%	AAD09829.1
☐	dopamine beta-hydroxylase precursor [Bos taurus]	39.2	39.2	100%	0.048	72%	ABG81467.1
☐	PREDICTED: dopamine beta-hydroxylase [Bison bison bison]	39.2	39.2	100%	0.048	72%	XP_010831066.1
☐	RecName: Full=Dopamine beta-hydroxylase; AltName: Full=Dopamine beta-n	39.2	39.2	100%	0.048	72%	P15101.2
☐	dopamine beta-hydroxylase precursor [Bos taurus]	39.2	39.2	100%	0.048	72%	NP_851338.1
☐	PREDICTED: dopamine beta-hydroxylase [Nannospalax galili]	39.2	39.2	100%	0.048	78%	XP_008842140.1
☐	PREDICTED: dopamine beta-hydroxylase [Rhinopithecus roxellana]	38.8	38.8	94%	0.066	76%	XP_010371175.1
☐	PREDICTED: dopamine beta-hydroxylase isoform X2 [Chlorocebus sabaeus]	38.8	38.8	94%	0.066	76%	XP_008003949.1
☐	PREDICTED: dopamine beta-hydroxylase [Ochotona princeps]	38.8	38.8	100%	0.066	72%	XP_004593508.1
☐	PREDICTED: dopamine beta-hydroxylase isoform X1 [Chlorocebus sabaeus]	38.8	38.8	94%	0.066	76%	XP_008003948.1
☐	PREDICTED: LOW QUALITY PROTEIN: dopamine beta-hydroxylase [Tursio	38.4	38.4	94%	0.090	76%	XP_004314127.1
☐	PREDICTED: dopamine beta-hydroxylase [Lipotes vexillifer]	38.4	38.4	94%	0.090	76%	XP_007453141.1
☐	PREDICTED: dopamine beta-hydroxylase [Balaenoptera acutorostrata scamn	38.4	38.4	94%	0.090	76%	XP_007194475.1
☐	PREDICTED: dopamine beta-hydroxylase [Physeter catodon]	38.4	38.4	94%	0.090	76%	XP_007111132.1
☐	PREDICTED: dopamine beta-hydroxylase [Mustela putorius furo]	38.4	38.4	94%	0.090	76%	XP_004757456.1
☐	PREDICTED: dopamine beta-hydroxylase [Orcinus orca]	38.4	38.4	94%	0.090	76%	XP_004285054.1
☐	PREDICTED: dopamine beta-hydroxylase [Galeopterus variegatus]	38.4	38.4	94%	0.090	76%	XP_008578902.1
☐	PREDICTED: dopamine beta-hydroxylase [Microtus ochrogaster]	38.4	38.4	94%	0.090	76%	XP_005346784.1
☐	dopamine beta-hydroxylase [Mus musculus]	38.4	38.4	94%	0.090	76%	NP_620392.2
☐	PREDICTED: dopamine beta-hydroxylase [Mesocricetus auratus]	38.4	38.4	94%	0.090	76%	XP_005085459.1
☐	PREDICTED: dopamine beta-hydroxylase [Leptonychotes weddellii]	38.0	38.0	94%	0.12	76%	XP_006746395.1
☐	Dopamine beta-hydroxylase [Pteropus alecto]	38.0	38.0	94%	0.12	76%	ELK07341.1
☐	PREDICTED: dopamine beta-hydroxylase [Chinchilla lanigera]	38.0	38.0	94%	0.12	76%	XP_005408512.1
☐	PREDICTED: LOW QUALITY PROTEIN: dopamine beta-hydroxylase [Pterop	38.0	38.0	94%	0.12	76%	XP_006918159.1
☐	PREDICTED: dopamine beta-hydroxylase [Chrysochloris asiatica]	37.5	37.5	94%	0.17	76%	XP_006863887.1
☐	PREDICTED: dopamine beta-hydroxylase [Ceratotherium simum simum]	37.5	37.5	94%	0.17	76%	XP_004423687.1

☐	PREDICTED: dopamine beta-hydroxylase [Octodon degus]	37.5	37.5	94%	0.17	76%	XP_004640601.1
☐	PREDICTED: dopamine beta-hydroxylase [Myotis brandtii]	37.1	37.1	94%	0.23	76%	XP_005871861.1
☐	PREDICTED: dopamine beta-hydroxylase [Capra hircus]	37.1	37.1	94%	0.23	76%	XP_005687409.1
☐	PREDICTED: dopamine beta-hydroxylase [Eptesicus fuscus]	37.1	37.1	94%	0.23	76%	XP_008150706.1
☐	PREDICTED: dopamine beta-hydroxylase [Loxodonta africana]	36.7	36.7	94%	0.31	76%	XP_003420517.1
☐	PREDICTED: dopamine beta-hydroxylase [Ornithorhynchus anatinus]	36.3	36.3	88%	0.43	75%	XP_001505587.2
☐	PREDICTED: dopamine beta-hydroxylase [Elephantulus edwardii]	35.4	35.4	94%	0.80	76%	XP_006900619.1
☐	PREDICTED: dopamine beta-hydroxylase [Sarcophilus harrisii]	35.4	35.4	94%	0.80	71%	XP_003757519.1
☐	PREDICTED: dopamine beta-hydroxylase [Equus przewalskii]	35.0	35.0	94%	1.1	71%	XP_008537782.1
☐	PREDICTED: dopamine beta-hydroxylase [Jaculus jaculus]	35.0	35.0	83%	1.1	80%	XP_004654117.1
☐	dopamine beta-hydroxylase [Equus caballus]	35.0	35.0	94%	1.1	71%	NP_001075239.1
☐	PREDICTED: dopamine beta-hydroxylase [Myotis davidii]	34.1	34.1	88%	2.0	75%	XP_006776660.1
☐	PREDICTED: dopamine beta-hydroxylase [Chrysemys picta bellii]	34.1	34.1	100%	2.0	67%	XP_005293531.2
☐	PREDICTED: dopamine beta-hydroxylase [Serinus canaria]	34.1	34.1	100%	2.0	67%	XP_009091623.1
☐	RecName: Full=Dopamine beta-hydroxylase; AltName: Full=Dopamine beta-n	34.1	34.1	94%	2.0	71%	Q05754.1
☐	dopamine beta hydroxylase [Rattus norvegicus]	34.1	34.1	94%	2.0	71%	EDL93440.1
☐	dopamine beta-hydroxylase [Rattus norvegicus]	34.1	34.1	94%	2.0	71%	NP_037290.2
☐	Dopamine beta-hydroxylase [Tauraco erythrolophus]	33.3	33.3	100%	3.7	67%	KFV13733.1
☐	PREDICTED: LOW QUALITY PROTEIN: dopamine beta-hydroxylase [Taurac	33.3	33.3	100%	3.7	67%	XP_009980321.1
☐	PREDICTED: dopamine beta-hydroxylase [Peromyscus maniculatus bairdii]	33.3	33.3	94%	3.7	71%	XP_006993176.1
☐	PREDICTED: dopamine beta-hydroxylase [Ictidomys tridecemlineatus]	32.9	32.9	94%	5.1	71%	XP_005337059.1
☐	PREDICTED: dopamine beta-hydroxylase [Tarsius syrichta]	32.9	32.9	94%	5.1	71%	XP_008068990.1
☐	PREDICTED: dopamine beta-hydroxylase isoform X2 [Cricetulus griseus]	32.9	32.9	94%	5.1	76%	XP_007618621.1
☐	dopamine beta-hydroxylase [Mus musculus]	32.9	32.9	94%	5.1	71%	AAB24330.1
☐	dopamine beta-hydroxylase-like protein [Cricetulus griseus]	32.9	32.9	94%	5.1	76%	ERE71366.1
☐	dopamine beta-hydroxylase-like protein [Cricetulus griseus]	32.9	32.9	94%	5.1	76%	ERE71365.1

⊟ Alignments

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dopamine beta-hydroxylase preprotein (AA -25 to 578) [Homo sapiens]

Sequence ID: emb|CAA31631.1| **Length:** 603 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 164 to 181 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
56.2 bits(125)	1e-07	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    RSLEAIDGSGLQMGLQRV  18
            RSLEAI+GSGLQMGLQRV
Sbjct  164  RSLEAINGSGLQMGLQRV  181
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Download ⌄ GenPept Graphics ▼ Next ▲ Previous ▲ Descriptions

DBH protein [Homo sapiens]

Sequence ID: gb|AAH17174.1| **Length:** 603 **Number of Matches:** 1

▷ See 3 more title(s)

Range 1: 164 to 181 GenPept Graphics ▼ Next Match ▲ Previous Match

Related Information

Gene - associated gene details

Score	Expect	Identities	Positives	Gaps
56.2 bits(125)	1e-07	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    RSLEAIDGSGLQMGLQRV  18
            RSLEAI+GSGLQMGLQRV
Sbjct  164  RSLEAINGSGLQMGLQRV  181
```

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: emb|CAA68285.1| **Length:** 603 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 164 to 181 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
56.2 bits(125)	1e-07	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    RSLEAIDGSGLQMGLQRV  18
            RSLEAI+GSGLQMGLQRV
Sbjct  164  RSLEAINGSGLQMGLQRV  181
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Homo sapiens dopamine beta-hydroxylase (dopamine beta-monooxygenase) [synthetic construct]

Sequence ID: gb|AAP36138.1| **Length:** 604 **Number of Matches:** 1

See 2 more title(s)

Related Information

Identical Proteins - Proteins identical to the subject

Range 1: 164 to 181 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
56.2 bits(125)	1e-07	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    RSLEAIDGSGLQMGLQRV  18
            RSLEAI+GSGLQMGLQRV
Sbjct  164  RSLEAINGSGLQMGLQRV  181
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

dopamine beta-hydroxylase precursor [Homo sapiens]

Sequence ID: ref|NP_000778.3| **Length:** 617 **Number of Matches:** 1

See 2 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

PubChem BioAssay - bioactivity screening

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 178 to 195 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
56.2 bits(125)	1e-07	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    RSLEAIDGSGLQMGLQRV  18
            RSLEAI+GSGLQMGLQRV
Sbjct  178  RSLEAINGSGLQMGLQRV  195
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - B9CS4HMC01R

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How to read this page   Blast report description

DBH_RSLEAINGSGLQMGLQRV_NonMod

RID B9CS4HMC01R (Expires on 01-14 12:54 pm)

Query ID	lcl|195719	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ ▷Citation
Query Length	18		

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

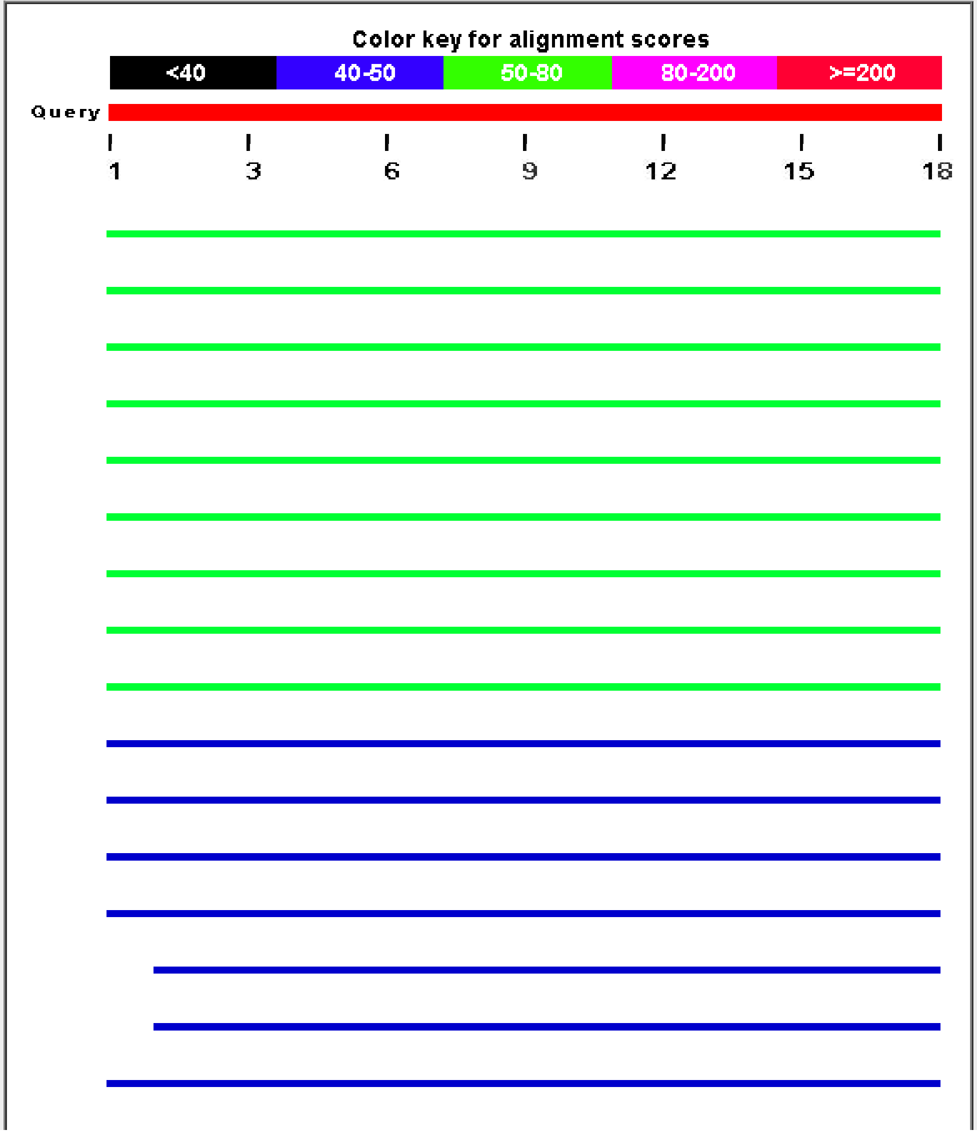
⊟ Graphic Summary

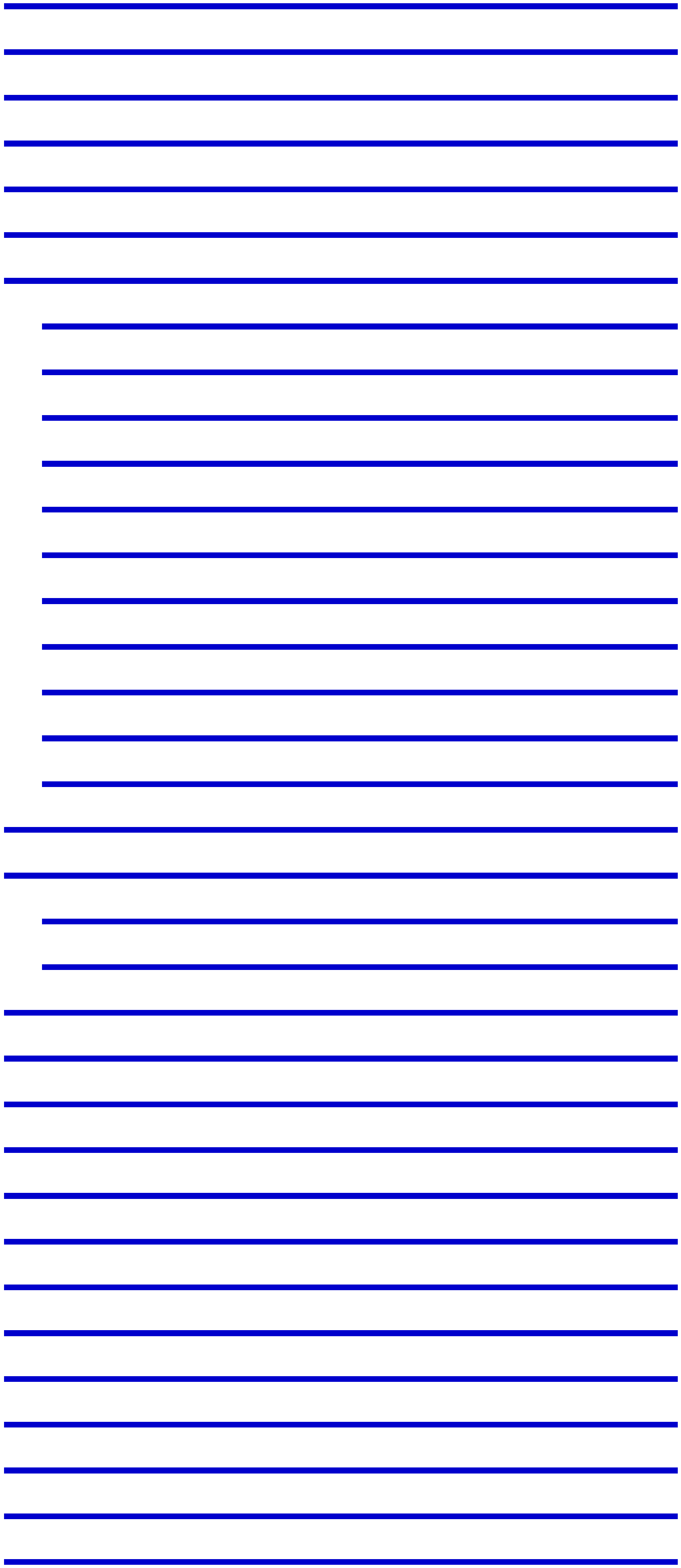
⊟ Show Conserved Domains

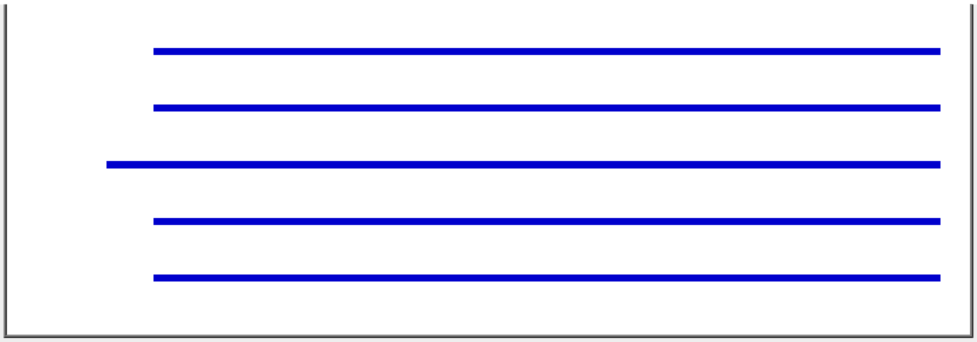
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	dopamine beta-hydroxylase preprotein (AA -25 to 578) [Homo sapi	58.7	58.7	100%	1e-08	100%	gi|30474|CAA31631.1
☐	DBH protein [Homo sapiens]	58.7	58.7	100%	1e-08	100%	gi|16877893|AAH17174.1
☐	unnamed protein product [Homo sapiens]	58.7	58.7	100%	1e-08	100%	gi|30456|CAA68285.1
☐	Homo sapiens dopamine beta-hydroxylase (dopamine beta-monoo	58.7	58.7	100%	1e-08	100%	gi|30583779|AAP36138.1
☐	dopamine beta-hydroxylase precursor [Homo sapiens]	58.7	58.7	100%	1e-08	100%	gi|116534900|NP_000778.3
☐	PREDICTED: dopamine beta-hydroxylase isoform X2 [Pan troglody	52.4	52.4	100%	2e-06	94%	gi|694937949|XP_009455932.1
☐	PREDICTED: dopamine beta-hydroxylase [Gorilla gorilla gorilla]	52.4	52.4	100%	2e-06	94%	gi|426363490|XP_004048873.1
☐	PREDICTED: dopamine beta-hydroxylase [Pongo abelii]	52.4	52.4	100%	2e-06	94%	gi|297685657|XP_002820399.1
☐	PREDICTED: dopamine beta-hydroxylase isoform X1 [Pan troglody	52.4	52.4	100%	2e-06	94%	gi|114627409|XP_520341.2
☐	PREDICTED: dopamine beta-hydroxylase isoform 1 [Nomascus leu	49.0	49.0	100%	3e-05	89%	gi|332255334|XP_003276787.1
☐	dopamine beta-hydroxylase [Sus scrofa]	47.3	47.3	100%	1e-04	89%	gi|71361891|AAZ30054.1
☐	PREDICTED: dopamine beta-hydroxylase [Sus scrofa]	47.3	47.3	100%	1e-04	89%	gi|335281176|XP_001927246.3
☐	PREDICTED: dopamine beta-hydroxylase [Ursus maritimus]	47.3	47.3	100%	1e-04	89%	gi|671033689|XP_008707666.1
☐	PREDICTED: dopamine beta-hydroxylase [Saimiri boliviensis bolivi	46.0	46.0	94%	3e-04	88%	gi|403301510|XP_003941430.1
☐	PREDICTED: LOW QUALITY PROTEIN: dopamine beta-hydroxylas	46.0	46.0	94%	3e-04	88%	gi|390458508|XP_003732129.1
☐	PREDICTED: dopamine beta-hydroxylase [Sorex araneus]	45.6	45.6	100%	4e-04	83%	gi|505839906|XP_004613476.1
☐	PREDICTED: dopamine beta-hydroxylase [Tupaia chinensis]	45.2	45.2	100%	5e-04	89%	gi|562872827|XP_006164329.1
☐	hypothetical protein EGM_06549 [Macaca fascicularis]	44.8	44.8	100%	7e-04	83%	gi|355752951|EHH56997.1
☐	hypothetical protein EGK_07229 [Macaca mulatta]	44.8	44.8	100%	7e-04	83%	gi|355567356|EHH23697.1
☐	PREDICTED: dopamine beta-hydroxylase [Felis catus]	44.8	44.8	100%	7e-04	83%	gi|410979427|XP_003996085.1
☐	PREDICTED: dopamine beta-hydroxylase [Macaca fascicularis]	44.8	44.8	100%	7e-04	83%	gi|544491671|XP_005580554.1
☐	PREDICTED: dopamine beta-hydroxylase [Papio anubis]	44.8	44.8	100%	7e-04	83%	gi|402896169|XP_003911179.1
☐	dopamine beta-hydroxylase [Macaca mulatta]	44.8	44.8	100%	7e-04	83%	gi|507588252|NP_001265274.1
☐	dopamine beta-hydroxylase [Canis lupus familiaris]	44.8	44.8	94%	7e-04	88%	gi|55742740|NP_001005263.1
☐	PREDICTED: dopamine beta-hydroxylase [Trichechus manatus lati	43.9	43.9	94%	0.001	88%	gi|471414372|XP_004388724.1
☐	PREDICTED: dopamine beta-hydroxylase [Odobenus rosmarus div	43.9	43.9	94%	0.001	88%	gi|472384135|XP_004411441.1
☐	PREDICTED: dopamine beta-hydroxylase [Fukomys damarensis]	43.9	43.9	94%	0.001	88%	gi|731276514|XP_010607223.1
☐	PREDICTED: dopamine beta-hydroxylase [Orycteropus afer afer]	43.9	43.9	94%	0.001	88%	gi|634885829|XP_007952494.1
☐							

	PREDICTED: dopamine beta-hydroxylase [Heterocephalus glaber]	43.9	43.9	94%	0.001	88%	gi|512975138|XP_004849647.1
☐	PREDICTED: dopamine beta-hydroxylase [Heterocephalus glaber]	43.9	43.9	94%	0.001	88%	gi|512857645|XP_004888900.1
☐	PREDICTED: dopamine beta-hydroxylase [Otolemur garnettii]	43.9	43.9	94%	0.001	88%	gi|395844543|XP_003795019.1
☐	PREDICTED: dopamine beta-hydroxylase [Cavia porcellus]	43.9	43.9	94%	0.001	88%	gi|348574542|XP_003473049.1
☐	Dopamine beta-hydroxylase [Fukomys damarensis]	43.9	43.9	94%	0.001	88%	gi|676265268|KFO21516.1
☐	Dopamine beta-hydroxylase [Heterocephalus glaber]	43.9	43.9	94%	0.001	88%	gi|351702674|EHB05593.1
☐	PREDICTED: dopamine beta-hydroxylase [Pantholops hodgsonii]	43.1	43.1	100%	0.003	83%	gi|556779765|XP_005984927.1
☐	PREDICTED: dopamine beta-hydroxylase [Bos mutus]	43.1	43.1	100%	0.003	83%	gi|555970958|XP_005897496.1
☐	PREDICTED: dopamine beta-hydroxylase-like [Ailuropoda melanole	43.1	43.1	94%	0.003	88%	gi|301770661|XP_002920753.1
☐	hypothetical protein PANDA_009520 [Ailuropoda melanoleuca]	43.1	43.1	94%	0.003	88%	gi|281349318|EFB24902.1
☐	Dopamine beta-hydroxylase [Bos mutus]	43.1	43.1	100%	0.003	83%	gi|440904711|ELR55184.1
☐	PREDICTED: LOW QUALITY PROTEIN: dopamine beta-hydroxylas	42.2	42.2	100%	0.005	78%	gi|591344199|XP_007099357.1
☐	PREDICTED: dopamine beta-hydroxylase [Bubalus bubalis]	42.2	42.2	100%	0.005	83%	gi|594077631|XP_006062530.1
☐	PREDICTED: dopamine beta-hydroxylase-like [Vicugna pacos]	41.8	41.8	100%	0.007	78%	gi|560995302|XP_006219741.1
☐	dopamine beta-hydroxylase [Bos taurus]	41.8	41.8	100%	0.007	78%	gi|162965|AAA30491.1
☐	dopamine beta-hydroxylase [Camelus ferus]	41.8	41.8	100%	0.007	78%	gi|528765060|EPY84719.1
☐	PREDICTED: dopamine beta-hydroxylase [Camelus ferus]	41.8	41.8	100%	0.007	78%	gi|560907230|XP_006179943.1
☐	dopamine beta-hydroxylase precursor (EC 1.14.17.1) [Bos taurus]	41.8	41.8	100%	0.007	78%	gi|162963|AAA30490.1
☐	dopamine beta-hydroxylase precursor [Bos taurus]	41.8	41.8	100%	0.007	78%	gi|4191614|AAD09829.1
☐	dopamine beta-hydroxylase precursor [Bos taurus]	41.8	41.8	100%	0.007	78%	gi|110665642|ABG81467.1
☐	RecName: Full=Dopamine beta-hydroxylase; AltName: Full=Dopam	41.8	41.8	100%	0.007	78%	gi|158931121|P15101.2
☐	dopamine beta-hydroxylase precursor [Bos taurus]	41.8	41.8	100%	0.007	78%	gi|30794286|NP_851338.1
☐	PREDICTED: dopamine beta-hydroxylase [Nannospalax galili]	41.8	41.8	100%	0.007	83%	gi|674070087|XP_008842140.1
☐	PREDICTED: dopamine beta-hydroxylase [Rhinopithecus roxellana	41.4	41.4	94%	0.009	82%	gi|724871980|XP_010371175.1
☐	PREDICTED: dopamine beta-hydroxylase isoform X2 [Chlorocebus	41.4	41.4	94%	0.009	82%	gi|635070261|XP_008003949.1
☐	PREDICTED: dopamine beta-hydroxylase [Ochotona princeps]	41.4	41.4	100%	0.009	78%	gi|504167697|XP_004593508.1
☐	PREDICTED: dopamine beta-hydroxylase isoform X1 [Chlorocebus	41.4	41.4	94%	0.009	82%	gi|635070259|XP_008003948.1
☐	PREDICTED: LOW QUALITY PROTEIN: dopamine beta-hydroxylas	40.9	40.9	94%	0.013	82%	gi|470606240|XP_004314127.1
☐	PREDICTED: dopamine beta-hydroxylase [Lipotes vexillifer]	40.9	40.9	94%	0.013	82%	gi|602680668|XP_007453141.1
☐	PREDICTED: dopamine beta-hydroxylase [Balaenoptera acutorostr	40.9	40.9	94%	0.013	82%	gi|594694468|XP_007194475.1
☐	PREDICTED: dopamine beta-hydroxylase [Physeter catodon]	40.9	40.9	94%	0.013	82%	gi|593731032|XP_007111132.1
☐	PREDICTED: dopamine beta-hydroxylase [Mustela putorius furo]	40.9	40.9	94%	0.013	82%	gi|511874860|XP_004757456.1
☐	PREDICTED: dopamine beta-hydroxylase [Orcinus orca]	40.9	40.9	94%	0.013	82%	gi|466083579|XP_004285054.1
☐	PREDICTED: dopamine beta-hydroxylase [Galeopterus variegatus]	40.9	40.9	94%	0.013	82%	gi|667294384|XP_008578902.1
☐	PREDICTED: dopamine beta-hydroxylase [Microtus ochrogaster]	40.9	40.9	94%	0.013	82%	gi|532005885|XP_005346784.1
☐	dopamine beta-hydroxylase [Mus musculus]	40.9	40.9	94%	0.013	82%	gi|110815861|NP_620392.2
☐	PREDICTED: dopamine beta-hydroxylase [Mesocricetus auratus]	40.9	40.9	94%	0.013	82%	gi|524971191|XP_005085459.1
☐	PREDICTED: dopamine beta-hydroxylase [Leptonychotes weddellii	40.5	40.5	94%	0.016	82%	gi|585190200|XP_006746395.1
☐	Dopamine beta-hydroxylase [Pteropus alecto]	40.5	40.5	94%	0.017	82%	gi|431898971|ELK07341.1
☐	PREDICTED: dopamine beta-hydroxylase [Chinchilla lanigera]	40.5	40.5	94%	0.018	82%	gi|533191305|XP_005408512.1
☐	PREDICTED: LOW QUALITY PROTEIN: dopamine beta-hydroxylas	40.5	40.5	94%	0.018	82%	gi|586526429|XP_006918159.1
☐	PREDICTED: dopamine beta-hydroxylase [Chrysochloris asiatica]	40.1	40.1	94%	0.024	82%	gi|586466542|XP_006863887.1
☐	PREDICTED: dopamine beta-hydroxylase [Ceratotherium simum si	40.1	40.1	94%	0.024	82%	gi|478498710|XP_004423687.1
☐	PREDICTED: dopamine beta-hydroxylase [Octodon degus]	40.1	40.1	94%	0.024	82%	gi|507685735|XP_004640601.1
☐	PREDICTED: dopamine beta-hydroxylase [Myotis brandtii]	39.7	39.7	94%	0.033	82%	gi|554554817|XP_005871861.1

☐	PREDICTED: dopamine beta-hydroxylase [Capra hircus]	39.7	39.7	94%	0.033	82%	gi|548487730|XP_005687409.1
☐	PREDICTED: dopamine beta-hydroxylase [Eptesicus fuscus]	39.7	39.7	94%	0.033	82%	gi|641721931|XP_008150706.1
☐	PREDICTED: dopamine beta-hydroxylase [Loxodonta africana]	39.2	39.2	94%	0.045	82%	gi|344297665|XP_003420517.1
☐	PREDICTED: dopamine beta-hydroxylase [Ornithorhynchus anatinu	38.8	38.8	88%	0.062	81%	gi|620943845|XP_001505587.2
☐	PREDICTED: dopamine beta-hydroxylase [Elephantulus edwardii]	38.0	38.0	94%	0.12	82%	gi|585713239|XP_006900619.1
☐	PREDICTED: dopamine beta-hydroxylase [Sarcophilus harrisii]	38.0	38.0	94%	0.12	76%	gi|395506397|XP_003757519.1
☐	PREDICTED: dopamine beta-hydroxylase [Equus przewalskii]	37.5	37.5	94%	0.16	76%	gi|664760398|XP_008537782.1
☐	PREDICTED: dopamine beta-hydroxylase [Jaculus jaculus]	37.5	37.5	83%	0.16	87%	gi|507540225|XP_004654117.1
☐	dopamine beta-hydroxylase [Equus caballus]	37.5	37.5	94%	0.16	76%	gi|126352385|NP_001075239.1
☐	PREDICTED: dopamine beta-hydroxylase [Myotis davidii]	36.7	36.7	88%	0.30	81%	gi|584064603|XP_006776660.1
☐	PREDICTED: dopamine beta-hydroxylase [Chrysemys picta bellii]	36.7	36.7	100%	0.30	72%	gi|641764396|XP_005293531.2
☐	PREDICTED: dopamine beta-hydroxylase [Serinus canaria]	36.7	36.7	100%	0.30	72%	gi|683921403|XP_009091623.1
☐	RecName: Full=Dopamine beta-hydroxylase; AltName: Full=Dopam	36.7	36.7	94%	0.30	76%	gi|729362|Q05754.1
☐	dopamine beta hydroxylase [Rattus norvegicus]	36.7	36.7	94%	0.30	76%	gi|149039220|EDL93440.1
☐	dopamine beta-hydroxylase [Rattus norvegicus]	36.7	36.7	94%	0.30	76%	gi|140970928|NP_037290.2
☐	Dopamine beta-hydroxylase [Tauraco erythrolophus]	35.8	35.8	100%	0.55	72%	gi|678144567|KFV13733.1
☐	PREDICTED: LOW QUALITY PROTEIN: dopamine beta-hydroxyla	35.8	35.8	100%	0.55	72%	gi|701335236|XP_009980321.1
☐	PREDICTED: dopamine beta-hydroxylase [Peromyscus maniculatu	35.8	35.8	94%	0.55	76%	gi|589961209|XP_006993176.1
☐	PREDICTED: dopamine beta-hydroxylase [Ictidomys tridecemlineat	35.4	35.4	94%	0.75	76%	gi|532102904|XP_005337059.1
☐	PREDICTED: dopamine beta-hydroxylase [Tarsius syrichta]	35.4	35.4	94%	0.75	76%	gi|640823891|XP_008068990.1
☐	PREDICTED: dopamine beta-hydroxylase isoform X2 [Cricetulus gr	35.4	35.4	94%	0.75	82%	gi|625254557|XP_007618621.1
☐	dopamine beta-hydroxylase [Mus musculus]	35.4	35.4	94%	0.75	76%	gi|260873|AAB24330.1
☐	dopamine beta-hydroxylase-like protein [Cricetulus griseus]	35.4	35.4	94%	0.75	82%	gi|537149913|ERE71366.1
☐	dopamine beta-hydroxylase-like protein [Cricetulus griseus]	35.4	35.4	94%	0.76	82%	gi|537149912|ERE71365.1
☐	PREDICTED: LOW QUALITY PROTEIN: dopamine beta-hydroxyla	34.1	34.1	100%	1.9	72%	gi|449478274|XP_004174400.1
☐	PREDICTED: dopamine beta-hydroxylase [Dasypus novemcinctus]	33.7	33.7	94%	2.6	76%	gi|488586293|XP_004478484.1
☐	PREDICTED: dopamine beta-hydroxylase isoform X1 [Monodelphis	33.7	33.7	94%	2.6	71%	gi|126297977|XP_001371885.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

dopamine beta-hydroxylase preprotein (AA -25 to 578) [Homo sapiens]

Sequence ID: gi|30474|emb|CAA31631.1| **Length:** 603 **Number of Matches:** 1

See 1 more title(s)

Range 1: 164 to 181 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
58.7 bits(131)	1e-08	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    RSLEAINGSGLQMGLQRV  18
            RSLEAINGSGLQMGLQRV
Sbjct  164  RSLEAINGSGLQMGLQRV  181
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

DBH protein [Homo sapiens]

Sequence ID: gi|16877893|gb|AAH17174.1| **Length:** 603 **Number of Matches:** 1

See 3 more title(s)

Range 1: 164 to 181 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps

Related Information

Gene - associated gene details

Identical Proteins - Proteins

58.7 bits(131)	1e-08	18/18(100%)	18/18(100%)	0/18(0%)

identical to the subject

```
Query  1    RSLEAINGSGLQMGLQRV  18
            RSLEAINGSGLQMGLQRV
Sbjct  164  RSLEAINGSGLQMGLQRV  181
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: gi|30456|emb|CAA68285.1| **Length:** 603 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 164 to 181 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
58.7 bits(131)	1e-08	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    RSLEAINGSGLQMGLQRV  18
            RSLEAINGSGLQMGLQRV
Sbjct  164  RSLEAINGSGLQMGLQRV  181
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Homo sapiens dopamine beta-hydroxylase (dopamine beta-monooxygenase) [synthetic construct]

Sequence ID: gi|30583779|gb|AAP36138.1| **Length:** 604 **Number of Matches:** 1

▷ See 2 more title(s)

Related Information

Identical Proteins - Proteins identical to the subject

Range 1: 164 to 181 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
58.7 bits(131)	1e-08	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    RSLEAINGSGLQMGLQRV  18
            RSLEAINGSGLQMGLQRV
Sbjct  164  RSLEAINGSGLQMGLQRV  181
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

dopamine beta-hydroxylase precursor [Homo sapiens]

Sequence ID: gi|116534900|ref|NP_000778.3| **Length:** 617 **Number of Matches:** 1

▷ See 2 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

PubChem BioAssay - bioactivity screening

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 178 to 195 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
58.7 bits(131)	1e-08	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    RSLEAINGSGLQMGLQRV  18
            RSLEAINGSGLQMGLQRV
Sbjct  178  RSLEAINGSGLQMGLQRV  195
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BTH1SCEE013

Your search parameters were adjusted to search for a short input sequence.

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F11_KDSVTETLPRVDRT_Mod

RID	BTH1SCEE013 (Expires on 01-20 15:45 pm)		
Query ID	lcl|22001	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	14	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

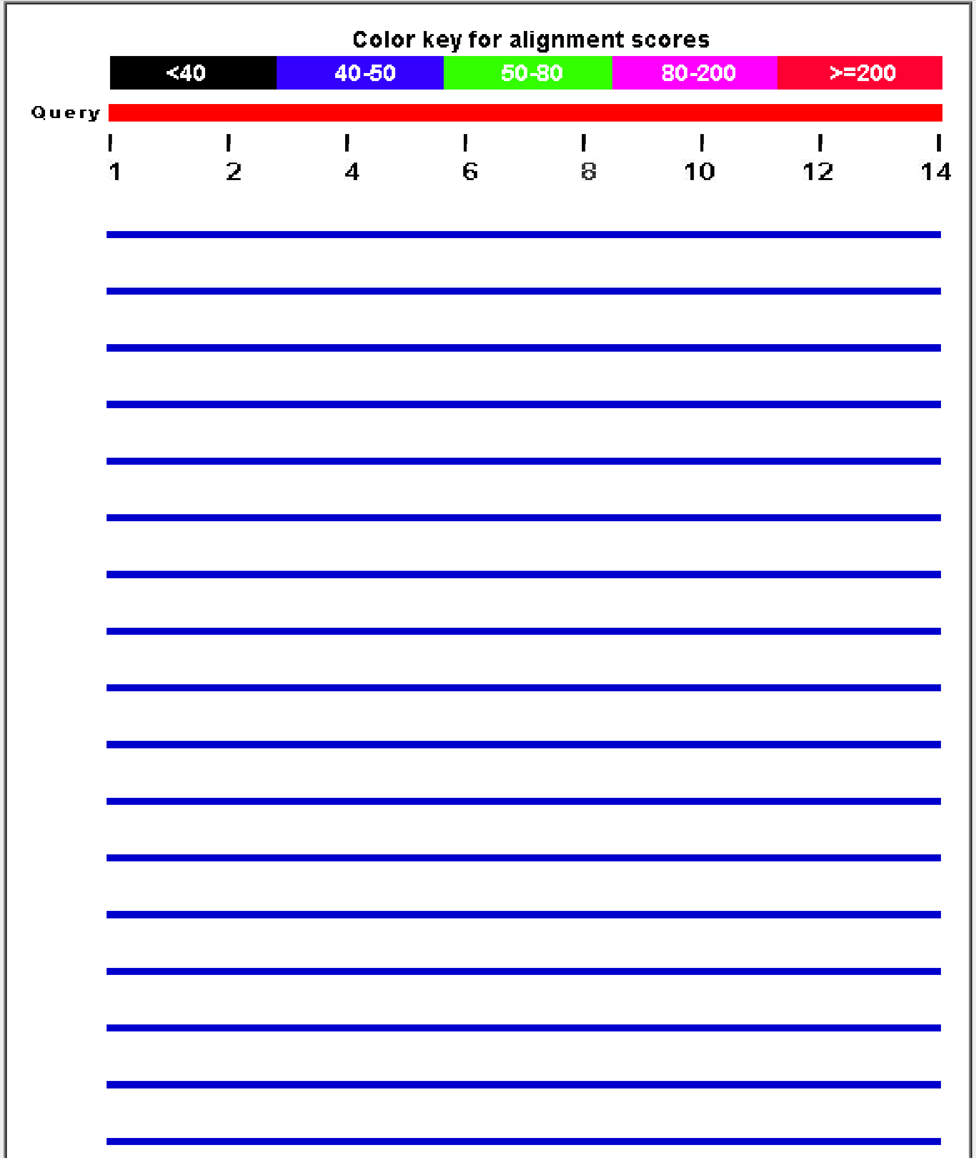
Graphic Summary

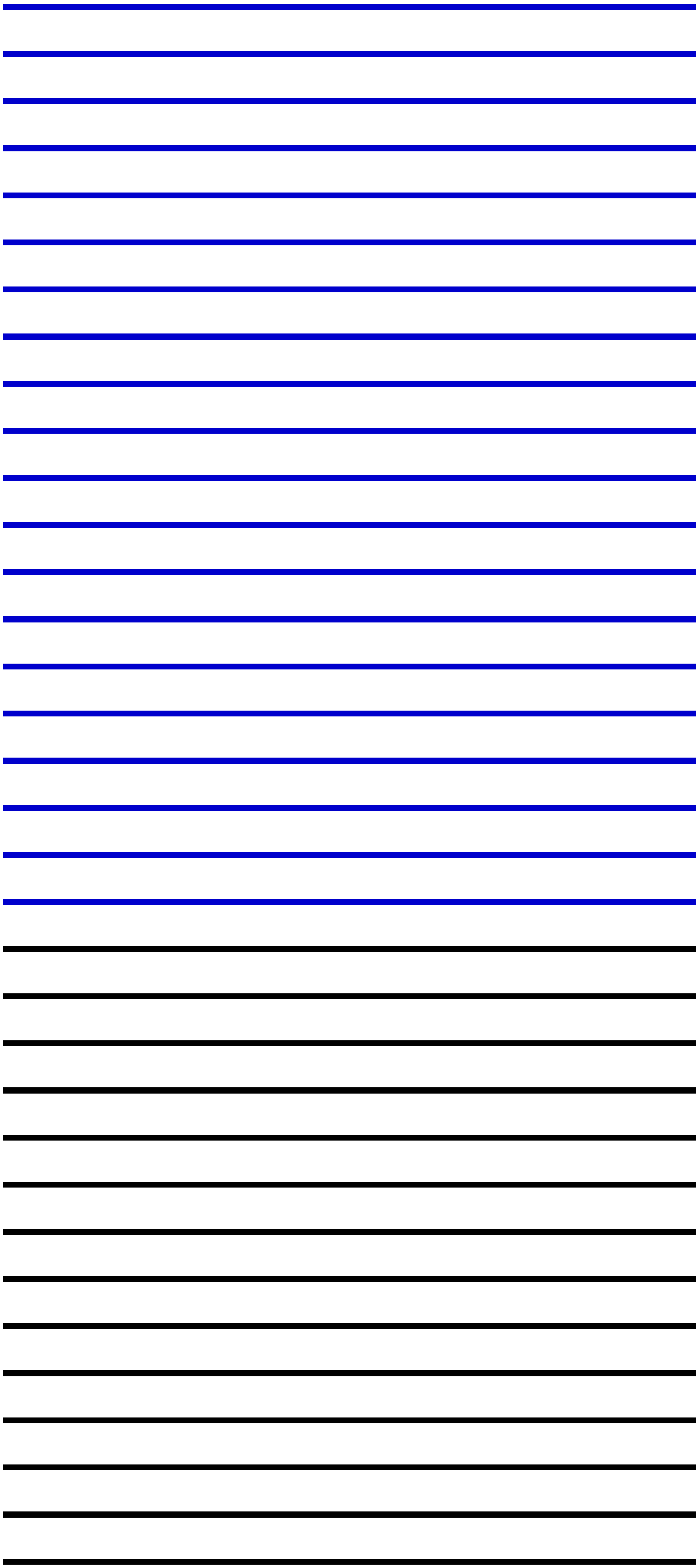
Show Conserved Domains

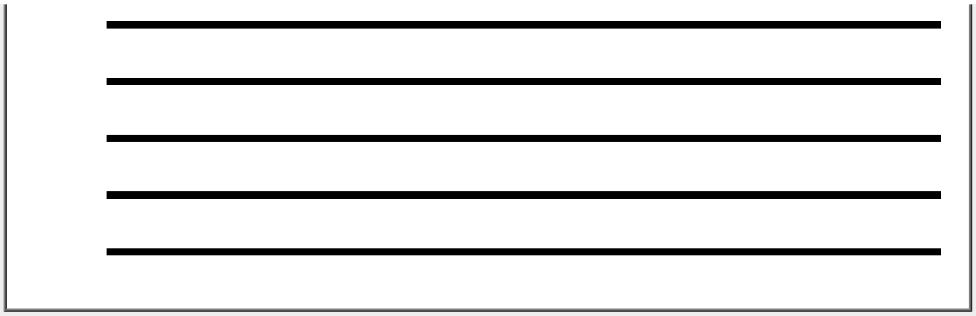
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: coagulation factor XI isoform X5 [Homo sapiens]	44.3	44.3	100%	6e-04	93%	gi|530377344|XP_005262882.1
☐	PREDICTED: coagulation factor XI isoform X4 [Homo sapiens]	44.3	44.3	100%	7e-04	93%	gi|530377342|XP_005262881.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]	44.3	44.3	100%	7e-04	93%	gi|675774870|XP_008975412.1
☐	PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes	44.3	44.3	100%	7e-04	93%	gi|694909938|XP_009446987.1
☐	PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]	44.3	44.3	100%	7e-04	93%	gi|530377340|XP_005262880.1
☐	platelet factor XI [Homo sapiens]	44.3	44.3	100%	7e-04	93%	gi|3258649|AAC24506.1
☐	PREDICTED: coagulation factor XI [Gorilla gorilla gorilla]	44.3	44.3	100%	7e-04	93%	gi|426346208|XP_004040776.1
☐	PREDICTED: coagulation factor XI isoform X3 [Saimiri bolivien	44.3	44.3	100%	7e-04	93%	gi|725582192|XP_010342663.1
☐	PREDICTED: coagulation factor XI isoform X4 [Pan troglodytes	44.3	44.3	100%	7e-04	93%	gi|694909936|XP_009446986.1
☐	PREDICTED: coagulation factor XI isoform X2 [Homo sapiens]	44.3	44.3	100%	7e-04	93%	gi|530377338|XP_005262879.1
☐	PREDICTED: coagulation factor XI isoform X2 [Rhinopithecus r	44.3	44.3	100%	7e-04	93%	gi|724897372|XP_010376291.1
☐	PREDICTED: coagulation factor XI isoform X2 [Papio anubis]	44.3	44.3	100%	7e-04	93%	gi|685544400|XP_009206295.1
☐	PREDICTED: coagulation factor XI isoform X2 [Chlorocebus sa	44.3	44.3	100%	7e-04	93%	gi|635046203|XP_007998683.1
☐	PREDICTED: coagulation factor XI isoform X2 [Macaca fascicu	44.3	44.3	100%	7e-04	93%	gi|544436077|XP_005556541.1
☐	PREDICTED: coagulation factor XI isoform X3 [Pan troglodytes	44.3	44.3	100%	7e-04	93%	gi|694909934|XP_009446985.1
☐	PREDICTED: coagulation factor XI isoform X6 [Homo sapiens]	44.3	44.3	100%	7e-04	93%	gi|578808899|XP_006714200.1
☐	PREDICTED: coagulation factor XI isoform X2 [Saimiri bolivien	44.3	44.3	100%	7e-04	93%	gi|725582190|XP_010342661.1
☐	hypothetical protein EGM_04467 [Macaca fascicularis]	44.3	44.3	100%	7e-04	93%	gi|355750969|EHH55296.1
☐	hypothetical protein EGK_16300 [Macaca mulatta]	44.3	44.3	100%	7e-04	93%	gi|355687768|EHH26352.1
☐	PREDICTED: coagulation factor XI isoform X1 [Rhinopithecus r	44.3	44.3	100%	7e-04	93%	gi|724897369|XP_010376290.1
☐	PREDICTED: coagulation factor XI isoform X1 [Chlorocebus sa	44.3	44.3	100%	7e-04	93%	gi|635046201|XP_007998681.1
☐	PREDICTED: coagulation factor XI [Callithrix jacchus]	44.3	44.3	100%	7e-04	93%	gi|296195030|XP_002745209.1
☐	coagulation factor XI [Homo sapiens]	44.3	44.3	100%	7e-04	93%	gi|180352|AAA51985.1
☐	PREDICTED: coagulation factor XI isoform X1 [Macaca fascicu	44.3	44.3	100%	7e-04	93%	gi|544436075|XP_005556540.1
☐	coagulation factor XI precursor [Homo sapiens]	44.3	44.3	100%	7e-04	93%	gi|4503627|NP_000119.1
☐	PREDICTED: coagulation factor XI isoform X1 [Saimiri bolivien	44.3	44.3	100%	7e-04	93%	gi|725582188|XP_010342660.1
☐	PREDICTED: coagulation factor XI isoform X1 [Papio anubis]	44.3	44.3	100%	7e-04	93%	gi|402871005|XP_003899481.1
☐	PREDICTED: coagulation factor XI [Nomascus leucogenys]	44.3	44.3	100%	7e-04	93%	gi|332244773|XP_003271548.1
☐	PREDICTED: coagulation factor XI [Pongo abelii]	44.3	44.3	100%	7e-04	93%	gi|297674804|XP_002815399.1

☐	PREDICTED: coagulation factor XI isoform X2 [Pan troglodytes	44.3	44.3	100%	7e-04	93%	gi|114597210|XP_001165847.1
☐	PREDICTED: coagulation factor XI isoform X1 [Pan troglodytes	44.3	44.3	100%	7e-04	93%	gi|694909931|XP_009446984.1
☐	PREDICTED: coagulation factor XI isoform X1 [Homo sapiens]	44.3	44.3	100%	7e-04	93%	gi|530377336|XP_005262878.1
☐	PREDICTED: coagulation factor XI-like [Macaca mulatta]	44.3	44.3	100%	7e-04	93%	gi|297293811|XP_001090398.2
☐	Coagulation factor XI [Myotis brandtii]	41.8	41.8	100%	0.004	93%	gi|521037558|EPQ19336.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [	41.8	41.8	100%	0.005	93%	gi|554587005|XP_005884913.1
☐	PREDICTED: coagulation factor XI [Tarsius syrichta]	40.1	40.1	100%	0.017	86%	gi|640821392|XP_008067645.1
☐	PREDICTED: coagulation factor XI [Otolemur garnettii]	40.1	40.1	100%	0.017	86%	gi|395840032|XP_003792872.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [	39.2	39.2	100%	0.032	86%	gi|586521035|XP_006926977.1
☐	PREDICTED: coagulation factor XI [Camelus bactrianus]	39.2	39.2	100%	0.033	86%	gi|743715881|XP_010951577.1
☐	PREDICTED: coagulation factor XI [Vicugna pacos]	39.2	39.2	100%	0.033	86%	gi|560951202|XP_006198143.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [	39.2	39.2	100%	0.033	86%	gi|744611375|XP_010994033.1
☐	coagulation factor XI precursor [Canis lupus familiaris]	39.2	39.2	100%	0.033	86%	gi|205361194|NP_001128595.1
☐	PREDICTED: coagulation factor XI isoform X2 [Leptonychotes	39.2	39.2	100%	0.033	86%	gi|585180453|XP_006741890.1
☐	PREDICTED: coagulation factor XI [Sorex araneus]	39.2	39.2	100%	0.033	86%	gi|505830321|XP_004610458.1
☐	PREDICTED: coagulation factor XI isoform 3 [Odobenus rosma	39.2	39.2	100%	0.033	86%	gi|472396395|XP_004417424.1
☐	PREDICTED: coagulation factor XI-like [Ailuropoda melanoleuc	39.2	39.2	100%	0.033	86%	gi|301776062|XP_002923450.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [	39.2	39.2	100%	0.033	86%	gi|591347751|XP_007099050.1
☐	PREDICTED: coagulation factor XI [Camelus ferus]	39.2	39.2	100%	0.033	86%	gi|560904135|XP_006178431.1
☐	PREDICTED: coagulation factor XI isoform X2 [Canis lupus fam	39.2	39.2	100%	0.033	86%	gi|545526400|XP_005629983.1
☐	PREDICTED: coagulation factor XI [Felis catus]	39.2	39.2	100%	0.033	86%	gi|410956035|XP_003984650.1
☐	PREDICTED: coagulation factor XI isoform X3 [Leptonychotes	39.2	39.2	100%	0.033	86%	gi|585180455|XP_006741891.1
☐	PREDICTED: coagulation factor XI isoform 2 [Odobenus rosma	39.2	39.2	100%	0.033	86%	gi|472396393|XP_004417423.1
☐	PREDICTED: coagulation factor XI isoform X1 [Leptonychotes	39.2	39.2	100%	0.033	86%	gi|585180451|XP_006741889.1
☐	PREDICTED: coagulation factor XI isoform X1 [Canis lupus fam	39.2	39.2	100%	0.033	86%	gi|545526398|XP_005629982.1
☐	PREDICTED: coagulation factor XI [Mustela putorius furo]	39.2	39.2	100%	0.033	86%	gi|511876760|XP_004758357.1
☐	PREDICTED: coagulation factor XI isoform 1 [Odobenus rosma	39.2	39.2	100%	0.033	86%	gi|472396391|XP_004417422.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [	39.2	39.2	100%	0.034	86%	gi|671035736|XP_008708722.1
☐	PREDICTED: coagulation factor XI [Octodon degus]	37.5	37.5	100%	0.12	79%	gi|507682719|XP_004639867.1
☐	PREDICTED: plasma kallikrein isoform X2 [Capra hircus]	36.7	36.7	100%	0.22	86%	gi|548524193|XP_005698801.1
☐	PREDICTED: plasma kallikrein [Bos mutus]	36.7	36.7	100%	0.23	86%	gi|555974157|XP_005899073.1
☐	PREDICTED: plasma kallikrein [Sorex araneus]	36.7	36.7	100%	0.23	86%	gi|505830323|XP_004610459.1
☐	Plasma kallikrein [Bos mutus]	36.7	36.7	100%	0.23	86%	gi|440903405|ELR54069.1
☐	PREDICTED: plasma kallikrein [Bison bison bison]	36.7	36.7	100%	0.23	86%	gi|742100671|XP_010834112.1
☐	plasma kallikrein precursor [Bos taurus]	36.7	36.7	100%	0.23	86%	gi|114052314|NP_001039817.1
☐	PREDICTED: plasma kallikrein [Bubalus bubalis]	36.7	36.7	100%	0.23	86%	gi|594073050|XP_006060351.1
☐	PREDICTED: plasma kallikrein [Pantholops hodgsonii]	36.7	36.7	100%	0.23	86%	gi|556754531|XP_005972630.1
☐	PREDICTED: plasma kallikrein isoform X1 [Capra hircus]	36.7	36.7	100%	0.23	86%	gi|548524191|XP_005698800.1
☐	PREDICTED: plasma kallikrein [Ovis aries]	36.7	36.7	100%	0.23	86%	gi|426256278|XP_004021768.1
☐	PREDICTED: plasma kallikrein [Cavia porcellus]	36.7	36.7	100%	0.23	86%	gi|348566841|XP_003469210.1
☐	PREDICTED: plasma kallikrein isoform X2 [Fukomys damarens	36.7	36.7	100%	0.23	86%	gi|731206513|XP_010618084.1
☐	PREDICTED: plasma kallikrein isoform X1 [Fukomys damarens	36.7	36.7	100%	0.23	86%	gi|731206510|XP_010618083.1
☐	Coagulation factor XI [Heterocephalus glaber]	35.8	35.8	100%	0.42	79%	gi|351708043|EHB10962.1
☐	PREDICTED: coagulation factor XI isoform X4 [Heterocephalus	35.8	35.8	100%	0.42	79%	gi|512982227|XP_004853110.1
☐	PREDICTED: coagulation factor XI isoform X3 [Heterocephalus	35.8	35.8	100%	0.42	79%	gi|512892520|XP_004897310.1

☐	PREDICTED: coagulation factor XI [Dasypus novemcinctus]	35.8	35.8	100%	0.43	79%	gi|488532217|XP_004457855.1
☐	PREDICTED: coagulation factor XI isoform X1 [Chinchilla lanig	35.8	35.8	100%	0.43	79%	gi|533115750|XP_005373485.1
☐	PREDICTED: coagulation factor XI isoform X2 [Heterocephalus	35.8	35.8	100%	0.43	79%	gi|512982223|XP_004853108.1
☐	PREDICTED: coagulation factor XI isoform X1 [Heterocephalus	35.8	35.8	100%	0.43	79%	gi|512892512|XP_004897308.1
☐	PREDICTED: coagulation factor XI isoform X1 [Heterocephalus	35.8	35.8	100%	0.43	79%	gi|512982221|XP_004853107.1
☐	PREDICTED: coagulation factor XI isoform X2 [Heterocephalus	35.8	35.8	100%	0.43	79%	gi|512892516|XP_004897309.1
☐	PREDICTED: coagulation factor XI [Cavia porcellus]	35.8	35.8	100%	0.43	79%	gi|348566839|XP_003469209.1
☐	PREDICTED: coagulation factor XI [Ictidomys tridecemlineatus]	35.4	35.4	100%	0.59	79%	gi|532087072|XP_005329248.1
☐	PREDICTED: coagulation factor XI [Tupaia chinensis]	35.0	35.0	100%	0.80	79%	gi|562864607|XP_006160530.1
☐	PREDICTED: coagulation factor XI [Chrysochloris asiatica]	34.6	34.6	85%	1.1	83%	gi|586451182|XP_006834518.1
☐	PREDICTED: plasma kallikrein [Mesocricetus auratus]	34.6	34.6	100%	1.1	79%	gi|524924656|XP_005066575.1
☐	prekallikrein [Canis lupus familiaris]	34.1	34.1	71%	1.4	100%	gi|555289929|BAO03248.1
☐	F11 protein [Bos taurus]	34.1	34.1	100%	1.5	79%	gi|86821856|AAI05428.1
☐	coagulation factor XI [Bos taurus]	34.1	34.1	100%	1.5	79%	gi|45861248|AAS78506.1
☐	PREDICTED: coagulation factor XI isoform X3 [Fukomys dama	34.1	34.1	100%	1.5	79%	gi|731206524|XP_010618089.1
☐	blood coagulation factor XI [Bos taurus]	34.1	34.1	100%	1.5	79%	gi|45758733|AAS76646.1
☐	PREDICTED: coagulation factor XI isoform X2 [Fukomys dama	34.1	34.1	100%	1.5	79%	gi|731206521|XP_010618088.1
☐	PREDICTED: coagulation factor XI [Equus caballus]	34.1	34.1	100%	1.5	79%	gi|149742758|XP_001490330.1
☐	PREDICTED: coagulation factor XI isoform 2 [Ceratotherium si	34.1	34.1	100%	1.5	79%	gi|478509096|XP_004428828.1
☐	PREDICTED: coagulation factor XI [Bison bison bison]	34.1	34.1	100%	1.5	79%	gi|742100675|XP_010834113.1
☐	PREDICTED: coagulation factor XI isoform X1 [Fukomys dama	34.1	34.1	100%	1.5	79%	gi|731206515|XP_010618085.1
☐	PREDICTED: coagulation factor XI [Nannospalax galili]	34.1	34.1	100%	1.5	79%	gi|674087872|XP_008851827.1
☐	PREDICTED: coagulation factor XI [Equus przewalskii]	34.1	34.1	100%	1.5	79%	gi|664778079|XP_008508352.1
☐	PREDICTED: coagulation factor XI [Bubalus bubalis]	34.1	34.1	100%	1.5	79%	gi|594073052|XP_006060352.1
☐	PREDICTED: coagulation factor XI isoform 1 [Ceratotherium si	34.1	34.1	100%	1.5	79%	gi|478509094|XP_004428827.1
☐	PREDICTED: coagulation factor XI [Bos mutus]	34.1	34.1	100%	1.5	79%	gi|555974149|XP_005899069.1

⊟ Alignments

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PREDICTED: coagulation factor XI isoform X5 [Homo sapiens]

Sequence ID: gi|530377344|ref|XP_005262882.1| **Length:** 395 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 79 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	6e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1   KDSVTETLPRVDRT  14
           KDSVTETLPRV+RT
Sbjct  79  KDSVTETLPRVNRT  92
```

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PREDICTED: coagulation factor XI isoform X4 [Homo sapiens]

Sequence ID: gi|530377342|ref|XP_005262881.1| **Length:** 534 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 79 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	7e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1   KDSVTETLPRVDRT  14
           KDSVTETLPRV+RT
Sbjct  79  KDSVTETLPRVNRT  92
```

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PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]

Sequence ID: gi|675774870|ref|XP_008975412.1| **Length:** 535 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 79 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	7e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1   KDSVTETLPRVDRT  14
           KDSVTETLPRV+RT
Sbjct  79  KDSVTETLPRVNRT  92
```

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PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes]

Sequence ID: gi|694909938|ref|XP_009446987.1| **Length:** 536 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 79 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	7e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1   KDSVTETLPRVDRT  14
           KDSVTETLPRV+RT
Sbjct  79  KDSVTETLPRVNRT  92
```

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PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]

Sequence ID: gi|530377340|ref|XP_005262880.1| **Length:** 536 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 79 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	7e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1   KDSVTETLPRVDRT  14
           KDSVTETLPRV+RT
Sbjct  79  KDSVTETLPRVNRT  92
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download

How to read this page Blast report description

F11_KDSVTETLPRVNRT_NonMod

RID	B94UZJ3W01R (Expires on 01-14 10:39 am)
Query ID	lcl|195779
Description	None
Molecule type	amino acid
Query Length	14

Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

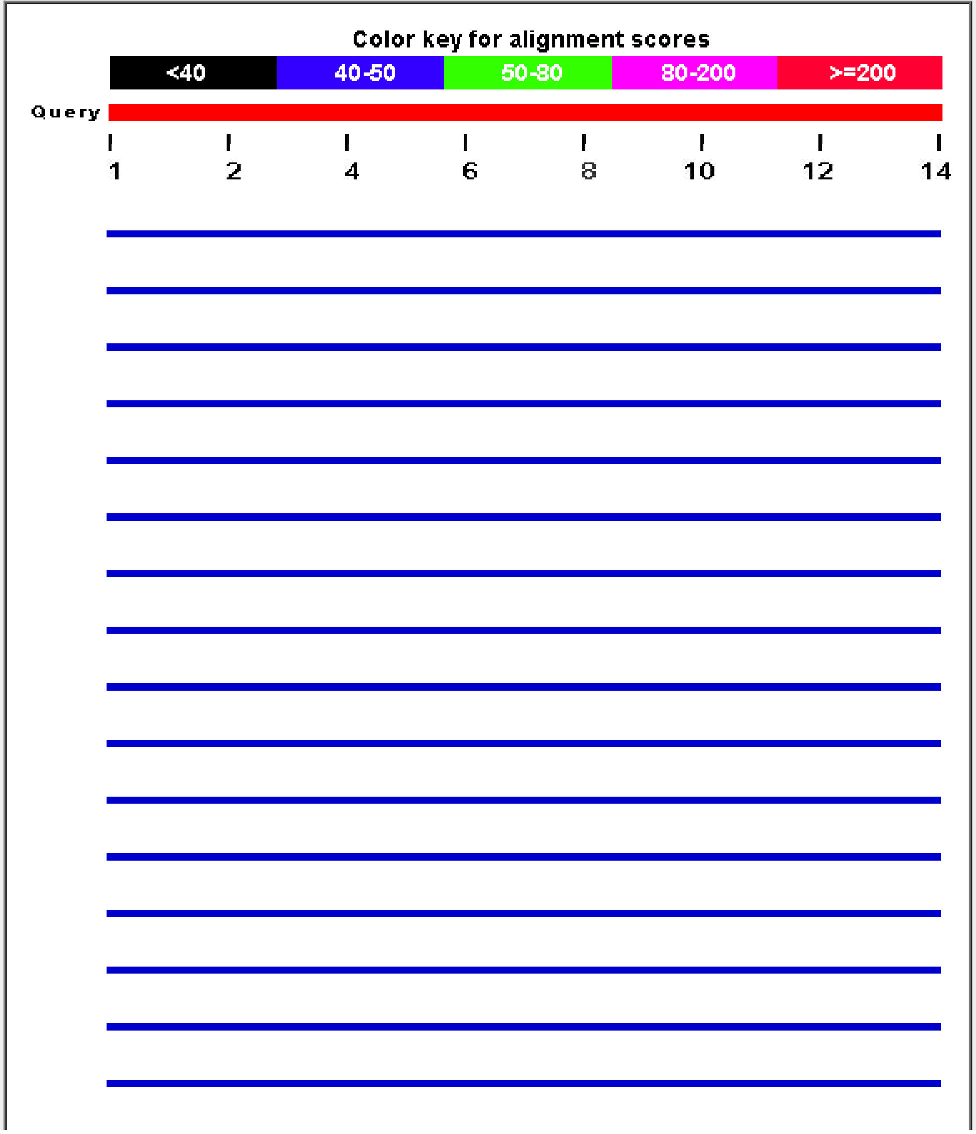
Graphic Summary

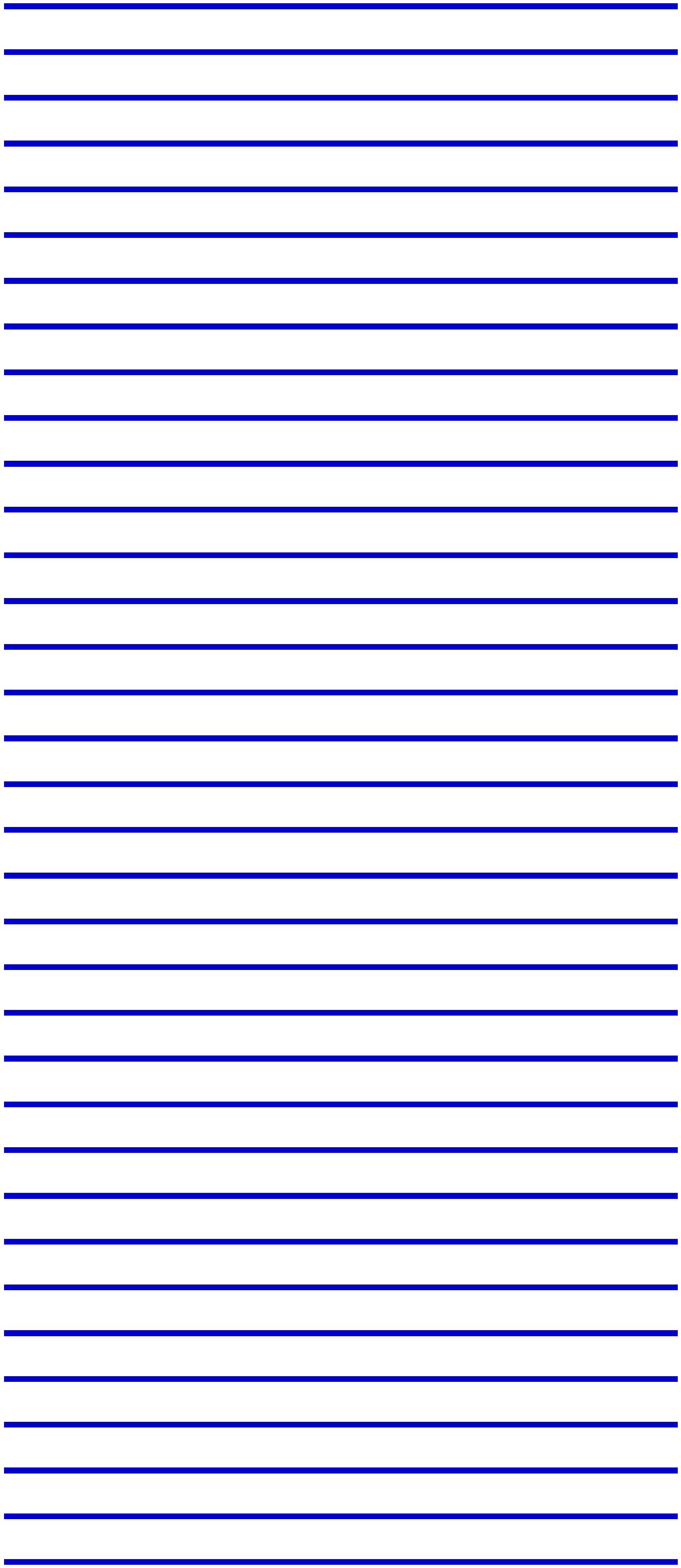
Show Conserved Domains

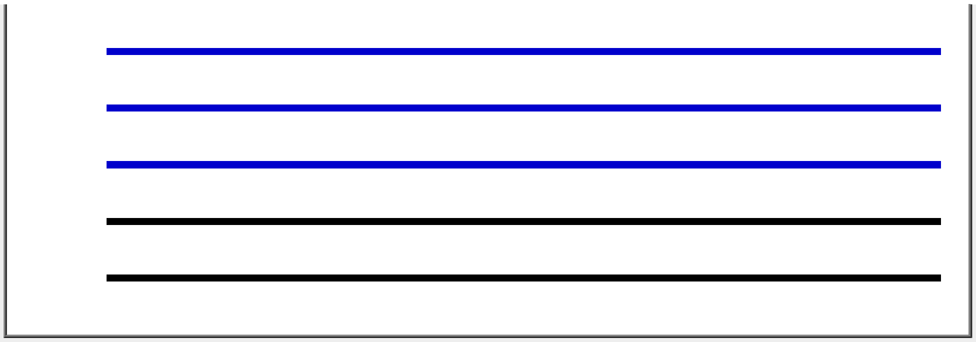
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: coagulation factor XI isoform X5 [Homo sapiens]	46.9	46.9	100%	9e-05	100%	gi|530377344|XP_005262882.1
☐	PREDICTED: coagulation factor XI isoform X4 [Homo sapiens]	46.9	46.9	100%	9e-05	100%	gi|530377342|XP_005262881.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]	46.9	46.9	100%	9e-05	100%	gi|675774870|XP_008975412.1
☐	PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes]	46.9	46.9	100%	9e-05	100%	gi|694909938|XP_009446987.1
☐	PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]	46.9	46.9	100%	9e-05	100%	gi|530377340|XP_005262880.1
☐	platelet factor XI [Homo sapiens]	46.9	46.9	100%	9e-05	100%	gi|3258649|AAC24506.1
☐	PREDICTED: coagulation factor XI [Gorilla gorilla gorilla]	46.9	46.9	100%	9e-05	100%	gi|426346208|XP_004040776.1
☐	PREDICTED: coagulation factor XI isoform X3 [Saimiri boliviensis b	46.9	46.9	100%	9e-05	100%	gi|725582192|XP_010342663.1
☐	PREDICTED: coagulation factor XI isoform X4 [Pan troglodytes]	46.9	46.9	100%	9e-05	100%	gi|694909936|XP_009446986.1
☐	PREDICTED: coagulation factor XI isoform X2 [Homo sapiens]	46.9	46.9	100%	9e-05	100%	gi|530377338|XP_005262879.1
☐	PREDICTED: coagulation factor XI isoform X2 [Rhinopithecus roxel	46.9	46.9	100%	9e-05	100%	gi|724897372|XP_010376291.1
☐	PREDICTED: coagulation factor XI isoform X2 [Papio anubis]	46.9	46.9	100%	9e-05	100%	gi|685544400|XP_009206295.1
☐	PREDICTED: coagulation factor XI isoform X2 [Chlorocebus sabae	46.9	46.9	100%	9e-05	100%	gi|635046203|XP_007998683.1
☐	PREDICTED: coagulation factor XI isoform X2 [Macaca fascicularis	46.9	46.9	100%	9e-05	100%	gi|544436077|XP_005556541.1
☐	PREDICTED: coagulation factor XI isoform X3 [Pan troglodytes]	46.9	46.9	100%	9e-05	100%	gi|694909934|XP_009446985.1
☐	PREDICTED: coagulation factor XI isoform X6 [Homo sapiens]	46.9	46.9	100%	9e-05	100%	gi|578808899|XP_006714200.1
☐	PREDICTED: coagulation factor XI isoform X2 [Saimiri boliviensis b	46.9	46.9	100%	9e-05	100%	gi|725582190|XP_010342661.1
☐	hypothetical protein EGM_04467 [Macaca fascicularis]	46.9	46.9	100%	9e-05	100%	gi|355750969|EHH55296.1
☐	hypothetical protein EGK_16300 [Macaca mulatta]	46.9	46.9	100%	9e-05	100%	gi|355687768|EHH26352.1
☐	PREDICTED: coagulation factor XI isoform X1 [Rhinopithecus roxel	46.9	46.9	100%	9e-05	100%	gi|724897369|XP_010376290.1
☐	PREDICTED: coagulation factor XI isoform X1 [Chlorocebus sabae	46.9	46.9	100%	9e-05	100%	gi|635046201|XP_007998681.1
☐	PREDICTED: coagulation factor XI [Callithrix jacchus]	46.9	46.9	100%	9e-05	100%	gi|296195030|XP_002745209.1
☐	coagulation factor XI [Homo sapiens]	46.9	46.9	100%	9e-05	100%	gi|180352|AAA51985.1
☐	PREDICTED: coagulation factor XI isoform X1 [Macaca fascicularis	46.9	46.9	100%	9e-05	100%	gi|544436075|XP_005556540.1
☐	coagulation factor XI precursor [Homo sapiens]	46.9	46.9	100%	9e-05	100%	gi|4503627|NP_000119.1
☐	PREDICTED: coagulation factor XI isoform X1 [Saimiri boliviensis b	46.9	46.9	100%	9e-05	100%	gi|725582188|XP_010342660.1
☐	PREDICTED: coagulation factor XI isoform X1 [Papio anubis]	46.9	46.9	100%	9e-05	100%	gi|402871005|XP_003899481.1
☐	PREDICTED: coagulation factor XI [Nomascus leucogenys]	46.9	46.9	100%	9e-05	100%	gi|332244773|XP_003271548.1
☐							

	PREDICTED: coagulation factor XI [Pongo abelii]	46.9	46.9	100%	9e-05	100%	gi|297674804|XP_002815399.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan troglodytes]	46.9	46.9	100%	9e-05	100%	gi|114597210|XP_001165847.1
☐	PREDICTED: coagulation factor XI isoform X1 [Pan troglodytes]	46.9	46.9	100%	9e-05	100%	gi|694909931|XP_009446984.1
☐	PREDICTED: coagulation factor XI isoform X1 [Homo sapiens]	46.9	46.9	100%	9e-05	100%	gi|530377336|XP_005262878.1
☐	PREDICTED: coagulation factor XI-like [Macaca mulatta]	46.9	46.9	100%	9e-05	100%	gi|297293811|XP_001090398.2
☐	PREDICTED: coagulation factor XI [Tarsius syrichta]	42.6	42.6	100%	0.002	93%	gi|640821392|XP_008067645.1
☐	PREDICTED: coagulation factor XI [Otolemur garnettii]	42.6	42.6	100%	0.002	93%	gi|395840032|XP_003792872.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Pte	41.8	41.8	100%	0.004	93%	gi|586521035|XP_006926977.1
☐	PREDICTED: coagulation factor XI [Vicugna pacos]	41.8	41.8	100%	0.005	93%	gi|560951202|XP_006198143.1
☐	coagulation factor XI precursor [Canis lupus familiaris]	41.8	41.8	100%	0.005	93%	gi|205361194|NP_001128595.1
☐	PREDICTED: coagulation factor XI isoform X2 [Leptonychotes wed	41.8	41.8	100%	0.005	93%	gi|585180453|XP_006741890.1
☐	PREDICTED: coagulation factor XI [Sorex araneus]	41.8	41.8	100%	0.005	93%	gi|505830321|XP_004610458.1
☐	PREDICTED: coagulation factor XI isoform 3 [Odobenus rosmarus	41.8	41.8	100%	0.005	93%	gi|472396395|XP_004417424.1
☐	PREDICTED: coagulation factor XI-like [Ailuropoda melanoleuca]	41.8	41.8	100%	0.005	93%	gi|301776062|XP_002923450.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Pan	41.8	41.8	100%	0.005	93%	gi|591347751|XP_007099050.1
☐	PREDICTED: coagulation factor XI [Camelus ferus]	41.8	41.8	100%	0.005	93%	gi|560904135|XP_006178431.1
☐	PREDICTED: coagulation factor XI isoform X2 [Canis lupus familiar	41.8	41.8	100%	0.005	93%	gi|545526400|XP_005629983.1
☐	PREDICTED: coagulation factor XI [Felis catus]	41.8	41.8	100%	0.005	93%	gi|410956035|XP_003984650.1
☐	PREDICTED: coagulation factor XI isoform X3 [Leptonychotes wed	41.8	41.8	100%	0.005	93%	gi|585180455|XP_006741891.1
☐	PREDICTED: coagulation factor XI isoform 2 [Odobenus rosmarus	41.8	41.8	100%	0.005	93%	gi|472396393|XP_004417423.1
☐	PREDICTED: coagulation factor XI isoform X1 [Leptonychotes wed	41.8	41.8	100%	0.005	93%	gi|585180451|XP_006741889.1
☐	PREDICTED: coagulation factor XI isoform X1 [Canis lupus familiar	41.8	41.8	100%	0.005	93%	gi|545526398|XP_005629982.1
☐	PREDICTED: coagulation factor XI [Mustela putorius furo]	41.8	41.8	100%	0.005	93%	gi|511876760|XP_004758357.1
☐	PREDICTED: coagulation factor XI isoform 1 [Odobenus rosmarus	41.8	41.8	100%	0.005	93%	gi|472396391|XP_004417422.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Urs	41.8	41.8	100%	0.005	93%	gi|671035736|XP_008708722.1
☐	PREDICTED: coagulation factor XI [Octodon degus]	40.1	40.1	100%	0.017	86%	gi|507682719|XP_004639867.1
☐	Coagulation factor XI [Myotis brandtii]	39.2	39.2	100%	0.029	86%	gi|521037558|EPQ19336.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [My	39.2	39.2	100%	0.031	86%	gi|554587005|XP_005884913.1
☐	PREDICTED: plasma kallikrein isoform X1 [Bos taurus]	38.4	38.4	100%	0.059	86%	gi|529009741|XP_005226045.1
☐	PREDICTED: plasma kallikrein isoform X2 [Capra hircus]	38.4	38.4	100%	0.059	86%	gi|548524193|XP_005698801.1
☐	Coagulation factor XI [Heterocephalus glaber]	38.4	38.4	100%	0.059	86%	gi|351708043|EHB10962.1
☐	PREDICTED: coagulation factor XI isoform X4 [Heterocephalus gla	38.4	38.4	100%	0.059	86%	gi|512982227|XP_004853110.1
☐	PREDICTED: coagulation factor XI isoform X3 [Heterocephalus gla	38.4	38.4	100%	0.059	86%	gi|512892520|XP_004897310.1
☐	PREDICTED: plasma kallikrein [Bos mutus]	38.4	38.4	100%	0.060	86%	gi|555974157|XP_005899073.1
☐	PREDICTED: coagulation factor XI [Dasypus novemcinctus]	38.4	38.4	100%	0.060	86%	gi|488532217|XP_004457855.1
☐	PREDICTED: coagulation factor XI isoform X1 [Chinchilla lanigera]	38.4	38.4	100%	0.060	86%	gi|533115750|XP_005373485.1
☐	PREDICTED: coagulation factor XI isoform X2 [Heterocephalus gla	38.4	38.4	100%	0.060	86%	gi|512982223|XP_004853108.1
☐	PREDICTED: coagulation factor XI isoform X1 [Heterocephalus gla	38.4	38.4	100%	0.060	86%	gi|512892512|XP_004897308.1
☐	PREDICTED: coagulation factor XI isoform X1 [Heterocephalus gla	38.4	38.4	100%	0.060	86%	gi|512982221|XP_004853107.1
☐	PREDICTED: coagulation factor XI isoform X2 [Heterocephalus gla	38.4	38.4	100%	0.060	86%	gi|512892516|XP_004897309.1
☐	PREDICTED: plasma kallikrein [Sorex araneus]	38.4	38.4	100%	0.060	86%	gi|505830323|XP_004610459.1
☐	PREDICTED: coagulation factor XI [Cavia porcellus]	38.4	38.4	100%	0.060	86%	gi|348566839|XP_003469209.1
☐	Plasma kallikrein [Bos mutus]	38.4	38.4	100%	0.060	86%	gi|440903405|ELR54069.1
☐	plasma kallikrein precursor [Bos taurus]	38.4	38.4	100%	0.060	86%	gi|114052314|NP_001039817.1
☐	PREDICTED: plasma kallikrein [Bubalus bubalis]	38.4	38.4	100%	0.060	86%	gi|594073050|XP_006060351.1

☐	PREDICTED: plasma kallikrein [Pantholops hodgsonii]	38.4	38.4	100%	0.060	86%	gi|556754531|XP_005972630.1
☐	PREDICTED: plasma kallikrein isoform X1 [Capra hircus]	38.4	38.4	100%	0.060	86%	gi|548524191|XP_005698800.1
☐	PREDICTED: plasma kallikrein [Ovis aries]	38.4	38.4	100%	0.060	86%	gi|426256278|XP_004021768.1
☐	PREDICTED: plasma kallikrein [Cavia porcellus]	38.4	38.4	100%	0.060	86%	gi|348566841|XP_003469210.1
☐	PREDICTED: plasma kallikrein isoform X2 [Fukomys damarensis]	38.4	38.4	100%	0.060	86%	gi|731206513|XP_010618084.1
☐	PREDICTED: plasma kallikrein isoform X1 [Fukomys damarensis]	38.4	38.4	100%	0.060	86%	gi|731206510|XP_010618083.1
☐	PREDICTED: coagulation factor XI [Ictidomys tridecemlineatus]	38.0	38.0	100%	0.082	86%	gi|532087072|XP_005329248.1
☐	PREDICTED: coagulation factor XI [Tupaia chinensis]	37.5	37.5	100%	0.11	86%	gi|562864607|XP_006160530.1
☐	PREDICTED: coagulation factor XI [Chrysochloris asiatica]	37.1	37.1	85%	0.16	92%	gi|586451182|XP_006834518.1
☐	F11 protein [Bos taurus]	36.7	36.7	100%	0.21	86%	gi|86821856|AAI05428.1
☐	coagulation factor XI [Bos taurus]	36.7	36.7	100%	0.21	86%	gi|45861248|AAS78506.1
☐	PREDICTED: coagulation factor XI isoform X3 [Fukomys damarens	36.7	36.7	100%	0.21	86%	gi|731206524|XP_010618089.1
☐	blood coagulation factor XI [Bos taurus]	36.7	36.7	100%	0.21	86%	gi|45758733|AAS76646.1
☐	PREDICTED: coagulation factor XI isoform X2 [Fukomys damarens	36.7	36.7	100%	0.21	86%	gi|731206521|XP_010618088.1
☐	PREDICTED: coagulation factor XI [Equus caballus]	36.7	36.7	100%	0.21	86%	gi|149742758|XP_001490330.1
☐	PREDICTED: coagulation factor XI isoform 2 [Ceratotherium simum	36.7	36.7	100%	0.21	86%	gi|478509096|XP_004428828.1
☐	PREDICTED: coagulation factor XI isoform X1 [Fukomys damarens	36.7	36.7	100%	0.21	86%	gi|731206515|XP_010618085.1
☐	PREDICTED: coagulation factor XI [Nannospalax galili]	36.7	36.7	100%	0.21	86%	gi|674087872|XP_008851827.1
☐	PREDICTED: coagulation factor XI [Equus przewalskii]	36.7	36.7	100%	0.21	86%	gi|664778079|XP_008508352.1
☐	PREDICTED: coagulation factor XI [Bubalus bubalis]	36.7	36.7	100%	0.21	86%	gi|594073052|XP_006060352.1
☐	PREDICTED: coagulation factor XI isoform 1 [Ceratotherium simum	36.7	36.7	100%	0.21	86%	gi|478509094|XP_004428827.1
☐	PREDICTED: coagulation factor XI [Bos mutus]	36.7	36.7	100%	0.21	86%	gi|555974149|XP_005899069.1
☐	coagulation factor XI precursor [Bos taurus]	36.7	36.7	100%	0.21	86%	gi|56710319|NP_001008665.1
☐	TPA: coagulation factor XI precursor [Bos taurus]	36.7	36.7	100%	0.21	86%	gi|296472409|DAA14524.1
☐	PREDICTED: coagulation factor XI [Mesocricetus auratus]	36.7	36.7	100%	0.21	86%	gi|524924928|XP_005066710.1
☐	PREDICTED: coagulation factor XI [Cricetulus griseus]	36.7	36.7	100%	0.21	86%	gi|354490732|XP_003507510.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Per	36.7	36.7	100%	0.22	86%	gi|589915357|XP_006971011.1

Alignments

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PREDICTED: coagulation factor XI isoform X5 [Homo sapiens]

Sequence ID: gi|530377344|ref|XP_005262882.1| **Length:** 395 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 79 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	9e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1   KDSVTETLPRVNRT  14
           KDSVTETLPRVNRT
Sbjct  79  KDSVTETLPRVNRT  92
```

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PREDICTED: coagulation factor XI isoform X4 [Homo sapiens]

Sequence ID: gi|530377342|ref|XP_005262881.1| **Length:** 534 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 79 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	9e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1   KDSVTETLPRVNRT  14
```

```
              KDSVTETLPRVNRT
Sbjct  79   KDSVTETLPRVNRT  92
```

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PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]

Sequence ID: gi|675774870|ref|XP_008975412.1| **Length:** 535 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 79 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	9e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KDSVTETLPRVNRT  14
              KDSVTETLPRVNRT
Sbjct  79   KDSVTETLPRVNRT  92
```

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PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes]

Sequence ID: gi|694909938|ref|XP_009446987.1| **Length:** 536 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 79 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	9e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KDSVTETLPRVNRT  14
              KDSVTETLPRVNRT
Sbjct  79   KDSVTETLPRVNRT  92
```

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PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]

Sequence ID: gi|530377340|ref|XP_005262880.1| **Length:** 536 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 79 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	9e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KDSVTETLPRVNRT  14
              KDSVTETLPRVNRT
Sbjct  79   KDSVTETLPRVNRT  92
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - BTH21AWC016

Your search parameters were adjusted to search for a short input sequence.

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F11_KGINYDSSVAKS_Mod

RID BTH21AWC016 (Expires on 01-20 15:45 pm)

Query ID lcl|28637
Description None
Molecule type amino acid
Query Length 12

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

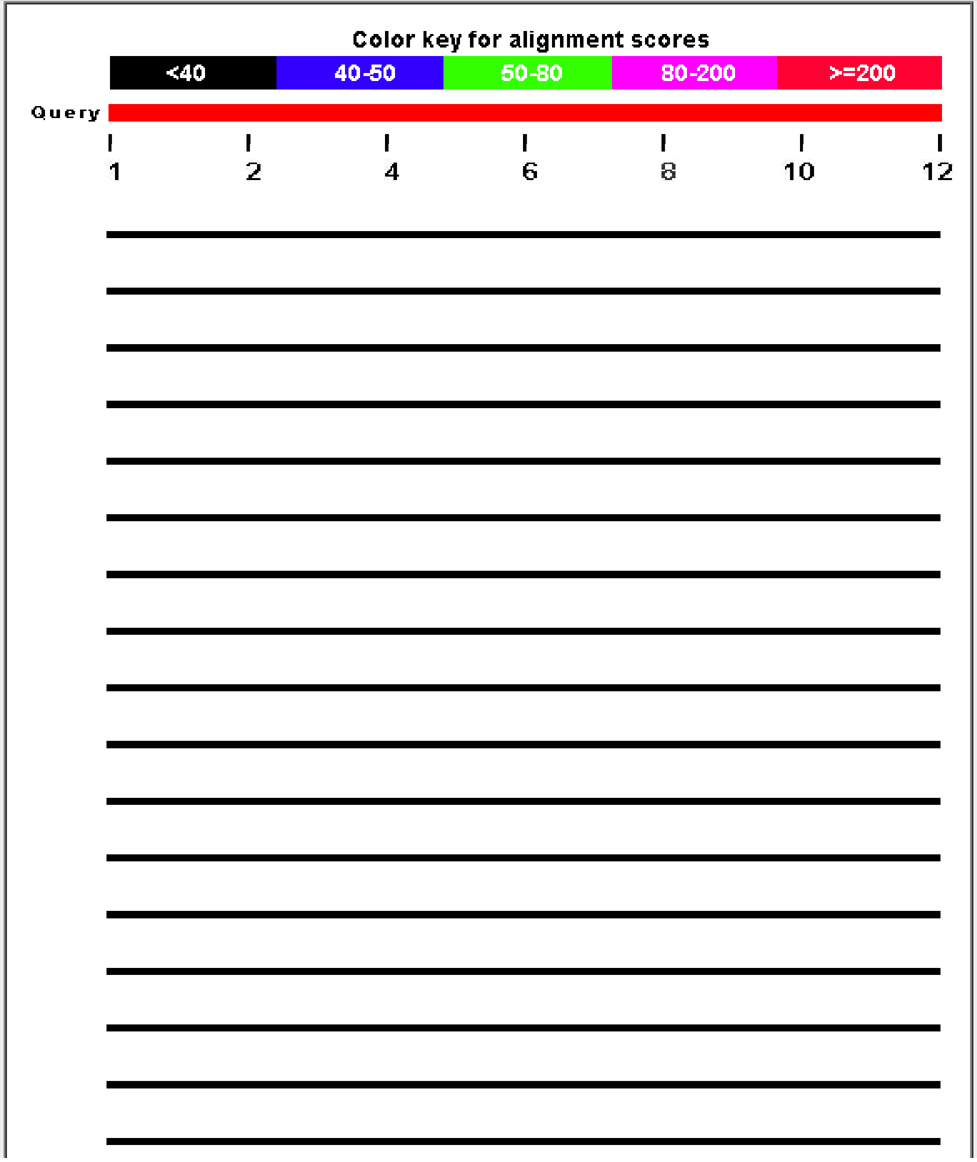
Graphic Summary

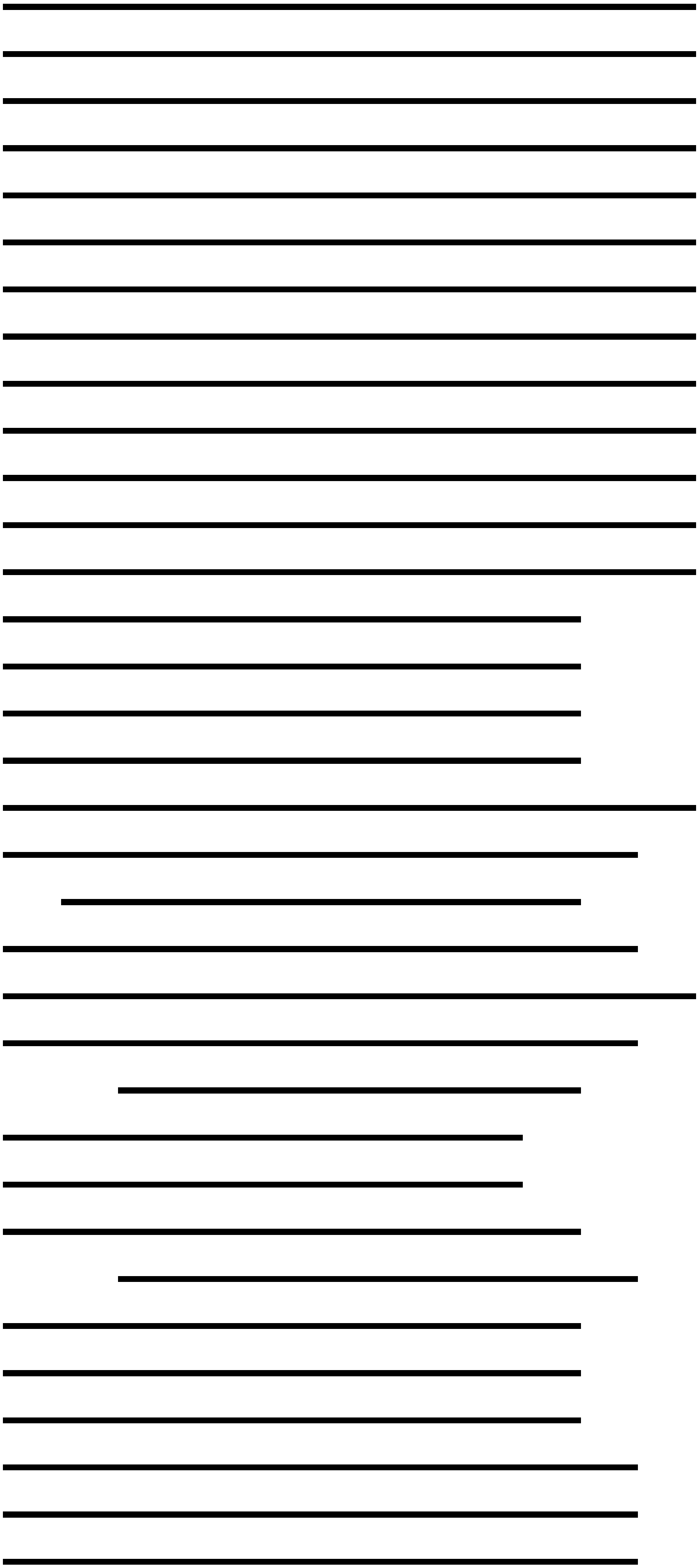
Show Conserved Domains

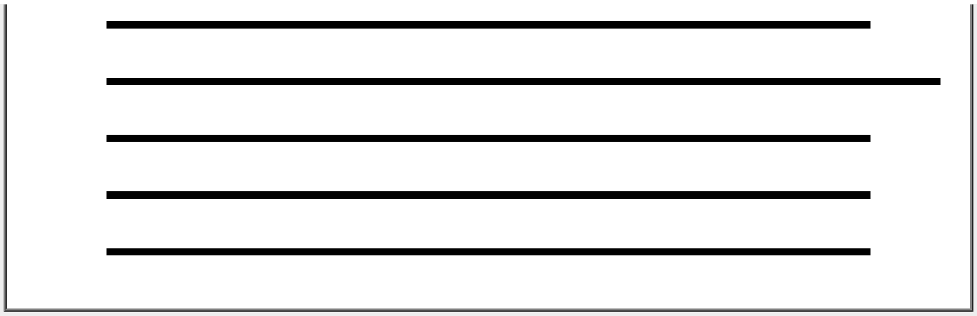
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: coagulation factor XI isoform X5 [Homo sapiens]	36.7	36.7	100%	0.18	92%	gi|530377344|XP_005262882.1
☐	PREDICTED: coagulation factor XI isoform X4 [Homo sapiens]	36.7	36.7	100%	0.18	92%	gi|530377342|XP_005262881.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]	36.7	36.7	100%	0.18	92%	gi|675774870|XP_008975412.1
☐	PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes	36.7	36.7	100%	0.18	92%	gi|694909938|XP_009446987.1
☐	PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]	36.7	36.7	100%	0.18	92%	gi|530377340|XP_005262880.1
☐	PREDICTED: coagulation factor XI [Gorilla gorilla gorilla]	36.7	36.7	100%	0.18	92%	gi|426346208|XP_004040776.1
☐	PREDICTED: coagulation factor XI isoform X4 [Pan troglodytes	36.7	36.7	100%	0.18	92%	gi|694909936|XP_009446986.1
☐	PREDICTED: coagulation factor XI isoform X2 [Homo sapiens]	36.7	36.7	100%	0.18	92%	gi|530377338|XP_005262879.1
☐	PREDICTED: coagulation factor XI isoform X3 [Pan troglodytes	36.7	36.7	100%	0.18	92%	gi|694909934|XP_009446985.1
☐	PREDICTED: coagulation factor XI isoform X6 [Homo sapiens]	36.7	36.7	100%	0.18	92%	gi|578808899|XP_006714200.1
☐	coagulation factor XI [Homo sapiens]	36.7	36.7	100%	0.18	92%	gi|180352|AAA51985.1
☐	coagulation factor XI precursor [Homo sapiens]	36.7	36.7	100%	0.18	92%	gi|4503627|NP_000119.1
☐	PREDICTED: coagulation factor XI [Nomascus leucogenys]	36.7	36.7	100%	0.18	92%	gi|332244773|XP_003271548.1
☐	PREDICTED: coagulation factor XI [Pongo abelii]	36.7	36.7	100%	0.18	92%	gi|297674804|XP_002815399.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan troglodytes	36.7	36.7	100%	0.18	92%	gi|114597210|XP_001165847.1
☐	PREDICTED: coagulation factor XI isoform X1 [Pan troglodytes	36.7	36.7	100%	0.18	92%	gi|694909931|XP_009446984.1
☐	PREDICTED: coagulation factor XI isoform X1 [Homo sapiens]	36.7	36.7	100%	0.18	92%	gi|530377336|XP_005262878.1
☐	PREDICTED: coagulation factor XI isoform X2 [Papio anubis]	32.9	32.9	100%	3.2	83%	gi|685544400|XP_009206295.1
☐	PREDICTED: coagulation factor XI isoform X2 [Chlorocebus sa	32.9	32.9	100%	3.2	83%	gi|635046203|XP_007998683.1
☐	PREDICTED: coagulation factor XI isoform X2 [Macaca fascicu	32.9	32.9	100%	3.2	83%	gi|544436077|XP_005556541.1
☐	PREDICTED: coagulation factor XI isoform X1 [Chlorocebus sa	32.9	32.9	100%	3.2	83%	gi|635046201|XP_007998681.1
☐	PREDICTED: coagulation factor XI isoform X1 [Macaca fascicu	32.9	32.9	100%	3.2	83%	gi|544436075|XP_005556540.1
☐	PREDICTED: coagulation factor XI isoform X1 [Papio anubis]	32.9	32.9	100%	3.2	83%	gi|402871005|XP_003899481.1
☐	PREDICTED: coagulation factor XI-like [Macaca mulatta]	32.9	32.9	100%	3.3	83%	gi|297293811|XP_001090398.2
☐	PREDICTED: coagulation factor XI isoform X3 [Saimiri bolivien	31.2	31.2	100%	11	75%	gi|725582192|XP_010342663.1
☐	PREDICTED: coagulation factor XI isoform X2 [Saimiri bolivien	31.2	31.2	100%	11	75%	gi|725582190|XP_010342661.1
☐	PREDICTED: coagulation factor XI isoform X1 [Saimiri bolivien	31.2	31.2	100%	11	75%	gi|725582188|XP_010342660.1
☐	PREDICTED: coagulation factor XI isoform X2 [Rhinopithecus r	30.3	30.3	100%	21	75%	gi|724897372|XP_010376291.1
☐	PREDICTED: coagulation factor XI isoform X1 [Rhinopithecus r	30.3	30.3	100%	21	75%	gi|724897369|XP_010376290.1

☐	PREDICTED: coagulation factor XI [Trichechus manatus latiros	30.3	30.3	100%	21	83%	gi|471399784|XP_004382857.1
☐	dNA polymerase [Clostridium sp. CAG:470]	29.1	29.1	83%	55	80%	gi|548192314|WP_022413014.1
☐	dNA polymerase [Clostridium sp. CAG:389]	29.1	29.1	83%	55	80%	gi|548291906|WP_022484756.1
☐	PREDICTED: uncharacterized protein LOC104705644 [Cameli	28.6	28.6	83%	65	80%	gi|727487947|XP_010419992.1
☐	PREDICTED: uncharacterized protein LOC104735395 [Cameli	28.6	28.6	83%	65	80%	gi|727562425|XP_010453485.1
☐	hypothetical protein EGK_16300 [Macaca mulatta]	28.6	28.6	100%	74	75%	gi|355687768|EHH26352.1
☐	PREDICTED: coagulation factor XI [Condylura cristata]	28.6	28.6	91%	74	82%	gi|507947527|XP_004682554.1
☐	putative uncharacterized protein [Bacteroides sp. CAG:927]	28.2	28.2	75%	98	89%	gi|514415610|WP_016563464.1
☐	PREDICTED: coagulation factor XI [Equus caballus]	28.2	28.2	91%	100	73%	gi|149742758|XP_001490330.1
☐	hypothetical protein EGM_04467 [Macaca fascicularis]	28.2	28.2	100%	100	75%	gi|355750969|EHH55296.1
☐	PREDICTED: coagulation factor XI [Equus przewalskii]	28.2	28.2	91%	100	73%	gi|664778079|XP_008508352.1
☐	hypothetical protein LOTGIDRAFT_157972 [Lottia gigantea]	28.2	28.2	66%	103	100%	gi|676439278|XP_009048802.1
☐	hypothetical protein [Capnocytophaga sp. oral taxon 326]	27.8	27.8	75%	129	89%	gi|736540851|WP_034555383.1
☐	hypothetical protein HMPREF9073_01445 [Capnocytophaga sp	27.8	27.8	75%	133	89%	gi|429176191|EKY17589.1
☐	hypothetical protein, conserved [Eimeria praecox]	27.8	27.8	83%	138	90%	gi|557213591|CDI86720.1
☐	ragB/SusD domain-containing protein [Bacteroides intestinalis	27.4	27.4	75%	186	89%	gi|548171327|WP_022393031.1
☐	3-phosphoshikimate 1-carboxyvinyltransferase [Bacillus cytotox	26.9	26.9	83%	250	80%	gi|500742744|WP_011984315.1
☐	3-phosphoshikimate 1-carboxyvinyltransferase [Roseburia sp.	26.9	26.9	83%	250	80%	gi|548338740|WP_022516325.1
☐	3-phosphoshikimate 1-carboxyvinyltransferase [Coprococcus sp	26.9	26.9	83%	250	80%	gi|547196965|WP_021938274.1
☐	hypothetical protein COCSADRAFT_93161 [Bipolaris sorokinia	26.9	26.9	91%	250	67%	gi|628072979|XP_007701143.1
☐	PREDICTED: coagulation factor XI isoform X3 [Mus musculus]	26.9	26.9	91%	252	73%	gi|568954471|XP_006509309.1
☐	PREDICTED: coagulation factor XI isoform X2 [Mus musculus]	26.9	26.9	91%	252	73%	gi|568954469|XP_006509308.1
☐	PREDICTED: coagulation factor XI isoform X1 [Mus musculus]	26.9	26.9	91%	252	73%	gi|568954467|XP_006509307.1
☐	PREDICTED: coagulation factor XI [Octodon degus]	26.9	26.9	100%	253	67%	gi|507682719|XP_004639867.1
☐	coagulation factor XI precursor [Mus musculus]	26.9	26.9	91%	253	73%	gi|21312500|NP_082342.1
☐	coagulation factor XI [Mus musculus]	26.9	26.9	91%	253	73%	gi|13811665|AAK40233.1
☐	PREDICTED: coagulation factor XI [Nannospalax galili]	26.9	26.9	91%	253	73%	gi|674087872|XP_008851827.1
☐	PREDICTED: coagulation factor XI [Callithrix jacchus]	26.9	26.9	91%	253	73%	gi|296195030|XP_002745209.1
☐	PREDICTED: coagulation factor XI [Mesocricetus auratus]	26.9	26.9	91%	253	73%	gi|524924928|XP_005066710.1
☐	PREDICTED: coagulation factor XI [Microtus ochrogaster]	26.9	26.9	91%	253	73%	gi|532039693|XP_005362704.1
☐	PREDICTED: coagulation factor XI [Cricetulus griseus]	26.9	26.9	91%	253	73%	gi|354490732|XP_003507510.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI	26.9	26.9	91%	254	73%	gi|589915357|XP_006971011.1
☐	plasma kallikrein-like protein [Cricetulus griseus]	26.9	26.9	91%	255	73%	gi|537243084|ERE87598.1
☐	hypothetical protein [Spirochaeta cellobiosiphila]	26.9	26.9	91%	256	73%	gi|655903408|WP_028973763.1
☐	hypothetical protein MVEG_11016 [Mortierella verticillata NRRL	26.5	26.5	75%	334	78%	gi|672818076|KFH62978.1
☐	UNKNOWN [Stylonychia lemnae]	26.5	26.5	83%	335	80%	gi|678318313|CDW85335.1
☐	glutamine synthetase [Clostridium thermocellum]	26.5	26.5	75%	340	89%	gi|489607843|WP_003512284.1
☐	dihydrolipoamide dehydrogenase [secondary endosymbiont of	26.5	26.5	75%	341	78%	gi|504701750|WP_014888852.1
☐	PREDICTED: coagulation factor XI [Vicugna pacos]	26.5	26.5	100%	344	67%	gi|560951202|XP_006198143.1
☐	PREDICTED: coagulation factor XI [Camelus ferus]	26.5	26.5	100%	344	67%	gi|560904135|XP_006178431.1
☐	regulatory factor X, other [Exophiala dermatitidis NIH/UT8656]	26.5	26.5	83%	346	70%	gi|684166392|XP_009157069.1
☐	hypothetical protein [Desulforegula conservatrix]	26.5	26.5	83%	347	70%	gi|653109506|WP_027359294.1
☐	PREDICTED: cyclin-Y-like protein 2 [Callithrix jacchus]	26.1	26.1	83%	434	70%	gi|675707925|XP_009007799.1
☐	PREDICTED: caffeic acid 3-O-methyltransferase-like [Malus do	26.1	26.1	100%	448	71%	gi|658063095|XP_008367461.1
☐	PREDICTED: cyclin-Y-like protein 2 [Callithrix jacchus]	26.1	26.1	83%	452	70%	gi|675709832|XP_009008189.1

☐	PREDICTED: caffeic acid 3-O-methyltransferase-like [Pyrus x b	26.1	26.1	100%	453	71%	gi|694444346|XP_009348698.1
☐	2-hydroxyglutaryl-CoA dehydratase [Dictyoglomus turgidum]	26.1	26.1	91%	453	82%	gi|501579763|WP_012584092.1
☐	2-hydroxyglutaryl-CoA dehydratase [Dictyoglomus thermophilu	26.1	26.1	91%	453	82%	gi|501543197|WP_012548312.1
☐	glutaminase [Sediminibacter sp. Hel_I_10]	26.1	26.1	83%	456	70%	gi|652357354|WP_026753496.1
☐	glutaminase [Psychroflexus tropicus]	26.1	26.1	83%	456	80%	gi|517867787|WP_019037995.1
☐	alpha-methylacyl-CoA racemase [Bacillus aurantiacus]	26.1	26.1	83%	457	70%	gi|737201816|WP_035187050.1
☐	growth hormone inducible transmembrane protein [Haemonchu	26.1	26.1	75%	457	78%	gi|560122294|CDJ93074.1
☐	hypothetical protein Y032_0061g3215 [Ancylostoma ceylanicur	26.1	26.1	75%	460	78%	gi|597859796|EYC09216.1
☐	hypothetical protein Y032_0061g3215 [Ancylostoma ceylanicur	26.1	26.1	75%	461	78%	gi|597859797|EYC09217.1
☐	BolA protein domain containing protein [Haemonchus contortus	26.1	26.1	75%	463	78%	gi|560117147|CDJ98221.1
☐	ankyrin [Legionella pneumophila]	26.1	26.1	91%	465	82%	gi|653016181|WP_027268203.1
☐	ankyrin [Legionella pneumophila]	26.1	26.1	91%	465	82%	gi|504656216|WP_014843318.1
☐	hypothetical protein C807_00689 [Lachnospiraceae bacterium :	26.1	26.1	75%	465	89%	gi|507774029|EOS32458.1
☐	PREDICTED: coagulation factor XI [Loxodonta africana]	26.1	26.1	100%	467	75%	gi|344281436|XP_003412485.1
☐	PREDICTED: metabotropic glutamate receptor 4-like [Saccoglo	26.1	26.1	66%	470	88%	gi|291240817|XP_002740314.1
☐	PREDICTED: probable GPI-anchored adhesin-like protein PGA	26.1	26.1	83%	472	53%	gi|665792957|XP_008544105.1
☐	PREDICTED: probable GPI-anchored adhesin-like protein PGA	26.1	26.1	83%	472	53%	gi|665792955|XP_008544104.1
☐	PREDICTED: probable GPI-anchored adhesin-like protein PGA	26.1	26.1	83%	472	53%	gi|665792953|XP_008544103.1
☐	PREDICTED: probable GPI-anchored adhesin-like protein PGA	26.1	26.1	83%	472	53%	gi|665792951|XP_008544102.1
☐	hypothetical protein [Klebsiella oxytoca]	25.7	25.7	58%	525	100%	gi|695790815|WP_032705039.1
☐	hypothetical protein [Streptococcus intermedius]	25.7	25.7	83%	532	80%	gi|489165200|WP_003074810.1
☐	PREDICTED: C-type lectin domain family 4 member C-like [Chl	25.7	25.7	58%	575	100%	gi|635064539|XP_007966340.1
☐	lipoprotein [Trabulsiella guamensis]	25.7	25.7	58%	587	100%	gi|740325027|WP_038162106.1
☐	threonine transporter RhtB [Bacillus endophyticus]	25.7	25.7	58%	609	100%	gi|518221703|WP_019391911.1
☐	hypothetical protein NECAME_17362 [Necator americanus]	25.7	25.7	58%	612	100%	gi|568297517|ETN83728.1
☐	cytochrome C [Burkholderia rhizoxinica]	25.7	25.7	66%	617	88%	gi|503200217|WP_013434878.1

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NCBI/ BLAST/ blastp suite/ Formatting Results - B94UCTUU01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download

How to read this page Blast report description

F11_KGINYNSSVAKS_NonMod

RID B94UCTUU01R (Expires on 01-14 10:38 am)

Query ID lcl|298721
Description None
Molecule type amino acid
Query Length 12

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

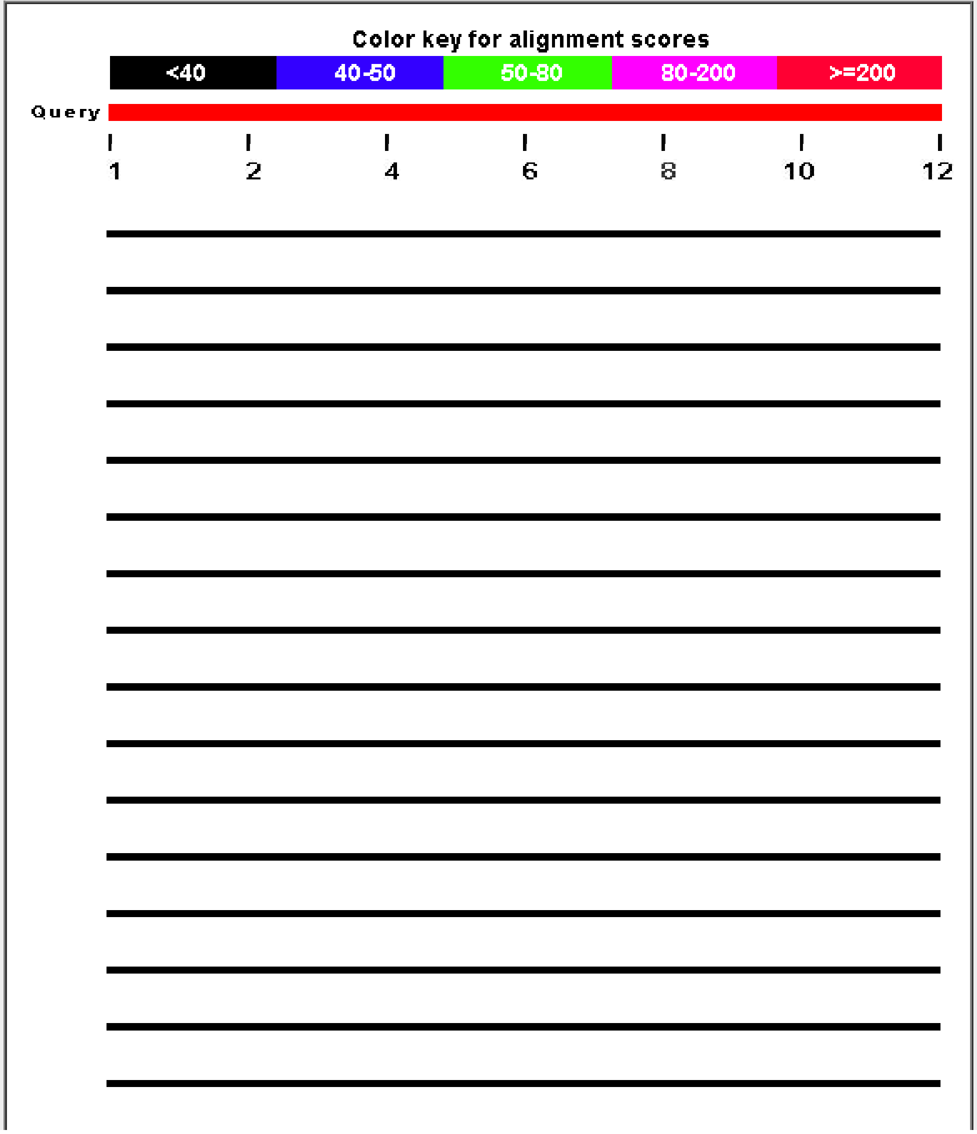
Graphic Summary

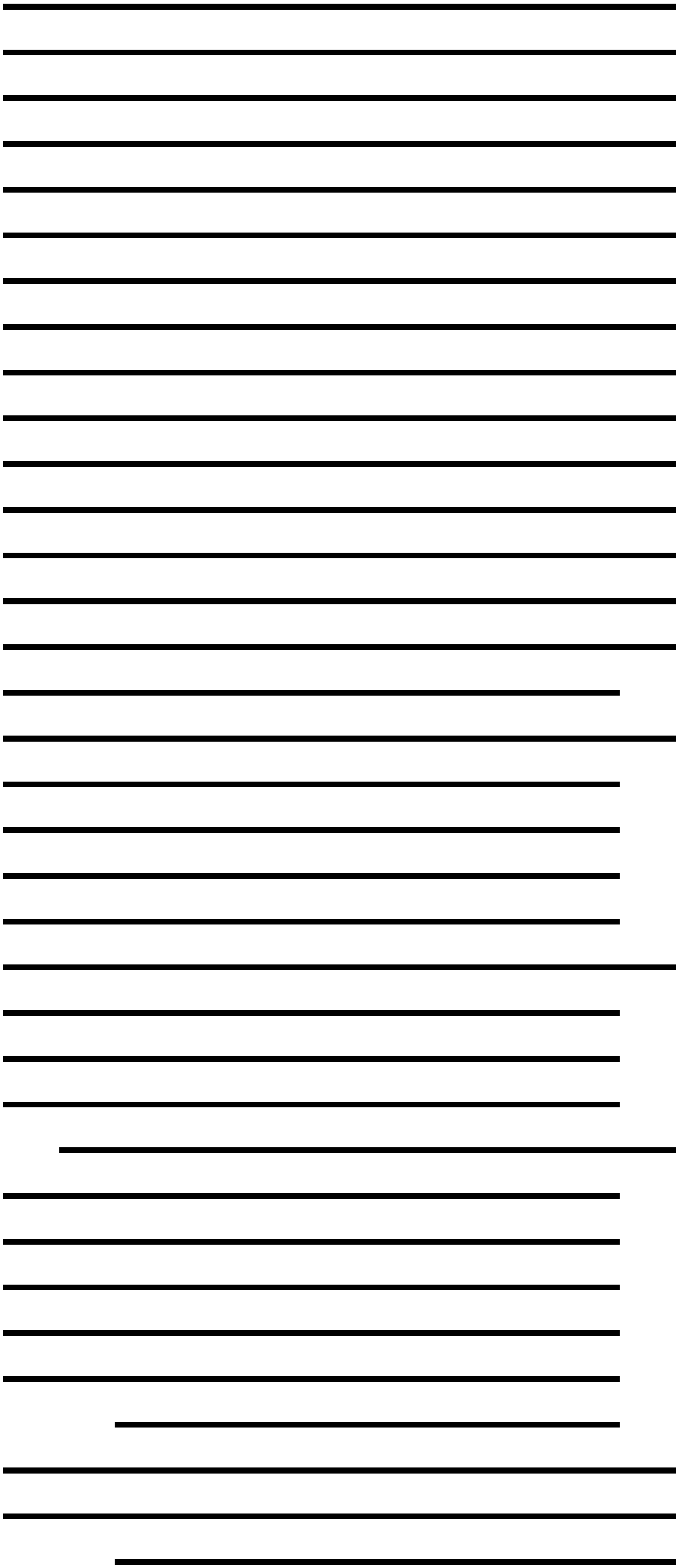
Show Conserved Domains

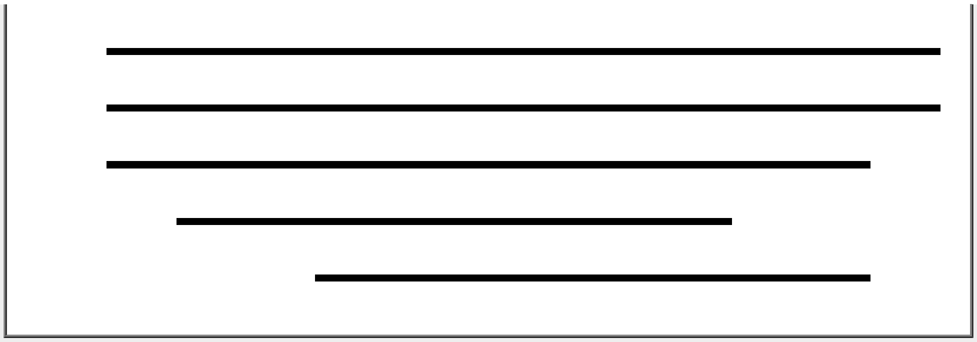
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: coagulation factor XI isoform X5 [Homo sapiens]	39.2	39.2	100%	0.024	100%	gi|530377344|XP_005262882.1
☐	PREDICTED: coagulation factor XI isoform X4 [Homo sapiens]	39.2	39.2	100%	0.025	100%	gi|530377342|XP_005262881.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]	39.2	39.2	100%	0.025	100%	gi|675774870|XP_008975412.1
☐	PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes]	39.2	39.2	100%	0.025	100%	gi|694909938|XP_009446987.1
☐	PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]	39.2	39.2	100%	0.025	100%	gi|530377340|XP_005262880.1
☐	PREDICTED: coagulation factor XI [Gorilla gorilla gorilla]	39.2	39.2	100%	0.025	100%	gi|426346208|XP_004040776.1
☐	PREDICTED: coagulation factor XI isoform X4 [Pan troglodytes]	39.2	39.2	100%	0.025	100%	gi|694909936|XP_009446986.1
☐	PREDICTED: coagulation factor XI isoform X2 [Homo sapiens]	39.2	39.2	100%	0.025	100%	gi|530377338|XP_005262879.1
☐	PREDICTED: coagulation factor XI isoform X3 [Pan troglodytes]	39.2	39.2	100%	0.025	100%	gi|694909934|XP_009446985.1
☐	PREDICTED: coagulation factor XI isoform X6 [Homo sapiens]	39.2	39.2	100%	0.025	100%	gi|578808899|XP_006714200.1
☐	coagulation factor XI [Homo sapiens]	39.2	39.2	100%	0.025	100%	gi|180352|AAA51985.1
☐	coagulation factor XI precursor [Homo sapiens]	39.2	39.2	100%	0.025	100%	gi|4503627|NP_000119.1
☐	PREDICTED: coagulation factor XI [Nomascus leucogenys]	39.2	39.2	100%	0.025	100%	gi|332244773|XP_003271548.1
☐	PREDICTED: coagulation factor XI [Pongo abelii]	39.2	39.2	100%	0.025	100%	gi|297674804|XP_002815399.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan troglodytes]	39.2	39.2	100%	0.025	100%	gi|114597210|XP_001165847.1
☐	PREDICTED: coagulation factor XI isoform X1 [Pan troglodytes]	39.2	39.2	100%	0.025	100%	gi|694909931|XP_009446984.1
☐	PREDICTED: coagulation factor XI isoform X1 [Homo sapiens]	39.2	39.2	100%	0.025	100%	gi|530377336|XP_005262878.1
☐	PREDICTED: coagulation factor XI isoform X2 [Papio anubis]	35.4	35.4	100%	0.46	92%	gi|685544400|XP_009206295.1
☐	PREDICTED: coagulation factor XI isoform X2 [Chlorocebus sabae	35.4	35.4	100%	0.46	92%	gi|635046203|XP_007998683.1
☐	PREDICTED: coagulation factor XI isoform X2 [Macaca fascicularis	35.4	35.4	100%	0.46	92%	gi|544436077|XP_005556541.1
☐	PREDICTED: coagulation factor XI isoform X1 [Chlorocebus sabae	35.4	35.4	100%	0.46	92%	gi|635046201|XP_007998681.1
☐	PREDICTED: coagulation factor XI isoform X1 [Macaca fascicularis	35.4	35.4	100%	0.46	92%	gi|544436075|XP_005556540.1
☐	PREDICTED: coagulation factor XI isoform X1 [Papio anubis]	35.4	35.4	100%	0.46	92%	gi|402871005|XP_003899481.1
☐	PREDICTED: coagulation factor XI-like [Macaca mulatta]	35.4	35.4	100%	0.46	92%	gi|297293811|XP_001090398.2
☐	PREDICTED: coagulation factor XI isoform X3 [Saimiri boliviensis b	33.7	33.7	100%	1.6	83%	gi|725582192|XP_010342663.1
☐	PREDICTED: coagulation factor XI isoform X2 [Saimiri boliviensis b	33.7	33.7	100%	1.6	83%	gi|725582190|XP_010342661.1
☐	PREDICTED: coagulation factor XI isoform X1 [Saimiri boliviensis b	33.7	33.7	100%	1.6	83%	gi|725582188|XP_010342660.1
☐	PREDICTED: coagulation factor XI isoform X2 [Rhinopithecus roxel	32.9	32.9	100%	3.1	83%	gi|724897372|XP_010376291.1
☐							

	PREDICTED: coagulation factor XI isoform X1 [Rhinopithecus roxel	32.9	32.9	100%	3.1	83%	gi|724897369|XP_010376290.1
☐	PREDICTED: coagulation factor XI [Trichechus manatus latirostris]	31.6	31.6	100%	7.9	83%	gi|471399784|XP_004382857.1
☐	hypothetical protein EGK_16300 [Macaca mulatta]	31.2	31.2	100%	11	83%	gi|355687768|EHH26352.1
☐	PREDICTED: coagulation factor XI [Equus caballus]	30.8	30.8	91%	15	82%	gi|149742758|XP_001490330.1
☐	hypothetical protein EGM_04467 [Macaca fascicularis]	30.8	30.8	100%	15	83%	gi|355750969|EHH55296.1
☐	PREDICTED: coagulation factor XI [Equus przewalskii]	30.8	30.8	91%	15	82%	gi|664778079|XP_008508352.1
☐	PREDICTED: coagulation factor XI isoform X3 [Mus musculus]	29.5	29.5	91%	37	82%	gi|568954471|XP_006509309.1
☐	PREDICTED: coagulation factor XI isoform X2 [Mus musculus]	29.5	29.5	91%	38	82%	gi|568954469|XP_006509308.1
☐	PREDICTED: coagulation factor XI isoform X1 [Mus musculus]	29.5	29.5	91%	38	82%	gi|568954467|XP_006509307.1
☐	PREDICTED: coagulation factor XI [Octodon degus]	29.5	29.5	100%	38	75%	gi|507682719|XP_004639867.1
☐	coagulation factor XI precursor [Mus musculus]	29.5	29.5	91%	38	82%	gi|21312500|NP_082342.1
☐	coagulation factor XI [Mus musculus]	29.5	29.5	91%	38	82%	gi|13811665|AAK40233.1
☐	PREDICTED: coagulation factor XI [Nannospalax galili]	29.5	29.5	91%	38	82%	gi|674087872|XP_008851827.1
☐	PREDICTED: coagulation factor XI [Callithrix jacchus]	29.5	29.5	91%	38	82%	gi|296195030|XP_002745209.1
☐	PREDICTED: coagulation factor XI [Mesocricetus auratus]	29.5	29.5	91%	38	82%	gi|524924928|XP_005066710.1
☐	PREDICTED: coagulation factor XI [Microtus ochrogaster]	29.5	29.5	91%	38	82%	gi|532039693|XP_005362704.1
☐	PREDICTED: coagulation factor XI [Cricetulus griseus]	29.5	29.5	91%	38	82%	gi|354490732|XP_003507510.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Per	29.5	29.5	91%	38	82%	gi|589915357|XP_006971011.1
☐	plasma kallikrein-like protein [Cricetulus griseus]	29.5	29.5	91%	38	82%	gi|537243084|ERE87598.1
☐	hypothetical protein MVEG_11016 [Mortierella verticillata NRRL 63	29.1	29.1	75%	49	89%	gi|672818076|KFH62978.1
☐	PREDICTED: coagulation factor XI [Vicugna pacos]	29.1	29.1	100%	51	75%	gi|560951202|XP_006198143.1
☐	PREDICTED: coagulation factor XI [Camelus ferus]	29.1	29.1	100%	51	75%	gi|560904135|XP_006178431.1
☐	glutaminase [Sediminibacter sp. Hel_I_10]	28.6	28.6	83%	68	80%	gi|652357354|WP_026753496.1
☐	PREDICTED: coagulation factor XI [Pantholops hodgsonii]	28.2	28.2	100%	95	75%	gi|556754529|XP_005972629.1
☐	PREDICTED: coagulation factor XI [Capra hircus]	28.2	28.2	100%	95	75%	gi|548524195|XP_005698802.1
☐	PREDICTED: coagulation factor XI [Condylura cristata]	28.2	28.2	91%	95	82%	gi|507947527|XP_004682554.1
☐	hypothetical protein [uncultured bacterium 270]	28.2	28.2	66%	96	100%	gi|285808506|ADC36029.1
☐	Methyl-accepting chemotaxis protein [Hoeflea phototrophica DFL-4	27.8	27.8	66%	128	100%	gi|685804179|EDQ33710.2
☐	methyl-accepting chemotaxis protein [Hoeflea phototrophica]	27.8	27.8	66%	129	100%	gi|494366291|WP_007196716.1
☐	PREDICTED: coagulation factor XI isoform 2 [Ceratotherium simum	27.8	27.8	91%	130	73%	gi|478509096|XP_004428828.1
☐	PREDICTED: coagulation factor XI [Jaculus jaculus]	27.8	27.8	100%	130	75%	gi|507565537|XP_004666428.1
☐	PREDICTED: coagulation factor XI isoform 1 [Ceratotherium simum	27.8	27.8	91%	130	73%	gi|478509094|XP_004428827.1
☐	PREDICTED: coagulation factor XI [Chrysochloris asiatica]	27.8	27.8	100%	130	67%	gi|586451182|XP_006834518.1
☐	PREDICTED: coagulation factor XI [Erinaceus europaeus]	27.8	27.8	100%	130	67%	gi|617577865|XP_007517757.1
☐	PREDICTED: coagulation factor XI [Orycteropus afer afer]	27.8	27.8	100%	130	67%	gi|634869242|XP_007946583.1
☐	hypothetical protein [Butyrivibrio sp. VCB2001]	27.8	27.8	75%	132	89%	gi|651419072|WP_026522039.1
☐	F11 protein [Bos taurus]	27.4	27.4	100%	173	75%	gi|86821856|AAI05428.1
☐	coagulation factor XI [Bos taurus]	27.4	27.4	100%	175	75%	gi|45861248|AAS78506.1
☐	blood coagulation factor XI [Bos taurus]	27.4	27.4	100%	176	75%	gi|45758733|AAS76646.1
☐	PREDICTED: coagulation factor XI [Ochotona princeps]	27.4	27.4	75%	176	89%	gi|504133468|XP_004579306.1
☐	PREDICTED: coagulation factor XI [Bubalus bubalis]	27.4	27.4	100%	176	75%	gi|594073052|XP_006060352.1
☐	PREDICTED: coagulation factor XI [Ictidomys tridecemlineatus]	27.4	27.4	91%	176	73%	gi|532087072|XP_005329248.1
☐	PREDICTED: coagulation factor XI [Bos mutus]	27.4	27.4	100%	176	75%	gi|555974149|XP_005899069.1
☐	coagulation factor XI precursor [Bos taurus]	27.4	27.4	100%	176	75%	gi|56710319|NP_001008665.1
☐	PREDICTED: coagulation factor XI [Loxodonta africana]	27.4	27.4	100%	176	75%	gi|344281436|XP_003412485.1

☐	TPA: coagulation factor XI precursor [Bos taurus]	27.4	27.4	100%	176	75%	gi|296472409|DAA14524.1
☐	PREDICTED: coagulation factor XI [Cavia porcellus]	27.4	27.4	91%	176	73%	gi|348566839|XP_003469209.1
☐	hypothetical protein COCMIDRAFT_82012 [Bipolaris oryzae ATCC	27.4	27.4	75%	179	89%	gi|627820471|XP_007683075.1
☐	hypothetical protein [Butyricimonas virosa]	26.9	26.9	75%	208	89%	gi|652947693|WP_027201158.1
☐	PREDICTED: uncharacterized protein LOC104705644 [Camelina sa	26.9	26.9	83%	217	80%	gi|727487947|XP_010419992.1
☐	PREDICTED: uncharacterized protein LOC104735395 [Camelina sa	26.9	26.9	83%	217	80%	gi|727562425|XP_010453485.1
☐	ABC transporter substrate-binding protein [Geobacter bremensis]	26.9	26.9	83%	233	59%	gi|652446890|WP_026841868.1
☐	peptidase U32 [Desulfobacter curvatus]	26.9	26.9	91%	237	82%	gi|522078314|WP_020589523.1
☐	peptidase U32 [Desulfobacter postgatei]	26.9	26.9	91%	237	82%	gi|490175138|WP_004073771.1
☐	Coagulation factor XI [Tupaia chinensis]	26.5	26.5	83%	322	80%	gi|444705646|ELW47049.1
☐	conserved hypothetical protein [Pyrenophora tritici-repentis Pt-1C-E	26.5	26.5	83%	322	56%	gi|189190382|XP_001931530.1
☐	PREDICTED: coagulation factor XI isoform X4 [Fukomys damarens	26.5	26.5	83%	325	80%	gi|731206526|XP_010618090.1
☐	PREDICTED: coagulation factor XI isoform X3 [Fukomys damarens	26.5	26.5	83%	325	80%	gi|731206524|XP_010618089.1
☐	PREDICTED: coagulation factor XI isoform X2 [Fukomys damarens	26.5	26.5	83%	325	80%	gi|731206521|XP_010618088.1
☐	PREDICTED: coagulation factor XI isoform X2 [Leptonychotes wed	26.5	26.5	83%	326	80%	gi|585180453|XP_006741890.1
☐	PREDICTED: coagulation factor XI isoform 3 [Odobenus rosmarus	26.5	26.5	83%	326	80%	gi|472396395|XP_004417424.1
☐	PREDICTED: coagulation factor XI isoform X1 [Fukomys damarens	26.5	26.5	83%	326	80%	gi|731206515|XP_010618085.1
☐	PREDICTED: coagulation factor XI [Otolemur garnettii]	26.5	26.5	75%	326	78%	gi|395840032|XP_003792872.1
☐	PREDICTED: coagulation factor XI isoform X3 [Leptonychotes wed	26.5	26.5	83%	326	80%	gi|585180455|XP_006741891.1
☐	PREDICTED: coagulation factor XI isoform 2 [Odobenus rosmarus	26.5	26.5	83%	326	80%	gi|472396393|XP_004417423.1
☐	PREDICTED: coagulation factor XI [Tupaia chinensis]	26.5	26.5	83%	326	80%	gi|562864607|XP_006160530.1
☐	PREDICTED: coagulation factor XI isoform X1 [Leptonychotes wed	26.5	26.5	83%	326	80%	gi|585180451|XP_006741889.1
☐	PREDICTED: coagulation factor XI isoform 1 [Odobenus rosmarus	26.5	26.5	83%	326	80%	gi|472396391|XP_004417422.1
☐	dNA polymerase [Clostridium sp. CAG:470]	26.5	26.5	83%	328	70%	gi|548192314|WP_022413014.1
☐	dNA polymerase [Clostridium sp. CAG:389]	26.5	26.5	83%	328	70%	gi|548291906|WP_022484756.1
☐	MULTISPECIES: TonB-linked outer membrane protein [Myroides]	26.5	26.5	75%	329	89%	gi|489076937|WP_002986882.1
☐	hypothetical protein TRIADDRAFT_53385 [Trichoplax adhaerens]	26.1	26.1	75%	419	78%	gi|195999058|XP_002109397.1

Alignments

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PREDICTED: coagulation factor XI isoform X5 [Homo sapiens]

Sequence ID: gi|530377344|ref|XP_005262882.1| **Length:** 395 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 121 to 132 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
39.2 bits(85)	0.024	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    KGINYNSSVAKS  12
            KGINYNSSVAKS
Sbjct  121  KGINYNSSVAKS  132
```

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PREDICTED: coagulation factor XI isoform X4 [Homo sapiens]

Sequence ID: gi|530377342|ref|XP_005262881.1| **Length:** 534 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 121 to 132 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
39.2 bits(85)	0.025	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    KGINYNSSVAKS  12
```

```
                KGINYNSSVAKS
Sbjct  121  KGINYNSSVAKS  132
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]

Sequence ID: gi|675774870|ref|XP_008975412.1| **Length:** 535 **Number of Matches:** 1

Range 1: 121 to 132 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
39.2 bits(85)	0.025	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    KGINYNSSVAKS  12
            KGINYNSSVAKS
Sbjct  121  KGINYNSSVAKS  132
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes]

Sequence ID: gi|694909938|ref|XP_009446987.1| **Length:** 536 **Number of Matches:** 1

Range 1: 121 to 132 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
39.2 bits(85)	0.025	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    KGINYNSSVAKS  12
            KGINYNSSVAKS
Sbjct  121  KGINYNSSVAKS  132
```

Related Information

Gene - associated gene details

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PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]

Sequence ID: gi|530377340|ref|XP_005262880.1| **Length:** 536 **Number of Matches:** 1

Range 1: 121 to 132 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
39.2 bits(85)	0.025	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    KGINYNSSVAKS  12
            KGINYNSSVAKS
Sbjct  121  KGINYNSSVAKS  132
```

Related Information

Gene - associated gene details

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

F11_KLETTVDYTDSQRPICLPSKG_Mod

RID BTH2AR3K013 (Expires on 01-20 15:46 pm)

Query ID lcl|42905
Description None
Molecule type amino acid
Query Length 21

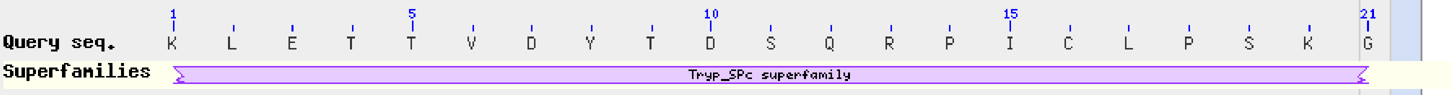
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

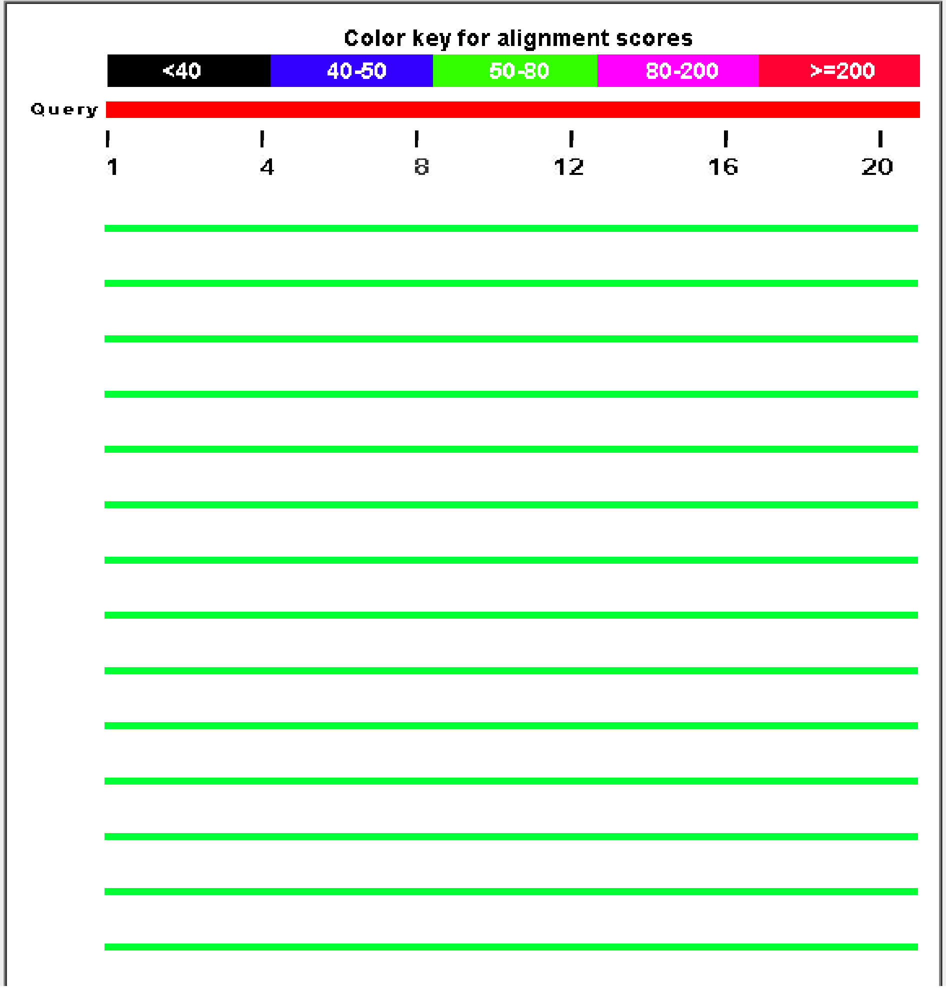
Show Conserved Domains

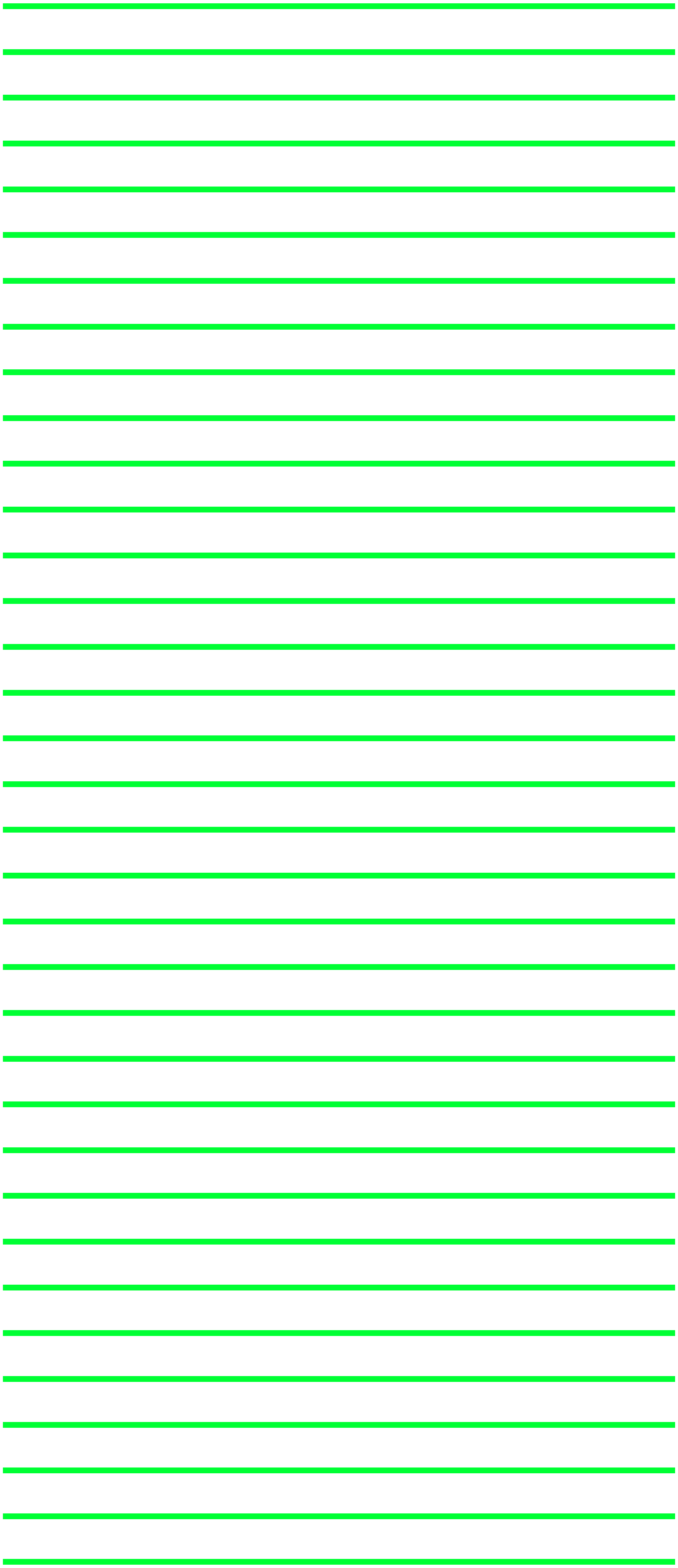
Putative conserved domains have been detected, click on the image below for detailed results.

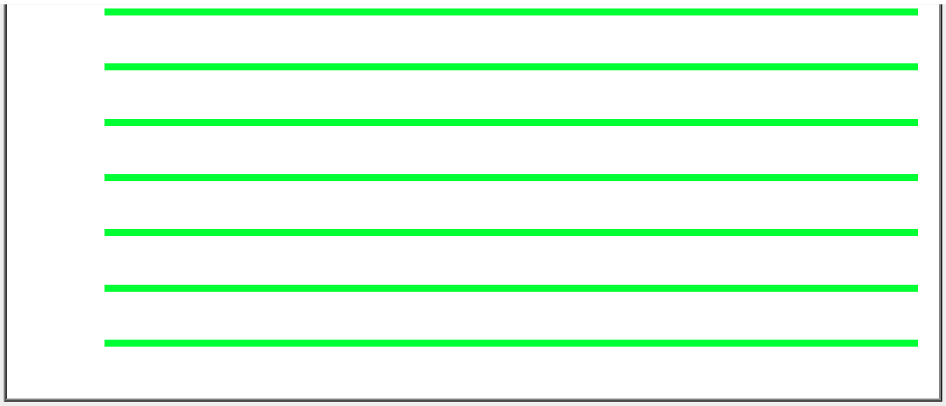


Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of The Fxia Catalytic Domain In Cor	67.7	67.7	100%	2e-11	95%	gi|56967287|1XX9_A
☐	Chain A, Factor Xia In Complex With The Inhibitor 3'-[(2s,4r)-6-	67.7	67.7	100%	2e-11	95%	gi|584579944|4NA7_A
☐	coagulation factor XI (plasma thromboplastin antecedent), isofo	67.7	67.7	100%	2e-11	95%	gi|119625025|EAX04620.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]	67.7	67.7	100%	2e-11	95%	gi|675774870|XP_008975412.1
☐	PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes	67.7	67.7	100%	2e-11	95%	gi|694909938|XP_009446987.1
☐	PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]	67.7	67.7	100%	2e-11	95%	gi|530377340|XP_005262880.1
☐	platelet factor XI [Homo sapiens]	67.7	67.7	100%	2e-11	95%	gi|3258649|AAC24506.1
☐	PREDICTED: coagulation factor XI [Gorilla gorilla gorilla]	67.7	67.7	100%	2e-11	95%	gi|426346208|XP_004040776.1
☐	PREDICTED: coagulation factor XI isoform X2 [Rhinopithecus r	67.7	67.7	100%	2e-11	95%	gi|724897372|XP_010376291.1
☐	PREDICTED: coagulation factor XI isoform X2 [Papio anubis]	67.7	67.7	100%	2e-11	95%	gi|685544400|XP_009206295.1
☐	PREDICTED: coagulation factor XI isoform X2 [Chlorocebus sa	67.7	67.7	100%	2e-11	95%	gi|635046203|XP_007998683.1
☐	PREDICTED: coagulation factor XI isoform X2 [Macaca fascicu	67.7	67.7	100%	2e-11	95%	gi|544436077|XP_005556541.1
☐	PREDICTED: coagulation factor XI isoform X3 [Pan troglodytes	67.7	67.7	100%	2e-11	95%	gi|694909934|XP_009446985.1
☐	PREDICTED: coagulation factor XI isoform X6 [Homo sapiens]	67.7	67.7	100%	2e-11	95%	gi|578808899|XP_006714200.1
☐	PREDICTED: coagulation factor XI isoform X2 [Saimiri boliviens	67.7	67.7	100%	2e-11	95%	gi|725582190|XP_010342661.1
☐	hypothetical protein EGM_04467 [Macaca fascicularis]	67.7	67.7	100%	2e-11	95%	gi|355750969|EHH55296.1
☐	hypothetical protein EGK_16300 [Macaca mulatta]	67.7	67.7	100%	2e-11	95%	gi|355687768|EHH26352.1
☐	PREDICTED: coagulation factor XI isoform X1 [Rhinopithecus r	67.7	67.7	100%	2e-11	95%	gi|724897369|XP_010376290.1
☐	PREDICTED: coagulation factor XI isoform X1 [Chlorocebus sa	67.7	67.7	100%	2e-11	95%	gi|635046201|XP_007998681.1
☐	coagulation factor XI [Homo sapiens]	67.7	67.7	100%	2e-11	95%	gi|180352|AAA51985.1
☐	PREDICTED: coagulation factor XI isoform X1 [Macaca fascicu	67.7	67.7	100%	2e-11	95%	gi|544436075|XP_005556540.1
☐	coagulation factor XI precursor [Homo sapiens]	67.7	67.7	100%	2e-11	95%	gi|4503627|NP_000119.1
☐	PREDICTED: coagulation factor XI isoform X1 [Saimiri boliviens	67.7	67.7	100%	2e-11	95%	gi|725582188|XP_010342660.1
☐	PREDICTED: coagulation factor XI isoform X1 [Papio anubis]	67.7	67.7	100%	2e-11	95%	gi|402871005|XP_003899481.1
☐	PREDICTED: coagulation factor XI [Nomascus leucogenys]	67.7	67.7	100%	2e-11	95%	gi|332244773|XP_003271548.1
☐	PREDICTED: coagulation factor XI [Pongo abelii]	67.7	67.7	100%	2e-11	95%	gi|297674804|XP_002815399.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan troglodytes	67.7	67.7	100%	2e-11	95%	gi|114597210|XP_001165847.1
☐	PREDICTED: coagulation factor XI isoform X1 [Pan troglodytes	67.7	67.7	100%	2e-11	95%	gi|694909931|XP_009446984.1

☐	PREDICTED: coagulation factor XI isoform X1 [Homo sapiens]	67.7	67.7	100%	2e-11	95%	gi|530377336|XP_005262878.1
☐	PREDICTED: coagulation factor XI-like [Macaca mulatta]	67.7	67.7	100%	2e-11	95%	gi|297293811|XP_001090398.2
☐	PREDICTED: coagulation factor XI [Ictidomys tridecemlineatus]	65.5	65.5	100%	1e-10	90%	gi|532087072|XP_005329248.1
☐	Chain A, Crystal Structure Of The Catalytic Domain Of The Coa	64.3	64.3	100%	3e-10	90%	gi|78101065|1ZHM_A
☐	Chain A, Crystal Structure Of The Catalytic Domain Of Coagula	64.3	64.3	100%	3e-10	90%	gi|78101066|1ZHP_A
☐	Chain A, Crystal Structure Of The Fxia Catalytic Domain In Cor	64.3	64.3	100%	3e-10	90%	gi|56967291|1XXD_A
☐	PREDICTED: coagulation factor XI isoform X3 [Chinchilla lanig	64.3	64.3	100%	3e-10	90%	gi|533115754|XP_005373487.1
☐	coagulation factor XI precursor [Oryctolagus cuniculus]	64.3	64.3	100%	3e-10	90%	gi|130502142|NP_001076261.1
☐	PREDICTED: coagulation factor XI isoform 2 [Ceratotherium si	64.3	64.3	100%	3e-10	90%	gi|478509096|XP_004428828.1
☐	PREDICTED: coagulation factor XI [Tarsius syrichta]	64.3	64.3	100%	3e-10	90%	gi|640821392|XP_008067645.1
☐	PREDICTED: coagulation factor XI isoform X1 [Chinchilla lanig	64.3	64.3	100%	3e-10	90%	gi|533115750|XP_005373485.1
☐	PREDICTED: coagulation factor XI isoform 1 [Ceratotherium si	64.3	64.3	100%	3e-10	90%	gi|478509094|XP_004428827.1
☐	PREDICTED: coagulation factor XI [Mesocricetus auratus]	64.3	64.3	100%	3e-10	90%	gi|524924928|XP_005066710.1
☐	PREDICTED: coagulation factor XI [Cavia porcellus]	64.3	64.3	100%	3e-10	90%	gi|348566839|XP_003469209.1
☐	PREDICTED: coagulation factor XI [Ochotona princeps]	63.0	63.0	100%	8e-10	90%	gi|504133468|XP_004579306.1
☐	PREDICTED: coagulation factor XI [Callithrix jacchus]	62.6	62.6	100%	1e-09	90%	gi|296195030|XP_002745209.1
☐	PREDICTED: coagulation factor XI [Erinaceus europaeus]	62.6	62.6	100%	1e-09	90%	gi|617577865|XP_007517757.1
☐	Chain A, Crystal Structure Of Factor Xia In Complex With Clava	62.1	62.1	100%	1e-09	90%	gi|217035335|3BG8_A
☐	Chain A, Factor Xia In Complex With A Clorophenyl-tetrazole Ir	62.1	62.1	100%	1e-09	90%	gi|383875445|3SOR_A
☐	Chain A, Factor Xi Catalytic Domain Complexed With N-((R)-1-	62.1	62.1	100%	1e-09	90%	gi|109157010|1ZPZ_A
☐	PREDICTED: coagulation factor XI [Sorex araneus]	61.7	61.7	100%	2e-09	86%	gi|505830321|XP_004610458.1
☐	PREDICTED: coagulation factor XI isoform X7 [Heterocephalus	61.3	61.3	100%	3e-09	86%	gi|512982233|XP_004853113.1
☐	PREDICTED: coagulation factor XI isoform X6 [Heterocephalus	61.3	61.3	100%	3e-09	86%	gi|512892532|XP_004897313.1
☐	PREDICTED: coagulation factor XI isoform X4 [Fukomys dama	61.3	61.3	100%	3e-09	86%	gi|731206526|XP_010618090.1
☐	PREDICTED: coagulation factor XI isoform X6 [Heterocephalus	61.3	61.3	100%	3e-09	86%	gi|512982231|XP_004853112.1
☐	PREDICTED: coagulation factor XI isoform X5 [Heterocephalus	61.3	61.3	100%	3e-09	86%	gi|512892528|XP_004897312.1
☐	PREDICTED: coagulation factor XI isoform X4 [Heterocephalus	61.3	61.3	100%	3e-09	86%	gi|512892524|XP_004897311.1
☐	PREDICTED: coagulation factor XI isoform X5 [Heterocephalus	61.3	61.3	100%	3e-09	86%	gi|512982229|XP_004853111.1
☐	PREDICTED: coagulation factor XI isoform X3 [Fukomys dama	61.3	61.3	100%	3e-09	86%	gi|731206524|XP_010618089.1
☐	Coagulation factor XI [Heterocephalus glaber]	61.3	61.3	100%	3e-09	86%	gi|351708043|EHB10962.1
☐	PREDICTED: coagulation factor XI isoform X4 [Heterocephalus	61.3	61.3	100%	3e-09	86%	gi|512982227|XP_004853110.1
☐	PREDICTED: coagulation factor XI isoform X3 [Heterocephalus	61.3	61.3	100%	3e-09	86%	gi|512892520|XP_004897310.1
☐	PREDICTED: coagulation factor XI isoform X2 [Fukomys dama	61.3	61.3	100%	3e-09	86%	gi|731206521|XP_010618088.1
☐	PREDICTED: coagulation factor XI isoform X1 [Fukomys dama	61.3	61.3	100%	3e-09	86%	gi|731206515|XP_010618085.1
☐	PREDICTED: coagulation factor XI [Nannospalax galili]	61.3	81.9	100%	3e-09	86%	gi|674087872|XP_008851827.1
☐	PREDICTED: coagulation factor XI isoform X2 [Heterocephalus	61.3	61.3	100%	3e-09	86%	gi|512982223|XP_004853108.1
☐	PREDICTED: coagulation factor XI isoform X1 [Heterocephalus	61.3	61.3	100%	3e-09	86%	gi|512892512|XP_004897308.1
☐	PREDICTED: coagulation factor XI isoform X1 [Heterocephalus	61.3	61.3	100%	3e-09	86%	gi|512982221|XP_004853107.1
☐	PREDICTED: coagulation factor XI isoform X2 [Heterocephalus	61.3	61.3	100%	3e-09	86%	gi|512892516|XP_004897309.1
☐	PREDICTED: coagulation factor XI [Dasypus novemcinctus]	60.9	60.9	100%	4e-09	86%	gi|488532217|XP_004457855.1
☐	PREDICTED: coagulation factor XI [Ovis aries]	60.9	60.9	100%	4e-09	86%	gi|426256280|XP_004021769.1
☐	Chain A, Factor Xia In Complex With The Inhibitor 4-{2-[(1s)-1-(	60.0	60.0	100%	7e-09	90%	gi|728055500|4TY6_A
☐	blood coagulation factor XI [Bos taurus]	60.0	60.0	100%	8e-09	86%	gi|45758733|AAS76646.1
☐	PREDICTED: coagulation factor XI [Bison bison bison]	60.0	60.0	100%	8e-09	86%	gi|742100675|XP_010834113.1
☐	PREDICTED: coagulation factor XI [Bos mutus]	60.0	60.0	100%	8e-09	86%	gi|555974149|XP_005899069.1
☐	PREDICTED: coagulation factor XI isoform X2 [Leptonychotes	59.6	59.6	100%	1e-08	81%	gi|585180453|XP_006741890.1

☐	PREDICTED: coagulation factor XI isoform 3 [Odobenus rosma	59.6	59.6	100%	1e-08	81%	gi|472396395|XP_004417424.1
☐	PREDICTED: coagulation factor XI-like [Ailuropoda melanoleuc	59.6	59.6	100%	1e-08	81%	gi|301776062|XP_002923450.1
☐	PREDICTED: coagulation factor XI [Lipotes vexillifer]	59.6	59.6	100%	1e-08	86%	gi|602712769|XP_007466613.1
☐	PREDICTED: coagulation factor XI [Balaenoptera acutorostrata	59.6	59.6	100%	1e-08	86%	gi|594650157|XP_007174042.1
☐	PREDICTED: coagulation factor XI [Physeter catodon]	59.6	59.6	100%	1e-08	86%	gi|593742188|XP_007126520.1
☐	PREDICTED: coagulation factor XI [Jaculus jaculus]	59.6	59.6	95%	1e-08	85%	gi|507565537|XP_004666428.1
☐	PREDICTED: coagulation factor XI isoform X3 [Leptonychotes v	59.6	59.6	100%	1e-08	81%	gi|585180455|XP_006741891.1
☐	PREDICTED: coagulation factor XI isoform 2 [Odobenus rosma	59.6	59.6	100%	1e-08	81%	gi|472396393|XP_004417423.1
☐	PREDICTED: coagulation factor XI [Orcinus orca]	59.6	59.6	100%	1e-08	86%	gi|466045508|XP_004277238.1
☐	PREDICTED: coagulation factor XI isoform X1 [Leptonychotes v	59.6	59.6	100%	1e-08	81%	gi|585180451|XP_006741889.1
☐	PREDICTED: coagulation factor XI [Mustela putorius furo]	59.6	59.6	100%	1e-08	81%	gi|511876760|XP_004758357.1
☐	PREDICTED: coagulation factor XI isoform 1 [Odobenus rosma	59.6	59.6	100%	1e-08	81%	gi|472396391|XP_004417422.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [	59.6	59.6	100%	1e-08	81%	gi|671035736|XP_008708722.1
☐	PREDICTED: coagulation factor XI [Equus caballus]	59.2	59.2	100%	2e-08	86%	gi|149742758|XP_001490330.1
☐	PREDICTED: coagulation factor XI [Camelus bactrianus]	59.2	59.2	100%	2e-08	86%	gi|743715881|XP_010951577.1
☐	PREDICTED: coagulation factor XI [Vicugna pacos]	59.2	59.2	100%	2e-08	86%	gi|560951202|XP_006198143.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [	59.2	59.2	100%	2e-08	86%	gi|744611375|XP_010994033.1
☐	PREDICTED: coagulation factor XI [Equus przewalskii]	59.2	59.2	100%	2e-08	86%	gi|664778079|XP_008508352.1
☐	PREDICTED: coagulation factor XI [Camelus ferus]	59.2	59.2	100%	2e-08	86%	gi|560904135|XP_006178431.1
☐	Chain A, Crystal Structure Of The Catalytic Domain Of Coagula	58.7	58.7	100%	2e-08	86%	gi|75765761|1ZJD_A
☐	Chain A, Factor Xi Catalytic Domain Complexed With 2-Guanid	58.7	58.7	100%	2e-08	86%	gi|109156985|1ZLR_A
☐	Chain A, Crystal Structure Of The Catalytic Domain Of Coagula	58.7	58.7	100%	2e-08	86%	gi|78101067|1ZHR_A
☐	PREDICTED: coagulation factor XI [Otolemur garnettii]	58.7	58.7	100%	2e-08	86%	gi|395840032|XP_003792872.1
☐	coagulation factor XI precursor [Canis lupus familiaris]	58.3	58.3	100%	3e-08	81%	gi|205361194|NP_001128595.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [	58.3	58.3	100%	3e-08	81%	gi|591347751|XP_007099050.1
☐	PREDICTED: coagulation factor XI isoform X2 [Canis lupus fan	58.3	58.3	100%	3e-08	81%	gi|545526400|XP_005629983.1

⊖ Alignments

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Chain A, Crystal Structure Of The Fxia Catalytic Domain In Complex With Ecotinm84r

Sequence ID: gi|56967287|pdb|1XX9|A **Length:** 238 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 98 to 118 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.7 bits(152)	2e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KLETTVDYTDSQRPICLPSKG  21
            KLETTV+YTDSQRPICLPSKG
Sbjct  98   KLETTVNYTDSQRPICLPSKG  118
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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Chain A, Factor Xia In Complex With The Inhibitor 3'-[(2s,4r)-6-carbamimidoyl- 4-methyl-4-phenyl-1,2,3,4-tetrahydroquinolin-2-yl]-4-carbamoyl-5'- [(3-methylbutanoyl)amino]biphenyl-2-carboxylic Acid

Sequence ID: gi|584579944|pdb|4NA7|A **Length:** 244 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 98 to 118 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins

67.7 bits(152)	2e-11	20/21(95%)	21/21(100%)	0/21(0%)

identical to the subject

```
Query  1    KLETTVDYTDSQRPICLPSKG  21
            KLETTV+YTDSQRPICLPSKG
Sbjct  98   KLETTVNYTDSQRPICLPSKG  118
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

coagulation factor XI (plasma thromboplastin antecedent), isoform CRA_b [Homo sapiens]

Sequence ID: gi|119625025|gb|EAX04620.1| **Length:** 470 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 330 to 350 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.7 bits(152)	2e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KLETTVDYTDSQRPICLPSKG  21
            KLETTV+YTDSQRPICLPSKG
Sbjct  330  KLETTVNYTDSQRPICLPSKG  350
```

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PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]

Sequence ID: gi|675774870|ref|XP_008975412.1| **Length:** 535 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 395 to 415 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.7 bits(152)	2e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KLETTVDYTDSQRPICLPSKG  21
            KLETTV+YTDSQRPICLPSKG
Sbjct  395  KLETTVNYTDSQRPICLPSKG  415
```

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PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes]

Sequence ID: gi|694909938|ref|XP_009446987.1| **Length:** 536 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 396 to 416 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.7 bits(152)	2e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KLETTVDYTDSQRPICLPSKG  21
            KLETTV+YTDSQRPICLPSKG
Sbjct  396  KLETTVNYTDSQRPICLPSKG  416
```

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVDEK6ZS01R

Your search parameters were adjusted to search for a short input sequence.

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F11_KLETTVDYTDSQRPICLPSKGDRN_Mod

RID BVDEK6ZS01R (Expires on 01-21 08:56 am)

Query ID lcl|24533
Description None
Molecule type amino acid
Query Length 24

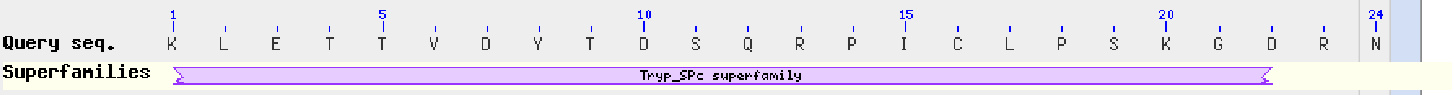
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

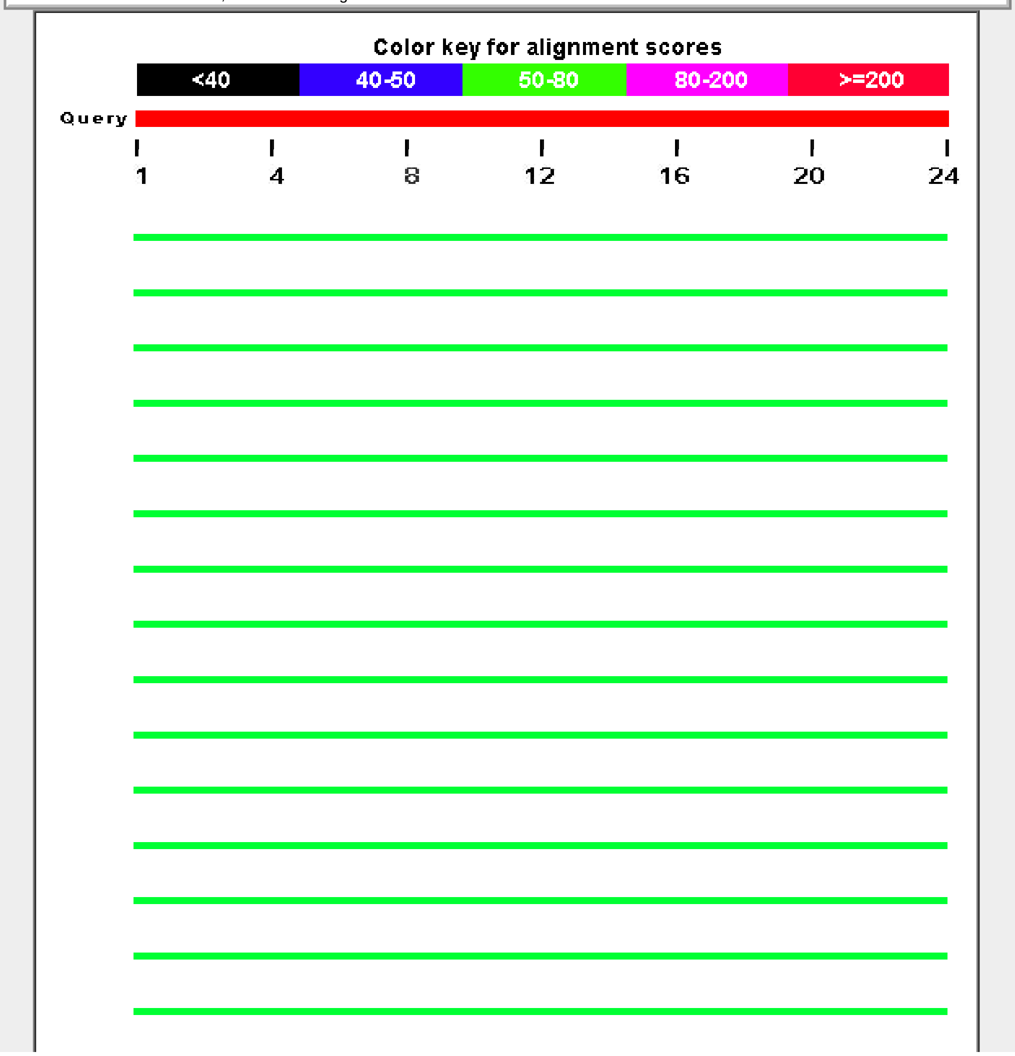
Show Conserved Domains

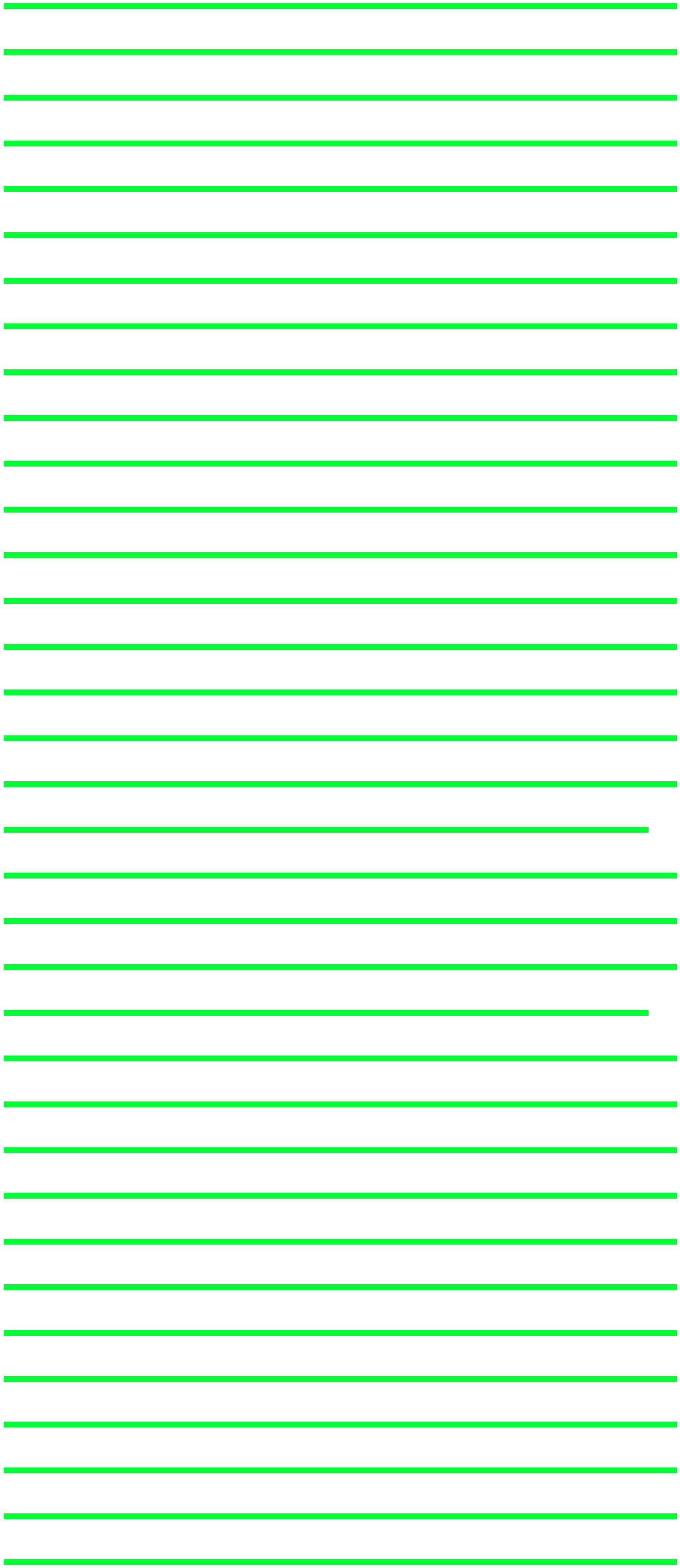
Putative conserved domains have been detected, click on the image below for detailed results.

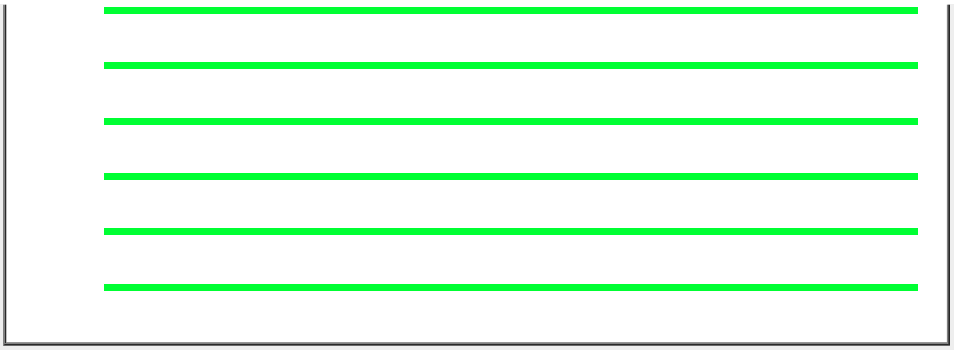


Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of The Fxia Catalytic Domain In Complex With Ecc	77.8	77.8	100%	8e-15	96%	1XX9_A
☐	Chain A, Factor Xia In Complex With The Inhibitor 3'-[(2s,4r)-6-carbamimidoyl	77.8	77.8	100%	8e-15	96%	4NA7_A
☐	coagulation factor XI (plasma thromboplastin antecedent), isoform CRA_b [Hc	77.8	77.8	100%	1e-14	96%	EAX04620.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]	77.8	77.8	100%	1e-14	96%	XP_008975412.1
☐	PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes]	77.8	77.8	100%	1e-14	96%	XP_009446987.1
☐	PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]	77.8	77.8	100%	1e-14	96%	XP_005262880.1
☐	platelet factor XI [Homo sapiens]	77.8	77.8	100%	1e-14	96%	AAC24506.1
☐	PREDICTED: coagulation factor XI [Gorilla gorilla gorilla]	77.8	77.8	100%	1e-14	96%	XP_004040776.1
☐	PREDICTED: coagulation factor XI isoform X2 [Rhinopithecus roxellana]	77.8	77.8	100%	1e-14	96%	XP_010376291.1
☐	PREDICTED: coagulation factor XI isoform X2 [Papio anubis]	77.8	77.8	100%	1e-14	96%	XP_009206295.1
☐	PREDICTED: coagulation factor XI isoform X2 [Chlorocebus sabaeus]	77.8	77.8	100%	1e-14	96%	XP_007998683.1
☐	PREDICTED: coagulation factor XI isoform X2 [Macaca fascicularis]	77.8	77.8	100%	1e-14	96%	XP_005556541.1
☐	PREDICTED: coagulation factor XI isoform X3 [Pan troglodytes]	77.8	77.8	100%	1e-14	96%	XP_009446985.1
☐	PREDICTED: coagulation factor XI isoform X6 [Homo sapiens]	77.8	77.8	100%	1e-14	96%	XP_006714200.1
☐	hypothetical protein EGM_04467 [Macaca fascicularis]	77.8	77.8	100%	1e-14	96%	EHH55296.1
☐	hypothetical protein EGK_16300 [Macaca mulatta]	77.8	77.8	100%	1e-14	96%	EHH26352.1
☐	PREDICTED: coagulation factor XI isoform X1 [Rhinopithecus roxellana]	77.8	77.8	100%	1e-14	96%	XP_010376290.1
☐	PREDICTED: coagulation factor XI isoform X1 [Chlorocebus sabaeus]	77.8	77.8	100%	1e-14	96%	XP_007998681.1
☐	coagulation factor XI [Homo sapiens]	77.8	77.8	100%	1e-14	96%	AAA51985.1
☐	PREDICTED: coagulation factor XI isoform X1 [Macaca fascicularis]	77.8	77.8	100%	1e-14	96%	XP_005556540.1
☐	coagulation factor XI precursor [Homo sapiens]	77.8	77.8	100%	1e-14	96%	NP_000119.1
☐	PREDICTED: coagulation factor XI isoform X1 [Papio anubis]	77.8	77.8	100%	1e-14	96%	XP_003899481.1
☐	PREDICTED: coagulation factor XI [Nomascus leucogenys]	77.8	77.8	100%	1e-14	96%	XP_003271548.1
☐	PREDICTED: coagulation factor XI [Pongo abelii]	77.8	77.8	100%	1e-14	96%	XP_002815399.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan troglodytes]	77.8	77.8	100%	1e-14	96%	XP_001165847.1
☐	PREDICTED: coagulation factor XI isoform X1 [Pan troglodytes]	77.8	77.8	100%	1e-14	96%	XP_009446984.1
☐	PREDICTED: coagulation factor XI isoform X1 [Homo sapiens]	77.8	77.8	100%	1e-14	96%	XP_005262878.1
☐	PREDICTED: coagulation factor XI-like [Macaca mulatta]	77.8	77.8	100%	1e-14	96%	XP_001090398.2
☐	PREDICTED: coagulation factor XI [Ictidomys tridecemlineatus]	75.7	75.7	100%	6e-14	92%	XP_005329248.1

☐	Chain A, Crystal Structure Of The Catalytic Domain Of The Coagulation Facto	74.4	74.4	100%	1e-13	92%	1ZHM_A
☐	Chain A, Crystal Structure Of The Catalytic Domain Of Coagulation Factor Xi	74.4	74.4	100%	1e-13	92%	1ZHP_A
☐	Chain A, Crystal Structure Of The Fxia Catalytic Domain In Complex With Mut	74.4	74.4	100%	1e-13	92%	1XXD_A
☐	PREDICTED: coagulation factor XI isoform X3 [Chinchilla lanigera]	74.4	74.4	100%	2e-13	92%	XP_005373487.1
☐	PREDICTED: coagulation factor XI isoform X2 [Saimiri boliviensis boliviensis]	74.4	74.4	95%	2e-13	96%	XP_010342661.1
☐	coagulation factor XI precursor [Oryctolagus cuniculus]	74.4	74.4	100%	2e-13	92%	NP_001076261.1
☐	PREDICTED: coagulation factor XI [Tarsius syrichta]	74.4	74.4	100%	2e-13	92%	XP_008067645.1
☐	PREDICTED: coagulation factor XI isoform X1 [Chinchilla lanigera]	74.4	74.4	100%	2e-13	92%	XP_005373485.1
☐	PREDICTED: coagulation factor XI isoform X1 [Saimiri boliviensis boliviensis]	74.4	74.4	95%	2e-13	96%	XP_010342660.1
☐	PREDICTED: coagulation factor XI [Mesocricetus auratus]	74.4	74.4	100%	2e-13	92%	XP_005066710.1
☐	PREDICTED: coagulation factor XI [Cavia porcellus]	74.4	74.4	100%	2e-13	92%	XP_003469209.1
☐	PREDICTED: coagulation factor XI [Erinaceus europaeus]	72.7	72.7	100%	6e-13	92%	XP_007517757.1
☐	Chain A, Factor Xia In Complex With A Clorophenyl-tetrazole Inhibitor [Homo	72.3	72.3	100%	7e-13	92%	3SOR_A
☐	Chain A, Factor Xi Catalytic Domain Complexed With N-((R)-1-(4- Bromophe	72.3	72.3	100%	7e-13	92%	1ZPZ_A
☐	PREDICTED: coagulation factor XI [Sorex araneus]	71.9	71.9	100%	1e-12	88%	XP_004610458.1
☐	PREDICTED: coagulation factor XI isoform X7 [Heterocephalus glaber]	71.5	71.5	100%	2e-12	88%	XP_004853113.1
☐	PREDICTED: coagulation factor XI isoform X6 [Heterocephalus glaber]	71.5	71.5	100%	2e-12	88%	XP_004897313.1
☐	PREDICTED: coagulation factor XI isoform X4 [Fukomys damarensis]	71.5	71.5	100%	2e-12	88%	XP_010618090.1
☐	PREDICTED: coagulation factor XI isoform X6 [Heterocephalus glaber]	71.5	71.5	100%	2e-12	88%	XP_004853112.1
☐	PREDICTED: coagulation factor XI isoform X5 [Heterocephalus glaber]	71.5	71.5	100%	2e-12	88%	XP_004897312.1
☐	PREDICTED: coagulation factor XI isoform X4 [Heterocephalus glaber]	71.5	71.5	100%	2e-12	88%	XP_004897311.1
☐	PREDICTED: coagulation factor XI isoform X5 [Heterocephalus glaber]	71.5	71.5	100%	2e-12	88%	XP_004853111.1
☐	PREDICTED: coagulation factor XI isoform X3 [Fukomys damarensis]	71.5	71.5	100%	2e-12	88%	XP_010618089.1
☐	Coagulation factor XI [Heterocephalus glaber]	71.5	71.5	100%	2e-12	88%	EHB10962.1
☐	PREDICTED: coagulation factor XI isoform X4 [Heterocephalus glaber]	71.5	71.5	100%	2e-12	88%	XP_004853110.1
☐	PREDICTED: coagulation factor XI isoform X3 [Heterocephalus glaber]	71.5	71.5	100%	2e-12	88%	XP_004897310.1
☐	PREDICTED: coagulation factor XI isoform X2 [Fukomys damarensis]	71.5	71.5	100%	2e-12	88%	XP_010618088.1
☐	PREDICTED: coagulation factor XI isoform X1 [Fukomys damarensis]	71.5	71.5	100%	2e-12	88%	XP_010618085.1
☐	PREDICTED: coagulation factor XI [Nannospalax galili]	71.5	92.0	100%	2e-12	88%	XP_008851827.1
☐	PREDICTED: coagulation factor XI isoform X2 [Heterocephalus glaber]	71.5	71.5	100%	2e-12	88%	XP_004853108.1
☐	PREDICTED: coagulation factor XI isoform X1 [Heterocephalus glaber]	71.5	71.5	100%	2e-12	88%	XP_004897308.1
☐	PREDICTED: coagulation factor XI isoform X1 [Heterocephalus glaber]	71.5	71.5	100%	2e-12	88%	XP_004853107.1
☐	PREDICTED: coagulation factor XI isoform X2 [Heterocephalus glaber]	71.5	71.5	100%	2e-12	88%	XP_004897309.1
☐	PREDICTED: coagulation factor XI isoform 2 [Ceratotherium simum simum]	71.0	71.0	100%	2e-12	88%	XP_004428828.1
☐	PREDICTED: coagulation factor XI isoform 1 [Ceratotherium simum simum]	71.0	71.0	100%	2e-12	88%	XP_004428827.1
☐	PREDICTED: coagulation factor XI [Ovis aries]	71.0	71.0	100%	2e-12	88%	XP_004021769.1
☐	Chain A, Factor Xia In Complex With The Inhibitor 4-{2-[(1s)-1-({[trans-4- (ami	70.2	70.2	100%	4e-12	92%	4TY6_A
☐	blood coagulation factor XI [Bos taurus]	70.2	70.2	100%	4e-12	88%	AAS76646.1
☐	PREDICTED: coagulation factor XI [Bison bison bison]	70.2	70.2	100%	4e-12	88%	XP_010834113.1
☐	PREDICTED: coagulation factor XI [Bos mutus]	70.2	70.2	100%	4e-12	88%	XP_005899069.1
☐	Chain A, Crystal Structure Of Factor Xia In Complex With Clavatadine A [Hom	69.8	69.8	100%	5e-12	88%	3BG8_A
☐	PREDICTED: coagulation factor XI [Ochotona princeps]	69.8	69.8	95%	6e-12	91%	XP_004579306.1
☐	PREDICTED: coagulation factor XI isoform X2 [Leptonychotes weddellii]	69.8	69.8	100%	6e-12	83%	XP_006741890.1
☐	PREDICTED: coagulation factor XI isoform 3 [Odobenus rosmarus divergens]	69.8	69.8	100%	6e-12	83%	XP_004417424.1
☐	PREDICTED: coagulation factor XI-like [Ailuropoda melanoleuca]	69.8	69.8	100%	6e-12	83%	XP_002923450.1
☐	PREDICTED: coagulation factor XI [Lipotes vexillifer]	69.8	69.8	100%	6e-12	88%	XP_007466613.1

☐	PREDICTED: coagulation factor XI [Balaenoptera acutorostrata scammoni]	69.8	69.8	100%	6e-12	88%	XP_007174042.1
☐	PREDICTED: coagulation factor XI [Physeter catodon]	69.8	69.8	100%	6e-12	88%	XP_007126520.1
☐	PREDICTED: coagulation factor XI [Jaculus jaculus]	69.8	69.8	95%	6e-12	87%	XP_004666428.1
☐	PREDICTED: coagulation factor XI isoform X3 [Leptonychotes weddellii]	69.8	69.8	100%	6e-12	83%	XP_006741891.1
☐	PREDICTED: coagulation factor XI isoform 2 [Odobenus rosmarus divergens]	69.8	69.8	100%	6e-12	83%	XP_004417423.1
☐	PREDICTED: coagulation factor XI [Orcinus orca]	69.8	69.8	100%	6e-12	88%	XP_004277238.1
☐	PREDICTED: coagulation factor XI isoform X1 [Leptonychotes weddellii]	69.8	69.8	100%	6e-12	83%	XP_006741889.1
☐	PREDICTED: coagulation factor XI [Mustela putorius furo]	69.8	69.8	100%	6e-12	83%	XP_004758357.1
☐	PREDICTED: coagulation factor XI isoform 1 [Odobenus rosmarus divergens]	69.8	69.8	100%	6e-12	83%	XP_004417422.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Ursus maritim	69.8	69.8	100%	6e-12	83%	XP_008708722.1
☐	PREDICTED: coagulation factor XI [Camelus bactrianus]	69.4	69.4	100%	9e-12	88%	XP_010951577.1
☐	PREDICTED: coagulation factor XI [Vicugna pacos]	69.4	69.4	100%	9e-12	88%	XP_006198143.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Camelus dron	69.4	69.4	100%	9e-12	88%	XP_010994033.1
☐	PREDICTED: coagulation factor XI [Callithrix jacchus]	69.4	69.4	95%	9e-12	91%	XP_002745209.1
☐	PREDICTED: coagulation factor XI [Camelus ferus]	69.4	69.4	100%	9e-12	88%	XP_006178431.1
☐	Chain A, Crystal Structure Of The Catalytic Domain Of Coagulation Factor Xi	68.9	68.9	100%	1e-11	88%	1ZJD_A
☐	Chain A, Factor Xi Catalytic Domain Complexed With 2-Guanidino-1-(4-(4,4,5	68.9	68.9	100%	1e-11	88%	1ZLR_A
☐	Chain A, Crystal Structure Of The Catalytic Domain Of Coagulation Factor Xi	68.9	68.9	100%	1e-11	88%	1ZHR_A
☐	coagulation factor XI precursor [Canis lupus familiaris]	68.5	68.5	100%	2e-11	83%	NP_001128595.1
☐	PREDICTED: coagulation factor XI [Dasypus novemcinctus]	68.5	68.5	100%	2e-11	83%	XP_004457855.1
☐	PREDICTED: coagulation factor XI isoform X2 [Canis lupus familiaris]	68.5	68.5	100%	2e-11	83%	XP_005629983.1
☐	PREDICTED: coagulation factor XI isoform X1 [Canis lupus familiaris]	68.5	68.5	100%	2e-11	83%	XP_005629982.1
☐	PREDICTED: coagulation factor XI [Trichechus manatus latirostris]	67.7	67.7	100%	3e-11	83%	XP_004382857.1
☐	PREDICTED: coagulation factor XI [Bubalus bubalis]	66.8	66.8	100%	6e-11	83%	XP_006060352.1
☐	PREDICTED: coagulation factor XI [Pantholops hodgsonii]	66.8	66.8	100%	6e-11	83%	XP_005972629.1

⊟ Alignments

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Chain A, Crystal Structure Of The Fxia Catalytic Domain In Complex With Ecotinm84r

Sequence ID: pdb|1XX9|A **Length:** 238 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 98 to 121 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.8 bits(176)	8e-15	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    KLETTVDYTDSQRPICLPSKGDRN  24
            KLETTV+YTDSQRPICLPSKGDRN
Sbjct  98   KLETTVNYTDSQRPICLPSKGDRN  121
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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Chain A, Factor Xia In Complex With The Inhibitor 3'-[(2s,4r)-6-carbamimidoyl- 4-methyl-4-phenyl-1,2,3,4-tetrahydroquinolin-2-yl]-4-carbamoyl-5'- [(3-methylbutanoyl)amino]biphenyl-2-carboxylic Acid

Sequence ID: pdb|4NA7|A **Length:** 244 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 98 to 121 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.8 bits(176)	8e-15	23/24(96%)	24/24(100%)	0/24(0%)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

```
Query  1    KLETTVDYTDSQRPICLPSKGDRN  24
            KLETTV+YTDSQRPICLPSKGDRN
Sbjct  98   KLETTVNYTDSQRPICLPSKGDRN  121
```

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coagulation factor XI (plasma thromboplastin antecedent), isoform CRA_b [Homo sapiens]

Sequence ID: gb|EAX04620.1| **Length:** 470 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 330 to 353 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.8 bits(176)	1e-14	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    KLETTVDYTDSQRPICLPSKGDRN  24
            KLETTV+YTDSQRPICLPSKGDRN
Sbjct  330  KLETTVNYTDSQRPICLPSKGDRN  353
```

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PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]

Sequence ID: ref|XP_008975412.1| **Length:** 535 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 395 to 418 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.8 bits(176)	1e-14	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    KLETTVDYTDSQRPICLPSKGDRN  24
            KLETTV+YTDSQRPICLPSKGDRN
Sbjct  395  KLETTVNYTDSQRPICLPSKGDRN  418
```

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PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes]

Sequence ID: ref|XP_009446987.1| **Length:** 536 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 396 to 419 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.8 bits(176)	1e-14	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    KLETTVDYTDSQRPICLPSKGDRN  24
            KLETTV+YTDSQRPICLPSKGDRN
Sbjct  396  KLETTVNYTDSQRPICLPSKGDRN  419
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download

How to read this page   Blast report description

F11_KLETTVNYTDSQRPICLPSKG_NonMod

RID B96432WD01R (Expires on 01-14 11:01 am)

Query ID lcl|229952
Description None
Molecule type amino acid
Query Length 21

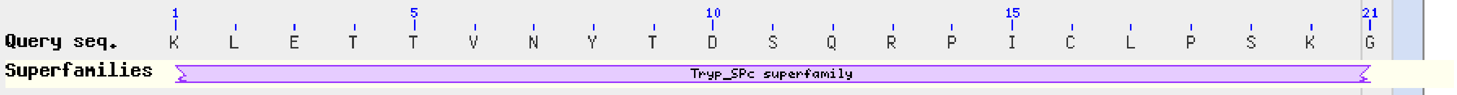
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

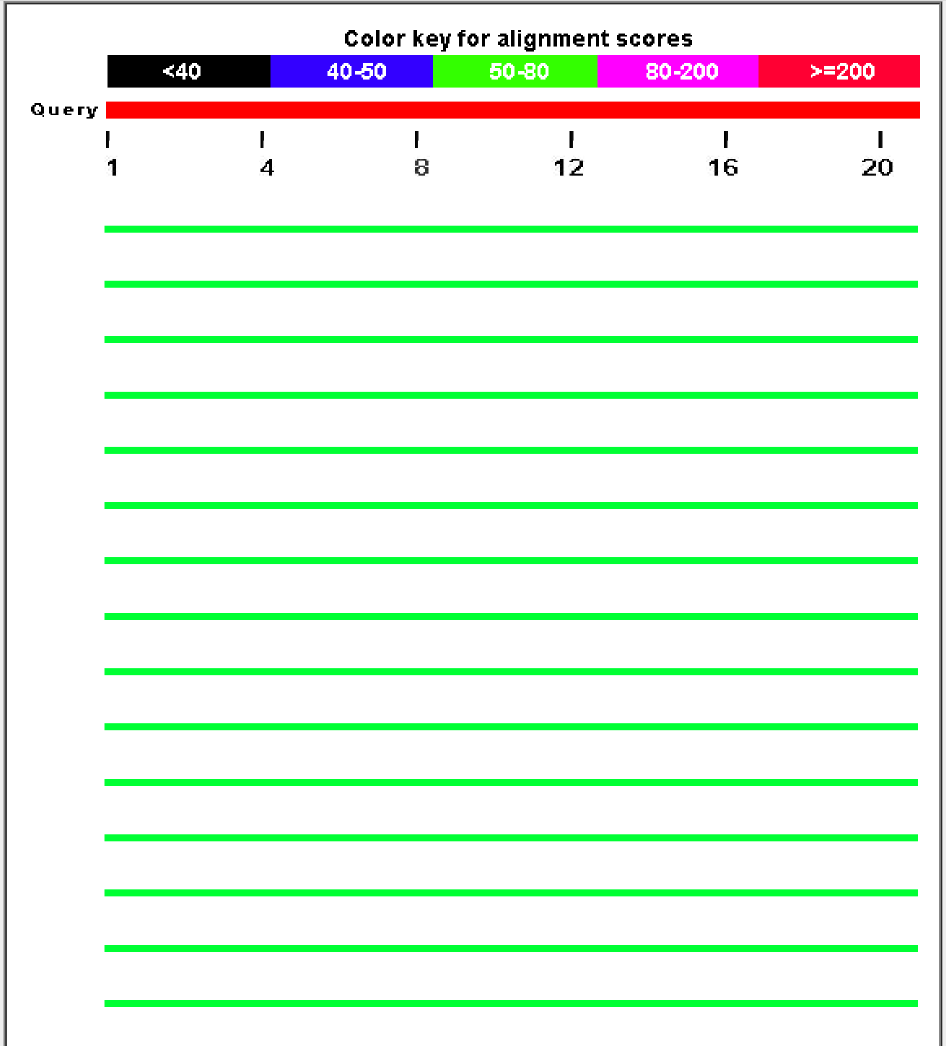
Show Conserved Domains

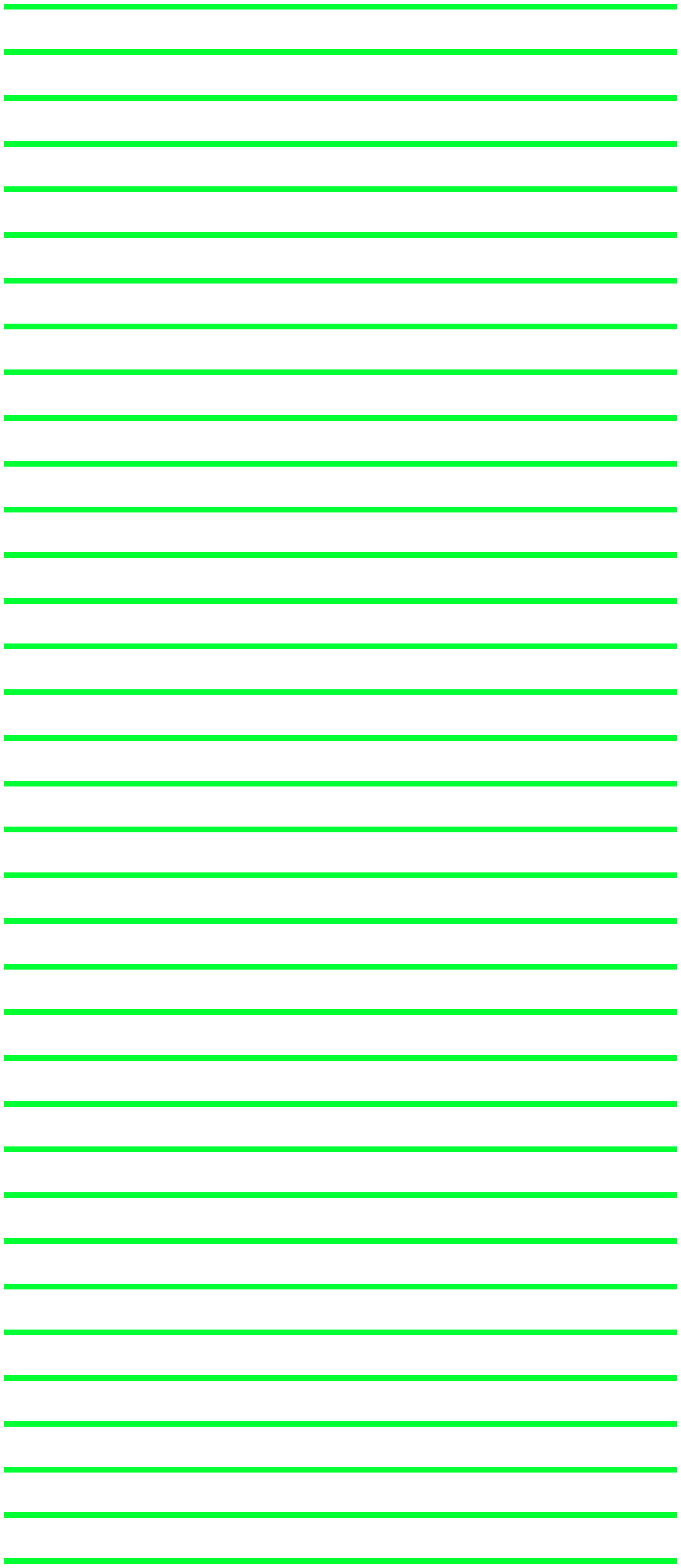
Putative conserved domains have been detected, click on the image below for detailed results.

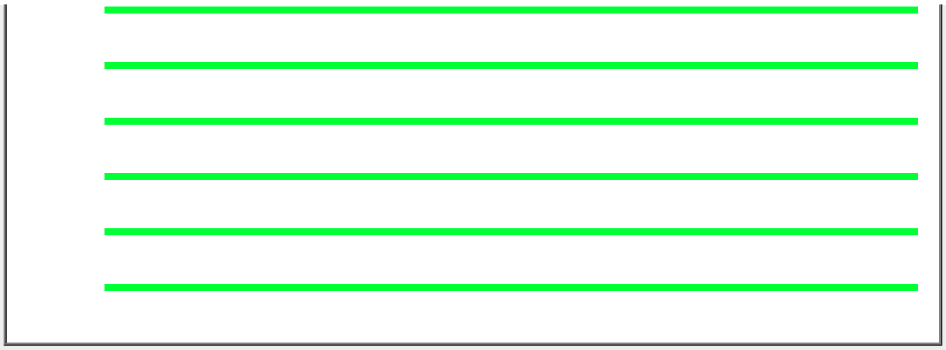


Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of The Fxia Catalytic Domain In Comple	70.2	70.2	100%	2e-12	100%	gi|56967287|1XX9_A
☐	Chain A, Factor Xia In Complex With The Inhibitor 3'-[(2s,4r)-6-carb	70.2	70.2	100%	2e-12	100%	gi|584579944|4NA7_A
☐	coagulation factor XI (plasma thromboplastin antecedent), isoform C	70.2	70.2	100%	3e-12	100%	gi|119625025|EAX04620.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]	70.2	70.2	100%	3e-12	100%	gi|675774870|XP_008975412.1
☐	PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes]	70.2	70.2	100%	3e-12	100%	gi|694909938|XP_009446987.1
☐	PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]	70.2	70.2	100%	3e-12	100%	gi|530377340|XP_005262880.1
☐	platelet factor XI [Homo sapiens]	70.2	70.2	100%	3e-12	100%	gi|3258649|AAC24506.1
☐	PREDICTED: coagulation factor XI [Gorilla gorilla gorilla]	70.2	70.2	100%	3e-12	100%	gi|426346208|XP_004040776.1
☐	PREDICTED: coagulation factor XI isoform X2 [Rhinopithecus roxel	70.2	70.2	100%	3e-12	100%	gi|724897372|XP_010376291.1
☐	PREDICTED: coagulation factor XI isoform X2 [Papio anubis]	70.2	70.2	100%	3e-12	100%	gi|685544400|XP_009206295.1
☐	PREDICTED: coagulation factor XI isoform X2 [Chlorocebus sabae	70.2	70.2	100%	3e-12	100%	gi|635046203|XP_007998683.1
☐	PREDICTED: coagulation factor XI isoform X2 [Macaca fascicularis	70.2	70.2	100%	3e-12	100%	gi|544436077|XP_005556541.1
☐	PREDICTED: coagulation factor XI isoform X3 [Pan troglodytes]	70.2	70.2	100%	3e-12	100%	gi|694909934|XP_009446985.1
☐	PREDICTED: coagulation factor XI isoform X6 [Homo sapiens]	70.2	70.2	100%	3e-12	100%	gi|578808899|XP_006714200.1
☐	PREDICTED: coagulation factor XI isoform X2 [Saimiri boliviensis b	70.2	70.2	100%	3e-12	100%	gi|725582190|XP_010342661.1
☐	hypothetical protein EGM_04467 [Macaca fascicularis]	70.2	70.2	100%	3e-12	100%	gi|355750969|EHH55296.1
☐	hypothetical protein EGK_16300 [Macaca mulatta]	70.2	70.2	100%	3e-12	100%	gi|355687768|EHH26352.1
☐	PREDICTED: coagulation factor XI isoform X1 [Rhinopithecus roxel	70.2	70.2	100%	3e-12	100%	gi|724897369|XP_010376290.1
☐	PREDICTED: coagulation factor XI isoform X1 [Chlorocebus sabae	70.2	70.2	100%	3e-12	100%	gi|635046201|XP_007998681.1
☐	coagulation factor XI [Homo sapiens]	70.2	70.2	100%	3e-12	100%	gi|180352|AAA51985.1
☐	PREDICTED: coagulation factor XI isoform X1 [Macaca fascicularis	70.2	70.2	100%	3e-12	100%	gi|544436075|XP_005556540.1
☐	coagulation factor XI precursor [Homo sapiens]	70.2	70.2	100%	3e-12	100%	gi|4503627|NP_000119.1
☐	PREDICTED: coagulation factor XI isoform X1 [Saimiri boliviensis b	70.2	70.2	100%	3e-12	100%	gi|725582188|XP_010342660.1
☐	PREDICTED: coagulation factor XI isoform X1 [Papio anubis]	70.2	70.2	100%	3e-12	100%	gi|402871005|XP_003899481.1
☐	PREDICTED: coagulation factor XI [Nomascus leucogenys]	70.2	70.2	100%	3e-12	100%	gi|332244773|XP_003271548.1
☐	PREDICTED: coagulation factor XI [Pongo abelii]	70.2	70.2	100%	3e-12	100%	gi|297674804|XP_002815399.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan troglodytes]	70.2	70.2	100%	3e-12	100%	gi|114597210|XP_001165847.1
☐	PREDICTED: coagulation factor XI isoform X1 [Pan troglodytes]	70.2	70.2	100%	3e-12	100%	gi|694909931|XP_009446984.1
☐	PREDICTED: coagulation factor XI isoform X1 [Homo sapiens]	70.2	70.2	100%	3e-12	100%	gi|530377336|XP_005262878.1

☐ PREDICTED: coagulation factor XI-like [Macaca mulatta]	70.2	70.2	100%	3e-12	100%	gi|297293811|XP_001090398.2
☐ PREDICTED: coagulation factor XI [Ictidomys tridecemlineatus]	68.1	68.1	100%	1e-11	95%	gi|532087072|XP_005329248.1
☐ Chain A, Crystal Structure Of The Catalytic Domain Of The Coagul	66.8	66.8	100%	3e-11	95%	gi|78101065|1ZHM_A
☐ Chain A, Crystal Structure Of The Catalytic Domain Of Coagulation	66.8	66.8	100%	3e-11	95%	gi|78101066|1ZHP_A
☐ Chain A, Crystal Structure Of The Fxia Catalytic Domain In Comple	66.8	66.8	100%	3e-11	95%	gi|56967291|1XXD_A
☐ PREDICTED: coagulation factor XI isoform X3 [Chinchilla lanigera]	66.8	66.8	100%	4e-11	95%	gi|533115754|XP_005373487.1
☐ coagulation factor XI precursor [Oryctolagus cuniculus]	66.8	66.8	100%	4e-11	95%	gi|130502142|NP_001076261.1
☐ PREDICTED: coagulation factor XI isoform 2 [Ceratotherium simu	66.8	66.8	100%	4e-11	95%	gi|478509096|XP_004428828.1
☐ PREDICTED: coagulation factor XI [Tarsius syrichta]	66.8	66.8	100%	4e-11	95%	gi|640821392|XP_008067645.1
☐ PREDICTED: coagulation factor XI isoform X1 [Chinchilla lanigera]	66.8	66.8	100%	4e-11	95%	gi|533115750|XP_005373485.1
☐ PREDICTED: coagulation factor XI isoform 1 [Ceratotherium simu	66.8	66.8	100%	4e-11	95%	gi|478509094|XP_004428827.1
☐ PREDICTED: coagulation factor XI [Mesocricetus auratus]	66.8	66.8	100%	4e-11	95%	gi|524924928|XP_005066710.1
☐ PREDICTED: coagulation factor XI [Cavia porcellus]	66.8	66.8	100%	4e-11	95%	gi|348566839|XP_003469209.1
☐ PREDICTED: coagulation factor XI [Callithrix jacchus]	65.1	65.1	100%	2e-10	95%	gi|296195030|XP_002745209.1
☐ Chain A, Crystal Structure Of Factor Xia In Complex With Clavatadi	64.7	64.7	100%	2e-10	95%	gi|217035335|3BG8_A
☐ Chain A, Factor Xia In Complex With A Clorophenyl-tetrazole Inhibi	64.7	64.7	100%	2e-10	95%	gi|383875445|3SOR_A
☐ Chain A, Factor Xi Catalytic Domain Complexed With N-((R)-1-(4-	64.7	64.7	100%	2e-10	95%	gi|109157010|1ZPZ_A
☐ PREDICTED: coagulation factor XI [Ochotona princeps]	64.7	64.7	100%	2e-10	90%	gi|504133468|XP_004579306.1
☐ PREDICTED: coagulation factor XI [Sorex araneus]	64.3	64.3	100%	3e-10	90%	gi|505830321|XP_004610458.1
☐ PREDICTED: coagulation factor XI isoform X7 [Heterocephalus gla	63.8	63.8	100%	4e-10	90%	gi|512982233|XP_004853113.1
☐ PREDICTED: coagulation factor XI isoform X6 [Heterocephalus gla	63.8	63.8	100%	4e-10	90%	gi|512892532|XP_004897313.1
☐ PREDICTED: coagulation factor XI isoform X4 [Fukomys damarens	63.8	63.8	100%	4e-10	90%	gi|731206526|XP_010618090.1
☐ PREDICTED: coagulation factor XI isoform X6 [Heterocephalus gla	63.8	63.8	100%	4e-10	90%	gi|512982231|XP_004853112.1
☐ PREDICTED: coagulation factor XI isoform X5 [Heterocephalus gla	63.8	63.8	100%	4e-10	90%	gi|512892528|XP_004897312.1
☐ PREDICTED: coagulation factor XI isoform X4 [Heterocephalus gla	63.8	63.8	100%	4e-10	90%	gi|512892524|XP_004897311.1
☐ PREDICTED: coagulation factor XI isoform X5 [Heterocephalus gla	63.8	63.8	100%	4e-10	90%	gi|512982229|XP_004853111.1
☐ PREDICTED: coagulation factor XI isoform X3 [Fukomys damarens	63.8	63.8	100%	4e-10	90%	gi|731206524|XP_010618089.1
☐ Coagulation factor XI [Heterocephalus glaber]	63.8	63.8	100%	4e-10	90%	gi|351708043|EHB10962.1
☐ PREDICTED: coagulation factor XI isoform X4 [Heterocephalus gla	63.8	63.8	100%	4e-10	90%	gi|512982227|XP_004853110.1
☐ PREDICTED: coagulation factor XI isoform X3 [Heterocephalus gla	63.8	63.8	100%	4e-10	90%	gi|512892520|XP_004897310.1
☐ PREDICTED: coagulation factor XI isoform X2 [Fukomys damarens	63.8	63.8	100%	4e-10	90%	gi|731206521|XP_010618088.1
☐ PREDICTED: coagulation factor XI isoform X1 [Fukomys damarens	63.8	63.8	100%	4e-10	90%	gi|731206515|XP_010618085.1
☐ PREDICTED: coagulation factor XI [Nannospalax galili]	63.8	84.4	100%	4e-10	90%	gi|674087872|XP_008851827.1
☐ PREDICTED: coagulation factor XI isoform X2 [Heterocephalus gla	63.8	63.8	100%	4e-10	90%	gi|512982223|XP_004853108.1
☐ PREDICTED: coagulation factor XI isoform X1 [Heterocephalus gla	63.8	63.8	100%	4e-10	90%	gi|512892512|XP_004897308.1
☐ PREDICTED: coagulation factor XI isoform X1 [Heterocephalus gla	63.8	63.8	100%	4e-10	90%	gi|512982221|XP_004853107.1
☐ PREDICTED: coagulation factor XI isoform X2 [Heterocephalus gla	63.8	63.8	100%	4e-10	90%	gi|512892516|XP_004897309.1
☐ PREDICTED: coagulation factor XI [Erinaceus europaeus]	63.8	63.8	100%	4e-10	90%	gi|617577865|XP_007517757.1
☐ PREDICTED: coagulation factor XI [Dasypus novemcinctus]	63.4	63.4	100%	6e-10	90%	gi|488532217|XP_004457855.1
☐ PREDICTED: coagulation factor XI [Ovis aries]	63.4	63.4	100%	6e-10	90%	gi|426256280|XP_004021769.1
☐ blood coagulation factor XI [Bos taurus]	62.6	62.6	100%	1e-09	90%	gi|45758733|AAS76646.1
☐ PREDICTED: coagulation factor XI [Bos mutus]	62.6	62.6	100%	1e-09	90%	gi|555974149|XP_005899069.1
☐ PREDICTED: coagulation factor XI isoform X2 [Leptonychotes wed	62.1	62.1	100%	2e-09	86%	gi|585180453|XP_006741890.1
☐ PREDICTED: coagulation factor XI isoform 3 [Odobenus rosmarus	62.1	62.1	100%	2e-09	86%	gi|472396395|XP_004417424.1
☐ PREDICTED: coagulation factor XI-like [Ailuropoda melanoleuca]	62.1	62.1	100%	2e-09	86%	gi|301776062|XP_002923450.1
☐ PREDICTED: coagulation factor XI [Lipotes vexillifer]	62.1	62.1	100%	2e-09	90%	gi|602712769|XP_007466613.1

☐	PREDICTED: coagulation factor XI [Balaenoptera acutorostrata sca	62.1	62.1	100%	2e-09	90%	gi|594650157|XP_007174042.1
☐	PREDICTED: coagulation factor XI [Physeter catodon]	62.1	62.1	100%	2e-09	90%	gi|593742188|XP_007126520.1
☐	PREDICTED: coagulation factor XI [Jaculus jaculus]	62.1	62.1	95%	2e-09	90%	gi|507565537|XP_004666428.1
☐	PREDICTED: coagulation factor XI isoform X3 [Leptonychotes wed	62.1	62.1	100%	2e-09	86%	gi|585180455|XP_006741891.1
☐	PREDICTED: coagulation factor XI isoform 2 [Odobenus rosmarus	62.1	62.1	100%	2e-09	86%	gi|472396393|XP_004417423.1
☐	PREDICTED: coagulation factor XI [Orcinus orca]	62.1	62.1	100%	2e-09	90%	gi|466045508|XP_004277238.1
☐	PREDICTED: coagulation factor XI isoform X1 [Leptonychotes wed	62.1	62.1	100%	2e-09	86%	gi|585180451|XP_006741889.1
☐	PREDICTED: coagulation factor XI [Mustela putorius furo]	62.1	62.1	100%	2e-09	86%	gi|511876760|XP_004758357.1
☐	PREDICTED: coagulation factor XI isoform 1 [Odobenus rosmarus	62.1	62.1	100%	2e-09	86%	gi|472396391|XP_004417422.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Urs	62.1	62.1	100%	2e-09	86%	gi|671035736|XP_008708722.1
☐	PREDICTED: coagulation factor XI [Equus caballus]	61.7	61.7	100%	2e-09	90%	gi|149742758|XP_001490330.1
☐	PREDICTED: coagulation factor XI [Vicugna pacos]	61.7	61.7	100%	2e-09	90%	gi|560951202|XP_006198143.1
☐	PREDICTED: coagulation factor XI [Equus przewalskii]	61.7	61.7	100%	2e-09	90%	gi|664778079|XP_008508352.1
☐	PREDICTED: coagulation factor XI [Camelus ferus]	61.7	61.7	100%	2e-09	90%	gi|560904135|XP_006178431.1
☐	Chain A, Crystal Structure Of The Catalytic Domain Of Coagulation	61.3	61.3	100%	2e-09	90%	gi|75765761|1ZJD_A
☐	Chain A, Factor Xi Catalytic Domain Complexed With 2-Guanidino-	61.3	61.3	100%	2e-09	90%	gi|109156985|1ZLR_A
☐	Chain A, Crystal Structure Of The Catalytic Domain Of Coagulation	61.3	61.3	100%	2e-09	90%	gi|78101067|1ZHR_A
☐	PREDICTED: coagulation factor XI [Otolemur garnettii]	61.3	61.3	100%	3e-09	90%	gi|395840032|XP_003792872.1
☐	coagulation factor XI precursor [Canis lupus familiaris]	60.9	60.9	100%	4e-09	86%	gi|205361194|NP_001128595.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Pan	60.9	60.9	100%	4e-09	86%	gi|591347751|XP_007099050.1
☐	PREDICTED: coagulation factor XI isoform X2 [Canis lupus familiar	60.9	60.9	100%	4e-09	86%	gi|545526400|XP_005629983.1
☐	PREDICTED: coagulation factor XI [Trichechus manatus latirostris]	60.9	60.9	95%	4e-09	90%	gi|471399784|XP_004382857.1
☐	PREDICTED: coagulation factor XI [Felis catus]	60.9	60.9	100%	4e-09	86%	gi|410956035|XP_003984650.1
☐	PREDICTED: coagulation factor XI isoform X1 [Canis lupus familiar	60.9	60.9	100%	4e-09	86%	gi|545526398|XP_005629982.1
☐	PREDICTED: coagulation factor XI [Cricetulus griseus]	60.4	60.4	100%	6e-09	86%	gi|354490732|XP_003507510.1

⊟ Alignments

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Chain A, Crystal Structure Of The Fxia Catalytic Domain In Complex With Ecotinm84r

Sequence ID: gi|56967287|pdb|1XX9|A **Length:** 238 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 98 to 118 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.2 bits(158)	2e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KLETTVNYTDSQRPICLPSKG  21
            KLETTVNYTDSQRPICLPSKG
Sbjct  98   KLETTVNYTDSQRPICLPSKG  118
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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Chain A, Factor Xia In Complex With The Inhibitor 3'-[(2s,4r)-6-carbamimidoyl- 4-methyl-4-phenyl-1,2,3,4-tetrahydroquinolin-2-yl]-4-carbamoyl-5'- [(3-methylbutanoyl)amino]biphenyl-2-carboxylic Acid

Sequence ID: gi|584579944|pdb|4NA7|A **Length:** 244 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 98 to 118 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.2 bits(158)	2e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KLETTVNYTDSQRPICLPSKG  21
            KLETTVNYTDSQRPICLPSKG
Sbjct  98   KLETTVNYTDSQRPICLPSKG  118
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

coagulation factor XI (plasma thromboplastin antecedent), isoform CRA_b [Homo sapiens]

Sequence ID: gi|119625025|gb|EAX04620.1| **Length:** 470 **Number of Matches:** 1

Range 1: 330 to 350 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.2 bits(158)	3e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KLETTVNYTDSQRPICLPSKG  21
            KLETTVNYTDSQRPICLPSKG
Sbjct  330  KLETTVNYTDSQRPICLPSKG  350
```

Related Information

Gene - associated gene details

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]

Sequence ID: gi|675774870|ref|XP_008975412.1| **Length:** 535 **Number of Matches:** 1

Range 1: 395 to 415 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.2 bits(158)	3e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KLETTVNYTDSQRPICLPSKG  21
            KLETTVNYTDSQRPICLPSKG
Sbjct  395  KLETTVNYTDSQRPICLPSKG  415
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes]

Sequence ID: gi|694909938|ref|XP_009446987.1| **Length:** 536 **Number of Matches:** 1

Range 1: 396 to 416 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.2 bits(158)	3e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KLETTVNYTDSQRPICLPSKG  21
            KLETTVNYTDSQRPICLPSKG
Sbjct  396  KLETTVNYTDSQRPICLPSKG  416
```

Related Information

Gene - associated gene details

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F11_KLETTVNYTDSQRPICLPSKGDRN_NonMod

RID B94V42ZZ01R (Expires on 01-14 10:39 am)

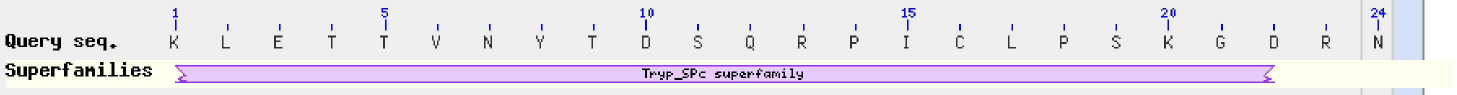
Query ID	lcl|304046	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	24		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

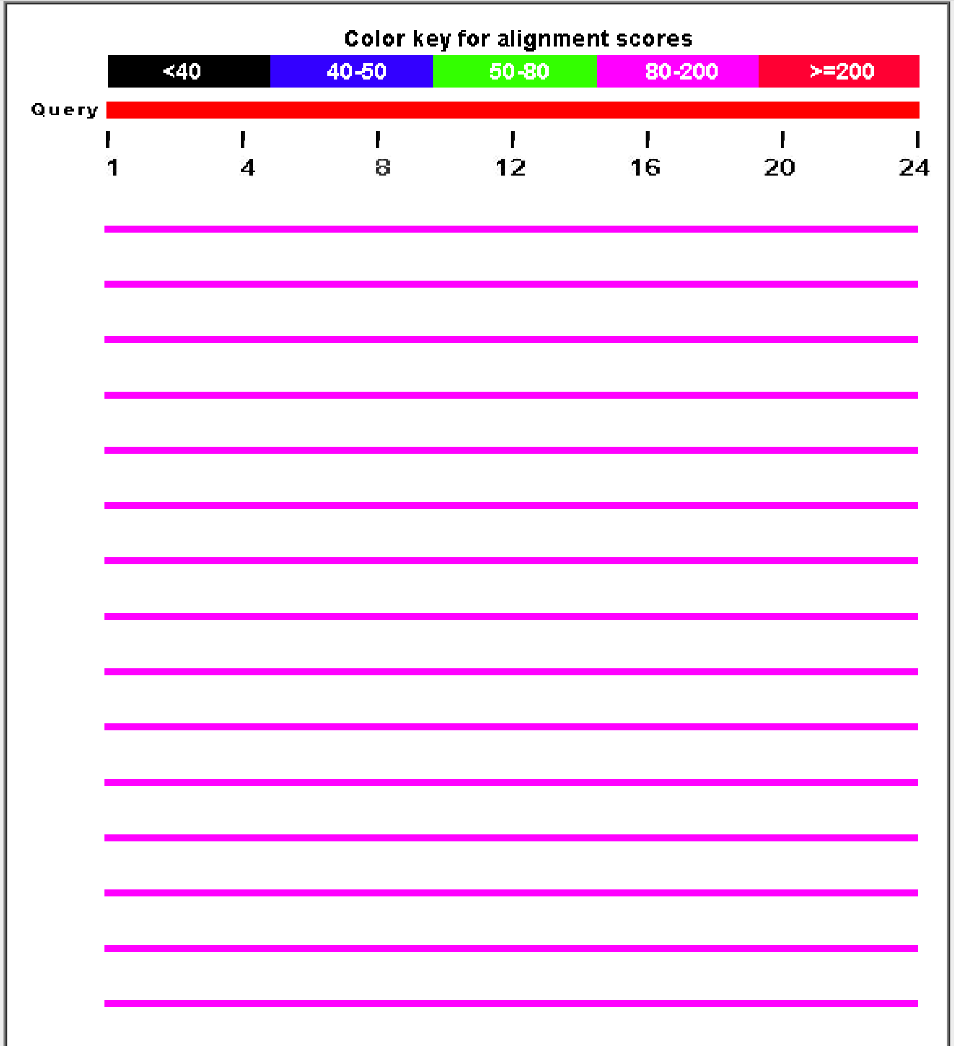
Show Conserved Domains

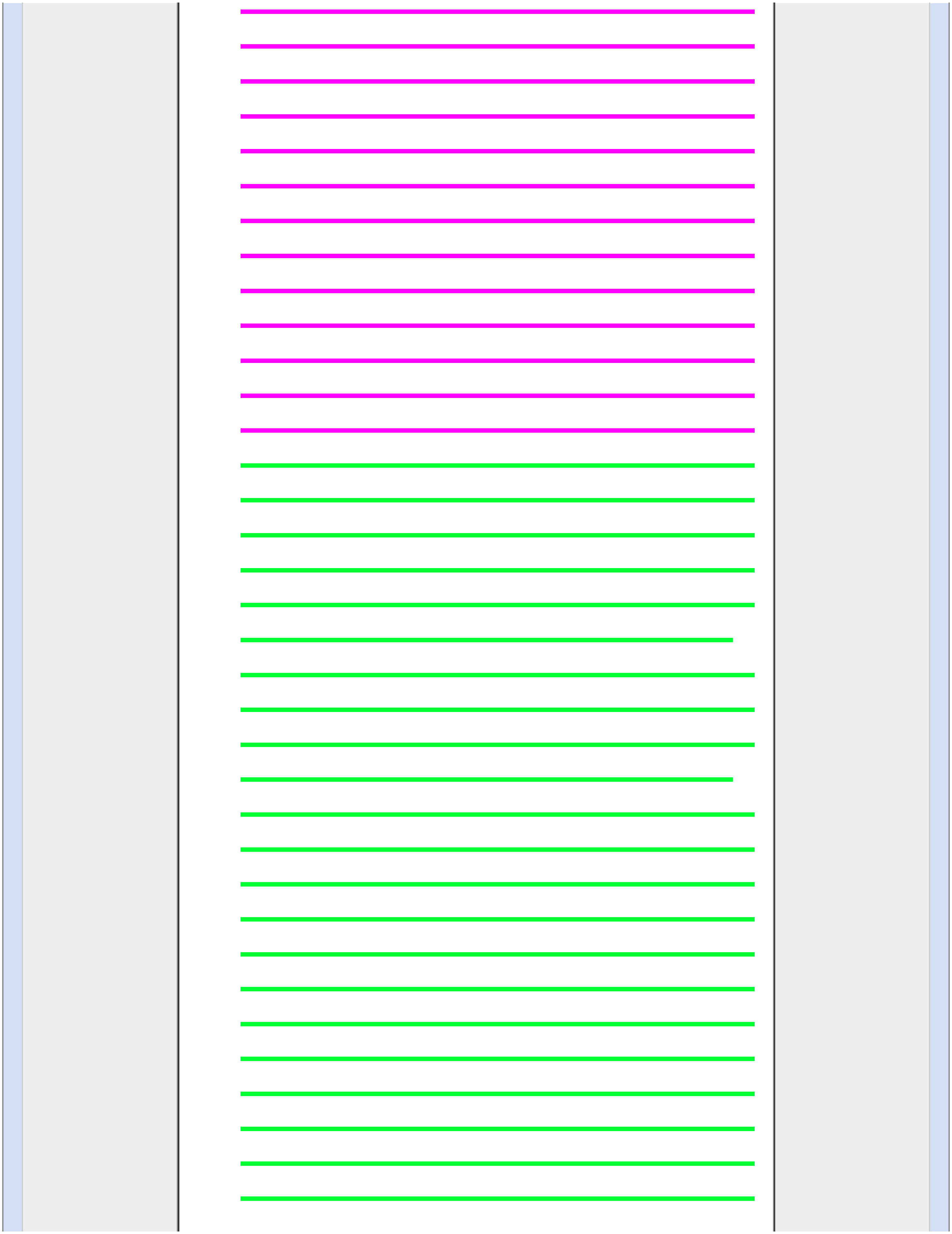
Putative conserved domains have been detected, click on the image below for detailed results.

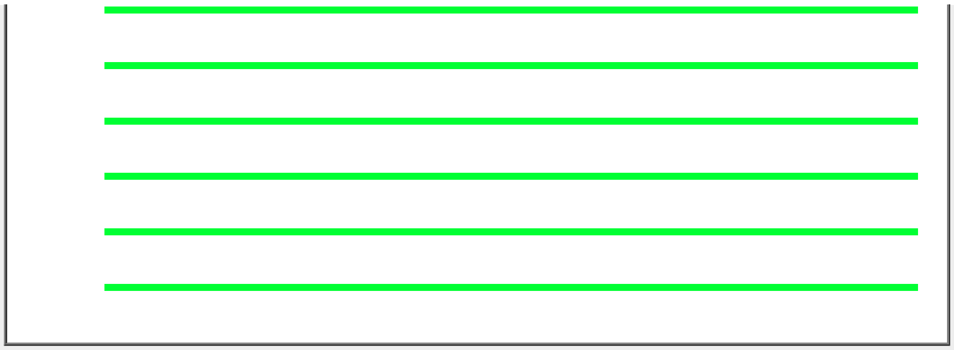


Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of The Fxia Catalytic Domain In Comple	80.4	80.4	100%	1e-15	100%	gi|56967287|1XX9_A
☐	Chain A, Factor Xia In Complex With The Inhibitor 3'-[(2s,4r)-6-carb	80.4	80.4	100%	1e-15	100%	gi|584579944|4NA7_A
☐	coagulation factor XI (plasma thromboplastin antecedent), isoform C	80.4	80.4	100%	1e-15	100%	gi|119625025|EAX04620.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]	80.4	80.4	100%	1e-15	100%	gi|675774870|XP_008975412.1
☐	PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes]	80.4	80.4	100%	1e-15	100%	gi|694909938|XP_009446987.1
☐	PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]	80.4	80.4	100%	1e-15	100%	gi|530377340|XP_005262880.1
☐	platelet factor XI [Homo sapiens]	80.4	80.4	100%	1e-15	100%	gi|3258649|AAC24506.1
☐	PREDICTED: coagulation factor XI [Gorilla gorilla gorilla]	80.4	80.4	100%	1e-15	100%	gi|426346208|XP_004040776.1
☐	PREDICTED: coagulation factor XI isoform X2 [Rhinopithecus roxel	80.4	80.4	100%	1e-15	100%	gi|724897372|XP_010376291.1
☐	PREDICTED: coagulation factor XI isoform X2 [Papio anubis]	80.4	80.4	100%	1e-15	100%	gi|685544400|XP_009206295.1
☐	PREDICTED: coagulation factor XI isoform X2 [Chlorocebus sabae	80.4	80.4	100%	1e-15	100%	gi|635046203|XP_007998683.1
☐	PREDICTED: coagulation factor XI isoform X2 [Macaca fascicularis	80.4	80.4	100%	1e-15	100%	gi|544436077|XP_005556541.1
☐	PREDICTED: coagulation factor XI isoform X3 [Pan troglodytes]	80.4	80.4	100%	1e-15	100%	gi|694909934|XP_009446985.1
☐	PREDICTED: coagulation factor XI isoform X6 [Homo sapiens]	80.4	80.4	100%	1e-15	100%	gi|578808899|XP_006714200.1
☐	hypothetical protein EGM_04467 [Macaca fascicularis]	80.4	80.4	100%	1e-15	100%	gi|355750969|EHH55296.1
☐	hypothetical protein EGK_16300 [Macaca mulatta]	80.4	80.4	100%	1e-15	100%	gi|355687768|EHH26352.1
☐	PREDICTED: coagulation factor XI isoform X1 [Rhinopithecus roxel	80.4	80.4	100%	1e-15	100%	gi|724897369|XP_010376290.1
☐	PREDICTED: coagulation factor XI isoform X1 [Chlorocebus sabae	80.4	80.4	100%	1e-15	100%	gi|635046201|XP_007998681.1
☐	coagulation factor XI [Homo sapiens]	80.4	80.4	100%	1e-15	100%	gi|180352|AAA51985.1
☐	PREDICTED: coagulation factor XI isoform X1 [Macaca fascicularis	80.4	80.4	100%	1e-15	100%	gi|544436075|XP_005556540.1
☐	coagulation factor XI precursor [Homo sapiens]	80.4	80.4	100%	1e-15	100%	gi|4503627|NP_000119.1
☐	PREDICTED: coagulation factor XI isoform X1 [Papio anubis]	80.4	80.4	100%	1e-15	100%	gi|402871005|XP_003899481.1
☐	PREDICTED: coagulation factor XI [Nomascus leucogenys]	80.4	80.4	100%	1e-15	100%	gi|332244773|XP_003271548.1
☐	PREDICTED: coagulation factor XI [Pongo abelii]	80.4	80.4	100%	1e-15	100%	gi|297674804|XP_002815399.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan troglodytes]	80.4	80.4	100%	1e-15	100%	gi|114597210|XP_001165847.1
☐	PREDICTED: coagulation factor XI isoform X1 [Pan troglodytes]	80.4	80.4	100%	1e-15	100%	gi|694909931|XP_009446984.1
☐	PREDICTED: coagulation factor XI isoform X1 [Homo sapiens]	80.4	80.4	100%	1e-15	100%	gi|530377336|XP_005262878.1
☐	PREDICTED: coagulation factor XI-like [Macaca mulatta]	80.4	80.4	100%	1e-15	100%	gi|297293811|XP_001090398.2
☐	PREDICTED: coagulation factor XI [Ictidomys tridecemlineatus]	78.3	78.3	100%	7e-15	96%	gi|532087072|XP_005329248.1

☐ Chain A, Crystal Structure Of The Catalytic Domain Of The Coagula	77.0	77.0	100%	2e-14	96%	gi|78101065|1ZHM_A
☐ Chain A, Crystal Structure Of The Catalytic Domain Of Coagulation	77.0	77.0	100%	2e-14	96%	gi|78101066|1ZHP_A
☐ Chain A, Crystal Structure Of The Fxia Catalytic Domain In Comple	77.0	77.0	100%	2e-14	96%	gi|56967291|1XXD_A
☐ PREDICTED: coagulation factor XI isoform X3 [Chinchilla lanigera]	77.0	77.0	100%	2e-14	96%	gi|533115754|XP_005373487.1
☐ PREDICTED: coagulation factor XI isoform X2 [Saimiri boliviensis b	77.0	77.0	95%	2e-14	100%	gi|725582190|XP_010342661.1
☐ coagulation factor XI precursor [Oryctolagus cuniculus]	77.0	77.0	100%	2e-14	96%	gi|130502142|NP_001076261.1
☐ PREDICTED: coagulation factor XI [Tarsius syrichta]	77.0	77.0	100%	2e-14	96%	gi|640821392|XP_008067645.1
☐ PREDICTED: coagulation factor XI isoform X1 [Chinchilla lanigera]	77.0	77.0	100%	2e-14	96%	gi|533115750|XP_005373485.1
☐ PREDICTED: coagulation factor XI isoform X1 [Saimiri boliviensis b	77.0	77.0	95%	2e-14	100%	gi|725582188|XP_010342660.1
☐ PREDICTED: coagulation factor XI [Mesocricetus auratus]	77.0	77.0	100%	2e-14	96%	gi|524924928|XP_005066710.1
☐ PREDICTED: coagulation factor XI [Cavia porcellus]	77.0	77.0	100%	2e-14	96%	gi|348566839|XP_003469209.1
☐ Chain A, Factor Xia In Complex With A Clorophenyl-tetrazole Inhibi	74.9	74.9	100%	8e-14	96%	gi|383875445|3SOR_A
☐ Chain A, Factor Xi Catalytic Domain Complexed With N-((R)-1-(4- E	74.9	74.9	100%	8e-14	96%	gi|109157010|1ZPZ_A
☐ PREDICTED: coagulation factor XI [Sorex araneus]	74.4	74.4	100%	1e-13	92%	gi|505830321|XP_004610458.1
☐ PREDICTED: coagulation factor XI isoform X7 [Heterocephalus glal	74.0	74.0	100%	2e-13	92%	gi|512982233|XP_004853113.1
☐ PREDICTED: coagulation factor XI isoform X6 [Heterocephalus glal	74.0	74.0	100%	2e-13	92%	gi|512892532|XP_004897313.1
☐ PREDICTED: coagulation factor XI isoform X4 [Fukomys damarens	74.0	74.0	100%	2e-13	92%	gi|731206526|XP_010618090.1
☐ PREDICTED: coagulation factor XI isoform X6 [Heterocephalus glal	74.0	74.0	100%	2e-13	92%	gi|512982231|XP_004853112.1
☐ PREDICTED: coagulation factor XI isoform X5 [Heterocephalus glal	74.0	74.0	100%	2e-13	92%	gi|512892528|XP_004897312.1
☐ PREDICTED: coagulation factor XI isoform X4 [Heterocephalus glal	74.0	74.0	100%	2e-13	92%	gi|512892524|XP_004897311.1
☐ PREDICTED: coagulation factor XI isoform X5 [Heterocephalus glal	74.0	74.0	100%	2e-13	92%	gi|512982229|XP_004853111.1
☐ PREDICTED: coagulation factor XI isoform X3 [Fukomys damarens	74.0	74.0	100%	2e-13	92%	gi|731206524|XP_010618089.1
☐ Coagulation factor XI [Heterocephalus glaber]	74.0	74.0	100%	2e-13	92%	gi|351708043|EHB10962.1
☐ PREDICTED: coagulation factor XI isoform X4 [Heterocephalus glal	74.0	74.0	100%	2e-13	92%	gi|512982227|XP_004853110.1
☐ PREDICTED: coagulation factor XI isoform X3 [Heterocephalus glal	74.0	74.0	100%	2e-13	92%	gi|512892520|XP_004897310.1
☐ PREDICTED: coagulation factor XI isoform X2 [Fukomys damarens	74.0	74.0	100%	2e-13	92%	gi|731206521|XP_010618088.1
☐ PREDICTED: coagulation factor XI isoform X1 [Fukomys damarens	74.0	74.0	100%	2e-13	92%	gi|731206515|XP_010618085.1
☐ PREDICTED: coagulation factor XI [Nannospalax galili]	74.0	94.6	100%	2e-13	92%	gi|674087872|XP_008851827.1
☐ PREDICTED: coagulation factor XI isoform X2 [Heterocephalus glal	74.0	74.0	100%	2e-13	92%	gi|512982223|XP_004853108.1
☐ PREDICTED: coagulation factor XI isoform X1 [Heterocephalus glal	74.0	74.0	100%	2e-13	92%	gi|512892512|XP_004897308.1
☐ PREDICTED: coagulation factor XI isoform X1 [Heterocephalus glal	74.0	74.0	100%	2e-13	92%	gi|512982221|XP_004853107.1
☐ PREDICTED: coagulation factor XI isoform X2 [Heterocephalus glal	74.0	74.0	100%	2e-13	92%	gi|512892516|XP_004897309.1
☐ PREDICTED: coagulation factor XI [Erinaceus europaeus]	74.0	74.0	100%	2e-13	92%	gi|617577865|XP_007517757.1
☐ PREDICTED: coagulation factor XI isoform 2 [Ceratotherium simum	73.6	73.6	100%	3e-13	92%	gi|478509096|XP_004428828.1
☐ PREDICTED: coagulation factor XI isoform 1 [Ceratotherium simum	73.6	73.6	100%	3e-13	92%	gi|478509094|XP_004428827.1
☐ PREDICTED: coagulation factor XI [Ovis aries]	73.6	73.6	100%	3e-13	92%	gi|426256280|XP_004021769.1
☐ blood coagulation factor XI [Bos taurus]	72.7	72.7	100%	6e-13	92%	gi|45758733|AAS76646.1
☐ PREDICTED: coagulation factor XI [Bos mutus]	72.7	72.7	100%	6e-13	92%	gi|555974149|XP_005899069.1
☐ Chain A, Crystal Structure Of Factor Xia In Complex With Clavatadi	72.3	72.3	100%	6e-13	92%	gi|217035335|3BG8_A
☐ PREDICTED: coagulation factor XI isoform X2 [Leptonychotes wed	72.3	72.3	100%	8e-13	88%	gi|585180453|XP_006741890.1
☐ PREDICTED: coagulation factor XI isoform 3 [Odobenus rosmarus	72.3	72.3	100%	8e-13	88%	gi|472396395|XP_004417424.1
☐ PREDICTED: coagulation factor XI-like [Ailuropoda melanoleuca]	72.3	72.3	100%	8e-13	88%	gi|301776062|XP_002923450.1
☐ PREDICTED: coagulation factor XI [Lipotes vexillifer]	72.3	72.3	100%	8e-13	92%	gi|602712769|XP_007466613.1
☐ PREDICTED: coagulation factor XI [Balaenoptera acutorostrata sca	72.3	72.3	100%	8e-13	92%	gi|594650157|XP_007174042.1
☐ PREDICTED: coagulation factor XI [Physeter catodon]	72.3	72.3	100%	8e-13	92%	gi|593742188|XP_007126520.1
☐ PREDICTED: coagulation factor XI [Jaculus jaculus]	72.3	72.3	95%	8e-13	91%	gi|507565537|XP_004666428.1

☐	PREDICTED: coagulation factor XI isoform X3 [Leptonychotes wed	72.3	72.3	100%	8e-13	88%	gi|585180455|XP_006741891.1
☐	PREDICTED: coagulation factor XI isoform 2 [Odobenus rosmarus	72.3	72.3	100%	8e-13	88%	gi|472396393|XP_004417423.1
☐	PREDICTED: coagulation factor XI [Orcinus orca]	72.3	72.3	100%	8e-13	92%	gi|466045508|XP_004277238.1
☐	PREDICTED: coagulation factor XI isoform X1 [Leptonychotes wed	72.3	72.3	100%	8e-13	88%	gi|585180451|XP_006741889.1
☐	PREDICTED: coagulation factor XI [Mustela putorius furo]	72.3	72.3	100%	8e-13	88%	gi|511876760|XP_004758357.1
☐	PREDICTED: coagulation factor XI isoform 1 [Odobenus rosmarus	72.3	72.3	100%	8e-13	88%	gi|472396391|XP_004417422.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Urs	72.3	72.3	100%	8e-13	88%	gi|671035736|XP_008708722.1
☐	PREDICTED: coagulation factor XI [Vicugna pacos]	71.9	71.9	100%	1e-12	92%	gi|560951202|XP_006198143.1
☐	PREDICTED: coagulation factor XI [Callithrix jacchus]	71.9	71.9	95%	1e-12	96%	gi|296195030|XP_002745209.1
☐	PREDICTED: coagulation factor XI [Camelus ferus]	71.9	71.9	100%	1e-12	92%	gi|560904135|XP_006178431.1
☐	Chain A, Crystal Structure Of The Catalytic Domain Of Coagulation	71.5	71.5	100%	1e-12	92%	gi|75765761|1ZJD_A
☐	Chain A, Factor Xi Catalytic Domain Complexed With 2-Guanidino-	71.5	71.5	100%	1e-12	92%	gi|109156985|1ZLR_A
☐	Chain A, Crystal Structure Of The Catalytic Domain Of Coagulation	71.5	71.5	100%	1e-12	92%	gi|78101067|1ZHR_A
☐	PREDICTED: coagulation factor XI [Ochotona princeps]	71.5	71.5	95%	2e-12	91%	gi|504133468|XP_004579306.1
☐	coagulation factor XI precursor [Canis lupus familiaris]	71.0	71.0	100%	2e-12	88%	gi|205361194|NP_001128595.1
☐	PREDICTED: coagulation factor XI [Dasypus novemcinctus]	71.0	71.0	100%	2e-12	88%	gi|488532217|XP_004457855.1
☐	PREDICTED: coagulation factor XI isoform X2 [Canis lupus familiar	71.0	71.0	100%	2e-12	88%	gi|545526400|XP_005629983.1
☐	PREDICTED: coagulation factor XI isoform X1 [Canis lupus familiar	71.0	71.0	100%	2e-12	88%	gi|545526398|XP_005629982.1
☐	Chain A, Factor Xia In Complex With The Inhibitor 4-{2-[(1s)-1-({[tra	70.2	70.2	100%	3e-12	92%	gi|728055500|4TY6_A
☐	PREDICTED: coagulation factor XI [Trichechus manatus latirostris]	70.2	70.2	100%	4e-12	88%	gi|471399784|XP_004382857.1
☐	PREDICTED: coagulation factor XI [Bubalus bubalis]	69.4	69.4	100%	8e-12	88%	gi|594073052|XP_006060352.1
☐	PREDICTED: coagulation factor XI [Pantholops hodgsonii]	69.4	69.4	100%	8e-12	88%	gi|556754529|XP_005972629.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Ech	69.4	69.4	100%	8e-12	88%	gi|507618988|XP_004696215.1
☐	coagulation factor XI precursor [Bos taurus]	69.4	69.4	100%	8e-12	88%	gi|56710319|NP_001008665.1
☐	TPA: coagulation factor XI precursor [Bos taurus]	69.4	69.4	100%	8e-12	88%	gi|296472409|DAA14524.1

⊟ Alignments

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Chain A, Crystal Structure Of The Fxia Catalytic Domain In Complex With Ecotinm84r

Sequence ID: gi|56967287|pdb|1XX9|A **Length:** 238 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 98 to 121 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	1e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KLETTVNYTDSQRPICLPSKGDRN  24
            KLETTVNYTDSQRPICLPSKGDRN
Sbjct  98   KLETTVNYTDSQRPICLPSKGDRN  121
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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Chain A, Factor Xia In Complex With The Inhibitor 3'-[(2s,4r)-6-carbamimidoyl- 4-methyl-4-phenyl-1,2,3,4-tetrahydroquinolin-2-yl]-4-carbamoyl-5'- [(3-methylbutanoyl)amino]biphenyl-2-carboxylic Acid

Sequence ID: gi|584579944|pdb|4NA7|A **Length:** 244 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 98 to 121 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	1e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KLETTVNYTDSQRPICLPSKGDRN  24
            KLETTVNYTDSQRPICLPSKGDRN
Sbjct  98   KLETTVNYTDSQRPICLPSKGDRN  121
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

coagulation factor XI (plasma thromboplastin antecedent), isoform CRA_b [Homo sapiens]

Sequence ID: gi|119625025|gb|EAX04620.1| **Length:** 470 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 330 to 353 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	1e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KLETTVNYTDSQRPICLPSKGDRN  24
            KLETTVNYTDSQRPICLPSKGDRN
Sbjct  330  KLETTVNYTDSQRPICLPSKGDRN  353
```

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PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]

Sequence ID: gi|675774870|ref|XP_008975412.1| **Length:** 535 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 395 to 418 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	1e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KLETTVNYTDSQRPICLPSKGDRN  24
            KLETTVNYTDSQRPICLPSKGDRN
Sbjct  395  KLETTVNYTDSQRPICLPSKGDRN  418
```

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PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes]

Sequence ID: gi|694909938|ref|XP_009446987.1| **Length:** 536 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 396 to 419 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	1e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KLETTVNYTDSQRPICLPSKGDRN  24
            KLETTVNYTDSQRPICLPSKGDRN
Sbjct  396  KLETTVNYTDSQRPICLPSKGDRN  419
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BTH2V5DS016

Your search parameters were adjusted to search for a short input sequence.

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F11_RVYSGILDQSEIKE_Mod

RID	BTH2V5DS016 (Expires on 01-20 15:46 pm)
Query ID	lcl|63587
Description	None
Molecule type	amino acid
Query Length	14

Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

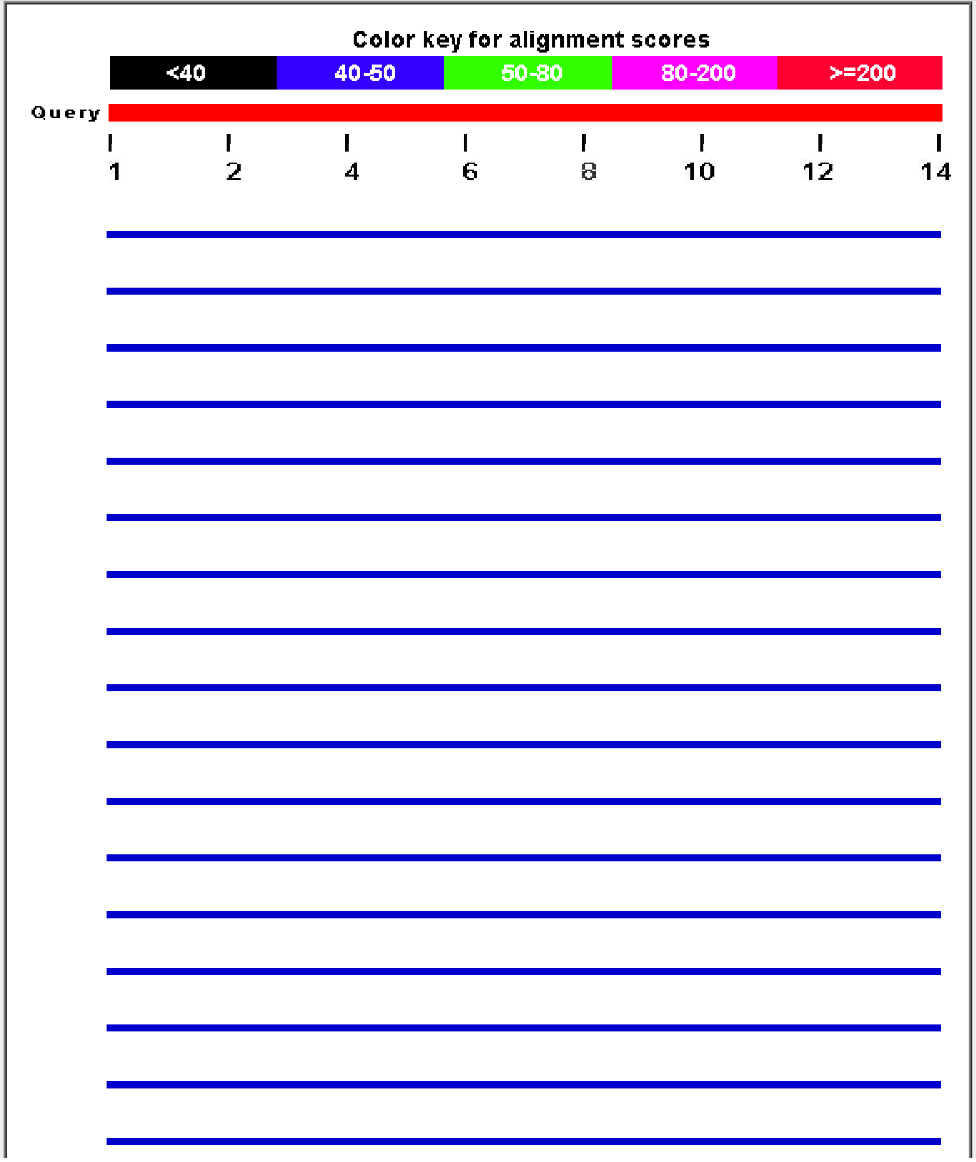
Graphic Summary

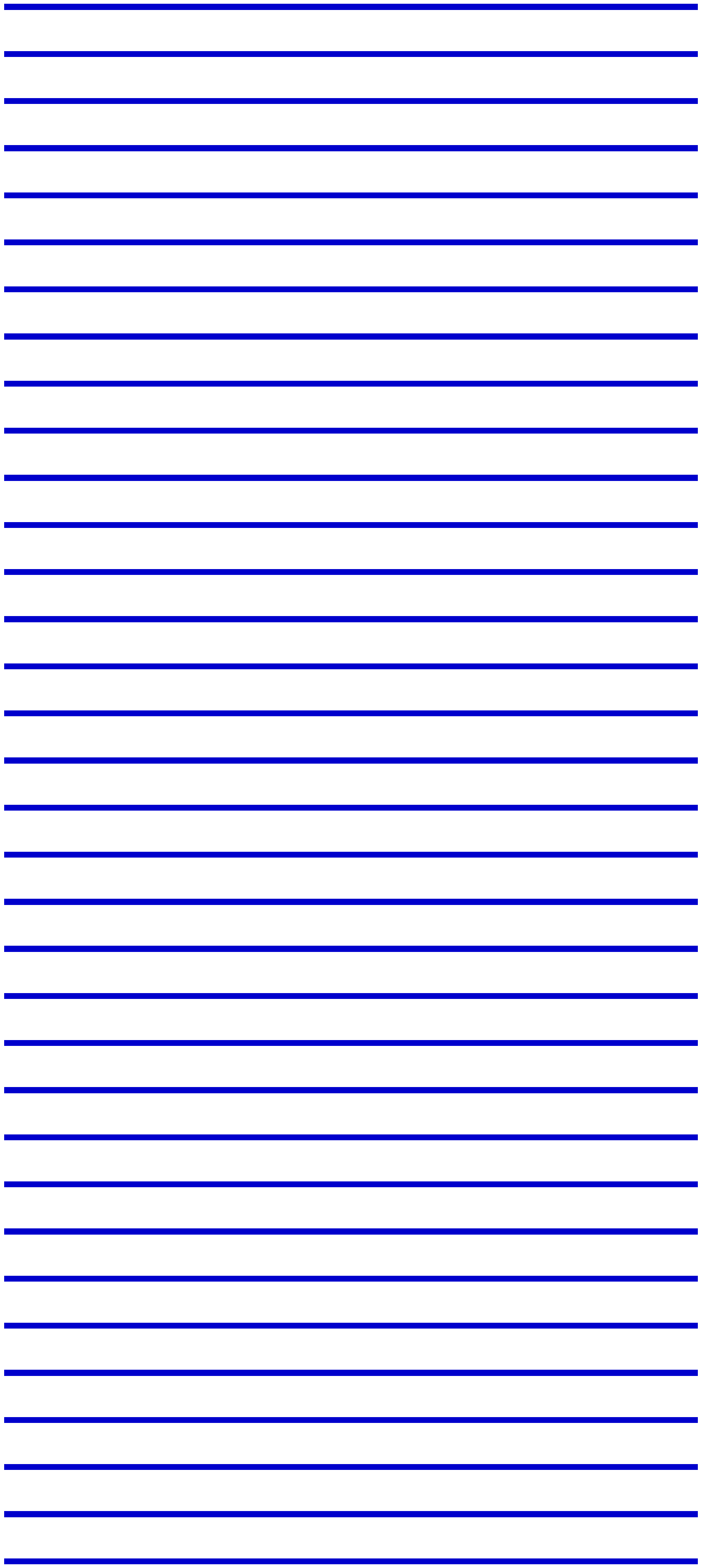
Show Conserved Domains

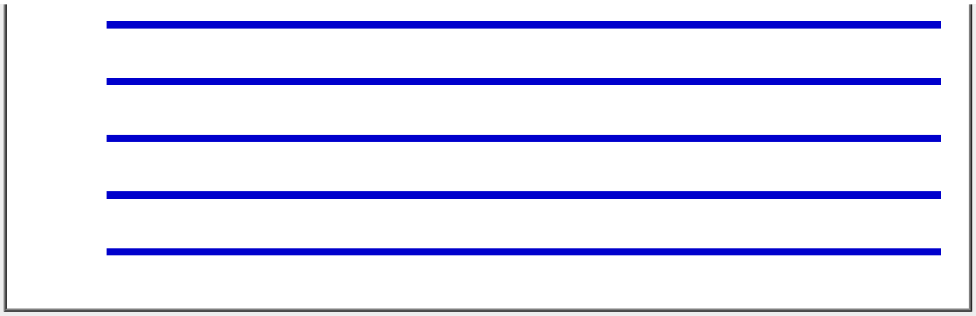
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	truncated coagulation factor XI [Bos taurus]	45.2	45.2	100%	4e-05	93%	gi|89338423|ABD67506.1
☐	coagulation factor XI [Bos taurus]	45.2	45.2	100%	5e-05	93%	gi|237637253|ACR07926.1
☐	coagulation factor XI [Bos taurus]	45.2	45.2	100%	8e-05	93%	gi|89338421|ABD67505.1
☐	Chain A, Crystal Structure Of Factor Xia In Complex With Clava	45.2	45.2	100%	3e-04	93%	gi|217035335|3BG8_A
☐	Chain A, Crystal Structure Of The Fxia Catalytic Domain In Cor	45.2	45.2	100%	3e-04	93%	gi|56967287|1XX9_A
☐	Chain A, Factor Xia In Complex With A Clorophenyl-tetrazole Ir	45.2	45.2	100%	3e-04	93%	gi|383875445|3SOR_A
☐	Chain A, Factor Xia In Complex With The Inhibitor 4-{2-[(1s)-1-(	45.2	45.2	100%	3e-04	93%	gi|728055500|4TY6_A
☐	Chain A, Factor Xia In Complex With The Inhibitor 3'-[(2s,4r)-6-	45.2	45.2	100%	3e-04	93%	gi|584579944|4NA7_A
☐	coagulation factor XI [Bos taurus]	45.2	45.2	100%	3e-04	93%	gi|45861248|AAS78506.1
☐	coagulation factor XI (plasma thromboplastin antecedent), isofo	45.2	45.2	100%	3e-04	93%	gi|119625025|EAX04620.1
☐	PREDICTED: coagulation factor XI isoform X4 [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|530377342|XP_005262881.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]	45.2	45.2	100%	3e-04	93%	gi|675774870|XP_008975412.1
☐	PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes	45.2	45.2	100%	3e-04	93%	gi|694909938|XP_009446987.1
☐	PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|530377340|XP_005262880.1
☐	platelet factor XI [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|3258649|AAC24506.1
☐	blood coagulation factor XI [Bos taurus]	45.2	45.2	100%	3e-04	93%	gi|45758733|AAS76646.1
☐	PREDICTED: coagulation factor XI [Gorilla gorilla gorilla]	45.2	45.2	100%	3e-04	93%	gi|426346208|XP_004040776.1
☐	PREDICTED: coagulation factor XI isoform X3 [Saimiri bolivien	45.2	45.2	100%	3e-04	93%	gi|725582192|XP_010342663.1
☐	PREDICTED: coagulation factor XI isoform X4 [Pan troglodytes	45.2	45.2	100%	3e-04	93%	gi|694909936|XP_009446986.1
☐	PREDICTED: coagulation factor XI isoform X2 [Homo sapiens]	45.2	45.2	100%	3e-04	93%	gi|530377338|XP_005262879.1
☐	PREDICTED: coagulation factor XI isoform X3 [Pan troglodytes	45.2	45.2	100%	4e-04	93%	gi|694909934|XP_009446985.1
☐	PREDICTED: coagulation factor XI isoform X6 [Homo sapiens]	45.2	45.2	100%	4e-04	93%	gi|578808899|XP_006714200.1
☐	PREDICTED: coagulation factor XI [Equus caballus]	45.2	45.2	100%	4e-04	93%	gi|149742758|XP_001490330.1
☐	PREDICTED: coagulation factor XI [Camelus bactrianus]	45.2	45.2	100%	4e-04	93%	gi|743715881|XP_010951577.1
☐	PREDICTED: coagulation factor XI [Vicugna pacos]	45.2	45.2	100%	4e-04	93%	gi|560951202|XP_006198143.1
☐	PREDICTED: coagulation factor XI isoform X2 [Saimiri bolivien	45.2	45.2	100%	4e-04	93%	gi|725582190|XP_010342661.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI	45.2	45.2	100%	4e-04	93%	gi|744611375|XP_010994033.1
☐	PREDICTED: coagulation factor XI [Bison bison bison]	45.2	45.2	100%	4e-04	93%	gi|742100675|XP_010834113.1
☐	PREDICTED: coagulation factor XI [Equus przewalskii]	45.2	45.2	100%	4e-04	93%	gi|664778079|XP_008508352.1

☐	PREDICTED: coagulation factor XI [Callithrix jacchus]	45.2	45.2	100%	4e-04	93%	gi|296195030|XP_002745209.1
☐	coagulation factor XI [Homo sapiens]	45.2	45.2	100%	4e-04	93%	gi|180352|AAA51985.1
☐	PREDICTED: coagulation factor XI [Camelus ferus]	45.2	45.2	100%	4e-04	93%	gi|560904135|XP_006178431.1
☐	PREDICTED: coagulation factor XI [Pantholops hodgsonii]	45.2	45.2	100%	4e-04	93%	gi|556754529|XP_005972629.1
☐	PREDICTED: coagulation factor XI [Condylura cristata]	45.2	45.2	100%	4e-04	93%	gi|507947527|XP_004682554.1
☐	PREDICTED: coagulation factor XI [Bos mutus]	45.2	45.2	100%	4e-04	93%	gi|555974149|XP_005899069.1
☐	PREDICTED: coagulation factor XI [Ovis aries]	45.2	45.2	100%	4e-04	93%	gi|426256280|XP_004021769.1
☐	coagulation factor XI precursor [Bos taurus]	45.2	45.2	100%	4e-04	93%	gi|56710319|NP_001008665.1
☐	coagulation factor XI precursor [Homo sapiens]	45.2	45.2	100%	4e-04	93%	gi|4503627|NP_000119.1
☐	PREDICTED: coagulation factor XI isoform X1 [Saimiri bolivien	45.2	45.2	100%	4e-04	93%	gi|725582188|XP_010342660.1
☐	PREDICTED: coagulation factor XI [Otolemur garnettii]	45.2	45.2	100%	4e-04	93%	gi|395840032|XP_003792872.1
☐	PREDICTED: coagulation factor XI [Loxodonta africana]	45.2	45.2	100%	4e-04	93%	gi|344281436|XP_003412485.1
☐	PREDICTED: coagulation factor XI [Nomascus leucogenys]	45.2	45.2	100%	4e-04	93%	gi|332244773|XP_003271548.1
☐	PREDICTED: coagulation factor XI [Pongo abelii]	45.2	45.2	100%	4e-04	93%	gi|297674804|XP_002815399.1
☐	TPA: coagulation factor XI precursor [Bos taurus]	45.2	45.2	100%	4e-04	93%	gi|296472409|DAA14524.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan troglodytes	45.2	45.2	100%	4e-04	93%	gi|114597210|XP_001165847.1
☐	PREDICTED: coagulation factor XI isoform X1 [Pan troglodytes	45.2	45.2	100%	4e-04	93%	gi|694909931|XP_009446984.1
☐	PREDICTED: coagulation factor XI isoform X1 [Homo sapiens]	45.2	45.2	100%	4e-04	93%	gi|530377336|XP_005262878.1
☐	PREDICTED: coagulation factor XI [Erinaceus europaeus]	45.2	45.2	100%	4e-04	93%	gi|617577865|XP_007517757.1
☐	blood coagulation factor XI [Bubalus bubalis]	41.8	41.8	100%	0.001	86%	gi|78093735|ABB19358.1
☐	blood coagulation factor XI [Bubalus bubalis]	41.8	41.8	100%	0.001	86%	gi|78146504|ABB22793.1
☐	blood coagulation factor XI [Bubalus bubalis]	41.8	41.8	100%	0.001	86%	gi|586972963|AHK06000.1
☐	Chain A, Crystal Structure Of The Catalytic Domain Of Coagula	42.6	42.6	100%	0.002	86%	gi|75765761|1ZJD_A
☐	Chain A, Crystal Structure Of The Catalytic Domain Of Coagula	42.6	42.6	100%	0.002	86%	gi|78101066|1ZHP_A
☐	Chain A, Crystal Structure Of The Fxia Catalytic Domain In Cor	42.6	42.6	100%	0.002	86%	gi|56967291|1XXD_A
☐	PREDICTED: coagulation factor XI isoform X2 [Rhinopithecus r	42.6	42.6	100%	0.002	86%	gi|724897372|XP_010376291.1
☐	PREDICTED: coagulation factor XI isoform X1 [Rhinopithecus r	42.6	42.6	100%	0.002	86%	gi|724897369|XP_010376290.1
☐	PREDICTED: coagulation factor XI [Balaenoptera acutorostrata	42.6	42.6	100%	0.002	86%	gi|594650157|XP_007174042.1
☐	PREDICTED: coagulation factor XI [Physeter catodon]	42.6	42.6	100%	0.002	86%	gi|593742188|XP_007126520.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI	42.6	42.6	100%	0.002	86%	gi|507618988|XP_004696215.1
☐	PREDICTED: coagulation factor XI [Orycteropus afer afer]	42.6	42.6	100%	0.002	86%	gi|634869242|XP_007946583.1
☐	PREDICTED: coagulation factor XI [Tarsius syrichta]	42.2	42.2	100%	0.003	86%	gi|640821392|XP_008067645.1
☐	Plasma kallikrein [Pteropus alecto]	41.8	41.8	92%	0.004	92%	gi|431902346|ELK08847.1
☐	Coagulation factor XI [Tupaia chinensis]	41.8	41.8	100%	0.005	86%	gi|444705646|ELW47049.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI	41.8	41.8	92%	0.005	92%	gi|586521035|XP_006926977.1
☐	coagulation factor XI precursor [Oryctolagus cuniculus]	41.8	41.8	100%	0.005	86%	gi|130502142|NP_001076261.1
☐	PREDICTED: coagulation factor XI [Dasypus novemcinctus]	41.8	41.8	100%	0.005	86%	gi|488532217|XP_004457855.1
☐	PREDICTED: coagulation factor XI isoform 2 [Ceratotherium sir	41.8	41.8	100%	0.005	86%	gi|478509096|XP_004428828.1
☐	PREDICTED: coagulation factor XI isoform 3 [Odobenus rosma	41.8	41.8	92%	0.005	92%	gi|472396395|XP_004417424.1
☐	PREDICTED: coagulation factor XI-like [Ailuropoda melanoleuc	41.8	41.8	92%	0.005	92%	gi|301776062|XP_002923450.1
☐	PREDICTED: coagulation factor XI [Bubalus bubalis]	41.8	41.8	100%	0.005	86%	gi|594073052|XP_006060352.1
☐	PREDICTED: coagulation factor XI [Capra hircus]	41.8	41.8	100%	0.005	86%	gi|548524195|XP_005698802.1
☐	PREDICTED: coagulation factor XI isoform 1 [Ceratotherium sir	41.8	41.8	100%	0.005	86%	gi|478509094|XP_004428827.1
☐	PREDICTED: coagulation factor XI isoform 2 [Odobenus rosma	41.8	41.8	92%	0.005	92%	gi|472396393|XP_004417423.1
☐	PREDICTED: coagulation factor XI [Tupaia chinensis]	41.8	41.8	100%	0.005	86%	gi|562864607|XP_006160530.1

☐	PREDICTED: coagulation factor XI [Mustela putorius furo]	41.8	41.8	92%	0.005	92%	gi|511876760|XP_004758357.1
☐	PREDICTED: coagulation factor XI isoform 1 [Odobenus rosma	41.8	41.8	92%	0.005	92%	gi|472396391|XP_004417422.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI	41.8	41.8	92%	0.005	92%	gi|671035736|XP_008708722.1
☐	PREDICTED: coagulation factor XI [Ictidomys tridecemlineatus]	41.4	41.4	100%	0.007	86%	gi|532087072|XP_005329248.1
☐	PREDICTED: coagulation factor XI [Lipotes vexillifer]	40.9	40.9	100%	0.009	86%	gi|602712769|XP_007466613.1
☐	PREDICTED: coagulation factor XI [Orcinus orca]	40.9	40.9	100%	0.009	86%	gi|466045508|XP_004277238.1
☐	PREDICTED: coagulation factor XI-like isoform X5 [Anas platyr	40.1	40.1	100%	0.017	86%	gi|514703781|XP_005009031.1
☐	PREDICTED: coagulation factor XI-like isoform X3 [Anas platyr	40.1	40.1	100%	0.017	86%	gi|514703777|XP_005009029.1
☐	Coagulation factor XI [Chlamydotis undulata macqueenii]	40.1	40.1	100%	0.017	86%	gi|677168326|KFP45777.1
☐	PREDICTED: plasma kallikrein isoform X2 [Struthio camelus au	40.1	40.1	100%	0.017	86%	gi|697488125|XP_009675004.1
☐	PREDICTED: coagulation factor XI-like [Chlamydotis undulata	40.1	40.1	100%	0.017	86%	gi|705703357|XP_010126720.1
☐	PREDICTED: coagulation factor XI-like isoform X2 [Anas platyr	40.1	40.1	100%	0.017	86%	gi|514703775|XP_005009028.1
☐	Plasma kallikrein [Struthio camelus australis]	40.1	40.1	100%	0.017	86%	gi|678215239|KFV82218.1
☐	Plasma kallikrein [Anas platyrhynchos]	40.1	40.1	100%	0.017	86%	gi|483525503|EOB09100.1
☐	PREDICTED: coagulation factor XI-like isoform X1 [Anas platyr	40.1	40.1	100%	0.017	86%	gi|514703773|XP_005009027.1
☐	PREDICTED: plasma kallikrein isoform X1 [Struthio camelus au	40.1	40.1	100%	0.017	86%	gi|697488121|XP_009675003.1
☐	PREDICTED: coagulation factor XI isoform X2 [Papio anubis]	39.7	39.7	100%	0.024	86%	gi|685544400|XP_009206295.1
☐	PREDICTED: coagulation factor XI isoform X2 [Chlorocebus sa	39.7	39.7	100%	0.024	86%	gi|635046203|XP_007998683.1
☐	PREDICTED: coagulation factor XI isoform X2 [Macaca fascicu	39.7	39.7	100%	0.024	86%	gi|544436077|XP_005556541.1
☐	hypothetical protein EGM_04467 [Macaca fascicularis]	39.7	39.7	100%	0.024	86%	gi|355750969|EHH55296.1
☐	hypothetical protein EGK_16300 [Macaca mulatta]	39.7	39.7	100%	0.024	86%	gi|355687768|EHH26352.1
☐	PREDICTED: coagulation factor XI isoform X1 [Chlorocebus sa	39.7	39.7	100%	0.024	86%	gi|635046201|XP_007998681.1
☐	PREDICTED: coagulation factor XI isoform X1 [Macaca fascicu	39.7	39.7	100%	0.024	86%	gi|544436075|XP_005556540.1
☐	PREDICTED: coagulation factor XI isoform X1 [Papio anubis]	39.7	39.7	100%	0.024	86%	gi|402871005|XP_003899481.1
☐	PREDICTED: coagulation factor XI-like [Macaca mulatta]	39.7	39.7	100%	0.024	86%	gi|297293811|XP_001090398.2
☐	Chain A, Factor Xi Catalytic Domain Complexed With N-((R)-1-	39.2	39.2	100%	0.030	86%	gi|109157010|1ZPZ_A

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NCBI/ BLAST/ blastp suite/ Formatting Results - B94V723E01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   Formatting options   Download

How to read this page   Blast report description

F11_RVYSGILNQSEIKE_NonMod

RID B94V723E01R (Expires on 01-14 10:39 am)

Query ID lcl|305543
Description None
Molecule type amino acid
Query Length 14

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

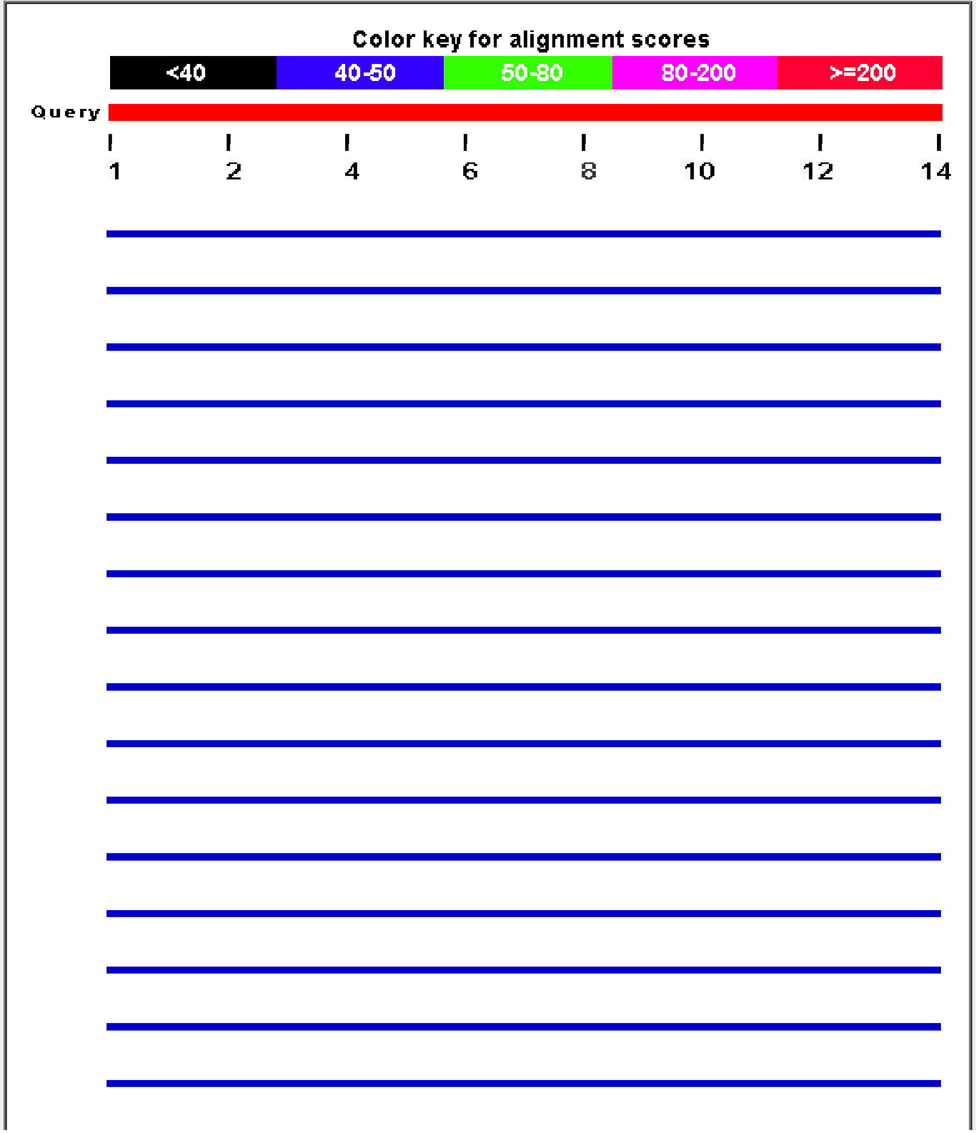
Graphic Summary

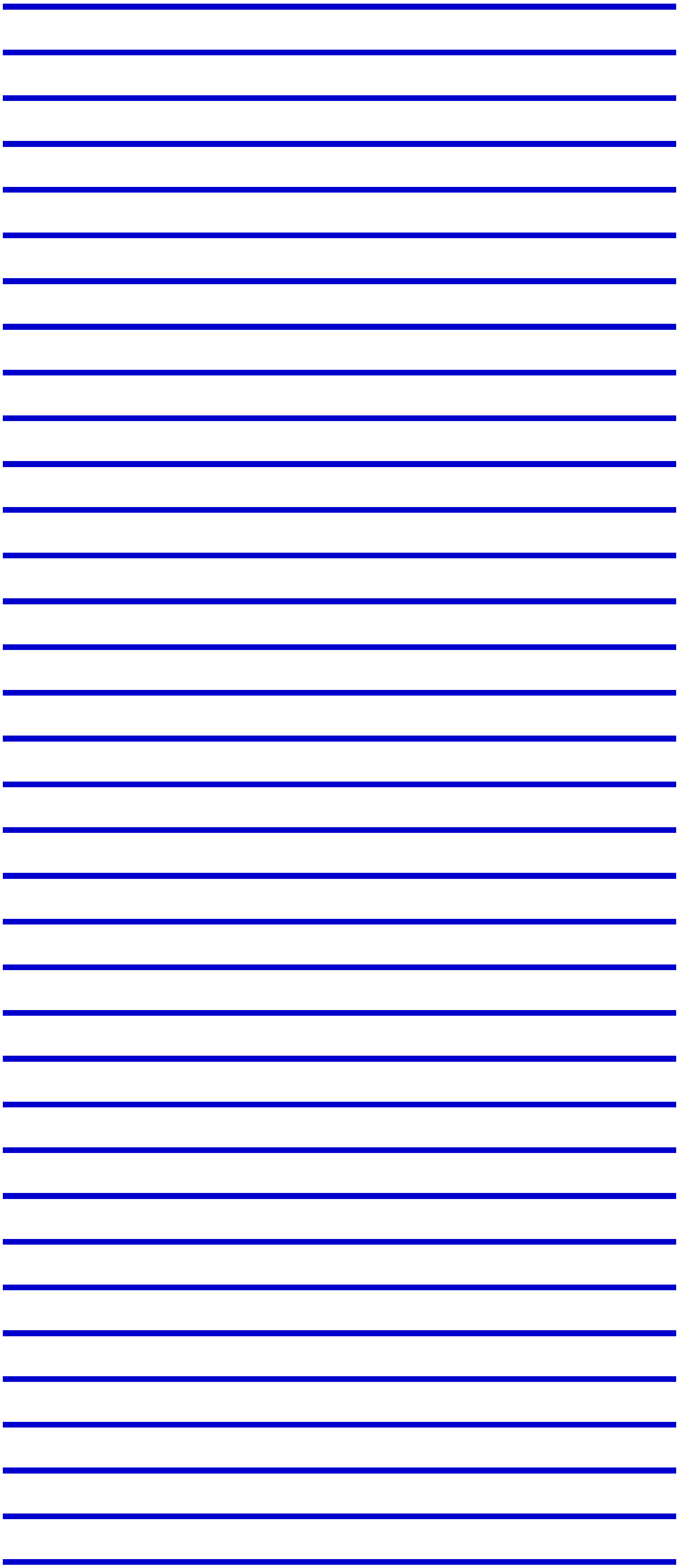
Show Conserved Domains

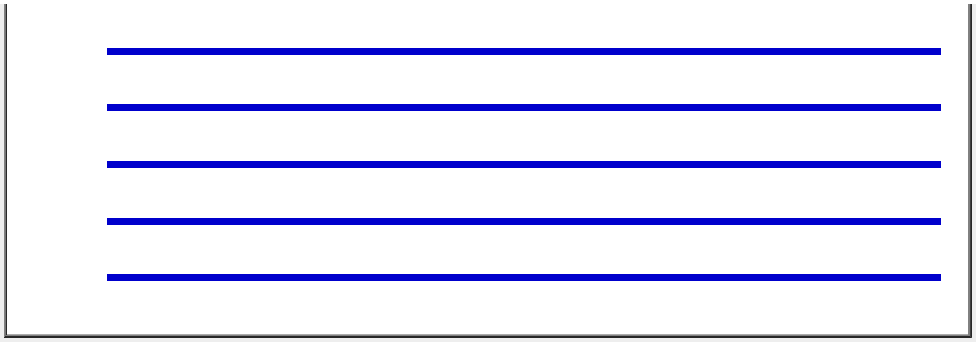
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	truncated coagulation factor XI [Bos taurus]	47.7	47.7	100%	4e-06	100%	gi|89338423|ABD67506.1
☐	coagulation factor XI [Bos taurus]	47.7	47.7	100%	6e-06	100%	gi|237637253|ACR07926.1
☐	coagulation factor XI [Bos taurus]	47.7	47.7	100%	8e-06	100%	gi|89338421|ABD67505.1
☐	Chain A, Crystal Structure Of Factor Xia In Complex With Clavatadi	47.7	47.7	100%	4e-05	100%	gi|217035335|3BG8_A
☐	Chain A, Crystal Structure Of The Fxia Catalytic Domain In Comple	47.7	47.7	100%	4e-05	100%	gi|56967287|1XX9_A
☐	Chain A, Factor Xia In Complex With A Clorophenyl-tetrazole Inhibi	47.7	47.7	100%	4e-05	100%	gi|383875445|3SOR_A
☐	Chain A, Factor Xia In Complex With The Inhibitor 4-{2-[(1s)-1-({[tra	47.7	47.7	100%	4e-05	100%	gi|728055500|4TY6_A
☐	Chain A, Factor Xia In Complex With The Inhibitor 3'-[(2s,4r)-6-carb	47.7	47.7	100%	4e-05	100%	gi|584579944|4NA7_A
☐	coagulation factor XI [Bos taurus]	47.7	47.7	100%	5e-05	100%	gi|45861248|AAS78506.1
☐	coagulation factor XI (plasma thromboplastin antecedent), isoform C	47.7	47.7	100%	5e-05	100%	gi|119625025|EAX04620.1
☐	PREDICTED: coagulation factor XI isoform X4 [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|530377342|XP_005262881.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan paniscus]	47.7	47.7	100%	5e-05	100%	gi|675774870|XP_008975412.1
☐	PREDICTED: coagulation factor XI isoform X5 [Pan troglodytes]	47.7	47.7	100%	5e-05	100%	gi|694909938|XP_009446987.1
☐	PREDICTED: coagulation factor XI isoform X3 [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|530377340|XP_005262880.1
☐	platelet factor XI [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|3258649|AAC24506.1
☐	blood coagulation factor XI [Bos taurus]	47.7	47.7	100%	5e-05	100%	gi|45758733|AAS76646.1
☐	PREDICTED: coagulation factor XI [Gorilla gorilla gorilla]	47.7	47.7	100%	5e-05	100%	gi|426346208|XP_004040776.1
☐	PREDICTED: coagulation factor XI isoform X3 [Saimiri boliviensis b	47.7	47.7	100%	5e-05	100%	gi|725582192|XP_010342663.1
☐	PREDICTED: coagulation factor XI isoform X4 [Pan troglodytes]	47.7	47.7	100%	5e-05	100%	gi|694909936|XP_009446986.1
☐	PREDICTED: coagulation factor XI isoform X2 [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|530377338|XP_005262879.1
☐	PREDICTED: coagulation factor XI isoform X3 [Pan troglodytes]	47.7	47.7	100%	5e-05	100%	gi|694909934|XP_009446985.1
☐	PREDICTED: coagulation factor XI isoform X6 [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|578808899|XP_006714200.1
☐	PREDICTED: coagulation factor XI [Equus caballus]	47.7	47.7	100%	5e-05	100%	gi|149742758|XP_001490330.1
☐	PREDICTED: coagulation factor XI [Vicugna pacos]	47.7	47.7	100%	5e-05	100%	gi|560951202|XP_006198143.1
☐	PREDICTED: coagulation factor XI isoform X2 [Saimiri boliviensis b	47.7	47.7	100%	5e-05	100%	gi|725582190|XP_010342661.1
☐	PREDICTED: coagulation factor XI [Equus przewalskii]	47.7	47.7	100%	5e-05	100%	gi|664778079|XP_008508352.1
☐	PREDICTED: coagulation factor XI [Callithrix jacchus]	47.7	47.7	100%	5e-05	100%	gi|296195030|XP_002745209.1
☐	coagulation factor XI [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|180352|AAA51985.1
☐							

	PREDICTED: coagulation factor XI [Camelus ferus]	47.7	47.7	100%	5e-05	100%	gi|560904135|XP_006178431.1
☐	PREDICTED: coagulation factor XI [Pantholops hodgsonii]	47.7	47.7	100%	5e-05	100%	gi|556754529|XP_005972629.1
☐	PREDICTED: coagulation factor XI [Condylura cristata]	47.7	47.7	100%	5e-05	100%	gi|507947527|XP_004682554.1
☐	PREDICTED: coagulation factor XI [Bos mutus]	47.7	47.7	100%	5e-05	100%	gi|555974149|XP_005899069.1
☐	PREDICTED: coagulation factor XI [Ovis aries]	47.7	47.7	100%	5e-05	100%	gi|426256280|XP_004021769.1
☐	coagulation factor XI precursor [Bos taurus]	47.7	47.7	100%	5e-05	100%	gi|56710319|NP_001008665.1
☐	coagulation factor XI precursor [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|4503627|NP_000119.1
☐	PREDICTED: coagulation factor XI isoform X1 [Saimiri boliviensis b	47.7	47.7	100%	5e-05	100%	gi|725582188|XP_010342660.1
☐	PREDICTED: coagulation factor XI [Otolemur garnettii]	47.7	47.7	100%	5e-05	100%	gi|395840032|XP_003792872.1
☐	PREDICTED: coagulation factor XI [Loxodonta africana]	47.7	47.7	100%	5e-05	100%	gi|344281436|XP_003412485.1
☐	PREDICTED: coagulation factor XI [Nomascus leucogenys]	47.7	47.7	100%	5e-05	100%	gi|332244773|XP_003271548.1
☐	PREDICTED: coagulation factor XI [Pongo abelii]	47.7	47.7	100%	5e-05	100%	gi|297674804|XP_002815399.1
☐	TPA: coagulation factor XI precursor [Bos taurus]	47.7	47.7	100%	5e-05	100%	gi|296472409|DAA14524.1
☐	PREDICTED: coagulation factor XI isoform X2 [Pan troglodytes]	47.7	47.7	100%	5e-05	100%	gi|114597210|XP_001165847.1
☐	PREDICTED: coagulation factor XI isoform X1 [Pan troglodytes]	47.7	47.7	100%	5e-05	100%	gi|694909931|XP_009446984.1
☐	PREDICTED: coagulation factor XI isoform X1 [Homo sapiens]	47.7	47.7	100%	5e-05	100%	gi|530377336|XP_005262878.1
☐	PREDICTED: coagulation factor XI [Erinaceus europaeus]	47.7	47.7	100%	5e-05	100%	gi|617577865|XP_007517757.1
☐	blood coagulation factor XI [Bubalus bubalis]	44.3	44.3	100%	1e-04	93%	gi|78093735|ABB19358.1
☐	blood coagulation factor XI [Bubalus bubalis]	44.3	44.3	100%	2e-04	93%	gi|78146504|ABB22793.1
☐	blood coagulation factor XI [Bubalus bubalis]	44.3	44.3	100%	2e-04	93%	gi|586972963|AHK06000.1
☐	Chain A, Crystal Structure Of The Catalytic Domain Of Coagulation	45.2	45.2	100%	3e-04	93%	gi|75765761|1ZJD_A
☐	Chain A, Crystal Structure Of The Catalytic Domain Of Coagulation	45.2	45.2	100%	3e-04	93%	gi|78101066|1ZHP_A
☐	Chain A, Crystal Structure Of The Fxia Catalytic Domain In Comple	45.2	45.2	100%	3e-04	93%	gi|56967291|1XXD_A
☐	PREDICTED: coagulation factor XI isoform X2 [Rhinopithecus roxel	45.2	45.2	100%	3e-04	93%	gi|724897372|XP_010376291.1
☐	PREDICTED: coagulation factor XI isoform X1 [Rhinopithecus roxel	45.2	45.2	100%	3e-04	93%	gi|724897369|XP_010376290.1
☐	PREDICTED: coagulation factor XI [Balaenoptera acutorostrata sca	45.2	45.2	100%	3e-04	93%	gi|594650157|XP_007174042.1
☐	PREDICTED: coagulation factor XI [Physeter catodon]	45.2	45.2	100%	3e-04	93%	gi|593742188|XP_007126520.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Ech	45.2	45.2	100%	3e-04	93%	gi|507618988|XP_004696215.1
☐	PREDICTED: coagulation factor XI [Orycteropus afer afer]	45.2	45.2	100%	3e-04	93%	gi|634869242|XP_007946583.1
☐	PREDICTED: coagulation factor XI [Tarsius syrichta]	44.8	44.8	100%	5e-04	93%	gi|640821392|XP_008067645.1
☐	Plasma kallikrein [Pteropus alecto]	44.3	44.3	92%	6e-04	100%	gi|431902346|ELK08847.1
☐	Coagulation factor XI [Tupaia chinensis]	44.3	44.3	100%	6e-04	93%	gi|444705646|ELW47049.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Pter	44.3	44.3	92%	6e-04	100%	gi|586521035|XP_006926977.1
☐	coagulation factor XI precursor [Oryctolagus cuniculus]	44.3	44.3	100%	6e-04	93%	gi|130502142|NP_001076261.1
☐	PREDICTED: coagulation factor XI [Dasypus novemcinctus]	44.3	44.3	100%	6e-04	93%	gi|488532217|XP_004457855.1
☐	PREDICTED: coagulation factor XI isoform 2 [Ceratotherium simum	44.3	44.3	100%	6e-04	93%	gi|478509096|XP_004428828.1
☐	PREDICTED: coagulation factor XI isoform 3 [Odobenus rosmarus	44.3	44.3	92%	6e-04	100%	gi|472396395|XP_004417424.1
☐	PREDICTED: coagulation factor XI-like [Ailuropoda melanoleuca]	44.3	44.3	92%	6e-04	100%	gi|301776062|XP_002923450.1
☐	PREDICTED: coagulation factor XI [Bubalus bubalis]	44.3	44.3	100%	6e-04	93%	gi|594073052|XP_006060352.1
☐	PREDICTED: coagulation factor XI [Capra hircus]	44.3	44.3	100%	6e-04	93%	gi|548524195|XP_005698802.1
☐	PREDICTED: coagulation factor XI isoform 1 [Ceratotherium simum	44.3	44.3	100%	6e-04	93%	gi|478509094|XP_004428827.1
☐	PREDICTED: coagulation factor XI isoform 2 [Odobenus rosmarus	44.3	44.3	92%	6e-04	100%	gi|472396393|XP_004417423.1
☐	PREDICTED: coagulation factor XI [Tupaia chinensis]	44.3	44.3	100%	6e-04	93%	gi|562864607|XP_006160530.1
☐	PREDICTED: coagulation factor XI [Mustela putorius furo]	44.3	44.3	92%	6e-04	100%	gi|511876760|XP_004758357.1
☐	PREDICTED: coagulation factor XI isoform 1 [Odobenus rosmarus	44.3	44.3	92%	6e-04	100%	gi|472396391|XP_004417422.1

☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Urs	44.3	44.3	92%	7e-04	100%	gi|671035736|XP_008708722.1
☐	PREDICTED: coagulation factor XI [Ictidomys tridecemlineatus]	43.9	43.9	100%	9e-04	93%	gi|532087072|XP_005329248.1
☐	PREDICTED: coagulation factor XI [Lipotes vexillifer]	43.5	43.5	100%	0.001	93%	gi|602712769|XP_007466613.1
☐	PREDICTED: coagulation factor XI [Orcinus orca]	43.5	43.5	100%	0.001	93%	gi|466045508|XP_004277238.1
☐	PREDICTED: coagulation factor XI isoform X2 [Papio anubis]	42.2	42.2	100%	0.003	93%	gi|685544400|XP_009206295.1
☐	PREDICTED: coagulation factor XI isoform X2 [Chlorocebus sabae	42.2	42.2	100%	0.003	93%	gi|635046203|XP_007998683.1
☐	PREDICTED: coagulation factor XI isoform X2 [Macaca fascicularis	42.2	42.2	100%	0.003	93%	gi|544436077|XP_005556541.1
☐	hypothetical protein EGM_04467 [Macaca fascicularis]	42.2	42.2	100%	0.003	93%	gi|355750969|EHH55296.1
☐	hypothetical protein EGK_16300 [Macaca mulatta]	42.2	42.2	100%	0.003	93%	gi|355687768|EHH26352.1
☐	PREDICTED: coagulation factor XI isoform X1 [Chlorocebus sabae	42.2	42.2	100%	0.003	93%	gi|635046201|XP_007998681.1
☐	PREDICTED: coagulation factor XI isoform X1 [Macaca fascicularis	42.2	42.2	100%	0.003	93%	gi|544436075|XP_005556540.1
☐	PREDICTED: coagulation factor XI isoform X1 [Papio anubis]	42.2	42.2	100%	0.003	93%	gi|402871005|XP_003899481.1
☐	PREDICTED: coagulation factor XI-like [Macaca mulatta]	42.2	42.2	100%	0.003	93%	gi|297293811|XP_001090398.2
☐	Chain A, Factor Xi Catalytic Domain Complexed With N-((R)-1-(4- E	41.8	41.8	100%	0.004	93%	gi|109157010|1ZPZ_A
☐	coagulation factor XI precursor [Canis lupus familiaris]	41.8	41.8	92%	0.005	92%	gi|205361194|NP_001128595.1
☐	PREDICTED: coagulation factor XI isoform X2 [Leptonychotes wed	41.8	41.8	92%	0.005	92%	gi|585180453|XP_006741890.1
☐	PREDICTED: coagulation factor XI [Sorex araneus]	41.8	41.8	100%	0.005	86%	gi|505830321|XP_004610458.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XI [Pan	41.8	41.8	92%	0.005	92%	gi|591347751|XP_007099050.1
☐	PREDICTED: coagulation factor XI isoform X2 [Canis lupus familiar	41.8	41.8	92%	0.005	92%	gi|545526400|XP_005629983.1
☐	PREDICTED: coagulation factor XI [Felis catus]	41.8	41.8	92%	0.005	92%	gi|410956035|XP_003984650.1
☐	PREDICTED: coagulation factor XI isoform X3 [Leptonychotes wed	41.8	41.8	92%	0.005	92%	gi|585180455|XP_006741891.1
☐	PREDICTED: coagulation factor XI [Chrysochloris asiatica]	41.8	41.8	100%	0.005	86%	gi|586451182|XP_006834518.1
☐	PREDICTED: coagulation factor XI isoform X1 [Leptonychotes wed	41.8	41.8	92%	0.005	92%	gi|585180451|XP_006741889.1
☐	PREDICTED: coagulation factor XI isoform X1 [Canis lupus familiar	41.8	41.8	92%	0.005	92%	gi|545526398|XP_005629982.1
☐	PREDICTED: coagulation factor XI-like isoform X5 [Anas platyrhyn	41.4	41.4	100%	0.006	86%	gi|514703781|XP_005009031.1
☐	PREDICTED: coagulation factor XI-like isoform X3 [Anas platyrhyn	41.4	41.4	100%	0.006	86%	gi|514703777|XP_005009029.1
☐	Coagulation factor XI [Chlamydotis undulata macqueenii]	41.4	41.4	100%	0.006	86%	gi|677168326|KFP45777.1

⊟ Alignments

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truncated coagulation factor XI [Bos taurus]

Sequence ID: gi|89338423|gb|ABD67506.1| **Length:** 34 **Number of Matches:** 1

▷ See 2 more title(s)

Range 1: 8 to 21 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	4e-06	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    RVYSGILNQSEIKE  14
            RVYSGILNQSEIKE
Sbjct  8    RVYSGILNQSEIKE  21
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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coagulation factor XI, partial [Bos taurus]

Sequence ID: gi|237637253|gb|ACR07926.1| **Length:** 41 **Number of Matches:** 1

Range 1: 8 to 21 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	6e-06	14/14(100%)	14/14(100%)	0/14(0%)

Related Information

```
Query  1    RVYSGILNQSEIKE  14
            RVYSGILNQSEIKE
Sbjct  8    RVYSGILNQSEIKE  21
```

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coagulation factor XI [Bos taurus]

Sequence ID: gi|89338421|gb|ABD67505.1| **Length:** 48 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 8 to 21 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	8e-06	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    RVYSGILNQSEIKE  14
            RVYSGILNQSEIKE
Sbjct  8    RVYSGILNQSEIKE  21
```

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Chain A, Crystal Structure Of Factor Xia In Complex With Clavatadine A

Sequence ID: gi|217035335|pdb|3BG8|A **Length:** 238 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 56 to 69 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	4e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    RVYSGILNQSEIKE  14
            RVYSGILNQSEIKE
Sbjct  56   RVYSGILNQSEIKE  69
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of The Fxia Catalytic Domain In Complex With Ecotinm84r

Sequence ID: gi|56967287|pdb|1XX9|A **Length:** 238 **Number of Matches:** 1

See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 56 to 69 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	4e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    RVYSGILNQSEIKE  14
            RVYSGILNQSEIKE
Sbjct  56   RVYSGILNQSEIKE  69
```

BLAST ®

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BVDM5A2W01R**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

F13B_KHGVIISSTVDTYEDGSSVEYRC_Mod

RID BVDM5A2W01R (Expires on 01-21 08:59 am)

Query ID lcl|73820

Description None

Molecule type amino acid

Query Length 23

Database Name nr

Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

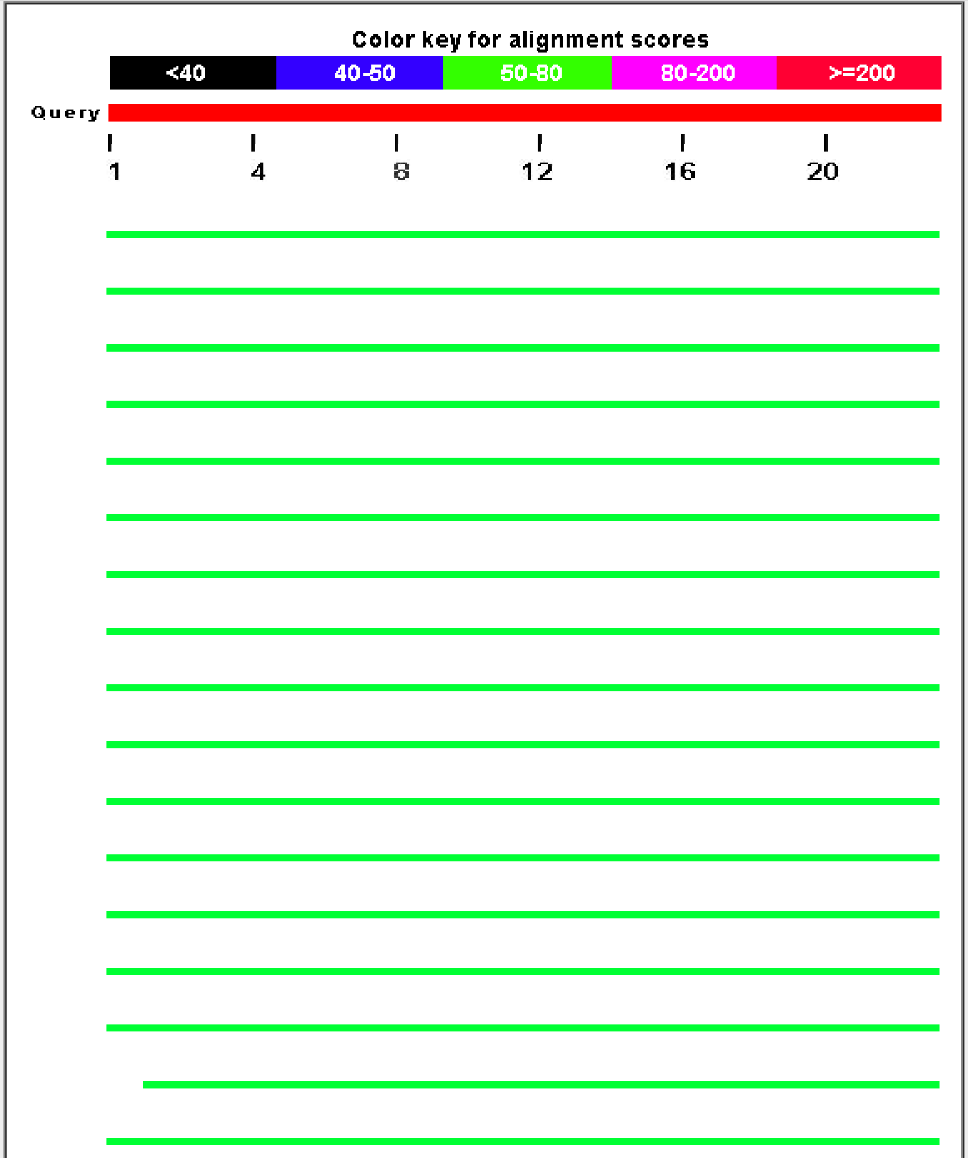
Graphic Summary

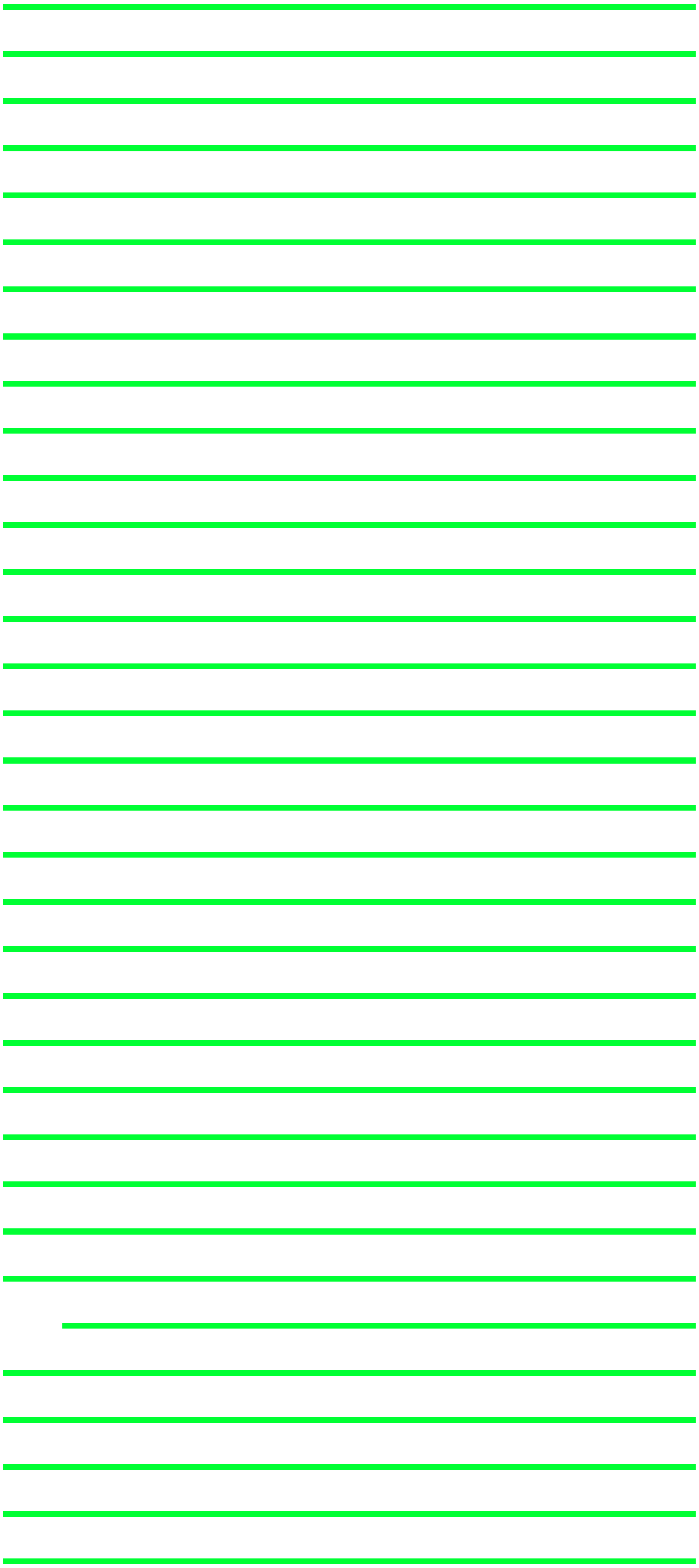
Show Conserved Domains

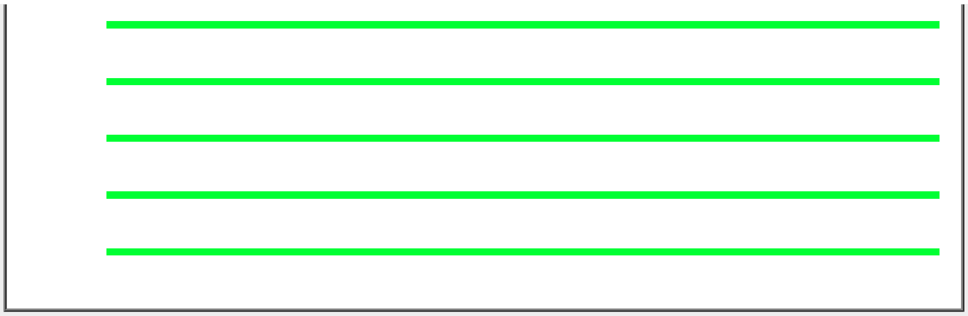
No putative conserved domains have been detected

Distribution of 200 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊖ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: coagulation factor XIII B chain isoform X4 [Pan troglodytes]	74.0	104	100%	2e-13	96%	XP_009438553.1
☐	PREDICTED: coagulation factor XIII B chain isoform X3 [Pan troglodytes]	74.0	104	100%	2e-13	96%	XP_009438550.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Homo sapiens]	74.0	104	100%	2e-13	96%	XP_005245011.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Pan troglodytes]	74.0	104	100%	2e-13	96%	XP_009438547.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Homo sapiens]	74.0	104	100%	2e-13	96%	XP_005245010.1
☐	factor XIII b subunit precursor [Homo sapiens]	74.0	104	100%	2e-13	96%	AAA88042.1
☐	coagulation factor XIIIb [Homo sapiens]	74.0	104	100%	2e-13	96%	AAA51821.1
☐	PREDICTED: coagulation factor XIII B chain [Gorilla gorilla gorilla]	74.0	104	100%	2e-13	96%	XP_004028140.1
☐	coagulation factor XIII, B polypeptide [Homo sapiens]	74.0	104	100%	2e-13	96%	AAT85802.1
☐	PREDICTED: coagulation factor XIII B chain [Pan paniscus]	74.0	104	100%	2e-13	96%	XP_003823128.1
☐	unnamed protein product [Homo sapiens]	74.0	104	100%	2e-13	96%	BAF83249.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Pan troglodytes]	74.0	104	100%	2e-13	96%	XP_001137074.1
☐	coagulation factor XIII B chain precursor [Homo sapiens]	74.0	104	100%	2e-13	96%	NP_001985.2
☐	PREDICTED: coagulation factor XIII B chain [Rhinopithecus roxellana]	70.2	101	100%	4e-12	91%	XP_010356755.1
☐	PREDICTED: coagulation factor XIII B chain [Nomascus leucogenys]	70.2	100	100%	4e-12	91%	XP_003264551.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XIII B chain [Pon	67.2	97.6	95%	4e-11	91%	XP_002809712.2
☐	PREDICTED: coagulation factor XIII B chain [Galeopterus variegatus]	66.4	96.7	100%	8e-11	87%	XP_008590154.1
☐	PREDICTED: coagulation factor XIII B chain isoform X4 [Chinchilla lanigera]	66.0	92.0	100%	1e-10	87%	XP_005375174.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Chinchilla lanigera]	66.0	92.0	100%	1e-10	87%	XP_005375172.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Chinchilla lanigera]	66.0	92.0	100%	1e-10	87%	XP_005375171.1
☐	PREDICTED: coagulation factor XIII B chain-like [Papio anubis]	63.8	63.8	100%	3e-10	87%	XP_009189228.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Chlorocebus sabaeu	63.8	95.0	100%	6e-10	87%	XP_007987269.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Chlorocebus sabaeu	63.8	95.0	100%	6e-10	87%	XP_007987268.1
☐	PREDICTED: coagulation factor XIII B chain isoform X4 [Macaca fascicularis]	63.4	94.6	100%	8e-10	87%	XP_005540366.1
☐	PREDICTED: coagulation factor XIII B chain isoform X3 [Macaca fascicularis]	63.4	94.6	100%	8e-10	87%	XP_005540365.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Macaca fascicularis]	63.4	94.6	100%	8e-10	87%	XP_005540364.1
☐	hypothetical protein EGM_01565 [Macaca fascicularis]	63.4	94.6	100%	8e-10	87%	EHH50697.1
☐	PREDICTED: coagulation factor XIII B chain isoform 2 [Macaca mulatta]	63.4	94.6	100%	8e-10	87%	XP_001111017.1
☐	PREDICTED: coagulation factor XIII B chain isoform X5 [Callithrix jacchus]	62.6	91.6	100%	2e-09	83%	XP_008983391.1

☐	PREDICTED: coagulation factor XIII B chain isoform X4 [Callithrix jacchus]	62.6	91.6	100%	2e-09	83%	XP_002760512.2
☐	PREDICTED: coagulation factor XIII B chain isoform X3 [Callithrix jacchus]	62.6	91.6	100%	2e-09	83%	XP_008983390.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Callithrix jacchus]	62.6	91.6	100%	2e-09	83%	XP_008983389.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Callithrix jacchus]	62.6	91.6	100%	2e-09	83%	XP_008983388.1
☐	Coagulation factor XIII B chain [Heterocephalus glaber]	61.3	87.0	100%	4e-09	83%	EHB10383.1
☐	PREDICTED: coagulation factor XIII B chain [Heterocephalus glaber]	61.3	87.0	100%	4e-09	83%	XP_004860190.1
☐	PREDICTED: coagulation factor XIII B chain [Heterocephalus glaber]	61.3	87.0	100%	4e-09	83%	XP_004896309.1
☐	PREDICTED: coagulation factor XIII B chain [Otolemur garnettii]	60.9	92.5	100%	6e-09	78%	XP_003792408.1
☐	PREDICTED: coagulation factor XIII B chain [Cavia porcellus]	59.6	85.7	100%	2e-08	78%	XP_003474759.1
☐	hypothetical protein PANDA_007949 [Ailuropoda melanoleuca]	59.2	88.7	100%	2e-08	78%	EFB29754.1
☐	PREDICTED: coagulation factor XIII B chain [Ursus maritimus]	59.2	90.8	100%	2e-08	78%	XP_008683305.1
☐	PREDICTED: coagulation factor XIII B chain [Equus caballus]	59.2	86.5	100%	2e-08	78%	XP_005608147.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Equus przewalskii]	59.2	86.5	100%	2e-08	78%	XP_008507405.1
☐	PREDICTED: coagulation factor XIII B chain [Condylura cristata]	59.2	110	100%	2e-08	78%	XP_004685543.1
☐	PREDICTED: coagulation factor XIII B chain-like [Ailuropoda melanoleuca]	59.2	88.7	100%	2e-08	78%	XP_002919322.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Equus przewalskii]	59.2	86.5	100%	2e-08	78%	XP_008507404.1
☐	PREDICTED: coagulation factor XIII B chain [Octodon degus]	58.3	106	91%	4e-08	86%	XP_004625499.1
☐	PREDICTED: coagulation factor XIII B chain [Canis lupus familiaris]	57.9	89.5	100%	6e-08	78%	XP_005622353.1
☐	PREDICTED: coagulation factor XIII B chain [Leptonychotes weddellii]	57.5	89.1	100%	8e-08	78%	XP_006734122.1
☐	PREDICTED: coagulation factor XIII B chain-like [Physeter catodon]	56.6	85.7	100%	1e-07	83%	XP_007106854.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Mustela putorius furc	56.6	86.5	100%	1e-07	74%	XP_004756256.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Saimiri boliviensis bo	56.6	87.0	100%	1e-07	74%	XP_010347048.1
☐	PREDICTED: coagulation factor XIII B chain [Lipotes vexillifer]	56.6	85.7	100%	1e-07	83%	XP_007459727.1
☐	PREDICTED: coagulation factor XIII B chain [Orcinus orca]	56.6	86.5	100%	1e-07	83%	XP_004285138.1
☐	PREDICTED: coagulation factor XIII B chain-like [Balaenoptera acutorostrata	56.6	85.7	100%	1e-07	83%	XP_007167347.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Mustela putorius furc	56.6	86.5	100%	1e-07	74%	XP_004756255.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Saimiri boliviensis bo	56.6	87.0	100%	1e-07	74%	XP_003938193.1
☐	PREDICTED: coagulation factor XIII B chain [Oryctolagus cuniculus]	55.8	84.8	100%	3e-07	74%	XP_008266934.1
☐	Coagulation factor XIII B chain [Pteropus alecto]	55.4	87.0	91%	4e-07	81%	ELK19109.1
☐	PREDICTED: coagulation factor XIII B chain [Pteropus alecto]	55.4	87.0	91%	4e-07	81%	XP_006904520.1
☐	PREDICTED: coagulation factor XIII B chain [Trichechus manatus latirostris]	54.9	81.4	100%	5e-07	74%	XP_004375387.1
☐	Coagulation factor XIII B chain [Fukomys damarensis]	54.5	80.2	91%	8e-07	81%	KFO28612.1
☐	PREDICTED: coagulation factor XIII B chain [Fukomys damarensis]	54.5	80.2	91%	8e-07	81%	XP_010633708.1
☐	PREDICTED: coagulation factor XIII B chain [Odobenus rosmarus divergens]	54.1	85.7	100%	1e-06	74%	XP_004415556.1
☐	PREDICTED: coagulation factor XIII B chain [Felis catus]	54.1	85.7	100%	1e-06	74%	XP_006943009.1
☐	PREDICTED: coagulation factor XIII B chain [Panthera tigris altaica]	54.1	85.7	100%	1e-06	74%	XP_007096339.1
☐	Coagulation factor XIII B chain [Tupaia chinensis]	53.2	82.7	100%	2e-06	70%	ELW57877.1
☐	PREDICTED: coagulation factor XIII B chain [Tupaia chinensis]	53.2	82.7	100%	2e-06	70%	XP_006155486.1
☐	PREDICTED: coagulation factor XIII B chain [Echinops telfairi]	52.8	52.8	100%	3e-06	74%	XP_004700122.1
☐	PREDICTED: coagulation factor XIII B chain [Orycteropus afer afer]	52.8	82.7	100%	3e-06	74%	XP_007939370.1
☐	hypothetical protein CB1_001441011 [Camelus ferus]	52.4	52.4	100%	4e-06	74%	EPY76298.1
☐	PREDICTED: coagulation factor XIII B chain isoform 2 [Dasypus novemcinctu	52.4	81.9	100%	4e-06	78%	XP_004476414.1
☐	PREDICTED: coagulation factor XIII B chain [Vicugna pacos]	52.4	81.9	100%	4e-06	74%	XP_006213311.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XIII B chain [Cam	52.4	81.9	100%	4e-06	74%	XP_010980486.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Camelus bactrianus]	52.4	81.9	100%	4e-06	74%	XP_010954592.1

☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Camelus bactrianus]	52.4	81.9	100%	4e-06	74%	XP_010954591.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XIII B chain [Cam	52.4	81.9	100%	4e-06	74%	XP_006191145.1
☐	PREDICTED: coagulation factor XIII B chain-like [Pantholops hodgsonii]	52.4	82.3	100%	4e-06	74%	XP_005979749.1
☐	PREDICTED: coagulation factor XIII B chain-like [Capra hircus]	52.4	82.3	100%	4e-06	74%	XP_005691104.1
☐	PREDICTED: coagulation factor XIII B chain isoform 1 [Dasypus novemcinctu	52.4	81.9	100%	4e-06	78%	XP_004476413.1
☐	PREDICTED: coagulation factor XIII B chain-like [Bos mutus]	52.4	82.3	100%	4e-06	74%	XP_005897275.1
☐	PREDICTED: coagulation factor XIII B chain [Bison bison bison]	52.4	105	100%	4e-06	74%	XP_010829438.1
☐	PREDICTED: coagulation factor XIII B chain-like [Bubalus bubalis]	51.1	81.0	100%	1e-05	74%	XP_006064953.1
☐	PREDICTED: coagulation factor XIII B chain [Nannospalax galili]	50.7	79.7	91%	1e-05	77%	XP_008829795.1
☐	PREDICTED: coagulation factor XIII B chain [Ceratotherium simum simum]	50.3	81.9	100%	2e-05	70%	XP_004439047.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XIII B chain [Ochc	50.3	81.4	100%	2e-05	70%	XP_004578856.1
☐	coagulation factor XIII B chain precursor [Bos taurus]	49.8	79.7	100%	3e-05	74%	NP_001033618.1
☐	PREDICTED: coagulation factor XIII B chain [Tarsius syrichta]	49.4	79.3	100%	4e-05	65%	XP_008062916.1
☐	PREDICTED: coagulation factor XIII B chain [Ovis aries]	49.0	78.9	100%	5e-05	70%	XP_004013974.1
☐	PREDICTED: coagulation factor XIII B chain [Peromyscus maniculatus bairdii]	48.6	74.7	100%	7e-05	70%	XP_006982468.1
☐	PREDICTED: coagulation factor XIII B chain [Elephantulus edwardii]	47.3	74.2	100%	2e-04	70%	XP_006892166.1
☐	PREDICTED: coagulation factor XIII B chain [Ictidomys tridecemlineatus]	47.3	73.8	100%	2e-04	65%	XP_005330450.1
☐	PREDICTED: coagulation factor XIII B chain [Jaculus jaculus]	46.9	76.4	100%	2e-04	70%	XP_004659583.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XIII B chain [Micro	46.9	76.4	82%	2e-04	74%	XP_005348510.1
☐	PREDICTED: coagulation factor XIII B chain [Sarcophilus harrisii]	46.0	78.1	95%	5e-04	64%	XP_003767597.1
☐	PREDICTED: coagulation factor XIII B chain [Cricetulus griseus]	45.6	74.7	82%	6e-04	74%	XP_003504725.2
☐	PREDICTED: coagulation factor XIII B chain [Sus scrofa]	44.8	74.7	100%	0.001	61%	XP_003361662.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Mus musculus]	44.3	74.7	91%	0.002	74%	XP_006529196.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Mus musculus]	44.3	74.7	91%	0.002	74%	XP_006529195.1
☐	B subunit of factor XIII [Mus musculus]	44.3	74.7	91%	0.002	74%	BAA00963.1
☐	Coagulation factor XIII, beta subunit [Mus musculus]	44.3	74.7	91%	0.002	74%	AAH30166.1

Alignments

Download GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

PREDICTED: coagulation factor XIII B chain isoform X4 [Pan troglodytes]

Sequence ID: ref|XP_009438553.1| **Length:** 613 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 483 to 505 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
74.0 bits(167)	2e-13	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    KHGVIISSTVDTYEDGSSVEYRC  23
            KHGVIISSTVDTYE+GSSVEYRC
Sbjct  483  KHGVIISSTVDTYENGSSVEYRC  505
```

Range 2: 367 to 377 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
30.3 bits(64)	51	9/11(82%)	9/11(81%)	0/11(0%)

```
Query  13   YEDGSSVEYRC  23
            Y  GSSVEYRC
Sbjct  367  YATGSSVEYRC  377
```

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PREDICTED: coagulation factor XIII B chain isoform X3 [Pan troglodytes]

Sequence ID: ref|XP_009438550.1| **Length:** 629 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 499 to 521 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
74.0 bits(167)	2e-13	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    KHGVIISSTVDTYEDGSSVEYRC  23
            KHGVIISSTVDTYE+GSSVEYRC
Sbjct  499  KHGVIISSTVDTYENGSSVEYRC  521
```

Range 2: 383 to 393 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
30.3 bits(64)	51	9/11(82%)	9/11(81%)	0/11(0%)

```
Query  13   YEDGSSVEYRC  23
            Y  GSSVEYRC
Sbjct  383  YATGSSVEYRC  393
```

Download GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

PREDICTED: coagulation factor XIII B chain isoform X2 [Homo sapiens]

Sequence ID: ref|XP_005245011.1| **Length:** 629 **Number of Matches:** 2

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 499 to 521 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
74.0 bits(167)	2e-13	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    KHGVIISSTVDTYEDGSSVEYRC  23
            KHGVIISSTVDTYE+GSSVEYRC
Sbjct  499  KHGVIISSTVDTYENGSSVEYRC  521
```

Range 2: 383 to 393 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
30.3 bits(64)	51	9/11(82%)	9/11(81%)	0/11(0%)

```
Query  13   YEDGSSVEYRC  23
            Y  GSSVEYRC
Sbjct  383  YATGSSVEYRC  393
```

Download GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

PREDICTED: coagulation factor XIII B chain isoform X2 [Pan troglodytes]

Sequence ID: ref|XP_009438547.1| **Length:** 660 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 530 to 552 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
74.0 bits(167)	2e-13	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    KHGVIISSTVDTYEDGSSVEYRC  23
            KHGVIISSTVDTYE+GSSVEYRC
Sbjct  530  KHGVIISSTVDTYENGSSVEYRC  552
```

Range 2: 414 to 424 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
30.3 bits(64)	51	9/11(82%)	9/11(81%)	0/11(0%)

```
Query  13   YEDGSSVEYRC  23
            Y  GSSVEYRC
Sbjct  414  YATGSSVEYRC  424
```

Download GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

PREDICTED: coagulation factor XIII B chain isoform X1 [Homo sapiens]

Sequence ID: ref|XP_005245010.1| **Length:** 660 **Number of Matches:** 2

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 530 to 552 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
74.0 bits(167)	2e-13	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    KHGVIISSTVDTYEDGSSVEYRC  23
            KHGVIISSTVDTYE+GSSVEYRC
Sbjct  530  KHGVIISSTVDTYENGSSVEYRC  552
```

Range 2: 414 to 424 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Identities	Positives	Gaps
30.3 bits(64)	51	9/11(82%)	9/11(81%)	0/11(0%)

```
Query  13   YEDGSSVEYRC  23
            Y  GSSVEYRC
Sbjct  414  YATGSSVEYRC  424
```

BLAST ®   Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - B94VMWFG01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   Formatting options   Download

How to read this page   Blast report description

F13B_KHGVIISSTVDTYENGSSVEYRC_NonMod

RID B94VMWFG01R (Expires on 01-14 10:39 am)

Query ID lcl|308111
Description None
Molecule type amino acid
Query Length 23

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

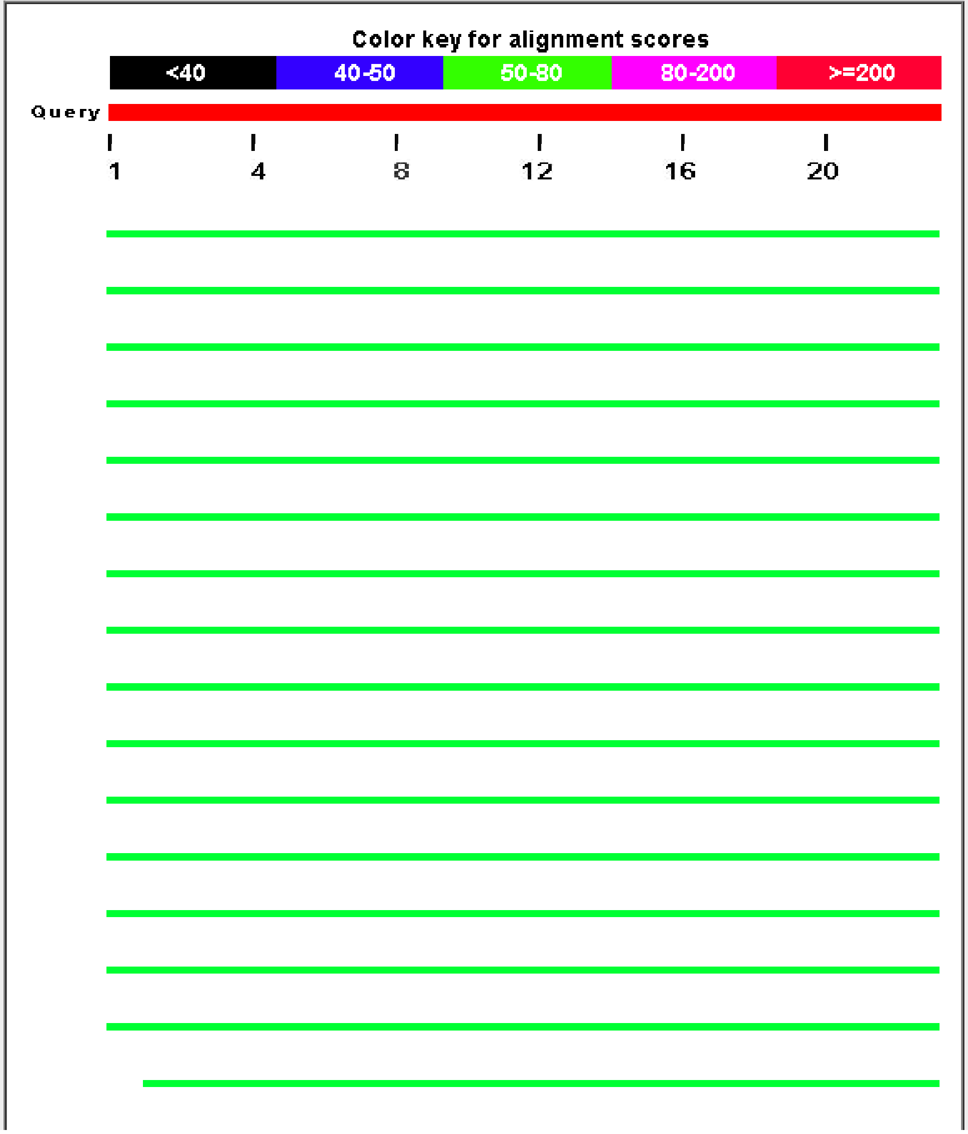
Graphic Summary

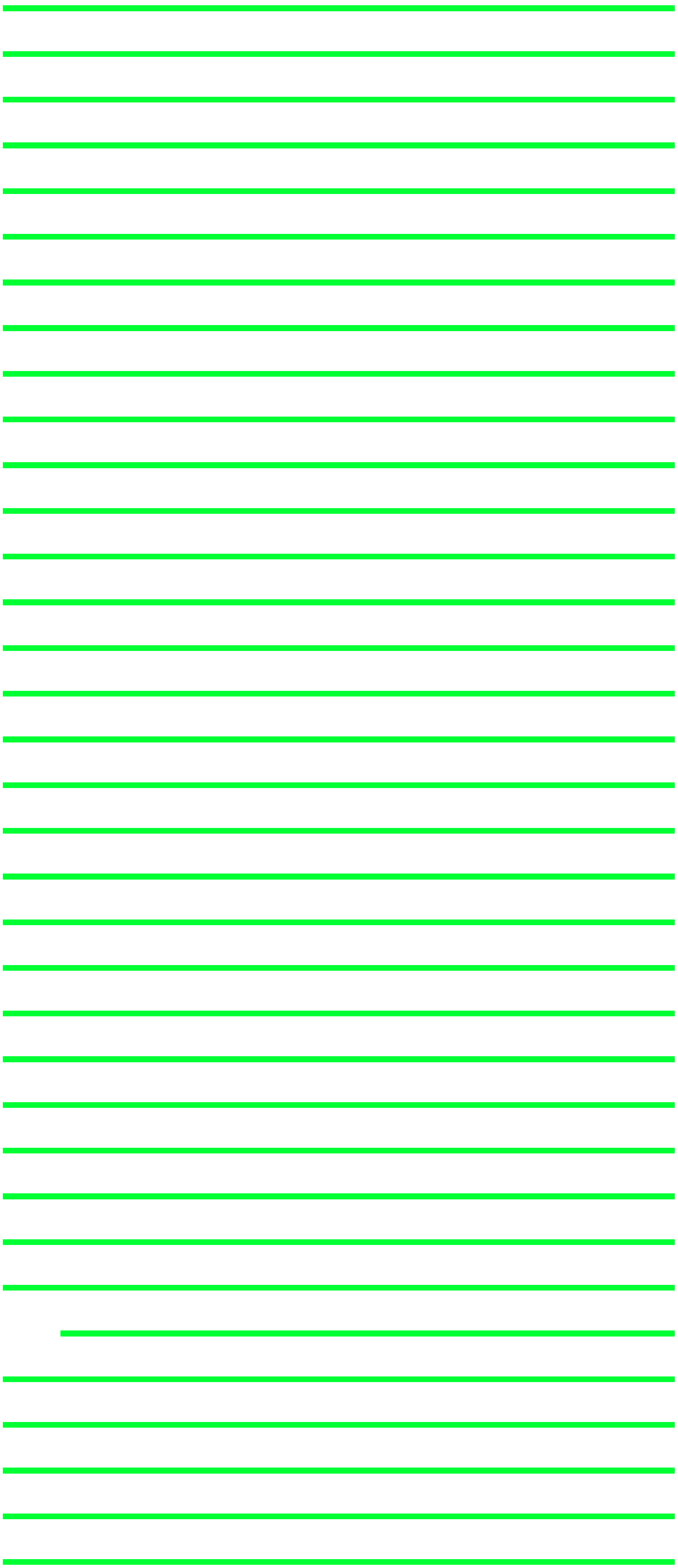
Show Conserved Domains

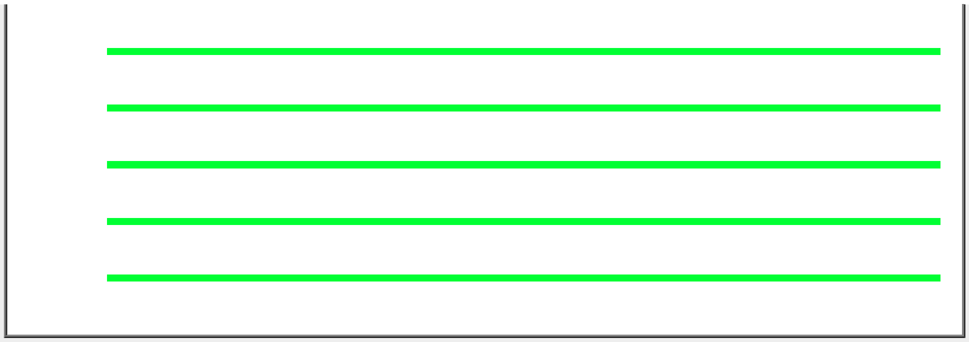
No putative conserved domains have been detected

Distribution of 200 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: coagulation factor XIII B chain isoform X4 [Pan troglo	76.6	108	100%	2e-14	100%	gi|694890887|XP_009438553.1
☐	PREDICTED: coagulation factor XIII B chain isoform X3 [Pan troglo	76.6	108	100%	2e-14	100%	gi|694890885|XP_009438550.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Homo sap	76.6	108	100%	2e-14	100%	gi|530364289|XP_005245011.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Pan troglo	76.6	108	100%	2e-14	100%	gi|694890883|XP_009438547.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Homo sap	76.6	108	100%	2e-14	100%	gi|530364287|XP_005245010.1
☐	factor XIII b subunit precursor [Homo sapiens]	76.6	108	100%	2e-14	100%	gi|182839|AAA88042.1
☐	coagulation factor XIIIb [Homo sapiens]	76.6	108	100%	2e-14	100%	gi|179417|AAA51821.1
☐	PREDICTED: coagulation factor XIII B chain [Gorilla gorilla gorilla]	76.6	108	100%	2e-14	100%	gi|426333135|XP_004028140.1
☐	coagulation factor XIII, B polypeptide [Homo sapiens]	76.6	108	100%	2e-14	100%	gi|50897468|AAT85802.1
☐	PREDICTED: coagulation factor XIII B chain [Pan paniscus]	76.6	108	100%	2e-14	100%	gi|397505134|XP_003823128.1
☐	unnamed protein product [Homo sapiens]	76.6	108	100%	2e-14	100%	gi|158254552|BAF83249.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Pan troglo	76.6	108	100%	2e-14	100%	gi|114571621|XP_001137074.1
☐	coagulation factor XIII B chain precursor [Homo sapiens]	76.6	108	100%	2e-14	100%	gi|110611237|NP_001985.2
☐	PREDICTED: coagulation factor XIII B chain [Rhinopithecus roxella	72.7	103	100%	5e-13	96%	gi|724966976|XP_010356755.1
☐	PREDICTED: coagulation factor XIII B chain [Nomascus leucogeny	72.7	104	100%	5e-13	96%	gi|332230735|XP_003264551.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XIII B c	69.8	101	95%	5e-12	95%	gi|395729264|XP_002809712.2
☐	PREDICTED: coagulation factor XIII B chain [Galeopterus variegatu	68.9	100	100%	1e-11	91%	gi|667327246|XP_008590154.1
☐	PREDICTED: coagulation factor XIII B chain isoform X4 [Chinchilla	68.5	95.9	100%	1e-11	91%	gi|533119447|XP_005375174.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Chinchilla	68.5	95.9	100%	1e-11	91%	gi|533119443|XP_005375172.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Chinchilla	68.5	95.9	100%	1e-11	91%	gi|533119441|XP_005375171.1
☐	PREDICTED: coagulation factor XIII B chain-like [Papio anubis]	66.4	66.4	100%	4e-11	91%	gi|685520465|XP_009189228.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Chloroceb	66.4	97.1	100%	7e-11	91%	gi|635131774|XP_007987269.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Chloroceb	66.4	97.1	100%	7e-11	91%	gi|635131772|XP_007987268.1
☐	PREDICTED: coagulation factor XIII B chain isoform X4 [Macaca fa	66.0	96.7	100%	1e-10	91%	gi|544399131|XP_005540366.1
☐	PREDICTED: coagulation factor XIII B chain isoform X3 [Macaca fa	66.0	96.7	100%	1e-10	91%	gi|544399129|XP_005540365.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Macaca fa	66.0	96.7	100%	1e-10	91%	gi|544399127|XP_005540364.1
☐	hypothetical protein EGM_01565 [Macaca fascicularis]	66.0	96.7	100%	1e-10	91%	gi|355746072|EHH50697.1
☐	PREDICTED: coagulation factor XIII B chain isoform 2 [Macaca mu	66.0	96.7	100%	1e-10	91%	gi|109018994|XP_001111017.1
☐							

	PREDICTED: coagulation factor XIII B chain isoform X5 [Callithrix ja	65.1	95.0	100%	2e-10	87%	gi|675747042|XP_008983391.1
☐	PREDICTED: coagulation factor XIII B chain isoform X4 [Callithrix ja	65.1	95.0	100%	2e-10	87%	gi|390477211|XP_002760512.2
☐	PREDICTED: coagulation factor XIII B chain isoform X3 [Callithrix ja	65.1	95.0	100%	2e-10	87%	gi|675747035|XP_008983390.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Callithrix ja	65.1	95.0	100%	2e-10	87%	gi|675747031|XP_008983389.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Callithrix ja	65.1	95.0	100%	2e-10	87%	gi|675747027|XP_008983388.1
☐	Coagulation factor XIII B chain [Heterocephalus glaber]	63.8	90.8	100%	5e-10	87%	gi|351707464|EHB10383.1
☐	PREDICTED: coagulation factor XIII B chain [Heterocephalus glabe	63.8	90.8	100%	5e-10	87%	gi|512997230|XP_004860190.1
☐	PREDICTED: coagulation factor XIII B chain [Heterocephalus glabe	63.8	90.8	100%	5e-10	87%	gi|512886082|XP_004896309.1
☐	PREDICTED: coagulation factor XIII B chain [Otolemur garnettii]	63.4	96.3	100%	7e-10	83%	gi|395839035|XP_003792408.1
☐	PREDICTED: coagulation factor XIII B chain [Cavia porcellus]	62.1	112	100%	2e-09	83%	gi|348577975|XP_003474759.1
☐	hypothetical protein PANDA_007949 [Ailuropoda melanoleuca]	61.7	92.5	100%	3e-09	83%	gi|281354170|EFB29754.1
☐	PREDICTED: coagulation factor XIII B chain [Ursus maritimus]	61.7	94.6	100%	3e-09	83%	gi|670984420|XP_008683305.1
☐	PREDICTED: coagulation factor XIII B chain [Equus caballus]	61.7	90.4	100%	3e-09	83%	gi|545210834|XP_005608147.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Equus prz	61.7	90.4	100%	3e-09	83%	gi|664776253|XP_008507405.1
☐	PREDICTED: coagulation factor XIII B chain [Condylura cristata]	61.7	94.2	100%	3e-09	83%	gi|507956228|XP_004685543.1
☐	PREDICTED: coagulation factor XIII B chain-like [Ailuropoda melan	61.7	92.5	100%	3e-09	83%	gi|301767820|XP_002919322.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Equus prz	61.7	90.4	100%	3e-09	83%	gi|664776251|XP_008507404.1
☐	PREDICTED: coagulation factor XIII B chain [Octodon degus]	60.9	112	91%	5e-09	90%	gi|507621809|XP_004625499.1
☐	PREDICTED: coagulation factor XIII B chain [Canis lupus familiaris]	60.4	93.3	100%	7e-09	83%	gi|545504208|XP_005622353.1
☐	PREDICTED: coagulation factor XIII B chain [Leptonychotes wedde	60.0	92.9	100%	1e-08	83%	gi|585163917|XP_006734122.1
☐	PREDICTED: coagulation factor XIII B chain-like [Physeter catodon	59.2	89.5	100%	2e-08	87%	gi|593721150|XP_007106854.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Mustela pu	59.2	90.4	100%	2e-08	78%	gi|511871277|XP_004756256.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Saimiri bo	59.2	90.8	100%	2e-08	78%	gi|725592693|XP_010347048.1
☐	PREDICTED: coagulation factor XIII B chain [Lipotes vexillifer]	59.2	89.5	100%	2e-08	87%	gi|602695339|XP_007459727.1
☐	PREDICTED: coagulation factor XIII B chain [Orcinus orca]	59.2	88.7	100%	2e-08	87%	gi|466083906|XP_004285138.1
☐	PREDICTED: coagulation factor XIII B chain-like [Balaenoptera acu	59.2	89.5	100%	2e-08	87%	gi|594625548|XP_007167347.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Mustela pu	59.2	90.4	100%	2e-08	78%	gi|511871274|XP_004756255.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Saimiri bo	59.2	90.8	100%	2e-08	78%	gi|403294438|XP_003938193.1
☐	PREDICTED: coagulation factor XIII B chain [Oryctolagus cuniculus	58.3	89.1	100%	4e-08	78%	gi|655861271|XP_008266934.1
☐	Coagulation factor XIII B chain [Pteropus alecto]	57.9	89.1	91%	5e-08	86%	gi|431921906|ELK19109.1
☐	PREDICTED: coagulation factor XIII B chain [Pteropus alecto]	57.9	89.1	91%	5e-08	86%	gi|586520298|XP_006904520.1
☐	PREDICTED: coagulation factor XIII B chain [Trichechus manatus l	57.5	85.3	100%	7e-08	78%	gi|471369745|XP_004375387.1
☐	Coagulation factor XIII B chain [Fukomys damarensis]	57.1	84.0	91%	1e-07	86%	gi|676274024|KFO28612.1
☐	PREDICTED: coagulation factor XIII B chain [Fukomys damarensis	57.1	84.0	91%	1e-07	86%	gi|731240651|XP_010633708.1
☐	PREDICTED: coagulation factor XIII B chain [Odobenus rosmarus d	56.6	89.5	100%	1e-07	78%	gi|472392562|XP_004415556.1
☐	PREDICTED: coagulation factor XIII B chain [Felis catus]	56.6	89.5	100%	1e-07	78%	gi|587018672|XP_006943009.1
☐	PREDICTED: coagulation factor XIII B chain [Panthera tigris altaica	56.6	89.5	100%	1e-07	78%	gi|591341832|XP_007096339.1
☐	Coagulation factor XIII B chain [Tupaia chinensis]	55.8	86.5	100%	3e-07	74%	gi|444717041|ELW57877.1
☐	PREDICTED: coagulation factor XIII B chain [Tupaia chinensis]	55.8	86.5	100%	3e-07	74%	gi|562853713|XP_006155486.1
☐	PREDICTED: coagulation factor XIII B chain [Echinops telfairi]	55.4	55.4	100%	4e-07	78%	gi|507635138|XP_004700122.1
☐	PREDICTED: coagulation factor XIII B chain [Orycteropus afer afer]	55.4	86.5	100%	4e-07	78%	gi|634849111|XP_007939370.1
☐	hypothetical protein CB1_001441011 [Camelus ferus]	54.9	54.9	100%	5e-07	78%	gi|528756639|EPY76298.1
☐	PREDICTED: coagulation factor XIII B chain isoform 2 [Dasypus nc	54.9	85.7	100%	5e-07	83%	gi|488581997|XP_004476414.1
☐	PREDICTED: coagulation factor XIII B chain [Vicugna pacos]	54.9	85.7	100%	5e-07	78%	gi|560982160|XP_006213311.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XIII B c	54.9	85.7	100%	5e-07	78%	gi|560930005|XP_006191145.1

☐	PREDICTED: coagulation factor XIII B chain-like [Pantholops hodg	54.9	86.1	100%	5e-07	78%	gi|556769078|XP_005979749.1
☐	PREDICTED: coagulation factor XIII B chain-like [Capra hircus]	54.9	86.1	100%	5e-07	78%	gi|548499616|XP_005691104.1
☐	PREDICTED: coagulation factor XIII B chain isoform 1 [Dasypus nc	54.9	85.7	100%	5e-07	83%	gi|488581995|XP_004476413.1
☐	PREDICTED: coagulation factor XIII B chain-like [Bos mutus]	54.9	86.1	100%	5e-07	78%	gi|555970508|XP_005897275.1
☐	PREDICTED: coagulation factor XIII B chain-like [Bubalus bubalis]	53.7	84.8	100%	1e-06	78%	gi|594082720|XP_006064953.1
☐	PREDICTED: coagulation factor XIII B chain [Nannospalax galili]	53.2	83.6	91%	2e-06	82%	gi|674047440|XP_008829795.1
☐	PREDICTED: coagulation factor XIII B chain [Ceratotherium simum	52.8	85.7	100%	3e-06	74%	gi|478529758|XP_004439047.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XIII B c	52.8	85.3	100%	3e-06	74%	gi|504132480|XP_004578856.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Bos tauru	52.4	83.6	100%	4e-06	78%	gi|528980931|XP_005217396.1
☐	coagulation factor XIII B chain precursor [Bos taurus]	52.4	83.6	100%	4e-06	78%	gi|84370091|NP_001033618.1
☐	PREDICTED: coagulation factor XIII B chain [Tarsius syrichta]	52.0	83.1	100%	5e-06	70%	gi|640812512|XP_008062916.1
☐	PREDICTED: coagulation factor XIII B chain [Ovis aries]	51.5	82.7	100%	7e-06	74%	gi|426240145|XP_004013974.1
☐	PREDICTED: coagulation factor XIII B chain [Peromyscus manicula	51.1	78.5	100%	9e-06	74%	gi|589939450|XP_006982468.1
☐	PREDICTED: coagulation factor XIII B chain [Elephantulus edwardi	49.8	98.2	100%	2e-05	74%	gi|585682032|XP_006892166.1
☐	PREDICTED: coagulation factor XIII B chain [Ictidomys tridecemline	49.8	76.4	100%	2e-05	70%	gi|532089507|XP_005330450.1
☐	PREDICTED: coagulation factor XIII B chain [Jaculus jaculus]	49.4	80.2	100%	3e-05	74%	gi|507551568|XP_004659583.1
☐	PREDICTED: LOW QUALITY PROTEIN: coagulation factor XIII B c	49.4	80.2	82%	3e-05	79%	gi|532009392|XP_005348510.1
☐	PREDICTED: coagulation factor XIII B chain [Sarcophilus harrisii]	48.6	81.9	95%	6e-05	68%	gi|395531053|XP_003767597.1
☐	PREDICTED: coagulation factor XIII B chain [Cricetulus griseus]	48.1	78.1	82%	9e-05	79%	gi|625203770|XP_003504725.2
☐	PREDICTED: coagulation factor XIII B chain [Sus scrofa]	47.3	76.8	100%	2e-04	65%	gi|335309500|XP_003361662.1
☐	PREDICTED: coagulation factor XIII B chain isoform X2 [Mus musc	46.9	78.5	91%	2e-04	79%	gi|568908131|XP_006529196.1
☐	PREDICTED: coagulation factor XIII B chain isoform X1 [Mus musc	46.9	78.5	91%	2e-04	79%	gi|568908129|XP_006529195.1
☐	B subunit of factor XIII [Mus musculus]	46.9	78.5	91%	2e-04	79%	gi|303652|BAA00963.1
☐	Coagulation factor XIII, beta subunit [Mus musculus]	46.9	78.5	91%	2e-04	79%	gi|20987307|AAH30166.1
☐	unnamed protein product [Mus musculus]	46.9	78.5	91%	2e-04	79%	gi|74143591|BAE28851.1
☐	coagulation factor XIII B chain precursor [Mus musculus]	46.9	78.5	91%	2e-04	79%	gi|224967112|NP_112441.2
☐	PREDICTED: coagulation factor XIII B chain [Loxodonta africana]	46.0	78.1	100%	4e-04	70%	gi|344277215|XP_003410399.1

Alignments

Download GenPept Graphics Sort by: 0 Next Previous Descriptions

PREDICTED: coagulation factor XIII B chain isoform X4 [Pan troglodytes]

Sequence ID: gi|694890887|ref|XP_009438553.1| **Length:** 613 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 483 to 505 GenPept Graphics Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(173)	2e-14	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    KHGVIISSTVDTYENGSSVEYRC  23
            KHGVIISSTVDTYENGSSVEYRC
Sbjct  483  KHGVIISSTVDTYENGSSVEYRC  505
```

Range 2: 367 to 377 GenPept Graphics Next Match Previous Match First Match

Score	Expect	Identities	Positives	Gaps
31.6 bits(67)	18	9/11(82%)	9/11(81%)	0/11(0%)

```
Query  13   YENGSSVEYRC  23
            Y  GSSVEYRC
Sbjct  367  YATGSSVEYRC  377
```

Download GenPept Graphics Sort by: 0 Next Previous Descriptions

PREDICTED: coagulation factor XIII B chain isoform X3 [Pan troglodytes]

Sequence ID: gi|694890885|ref|XP_009438550.1| **Length:** 629 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 499 to 521 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(173)	2e-14	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    KHGVIISSTVDTYENGSSVEYRC  23
            KHGVIISSTVDTYENGSSVEYRC
Sbjct  499  KHGVIISSTVDTYENGSSVEYRC  521
```

Range 2: 383 to 393 GenPept Graphics

▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
31.6 bits(67)	18	9/11(82%)	9/11(81%)	0/11(0%)

```
Query  13   YENGSSVEYRC  23
            Y  GSSVEYRC
Sbjct  383  YATGSSVEYRC  393
```

Download GenPept Graphics **Sort by:** 0 ▼ Next ▲ Previous ▲ Descriptions

PREDICTED: coagulation factor XIII B chain isoform X2 [Homo sapiens]

Sequence ID: gi|530364289|ref|XP_005245011.1| **Length:** 629 **Number of Matches:** 2

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 499 to 521 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(173)	2e-14	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    KHGVIISSTVDTYENGSSVEYRC  23
            KHGVIISSTVDTYENGSSVEYRC
Sbjct  499  KHGVIISSTVDTYENGSSVEYRC  521
```

Range 2: 383 to 393 GenPept Graphics

▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
31.6 bits(67)	18	9/11(82%)	9/11(81%)	0/11(0%)

```
Query  13   YENGSSVEYRC  23
            Y  GSSVEYRC
Sbjct  383  YATGSSVEYRC  393
```

Download GenPept Graphics **Sort by:** 0 ▼ Next ▲ Previous ▲ Descriptions

PREDICTED: coagulation factor XIII B chain isoform X2 [Pan troglodytes]

Sequence ID: gi|694890883|ref|XP_009438547.1| **Length:** 660 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 530 to 552 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(173)	2e-14	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    KHGVIISSTVDTYENGSSVEYRC  23
            KHGVIISSTVDTYENGSSVEYRC
Sbjct  530  KHGVIISSTVDTYENGSSVEYRC  552
```

Range 2: 414 to 424 GenPept Graphics

▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
31.6 bits(67)	18	9/11(82%)	9/11(81%)	0/11(0%)

```
Query  13   YENGSSVEYRC  23
            Y  GSSVEYRC
Sbjct  414  YATGSSVEYRC  424
```

Download GenPept Graphics **Sort by:** 0 ▼ Next ▲ Previous ▲ Descriptions

PREDICTED: coagulation factor XIII B chain isoform X1 [Homo sapiens]

Sequence ID: gi|530364287|ref|XP_005245010.1| **Length:** 660 **Number of Matches:** 2

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 530 to 552 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(173)	2e-14	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    KHGVIISSTVDTYENGSSVEYRC  23
            KHGVIISSTVDTYENGSSVEYRC
Sbjct  530  KHGVIISSTVDTYENGSSVEYRC  552
```

Range 2: 414 to 424 GenPept Graphics

▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
31.6 bits(67)	18	9/11(82%)	9/11(81%)	0/11(0%)

```
Query  13   YENGSSVEYRC  23
```

```
            Y  GSSVEYRC
Sbjct  414  YATGSSVEYRC  424
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

FBLN1_RCATPHGDDASLEATFVKRC_Mod

RID BVDGPM5A01R (Expires on 01-21 08:57 am)

Query ID lcl|44843
Description None
Molecule type amino acid
Query Length 20

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

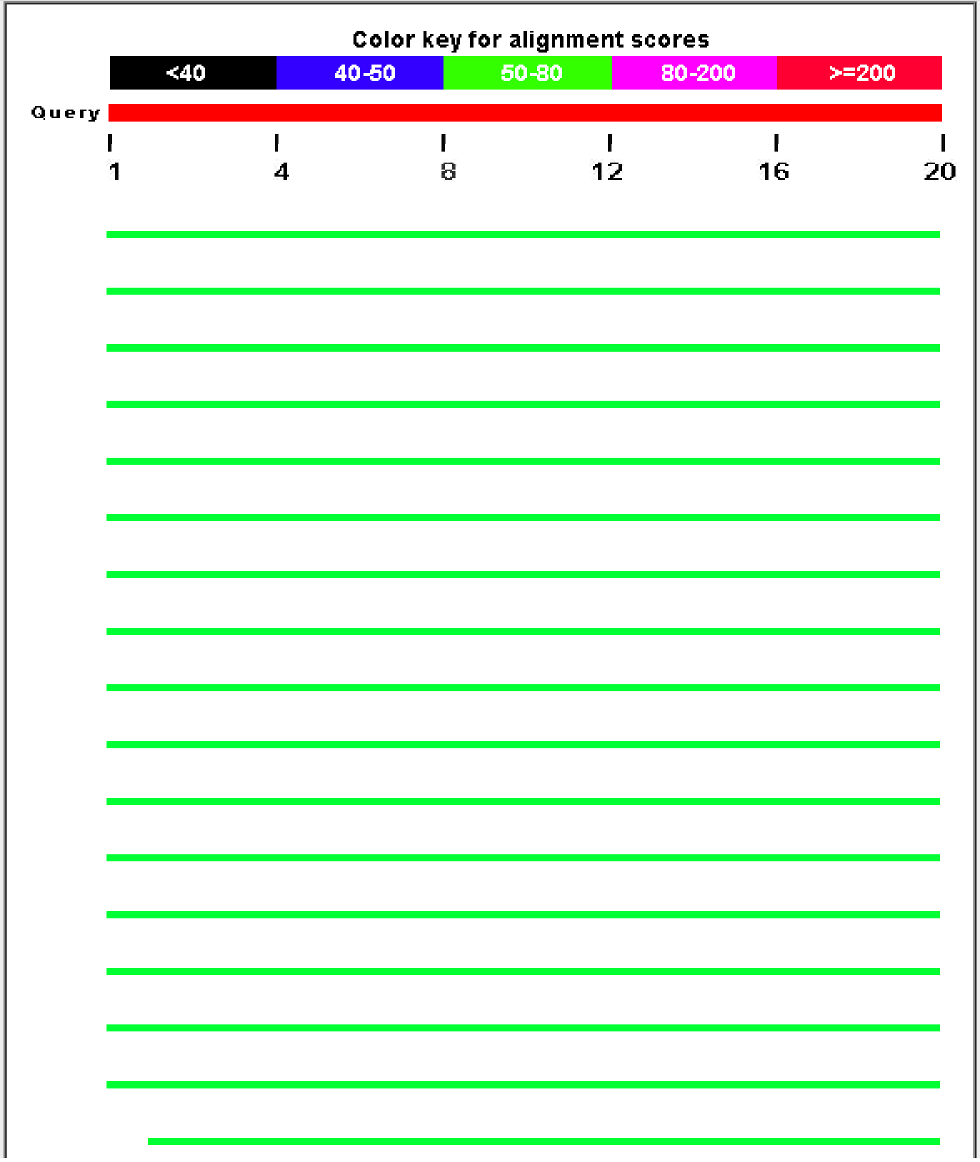
Graphic Summary

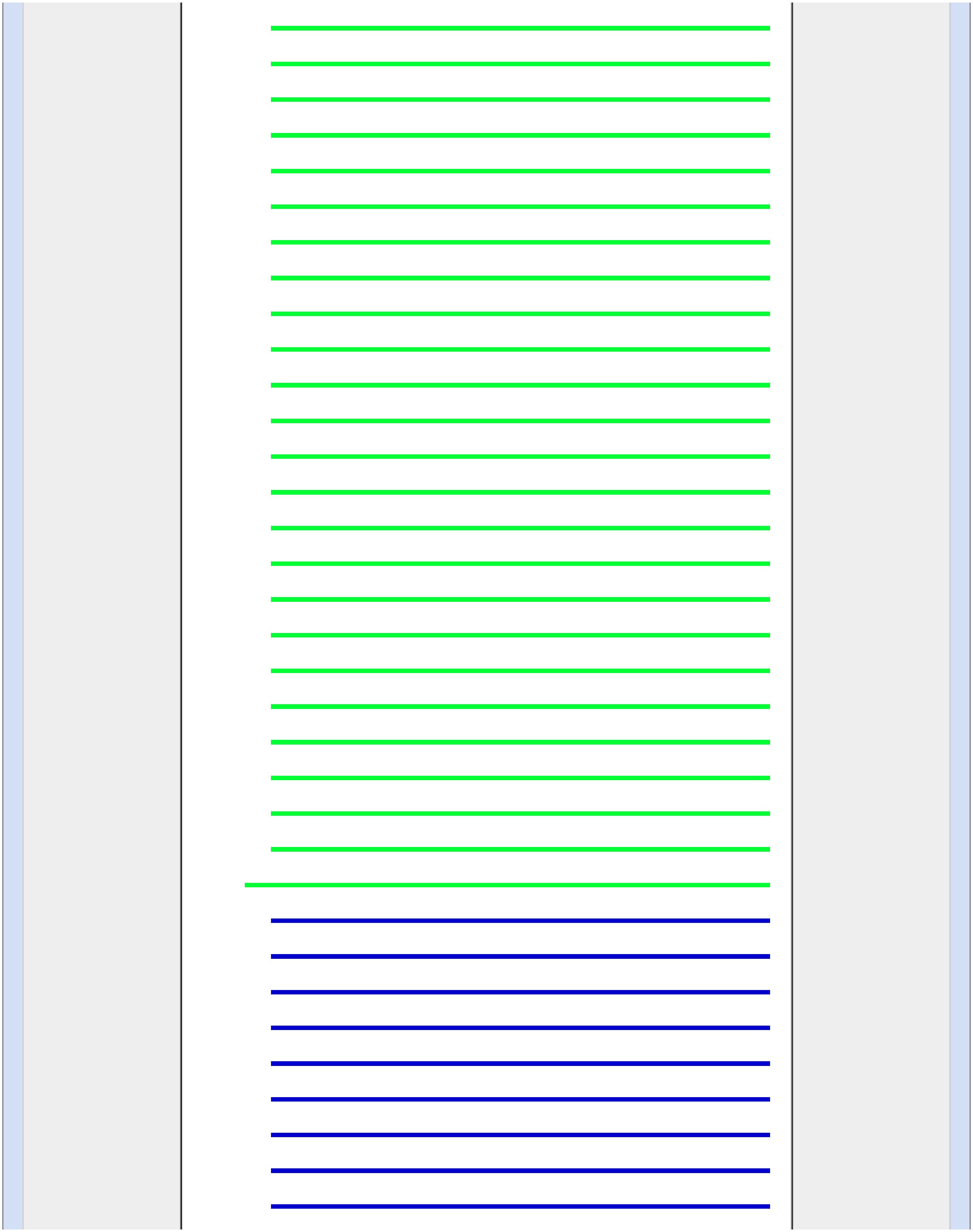
Show Conserved Domains

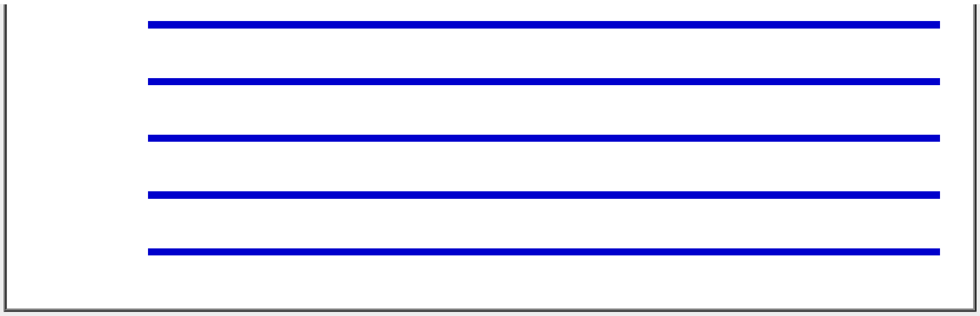
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	fibulin-1 isoform A precursor [Homo sapiens]	64.7	64.7	100%	2e-10	95%	NP_006478.2
☐	fibulin-1 A [Homo sapiens]	64.7	64.7	100%	2e-10	95%	CAA37770.1
☐	fibulin 1, isoform CRA_b [Homo sapiens]	64.7	64.7	100%	2e-10	95%	EAW73386.1
☐	fibulin 1 precursor, splice form B - human [Homo sapiens]	64.7	64.7	100%	2e-10	95%	B36346
☐	fibulin-1 isoform B precursor [Homo sapiens]	64.7	64.7	100%	2e-10	95%	NP_006476.2
☐	unnamed protein product [Homo sapiens]	64.7	64.7	100%	2e-10	95%	BAG62463.1
☐	fibulin-1 isoform C precursor [Homo sapiens]	64.7	64.7	100%	2e-10	95%	NP_001987.2
☐	Fibulin 1 [Homo sapiens]	64.7	64.7	100%	2e-10	95%	AAH22497.1
☐	fibulin-1 C [Homo sapiens]	64.7	64.7	100%	2e-10	95%	CAA37772.1
☐	fibulin 1 [synthetic construct]	64.7	64.7	100%	2e-10	95%	ABM84973.1
☐	fibulin 1, isoform CRA_f [Homo sapiens]	64.7	64.7	100%	2e-10	95%	EAW73390.1
☐	fibulin-1 isoform D precursor [Homo sapiens]	64.7	64.7	100%	2e-10	95%	AAK37822.1
☐	RecName: Full=Fibulin-1; Short=FIBL-1; Flags: Precursor [Homo sapiens]	64.7	64.7	100%	2e-10	95%	P23142.4
☐	fibulin-1 isoform D precursor [Homo sapiens]	64.7	64.7	100%	2e-10	95%	NP_006477.2
☐	PREDICTED: fibulin-1 isoform X1 [Pan paniscus]	61.7	61.7	100%	2e-09	90%	XP_003812435.1
☐	PREDICTED: fibulin-1 [Pan troglodytes]	61.7	61.7	100%	2e-09	90%	XP_009436873.1
☐	PREDICTED: fibulin-1 [Nomascus leucogenys]	61.3	61.3	95%	3e-09	95%	XP_003281320.2
☐	PREDICTED: fibulin-1 [Mustela putorius furo]	61.3	61.3	95%	3e-09	95%	XP_004813974.1
☐	PREDICTED: fibulin-1 [Mustela putorius furo]	61.3	61.3	95%	3e-09	95%	XP_004771346.1
☐	PREDICTED: fibulin-1 [Pongo abelii]	61.3	61.3	95%	3e-09	95%	XP_009232751.1
☐	PREDICTED: fibulin-1 [Gorilla gorilla gorilla]	58.3	58.3	95%	3e-08	89%	XP_004063688.1
☐	PREDICTED: fibulin-1 isoform 2 [Odobenus rosmarus divergens]	58.3	58.3	95%	3e-08	89%	XP_004415897.1
☐	PREDICTED: fibulin-1 [Otolemur garnettii]	58.3	58.3	95%	3e-08	89%	XP_003783160.1
☐	PREDICTED: fibulin-1 isoform 1 [Odobenus rosmarus divergens]	58.3	58.3	95%	3e-08	89%	XP_004415896.1
☐	PREDICTED: fibulin-1 isoform X4 [Rhinopithecus roxellana]	57.9	57.9	95%	4e-08	89%	XP_010365649.1
☐	PREDICTED: fibulin-1 isoform X3 [Rhinopithecus roxellana]	57.9	57.9	95%	4e-08	89%	XP_010365573.1
☐	PREDICTED: fibulin-1 isoform X2 [Rhinopithecus roxellana]	57.9	57.9	95%	4e-08	89%	XP_010365494.1
☐	PREDICTED: fibulin-1 isoform X1 [Rhinopithecus roxellana]	57.9	57.9	95%	4e-08	89%	XP_010365413.1
☐	PREDICTED: fibulin-1-like [Leptonychotes weddellii]	54.9	54.9	95%	4e-07	84%	XP_006743570.1

☐	PREDICTED: fibulin-1 [Ursus maritimus]	54.9	54.9	95%	4e-07	84%	XP_008701224.1
☐	PREDICTED: fibulin-1 [Saimiri boliviensis boliviensis]	54.1	54.1	95%	8e-07	84%	XP_003932799.1
☐	PREDICTED: fibulin-1 isoform X2 [Canis lupus familiaris]	54.1	54.1	95%	8e-07	84%	XP_005625812.1
☐	PREDICTED: fibulin-1 isoform X1 [Canis lupus familiaris]	54.1	54.1	95%	8e-07	84%	XP_005625811.1
☐	PREDICTED: fibulin-1 isoform X3 [Chlorocebus sabaeus]	53.2	53.2	95%	1e-06	84%	XP_007974271.1
☐	RecName: Full=Fibulin-1; Short=FIBL-1 [Chlorocebus aethiops]	53.2	53.2	95%	1e-06	84%	Q8MJJ9.1
☐	PREDICTED: fibulin-1 [Macaca fascicularis]	53.2	53.2	95%	1e-06	84%	XP_005567067.1
☐	PREDICTED: fibulin-1 isoform X2 [Chlorocebus sabaeus]	53.2	53.2	95%	1e-06	84%	XP_007974270.1
☐	PREDICTED: fibulin-1 isoform X1 [Chlorocebus sabaeus]	53.2	53.2	95%	1e-06	84%	XP_007974269.1
☐	PREDICTED: fibulin-1 isoform 2 [Macaca mulatta]	53.2	53.2	95%	1e-06	84%	XP_001109966.2
☐	PREDICTED: fibulin-1 isoform X2 [Vicugna pacos]	52.0	52.0	95%	4e-06	84%	XP_006212641.1
☐	PREDICTED: fibulin-1 isoform X1 [Vicugna pacos]	52.0	52.0	95%	4e-06	84%	XP_006212640.1
☐	PREDICTED: fibulin-1 [Loxodonta africana]	50.3	50.3	100%	1e-05	80%	XP_010598758.1
☐	PREDICTED: fibulin-1 [Papio anubis]	49.8	49.8	95%	2e-05	79%	XP_003905746.1
☐	PREDICTED: fibulin-1 [Physeter catodon]	49.4	49.4	95%	3e-05	79%	XP_007128800.1
☐	PREDICTED: fibulin-1 [Callithrix jacchus]	49.4	49.4	95%	3e-05	79%	XP_008978454.1
☐	PREDICTED: fibulin-1 isoform X2 [Bison bison bison]	49.0	49.0	95%	4e-05	79%	XP_010835915.1
☐	PREDICTED: fibulin-1 isoform X1 [Bison bison bison]	49.0	49.0	95%	4e-05	79%	XP_010835914.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1-like [Oryctolagus cuniculus]	49.0	49.0	95%	4e-05	79%	XP_008251212.1
☐	Fibulin-1 [Bos mutus]	49.0	49.0	95%	4e-05	79%	ELR55943.1
☐	TPA: fibulin 1 [Bos taurus]	49.0	49.0	95%	4e-05	79%	DAA29013.1
☐	fibulin-1 precursor [Bos taurus]	49.0	49.0	95%	4e-05	79%	NP_001091498.1
☐	PREDICTED: fibulin-1 [Bos mutus]	49.0	49.0	95%	4e-05	79%	XP_005896425.1
☐	PREDICTED: fibulin-1 [Bubalus bubalis]	49.0	49.0	95%	4e-05	79%	XP_006063368.1
☐	PREDICTED: fibulin-1 [Felis catus]	48.6	48.6	95%	5e-05	79%	XP_006934231.1
☐	PREDICTED: fibulin-1 [Equus caballus]	48.6	48.6	95%	5e-05	79%	XP_005606874.1
☐	PREDICTED: fibulin-1 [Pantholops hodgsonii]	48.6	48.6	95%	5e-05	79%	XP_005958536.1
☐	PREDICTED: fibulin-1 [Balaenoptera acutorostrata scammoni]	47.7	47.7	95%	1e-04	79%	XP_007189256.1
☐	PREDICTED: fibulin-1 isoform 2 [Ceratotherium simum simum]	46.9	46.9	95%	2e-04	79%	XP_004438039.1
☐	PREDICTED: fibulin-1 isoform 1 [Ceratotherium simum simum]	46.9	46.9	95%	2e-04	79%	XP_004438038.1
☐	PREDICTED: fibulin-1-like [Tursiops truncatus]	46.4	46.4	95%	3e-04	74%	XP_004326152.1
☐	PREDICTED: fibulin-1 isoform X4 [Lipotes vexillifer]	46.4	46.4	95%	3e-04	74%	XP_007453975.1
☐	PREDICTED: fibulin-1 isoform X3 [Lipotes vexillifer]	46.4	46.4	95%	3e-04	74%	XP_007453974.1
☐	PREDICTED: fibulin-1 isoform X2 [Lipotes vexillifer]	46.4	46.4	95%	3e-04	74%	XP_007453973.1
☐	PREDICTED: fibulin-1 isoform X1 [Lipotes vexillifer]	46.4	46.4	95%	3e-04	74%	XP_007453972.1
☐	PREDICTED: fibulin-1 isoform 2 [Trichechus manatus latirostris]	46.0	46.0	95%	4e-04	75%	XP_004380068.1
☐	PREDICTED: fibulin-1 isoform 1 [Trichechus manatus latirostris]	46.0	46.0	95%	4e-04	75%	XP_004380067.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1 [Cavia porcellus]	45.6	45.6	95%	5e-04	74%	XP_004999606.1
☐	PREDICTED: fibulin-1 [Octodon degus]	45.6	45.6	95%	5e-04	74%	XP_004642514.1
☐	PREDICTED: fibulin-1 isoform X2 [Sus scrofa]	45.2	45.2	95%	7e-04	74%	XP_005663793.1
☐	PREDICTED: fibulin-1 isoform X1 [Sus scrofa]	45.2	45.2	95%	7e-04	74%	XP_003126003.3
☐	PREDICTED: fibulin-1 isoform X2 [Camelus ferus]	43.9	43.9	95%	0.002	74%	XP_006176723.1
☐	PREDICTED: fibulin-1 isoform X1 [Camelus ferus]	43.9	43.9	95%	0.002	74%	XP_006176722.1
☐	PREDICTED: fibulin-1 [Tupaia chinensis]	43.9	43.9	95%	0.002	74%	XP_006164720.1
☐	PREDICTED: fibulin-1 [Camelus dromedarius]	43.9	43.9	95%	0.002	74%	XP_010981727.1

☐	fibulin-1 isoform C precursor [Camelus ferus]	43.9	43.9	95%	0.002	74%	EPY87041.1
☐	Fibulin-1 [Tupaia chinensis]	43.9	43.9	95%	0.002	74%	ELV12523.1
☐	PREDICTED: fibulin-1 isoform X2 [Chinchilla lanigera]	43.5	43.5	95%	0.002	74%	XP_005379549.1
☐	PREDICTED: fibulin-1 isoform X1 [Chinchilla lanigera]	43.5	43.5	95%	0.002	74%	XP_005379548.1
☐	PREDICTED: fibulin-1 isoform X2 [Erinaceus europaeus]	43.1	43.1	95%	0.003	74%	XP_007531965.1
☐	PREDICTED: fibulin-1 isoform X1 [Erinaceus europaeus]	43.1	43.1	95%	0.003	74%	XP_007531964.1
☐	PREDICTED: fibulin-1-like [Capra hircus]	42.6	42.6	95%	0.005	68%	XP_005681284.1
☐	PREDICTED: fibulin-1 [Ovis aries]	42.6	42.6	95%	0.005	68%	XP_004007703.1
☐	PREDICTED: fibulin-1 [Tarsius syrichta]	41.8	41.8	95%	0.009	68%	XP_008053358.1
☐	PREDICTED: fibulin-1 [Orcinus orca]	41.8	41.8	95%	0.009	68%	XP_004279635.1
☐	PREDICTED: fibulin-1 [Ictidomys tridecemlineatus]	40.9	40.9	95%	0.016	68%	XP_005335099.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1-like [Galeopterus variegatus	40.1	40.1	95%	0.030	74%	XP_008579007.1
☐	PREDICTED: fibulin-1 isoform X2 [Fukomys damarensis]	39.2	39.2	95%	0.056	68%	XP_010632637.1
☐	PREDICTED: fibulin-1 isoform X1 [Fukomys damarensis]	39.2	39.2	95%	0.056	68%	XP_010632636.1
☐	PREDICTED: fibulin-1 [Pteropus alecto]	38.8	38.8	95%	0.076	68%	XP_006917380.1
☐	PREDICTED: fibulin-1 isoform X2 [Ochotona princeps]	38.4	38.4	95%	0.10	68%	XP_004589482.1
☐	PREDICTED: fibulin-1 isoform X1 [Ochotona princeps]	38.4	38.4	95%	0.10	68%	XP_004589481.1
☐	PREDICTED: fibulin-1 isoform X4 [Microtus ochrogaster]	37.5	37.5	95%	0.19	63%	XP_005354460.1
☐	PREDICTED: fibulin-1 isoform X3 [Microtus ochrogaster]	37.5	37.5	95%	0.19	63%	XP_005354459.1
☐	PREDICTED: fibulin-1 isoform X2 [Microtus ochrogaster]	37.5	37.5	95%	0.19	63%	XP_005354458.1
☐	PREDICTED: fibulin-1 isoform X1 [Microtus ochrogaster]	37.5	37.5	95%	0.19	63%	XP_005354457.1
☐	PREDICTED: fibulin-1 [Eptesicus fuscus]	35.4	35.4	95%	0.90	68%	XP_008153634.1
☐	PREDICTED: fibulin-1 [Jaculus jaculus]	34.6	34.6	75%	1.7	67%	XP_004650445.1
☐	PREDICTED: fibulin-1 isoform X2 [Peromyscus maniculatus bairdii]	34.6	34.6	95%	1.7	58%	XP_006980340.1
☐	PREDICTED: fibulin-1 isoform X1 [Peromyscus maniculatus bairdii]	34.6	34.6	95%	1.7	58%	XP_006980339.1
☐	PREDICTED: fibulin-1 [Myotis brandtii]	34.1	34.1	60%	2.3	83%	XP_005886100.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

fibulin-1 isoform A precursor [Homo sapiens]

Sequence ID: ref|NP_006478.2| **Length:** 566 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 90 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
64.7 bits(145)	2e-10	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    RCATPHGDDASLEATFVKRC  20
            RCATPHGD+ASLEATFVKRC
Sbjct  90   RCATPHGDNASLEATFVKRC  109
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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fibulin-1 A [Homo sapiens]

Sequence ID: emb|CAA37770.1| **Length:** 566 **Number of Matches:** 1

Range 1: 90 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
64.7 bits(145)	2e-10	19/20(95%)	20/20(100%)	0/20(0%)

Related Information

Gene - associated gene details

```
Query  1     RCATPHGDDASLEATFVKRC  20
             RCATPHGD+ASLEATFVKRC
Sbjct  90    RCATPHGDNASLEATFVKRC  109
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

fibulin 1, isoform CRA_b, partial [Homo sapiens]

Sequence ID: gb|EAW73386.1| **Length:** 581 **Number of Matches:** 1

Range 1: 90 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
64.7 bits(145)	2e-10	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1     RCATPHGDDASLEATFVKRC  20
             RCATPHGD+ASLEATFVKRC
Sbjct  90    RCATPHGDNASLEATFVKRC  109
```

Related Information

Gene - associated gene details

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fibulin 1 precursor, splice form B - human

Sequence ID: pir||B36346 **Length:** 601 **Number of Matches:** 1

See 2 more title(s)

Range 1: 90 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
64.7 bits(145)	2e-10	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1     RCATPHGDDASLEATFVKRC  20
             RCATPHGD+ASLEATFVKRC
Sbjct  90    RCATPHGDNASLEATFVKRC  109
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

fibulin-1 isoform B precursor [Homo sapiens]

Sequence ID: ref|NP_006476.2| **Length:** 601 **Number of Matches:** 1

See 1 more title(s)

Range 1: 90 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
64.7 bits(145)	2e-10	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1     RCATPHGDDASLEATFVKRC  20
             RCATPHGD+ASLEATFVKRC
Sbjct  90    RCATPHGDNASLEATFVKRC  109
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

FBLN1_RCATPHGDNASLEATFVKRC_NonMod

RID B94W0NM901R (Expires on 01-14 10:39 am)

Query ID lcl|202649
Description None
Molecule type amino acid
Query Length 20

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

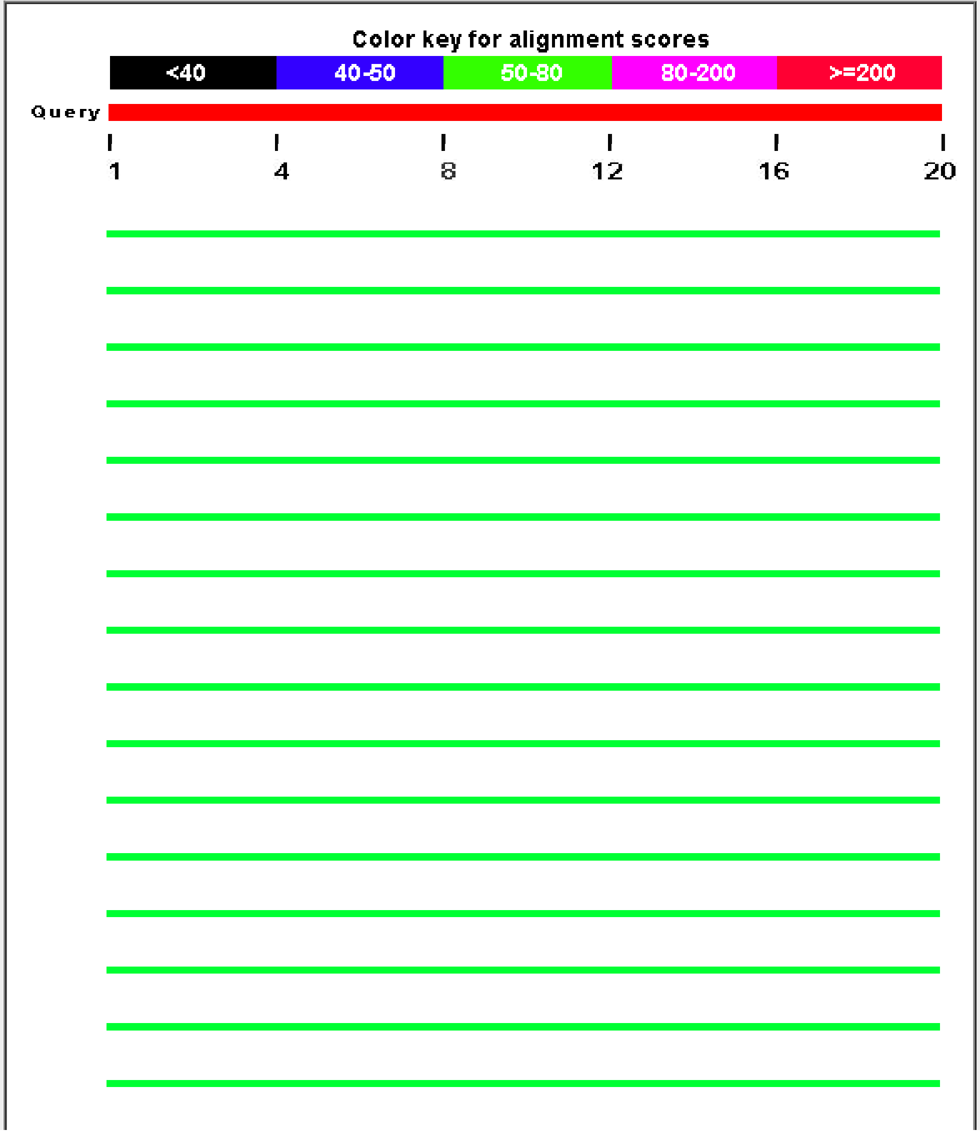
Graphic Summary

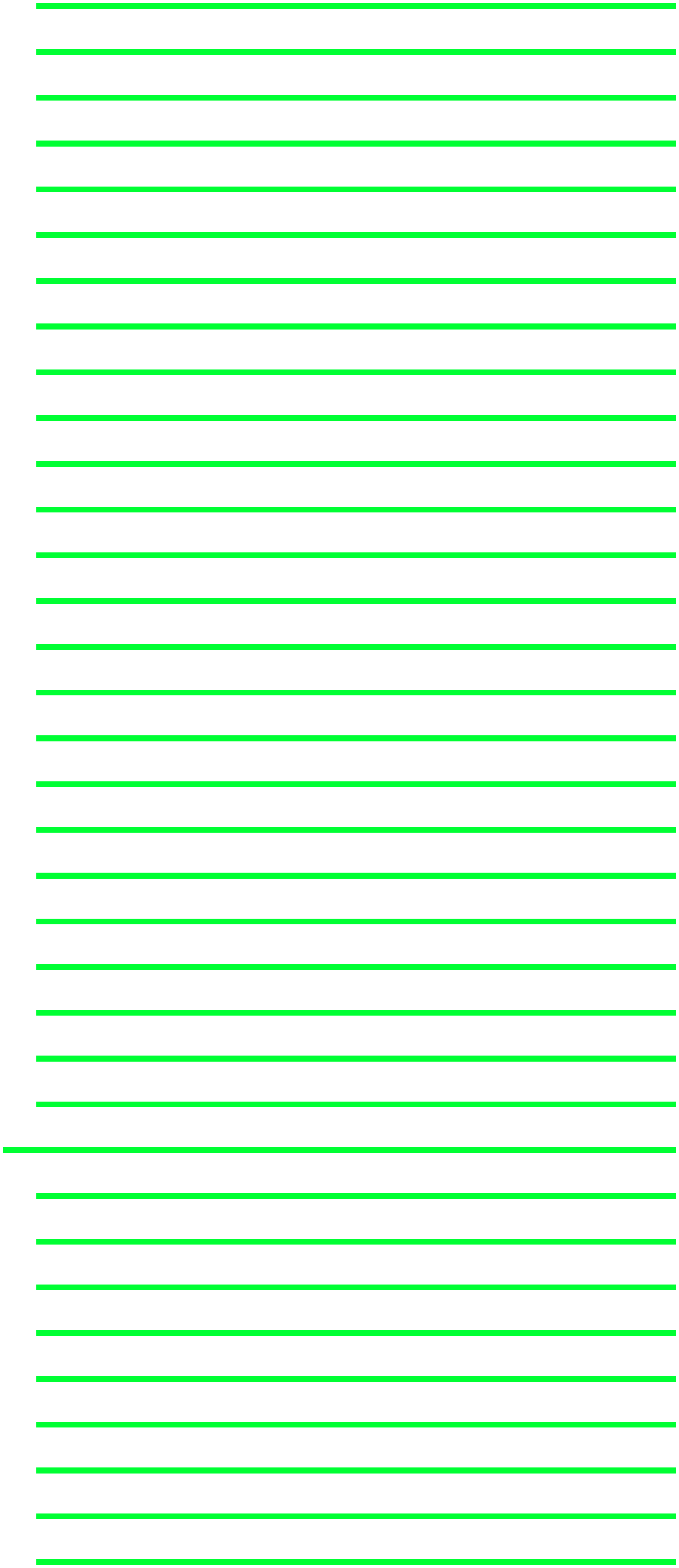
Show Conserved Domains

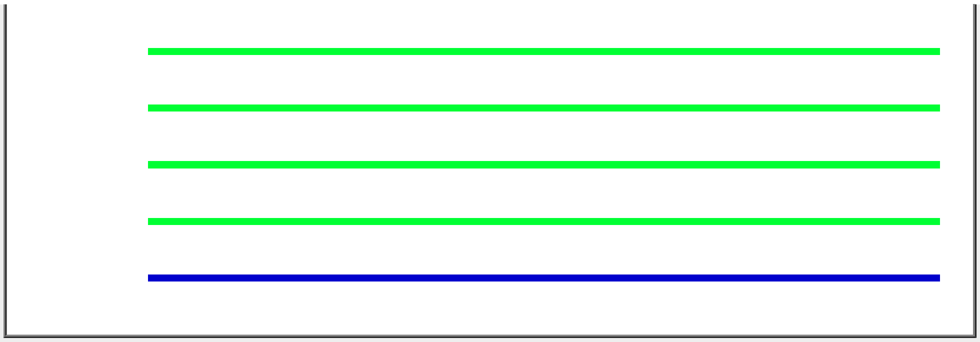
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	fibulin-1 isoform A precursor [Homo sapiens]	67.2	67.2	100%	2e-11	100%	gi|34734068|NP_006478.2
☐	fibulin-1 A [Homo sapiens]	67.2	67.2	100%	2e-11	100%	gi|31415|CAA37770.1
☐	fibulin 1, isoform CRA_b [Homo sapiens]	67.2	67.2	100%	2e-11	100%	gi|119593792|EAW73386.1
☐	fibulin 1 precursor, splice form B - human [Homo sapiens]	67.2	67.2	100%	2e-11	100%	gi|106017|B36346
☐	fibulin-1 isoform B precursor [Homo sapiens]	67.2	67.2	100%	2e-11	100%	gi|34734064|NP_006476.2
☐	unnamed protein product [Homo sapiens]	67.2	67.2	100%	2e-11	100%	gi|194374697|BAG62463.1
☐	fibulin-1 isoform C precursor [Homo sapiens]	67.2	67.2	100%	3e-11	100%	gi|34734062|NP_001987.2
☐	Fibulin 1 [Homo sapiens]	67.2	67.2	100%	3e-11	100%	gi|18490682|AAH22497.1
☐	fibulin-1 C [Homo sapiens]	67.2	67.2	100%	3e-11	100%	gi|31419|CAA37772.1
☐	fibulin 1 [synthetic construct]	67.2	67.2	100%	3e-11	100%	gi|123994743|ABM84973.1
☐	fibulin 1, isoform CRA_f [Homo sapiens]	67.2	67.2	100%	3e-11	100%	gi|119593796|EAW73390.1
☐	fibulin-1 isoform D precursor [Homo sapiens]	67.2	67.2	100%	3e-11	100%	gi|13661193|AAK37822.1
☐	RecName: Full=Fibulin-1; Short=FIBL-1; Flags: Precursor [Homo sa	67.2	67.2	100%	3e-11	100%	gi|215274249|P23142.4
☐	fibulin-1 isoform D precursor [Homo sapiens]	67.2	67.2	100%	3e-11	100%	gi|34734066|NP_006477.2
☐	PREDICTED: fibulin-1 isoform X1 [Pan paniscus]	64.3	64.3	100%	3e-10	95%	gi|397482444|XP_003812435.1
☐	PREDICTED: fibulin-1 [Pan troglodytes]	64.3	64.3	100%	3e-10	95%	gi|694983727|XP_009436873.1
☐	PREDICTED: fibulin-1 [Nomascus leucogenys]	63.8	63.8	95%	4e-10	100%	gi|441618218|XP_003281320.2
☐	PREDICTED: fibulin-1 [Mustela putorius furo]	63.8	63.8	95%	4e-10	100%	gi|511992630|XP_004813974.1
☐	PREDICTED: fibulin-1 [Mustela putorius furo]	63.8	63.8	95%	4e-10	100%	gi|511903702|XP_004771346.1
☐	PREDICTED: fibulin-1 [Pongo abelii]	63.8	63.8	95%	4e-10	100%	gi|686764893|XP_009232751.1
☐	PREDICTED: fibulin-1 [Gorilla gorilla gorilla]	60.9	60.9	95%	4e-09	95%	gi|426394827|XP_004063688.1
☐	PREDICTED: fibulin-1 isoform 2 [Odobenus rosmarus divergens]	60.9	60.9	95%	4e-09	95%	gi|472393253|XP_004415897.1
☐	PREDICTED: fibulin-1 [Otolemur garnettii]	60.9	60.9	95%	4e-09	95%	gi|395819580|XP_003783160.1
☐	PREDICTED: fibulin-1 isoform 1 [Odobenus rosmarus divergens]	60.9	60.9	95%	4e-09	95%	gi|472393251|XP_004415896.1
☐	PREDICTED: fibulin-1 isoform X4 [Rhinopithecus roxellana]	60.4	60.4	95%	5e-09	95%	gi|724795561|XP_010365649.1
☐	PREDICTED: fibulin-1 isoform X3 [Rhinopithecus roxellana]	60.4	60.4	95%	5e-09	95%	gi|724795558|XP_010365573.1
☐	PREDICTED: fibulin-1 isoform X2 [Rhinopithecus roxellana]	60.4	60.4	95%	5e-09	95%	gi|724795555|XP_010365494.1
☐	PREDICTED: fibulin-1 isoform X1 [Rhinopithecus roxellana]	60.4	60.4	95%	5e-09	95%	gi|724795552|XP_010365413.1
☐							

	PREDICTED: fibulin-1-like [Leptonychotes weddellii]	57.5	57.5	95%	5e-08	89%	gi|585183989|XP_006743570.1
☐	PREDICTED: fibulin-1 [Ursus maritimus]	57.5	57.5	95%	5e-08	89%	gi|671020810|XP_008701224.1
☐	PREDICTED: fibulin-1 [Saimiri boliviensis boliviensis]	56.6	56.6	95%	1e-07	89%	gi|403282742|XP_003932799.1
☐	PREDICTED: fibulin-1 isoform X2 [Canis lupus familiaris]	56.6	56.6	95%	1e-07	89%	gi|545514461|XP_005625812.1
☐	PREDICTED: fibulin-1 isoform X1 [Canis lupus familiaris]	56.6	56.6	95%	1e-07	89%	gi|545514459|XP_005625811.1
☐	PREDICTED: fibulin-1 isoform X3 [Chlorocebus sabaeus]	55.8	55.8	95%	2e-07	89%	gi|635102866|XP_007974271.1
☐	RecName: Full=Fibulin-1; Short=FIBL-1 [Chlorocebus aethiops]	55.8	55.8	95%	2e-07	89%	gi|30580425|Q8MJJ9.1
☐	PREDICTED: fibulin-1 [Macaca fascicularis]	55.8	55.8	95%	2e-07	89%	gi|544461232|XP_005567067.1
☐	PREDICTED: fibulin-1 isoform X2 [Chlorocebus sabaeus]	55.8	55.8	95%	2e-07	89%	gi|635102864|XP_007974270.1
☐	PREDICTED: fibulin-1 isoform X1 [Chlorocebus sabaeus]	55.8	55.8	95%	2e-07	89%	gi|635102862|XP_007974269.1
☐	PREDICTED: fibulin-1 isoform 2 [Macaca mulatta]	55.8	55.8	95%	2e-07	89%	gi|297261301|XP_001109966.2
☐	PREDICTED: fibulin-1 isoform X2 [Vicugna pacos]	54.5	54.5	95%	5e-07	89%	gi|560980789|XP_006212641.1
☐	PREDICTED: fibulin-1 isoform X1 [Vicugna pacos]	54.5	54.5	95%	5e-07	89%	gi|560980787|XP_006212640.1
☐	PREDICTED: fibulin-1 [Loxodonta africana]	52.8	52.8	100%	2e-06	85%	gi|731510789|XP_010598758.1
☐	PREDICTED: fibulin-1 [Papio anubis]	52.4	52.4	95%	2e-06	84%	gi|402884556|XP_003905746.1
☐	PREDICTED: fibulin-1 [Physeter catodon]	52.0	52.0	95%	4e-06	84%	gi|593746998|XP_007128800.1
☐	PREDICTED: fibulin-1 [Callithrix jacchus]	52.0	52.0	95%	4e-06	84%	gi|675641753|XP_008978454.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1-like [Oryctolagus	51.5	51.5	95%	5e-06	84%	gi|655899479|XP_008251212.1
☐	Fibulin-1 [Bos mutus]	51.5	51.5	95%	5e-06	84%	gi|440905574|ELR55943.1
☐	TPA: fibulin 1 [Bos taurus]	51.5	51.5	95%	5e-06	84%	gi|296486900|DAA29013.1
☐	fibulin-1 precursor [Bos taurus]	51.5	51.5	95%	5e-06	84%	gi|148232266|NP_001091498.1
☐	PREDICTED: fibulin-1 [Bos mutus]	51.5	51.5	95%	5e-06	84%	gi|555968788|XP_005896425.1
☐	PREDICTED: fibulin-1 [Bubalus bubalis]	51.5	51.5	95%	5e-06	84%	gi|594079384|XP_006063368.1
☐	PREDICTED: fibulin-1 [Felis catus]	51.1	51.1	95%	7e-06	84%	gi|586993905|XP_006934231.1
☐	PREDICTED: fibulin-1 [Equus caballus]	51.1	51.1	95%	7e-06	84%	gi|545206896|XP_005606874.1
☐	PREDICTED: fibulin-1 [Pantholops hodgsonii]	51.1	51.1	95%	7e-06	84%	gi|556725504|XP_005958536.1
☐	PREDICTED: fibulin-1 [Balaenoptera acutorostrata scammoni]	50.3	50.3	95%	1e-05	84%	gi|594683418|XP_007189256.1
☐	PREDICTED: fibulin-1-like [Tursiops truncatus]	49.0	49.0	95%	3e-05	79%	gi|470643167|XP_004326152.1
☐	PREDICTED: fibulin-1 isoform X4 [Lipotes vexillifer]	49.0	49.0	95%	4e-05	79%	gi|602683431|XP_007453975.1
☐	PREDICTED: fibulin-1 isoform X3 [Lipotes vexillifer]	49.0	49.0	95%	4e-05	79%	gi|602683429|XP_007453974.1
☐	PREDICTED: fibulin-1 isoform X2 [Lipotes vexillifer]	49.0	49.0	95%	4e-05	79%	gi|602683427|XP_007453973.1
☐	PREDICTED: fibulin-1 isoform X1 [Lipotes vexillifer]	49.0	49.0	95%	4e-05	79%	gi|602683425|XP_007453972.1
☐	PREDICTED: fibulin-1 isoform 2 [Trichechus manatus latirostris]	48.6	48.6	95%	5e-05	80%	gi|471390788|XP_004380068.1
☐	PREDICTED: fibulin-1 isoform 1 [Trichechus manatus latirostris]	48.6	48.6	95%	5e-05	80%	gi|471390784|XP_004380067.1
☐	PREDICTED: fibulin-1 isoform 2 [Ceratotherium simum simum]	48.1	48.1	95%	7e-05	79%	gi|478527715|XP_004438039.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1 [Cavia porcellus]	48.1	48.1	95%	7e-05	79%	gi|514443922|XP_004999606.1
☐	PREDICTED: fibulin-1 isoform 1 [Ceratotherium simum simum]	48.1	48.1	95%	7e-05	79%	gi|478527713|XP_004438038.1
☐	PREDICTED: fibulin-1 [Octodon degus]	48.1	48.1	95%	7e-05	79%	gi|507693081|XP_004642514.1
☐	PREDICTED: fibulin-1 isoform X2 [Sus scrofa]	47.7	47.7	95%	9e-05	79%	gi|545824398|XP_005663793.1
☐	PREDICTED: fibulin-1 isoform X1 [Sus scrofa]	47.7	47.7	95%	9e-05	79%	gi|350583711|XP_003126003.3
☐	PREDICTED: fibulin-1 isoform X2 [Camelus ferus]	46.4	46.4	95%	2e-04	79%	gi|560900629|XP_006176723.1
☐	PREDICTED: fibulin-1 isoform X1 [Camelus ferus]	46.4	46.4	95%	2e-04	79%	gi|560900627|XP_006176722.1
☐	PREDICTED: fibulin-1 [Tupaia chinensis]	46.4	46.4	95%	2e-04	79%	gi|562873654|XP_006164720.1
☐	fibulin-1 isoform C precursor [Camelus ferus]	46.4	46.4	95%	2e-04	79%	gi|528767382|EPY87041.1
☐	Fibulin-1 [Tupaia chinensis]	46.4	46.4	95%	3e-04	79%	gi|444519033|ELV12523.1

☐	PREDICTED: fibulin-1 isoform X2 [Chinchilla lanigera]	46.0	46.0	95%	3e-04	79%	gi|533128844|XP_005379549.1
☐	PREDICTED: fibulin-1 isoform X1 [Chinchilla lanigera]	46.0	46.0	95%	3e-04	79%	gi|533128842|XP_005379548.1
☐	PREDICTED: fibulin-1 isoform X2 [Erinaceus europaeus]	45.6	45.6	95%	5e-04	79%	gi|617642052|XP_007531965.1
☐	PREDICTED: fibulin-1 isoform X1 [Erinaceus europaeus]	45.6	45.6	95%	5e-04	79%	gi|617642049|XP_007531964.1
☐	PREDICTED: fibulin-1-like [Capra hircus]	45.2	45.2	95%	6e-04	74%	gi|548468863|XP_005681284.1
☐	PREDICTED: fibulin-1 [Ovis aries]	45.2	45.2	95%	7e-04	74%	gi|426227186|XP_004007703.1
☐	PREDICTED: fibulin-1 [Tarsius syrichta]	44.3	44.3	95%	0.001	74%	gi|640794658|XP_008053358.1
☐	PREDICTED: fibulin-1 [Orcinus orca]	44.3	44.3	95%	0.001	74%	gi|466057370|XP_004279635.1
☐	PREDICTED: fibulin-1 [Ictidomys tridecemlineatus]	43.5	43.5	95%	0.002	74%	gi|532098910|XP_005335099.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1-like [Galeopterus	41.8	41.8	95%	0.008	74%	gi|667294707|XP_008579007.1
☐	PREDICTED: fibulin-1 [Pteropus alecto]	41.4	41.4	95%	0.011	74%	gi|586524847|XP_006917380.1
☐	PREDICTED: fibulin-1 isoform X2 [Fukomys damarensis]	40.9	40.9	95%	0.015	68%	gi|731238270|XP_010632637.1
☐	PREDICTED: fibulin-1 isoform X1 [Fukomys damarensis]	40.9	40.9	95%	0.015	68%	gi|731238268|XP_010632636.1
☐	PREDICTED: fibulin-1 isoform X4 [Microtus ochrogaster]	40.1	40.1	95%	0.028	68%	gi|532022189|XP_005354460.1
☐	PREDICTED: fibulin-1 isoform X3 [Microtus ochrogaster]	40.1	40.1	95%	0.028	68%	gi|532022187|XP_005354459.1
☐	PREDICTED: fibulin-1 isoform X2 [Ochotona princeps]	40.1	40.1	95%	0.028	68%	gi|504155089|XP_004589482.1
☐	PREDICTED: fibulin-1 isoform X2 [Microtus ochrogaster]	40.1	40.1	95%	0.028	68%	gi|532022185|XP_005354458.1
☐	PREDICTED: fibulin-1 isoform X1 [Microtus ochrogaster]	40.1	40.1	95%	0.028	68%	gi|532022183|XP_005354457.1
☐	PREDICTED: fibulin-1 isoform X1 [Ochotona princeps]	40.1	40.1	95%	0.028	68%	gi|504155087|XP_004589481.1
☐	PREDICTED: fibulin-1 [Eptesicus fuscus]	38.0	38.0	95%	0.13	74%	gi|641727121|XP_008153634.1
☐	PREDICTED: fibulin-1 [Jaculus jaculus]	37.1	37.1	75%	0.25	73%	gi|507532747|XP_004650445.1
☐	PREDICTED: fibulin-1 isoform X2 [Peromyscus maniculatus bairdii]	37.1	37.1	95%	0.25	63%	gi|589935133|XP_006980340.1
☐	PREDICTED: fibulin-1 isoform X1 [Peromyscus maniculatus bairdii]	37.1	37.1	95%	0.25	63%	gi|589935131|XP_006980339.1
☐	PREDICTED: fibulin-1 [Myotis brandtii]	36.7	36.7	60%	0.34	92%	gi|554589517|XP_005886100.1
☐	PREDICTED: fibulin-1 [Myotis davidii]	36.3	36.3	95%	0.46	68%	gi|584059500|XP_006774235.1
☐	Fibulin-1 [Cricetulus griseus]	34.1	34.1	95%	2.1	60%	gi|344257685|EGW13789.1
☐	PREDICTED: fibulin-1 isoform X2 [Cricetulus griseus]	34.1	34.1	95%	2.1	60%	gi|625255711|XP_007619196.1

Alignments

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fibulin-1 isoform A precursor [Homo sapiens]

Sequence ID: gi|34734068|ref|NP_006478.2| **Length:** 566 **Number of Matches:** 1

▶ See 1 more title(s)

Range 1: 90 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.2 bits(151)	2e-11	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    RCATPHGDNASLEATFVKRC  20
            RCATPHGDNASLEATFVKRC
Sbjct  90   RCATPHGDNASLEATFVKRC  109
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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fibulin-1 A [Homo sapiens]

Sequence ID: gi|31415|emb|CAA37770.1| **Length:** 566 **Number of Matches:** 1

Range 1: 90 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.2 bits(151)	2e-11	20/20(100%)	20/20(100%)	0/20(0%)

Related Information

Gene - associated gene details

```
Query  1    RCATPHGDNASLEATFVKRC  20
            RCATPHGDNASLEATFVKRC
Sbjct  90   RCATPHGDNASLEATFVKRC  109
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

fibulin 1, isoform CRA_b, partial [Homo sapiens]

Sequence ID: gi|119593792|gb|EAW73386.1| **Length:** 581 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 90 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.2 bits(151)	2e-11	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    RCATPHGDNASLEATFVKRC  20
            RCATPHGDNASLEATFVKRC
Sbjct  90   RCATPHGDNASLEATFVKRC  109
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

fibulin 1 precursor, splice form B - human

Sequence ID: gi|106017|pir||B36346 **Length:** 601 **Number of Matches:** 1

See 2 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 90 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.2 bits(151)	2e-11	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    RCATPHGDNASLEATFVKRC  20
            RCATPHGDNASLEATFVKRC
Sbjct  90   RCATPHGDNASLEATFVKRC  109
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

fibulin-1 isoform B precursor [Homo sapiens]

Sequence ID: gi|34734064|ref|NP_006476.2| **Length:** 601 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 90 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.2 bits(151)	2e-11	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    RCATPHGDNASLEATFVKRC  20
            RCATPHGDNASLEATFVKRC
Sbjct  90   RCATPHGDNASLEATFVKRC  109
```

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FBLN1_RNCQDIDECVTGIHDCSIDETCFNIQGGFRC_Mod

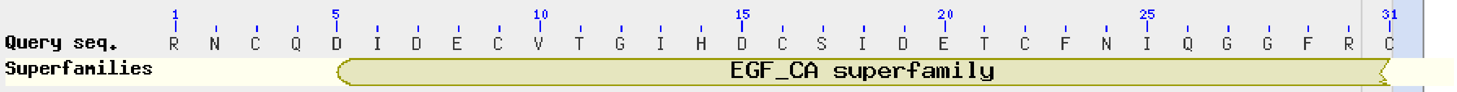
RID	BVDPEYVE01R (Expires on 01-21 09:00 am)		
Query ID	lcl|97178	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	31	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

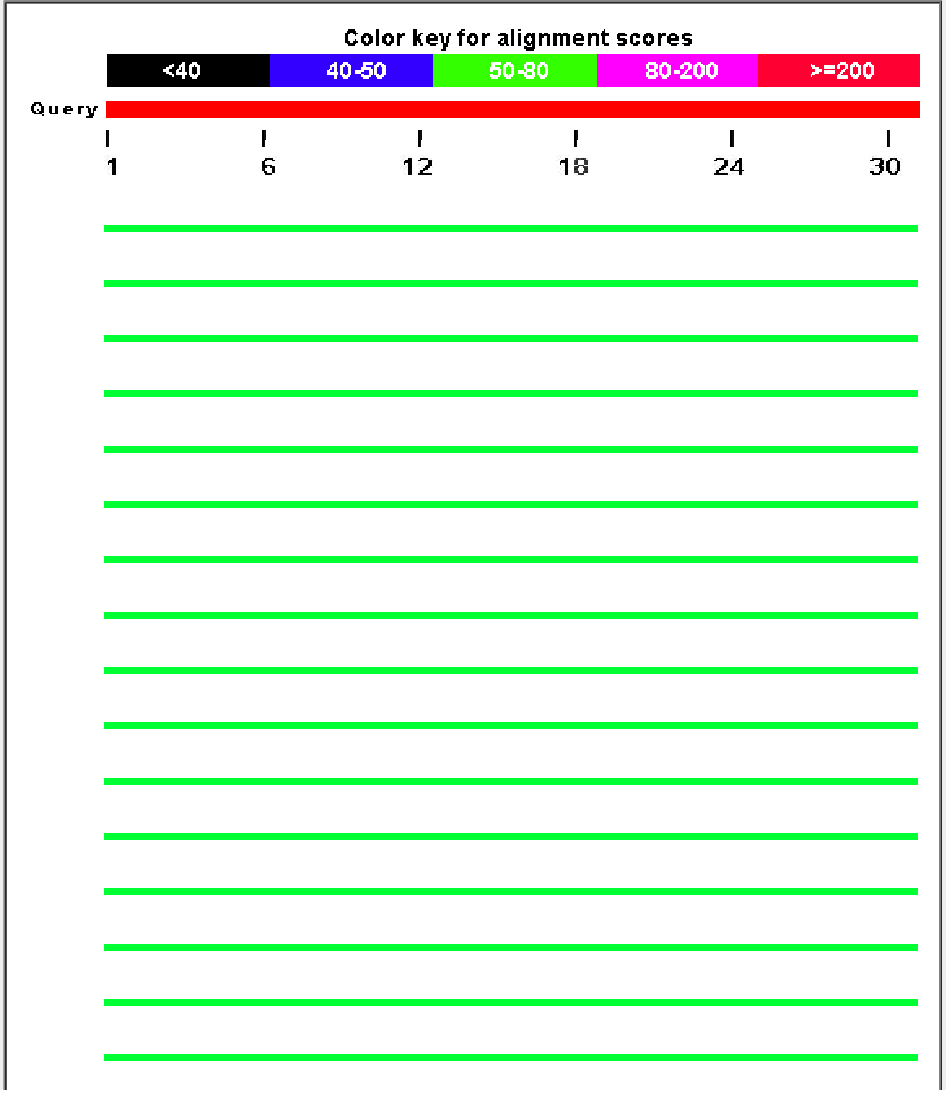
Show Conserved Domains

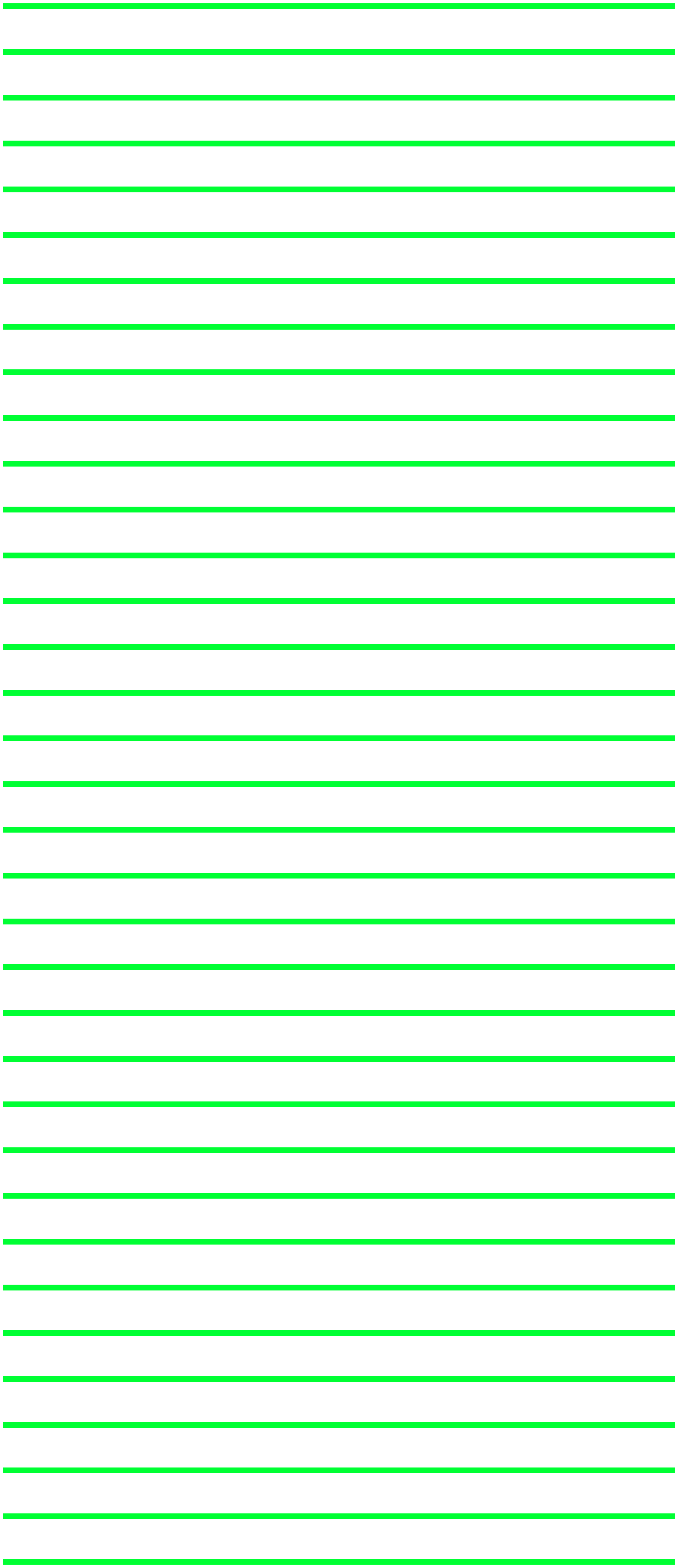
Putative conserved domains have been detected, click on the image below for detailed results.

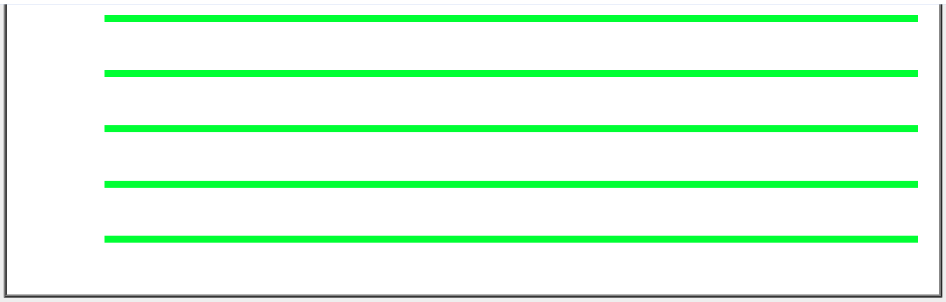


Distribution of 291 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Mus musculus]	63.2	63.2	100%	4e-11	90%	BAE35396.1
☐	PREDICTED: fibulin-1-like [Papio anubis]	64.3	64.3	100%	7e-11	94%	XP_009215764.1
☐	PREDICTED: fibulin-1 [Oryctolagus cuniculus]	62.8	62.8	100%	8e-11	87%	XP_008250507.1
☐	PREDICTED: fibulin-1 [Bubalus bubalis]	65.1	141	100%	8e-11	94%	XP_006063368.1
☐	PREDICTED: fibulin-1 [Ovis aries]	65.1	140	100%	9e-11	94%	XP_004007703.1
☐	fibulin-1 isoform C precursor [Camelus ferus]	64.7	103	100%	9e-11	90%	EPY87041.1
☐	PREDICTED: fibulin-1 [Pongo abelii]	64.7	142	100%	9e-11	94%	XP_009232751.1
☐	PREDICTED: fibulin-1 [Mustela putorius furo]	64.3	140	100%	1e-10	94%	XP_004771346.1
☐	PREDICTED: fibulin-1 isoform X2 [Erinaceus europaeus]	64.3	142	100%	1e-10	94%	XP_007531965.1
☐	PREDICTED: fibulin-1 [Ictidomys tridecemlineatus]	64.3	144	100%	1e-10	94%	XP_005335099.1
☐	PREDICTED: fibulin-1 isoform X2 [Rhinopithecus roxellana]	64.3	141	100%	1e-10	94%	XP_010365494.1
☐	RecName: Full=Fibulin-1; Short=FIBL-1 [Chlorocebus aethiops]	64.3	140	100%	1e-10	94%	Q8MJJ9.1
☐	PREDICTED: fibulin-1 isoform 2 [Trichechus manatus latirostris]	64.3	142	100%	1e-10	94%	XP_004380068.1
☐	PREDICTED: fibulin-1 isoform X2 [Nannospalax galili]	64.3	143	100%	1e-10	94%	XP_008842913.1
☐	PREDICTED: fibulin-1 isoform X4 [Lipotes vexillifer]	64.3	137	100%	1e-10	94%	XP_007453975.1
☐	PREDICTED: fibulin-1 [Mustela putorius furo]	64.3	140	100%	1e-10	94%	XP_004813974.1
☐	PREDICTED: fibulin-1 isoform X2 [Canis lupus familiaris]	64.3	142	100%	1e-10	94%	XP_005625812.1
☐	fibulin-1 isoform C precursor [Homo sapiens]	64.3	141	100%	1e-10	94%	NP_001987.2
☐	unnamed protein product [Homo sapiens]	64.3	141	100%	1e-10	94%	BAG62463.1
☐	PREDICTED: fibulin-1 [Macaca fascicularis]	64.3	141	100%	1e-10	94%	XP_005567067.1
☐	PREDICTED: fibulin-1 isoform X3 [Lipotes vexillifer]	64.3	137	100%	1e-10	94%	XP_007453974.1
☐	PREDICTED: fibulin-1 [Elephantulus edwardii]	64.3	140	100%	1e-10	94%	XP_006888093.1
☐	PREDICTED: fibulin-1 [Gorilla gorilla gorilla]	64.3	141	100%	1e-10	94%	XP_004063688.1
☐	PREDICTED: fibulin-1 [Physeter catodon]	64.3	137	100%	1e-10	94%	XP_007128800.1
☐	PREDICTED: fibulin-1 [Balaenoptera acutorostrata scammoni]	64.3	137	100%	1e-10	94%	XP_007189256.1
☐	unnamed protein product [Homo sapiens]	64.3	141	100%	1e-10	94%	BAC11705.1
☐	PREDICTED: fibulin-1 [Otolemur garnettii]	64.3	145	100%	1e-10	94%	XP_003783160.1
☐	fibulin 1, isoform CRA_f [Homo sapiens]	64.3	141	100%	1e-10	94%	EAW73390.1
☐	PREDICTED: fibulin-1-like [Leptonychotes weddellii]	63.9	140	100%	1e-10	94%	XP_006743570.1
☐	PREDICTED: fibulin-1 isoform X1 [Pan paniscus]	64.3	141	100%	1e-10	94%	XP_003812435.1

☐	PREDICTED: fibulin-1 [Orcinus orca]	64.3	137	100%	1e-10	94%	XP_004279635.1
☐	PREDICTED: fibulin-1 isoform 2 [Macaca mulatta]	64.3	141	100%	1e-10	94%	XP_001109966.2
☐	PREDICTED: fibulin-1 isoform 2 [Odobenus rosmarus divergens]	64.3	140	100%	1e-10	94%	XP_004415897.1
☐	PREDICTED: fibulin-1 [Loxodonta africana]	63.9	142	100%	1e-10	94%	XP_010598758.1
☐	PREDICTED: fibulin-1 [Chrysochloris asiatica]	63.9	141	100%	1e-10	94%	XP_006866955.1
☐	PREDICTED: fibulin-1 [Tarsius syrichta]	63.9	142	100%	1e-10	94%	XP_008053358.1
☐	PREDICTED: fibulin-1 isoform X1 [Erinaceus europaeus]	63.9	141	100%	2e-10	94%	XP_007531964.1
☐	PREDICTED: fibulin-1 isoform 1 [Trichechus manatus latirostris]	63.9	141	100%	2e-10	94%	XP_004380067.1
☐	PREDICTED: fibulin-1 [Nomascus leucogenys]	63.9	141	100%	2e-10	94%	XP_003281320.2
☐	PREDICTED: fibulin-1 isoform X2 [Ochotona princeps]	63.9	141	100%	2e-10	90%	XP_004589482.1
☐	PREDICTED: fibulin-1 isoform X1 [Canis lupus familiaris]	63.9	141	100%	2e-10	94%	XP_005625811.1
☐	PREDICTED: fibulin-1 [Octodon degus]	63.9	143	100%	2e-10	90%	XP_004642514.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1-like [Galeopterus variegatu	63.9	139	100%	2e-10	94%	XP_008579007.1
☐	PREDICTED: fibulin-1 isoform X3 [Rhinopithecus roxellana]	63.9	140	100%	2e-10	94%	XP_010365573.1
☐	PREDICTED: fibulin-1 isoform X1 [Nannospalax galili]	63.9	142	100%	2e-10	94%	XP_008842912.1
☐	PREDICTED: fibulin-1 [Galeopterus variegatus]	63.2	138	100%	2e-10	94%	XP_008562356.1
☐	PREDICTED: fibulin-1 isoform X1 [Rhinopithecus roxellana]	63.9	140	100%	2e-10	94%	XP_010365413.1
☐	fibulin 1, isoform CRA_b [Homo sapiens]	63.5	140	100%	2e-10	94%	EAW73386.1
☐	PREDICTED: fibulin-1 isoform 1 [Odobenus rosmarus divergens]	63.9	140	100%	2e-10	94%	XP_004415896.1
☐	PREDICTED: fibulin-1 isoform X2 [Lipotes vexillifer]	63.9	137	100%	2e-10	94%	XP_007453973.1
☐	PREDICTED: fibulin-1 isoform X1 [Lipotes vexillifer]	63.9	137	100%	2e-10	94%	XP_007453972.1
☐	fibulin-1 isoform B precursor [Homo sapiens]	63.9	140	100%	2e-10	94%	NP_006476.2
☐	PREDICTED: fibulin-1 [Pan troglodytes]	63.9	141	100%	2e-10	94%	XP_009436873.1
☐	RecName: Full=Fibulin-1; Short=FIBL-1; Flags: Precursor [Homo sapiens]	63.9	141	100%	2e-10	94%	P23142.4
☐	fibulin-1 isoform D precursor [Homo sapiens]	63.9	141	100%	2e-10	94%	NP_006477.2
☐	PREDICTED: fibulin-1 [Jaculus jaculus]	63.9	144	100%	2e-10	94%	XP_004650445.1
☐	fibulin-1 isoform A precursor [Homo sapiens]	63.5	140	100%	2e-10	94%	NP_006478.2
☐	PREDICTED: fibulin-1 [Equus caballus]	63.9	141	100%	2e-10	90%	XP_005606874.1
☐	PREDICTED: fibulin-1 isoform X4 [Rhinopithecus roxellana]	63.5	140	100%	2e-10	94%	XP_010365649.1
☐	unknown [Homo sapiens]	63.5	140	100%	2e-10	94%	AAG17241.1
☐	PREDICTED: fibulin-1 isoform X2 [Camelus ferus]	63.5	139	100%	2e-10	90%	XP_006176723.1
☐	PREDICTED: fibulin-1 isoform X2 [Pan paniscus]	63.5	140	100%	2e-10	94%	XP_008963042.1
☐	PREDICTED: fibulin-1 isoform X2 [Chinchilla lanigera]	63.5	141	100%	2e-10	90%	XP_005379549.1
☐	PREDICTED: fibulin-1-like [Echinops telfairi]	63.5	142	100%	2e-10	90%	XP_004700279.1
☐	PREDICTED: fibulin-1 isoform X2 [Vicugna pacos]	63.5	140	100%	2e-10	90%	XP_006212641.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1 [Cavia porcellus]	63.5	142	100%	2e-10	90%	XP_004999606.1
☐	PREDICTED: fibulin-1 isoform X1 [Ochotona princeps]	63.5	141	100%	2e-10	90%	XP_004589481.1
☐	PREDICTED: fibulin-1 [Felis catus]	63.5	141	100%	2e-10	90%	XP_006934231.1
☐	PREDICTED: fibulin-1 [Tupaia chinensis]	63.5	139	100%	2e-10	90%	XP_006164720.1
☐	PREDICTED: fibulin-1 [Camelus dromedarius]	63.5	139	100%	2e-10	90%	XP_010981727.1
☐	PREDICTED: fibulin-1 isoform X1 [Camelus ferus]	63.5	139	100%	2e-10	90%	XP_006176722.1
☐	PREDICTED: fibulin-1 isoform X1 [Chinchilla lanigera]	63.5	140	100%	3e-10	90%	XP_005379548.1
☐	PREDICTED: fibulin-1 [Equus przewalskii]	63.2	140	100%	3e-10	90%	XP_008529127.1
☐	PREDICTED: fibulin-1 isoform X1 [Vicugna pacos]	63.2	140	100%	3e-10	90%	XP_006212640.1
☐	PREDICTED: fibulin-1 isoform X2 [Sorex araneus]	63.2	142	100%	3e-10	87%	XP_004610628.1
☐	Fibulin-1 [Heterocephalus glaber]	63.2	101	100%	3e-10	94%	EHB13219.1

☐	PREDICTED: fibulin-1 isoform 2 [Ceratotherium simum simum]	63.2	140	100%	3e-10	90%	XP_004438039.1
☐	PREDICTED: fibulin-1 isoform X1 [Sorex araneus]	63.2	141	100%	3e-10	87%	XP_004610627.1
☐	Fibulin-1 [Tupaia chinensis]	63.2	101	100%	4e-10	90%	ELV12523.1
☐	PREDICTED: fibulin-1 isoform 1 [Ceratotherium simum simum]	62.8	140	100%	4e-10	90%	XP_004438038.1
☐	PREDICTED: fibulin-1 isoform X2 [Heterocephalus glaber]	62.8	142	100%	4e-10	94%	XP_004845455.1
☐	PREDICTED: fibulin-1 isoform X1 [Heterocephalus glaber]	62.4	141	100%	5e-10	94%	XP_004845454.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1 [Myotis lucifugus]	62.4	138	100%	5e-10	90%	XP_006104607.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1 [Heterocephalus glaber]	62.4	137	100%	5e-10	94%	XP_004900841.1
☐	fibulin-1 C [Homo sapiens]	62.4	139	100%	6e-10	90%	CAA37772.1
☐	PREDICTED: fibulin-1 [Orycteropus afer afer]	62.4	140	100%	6e-10	90%	XP_007953835.1
☐	Fibulin 1 [Homo sapiens]	62.0	139	96%	7e-10	93%	AAH22497.1
☐	PREDICTED: fibulin-1 [Bos mutus]	62.4	138	100%	7e-10	90%	XP_005896425.1
☐	PREDICTED: fibulin-1 isoform X2 [Chlorocebus sabaeus]	62.0	139	100%	7e-10	90%	XP_007974270.1
☐	fibulin 1 [synthetic construct]	62.0	139	96%	7e-10	93%	ABM84973.1
☐	Fibulin-1 [Cricetulus griseus]	62.0	143	100%	7e-10	90%	EGW13789.1
☐	PREDICTED: fibulin-1 isoform X2 [Sus scrofa]	62.0	137	100%	7e-10	90%	XP_005663793.1
☐	fibulin-1 isoform D precursor [Homo sapiens]	62.0	139	100%	8e-10	90%	AAK37822.1
☐	PREDICTED: fibulin-1 isoform X2 [Peromyscus maniculatus bairdii]	62.0	142	100%	8e-10	90%	XP_006980340.1
☐	PREDICTED: fibulin-1 [Eptesicus fuscus]	62.0	137	100%	8e-10	90%	XP_008153634.1
☐	fibulin-1 isoform 2 [Cricetulus griseus]	62.0	143	100%	8e-10	90%	ERE86479.1
☐	fibulin 1 precursor, splice form B - human [Homo sapiens]	62.0	139	100%	8e-10	90%	B36346
☐	PREDICTED: fibulin-1 isoform X2 [Bison bison bison]	62.0	137	100%	8e-10	90%	XP_010835915.1
☐	PREDICTED: fibulin-1 [Myotis davidii]	62.0	137	100%	8e-10	90%	XP_006774235.1
☐	unnamed protein product [Mus musculus]	62.0	144	100%	8e-10	90%	BAC39669.1

⊟ Alignments

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unnamed protein product [Mus musculus]

Sequence ID: dbj|BAE35396.1| **Length:** 228 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 46 to 76 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
63.2 bits(152)	4e-11	Compositional matrix adjust.	28/31(90%)	30/31(96%)	0/31(0%)

```
Query  1    RNCQDIDECVTGIHDCSIDETCFNIQGGFRC  31
            RNCQDIDECVTGIH+CSI+ETCFNIQG FRC
Sbjct  46   RNCQDIDECVTGIHNCSINETCFNIQGSFRC  76
```

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PREDICTED: fibulin-1-like, partial [Papio anubis]

Sequence ID: ref|XP_009215764.1| **Length:** 451 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 269 to 299 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
64.3 bits(155)	7e-11	Compositional matrix adjust.	29/31(94%)	31/31(100%)	0/31(0%)

```
Query  1     RNCQDIDECVTGIHDCSIDETCFNIQGGFRC  31
             RNCQDIDECVTGIH+CSI+ETCFNIQGGFRC
Sbjct  269   RNCQDIDECVTGIHNCSINETCFNIQGGFRC  299
```

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PREDICTED: fibulin-1, partial [Oryctolagus cuniculus]

Sequence ID: ref|XP_008250507.1| **Length:** 246 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 64 to 94 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
62.8 bits(151)	8e-11	Compositional matrix adjust.	27/31(87%)	30/31(96%)	0/31(0%)

```
Query  1   RNCQDIDECVTGIHDCSIDETCFNIQGGFRC  31
           RNCQDIDECVTG+H+CSI+ETCFNIQG FRC
Sbjct  64  RNCQDIDECVTGVHNCSINETCFNIQGSFRC  94
```

Download ⌄ GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

PREDICTED: fibulin-1 [Bubalus bubalis]

Sequence ID: ref|XP_006063368.1| **Length:** 944 **Number of Matches:** 3

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 762 to 792 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
65.1 bits(157)	8e-11	Compositional matrix adjust.	29/31(94%)	31/31(100%)	0/31(0%)

```
Query  1    RNCQDIDECVTGIHDCSIDETCFNIQGGFRC  31
            RNCQDIDECVTGIH+CSI+ETCFNIQGGFRC
Sbjct  762  RNCQDIDECVTGIHNCSINETCFNIQGGFRC  792
```

Range 2: 454 to 483 GenPept Graphics

▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Method	Identities	Positives	Gaps
38.5 bits(88)	0.12	Compositional matrix adjust.	14/30(47%)	22/30(73%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHDCSIDETCFNIQGGFRC  31
            +C+D++EC+TG  +C + E+C N  G FRC
Sbjct  454  SCEDVNECITGSQNCRLGESCINTVGSFRC  483
```

Range 3: 500 to 529 GenPept Graphics

▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Method	Identities	Positives	Gaps
37.7 bits(86)	0.19	Compositional matrix adjust.	17/30(57%)	21/30(70%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHDCSIDETCFNIQGGFRC  31
            +C+DIDEC +GIH+C  D  C N  G FRC
Sbjct  500  DCKDIDECESGIHNCLPDFICQNTLGSFRC  529
```

Download ⌄ GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

PREDICTED: fibulin-1 [Ovis aries]

Sequence ID: ref|XP_004007703.1| **Length:** 953 **Number of Matches:** 3

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Range 1: 771 to 801 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
65.1 bits(157)	9e-11	Compositional matrix adjust.	29/31(94%)	31/31(100%)	0/31(0%)

```
Query  1    RNCQDIDECVTGIHDCSIDETCFNIQGGFRC  31
            RNCQDIDECVTGIH+CSI+ETCFNIQGGFRC
Sbjct  771  RNCQDIDECVTGIHNCSINETCFNIQGGFRC  801
```

Range 2: 508 to 537 GenPept Graphics

▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Method	Identities	Positives	Gaps
37.7 bits(86)	0.20	Compositional matrix adjust.	17/30(57%)	21/30(70%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHDCSIDETCFNIQGGFRC  31
            +C+DIDEC +GIH+C  D  C N  G FRC
Sbjct  508  DCKDIDECESGIHNCLPDFICQNTLGSFRC  537
```

Range 3: 462 to 491 GenPept Graphics

▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Method	Identities	Positives	Gaps
37.4 bits(85)	0.25	Compositional matrix adjust.	14/30(47%)	21/30(70%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHDCSIDETCFNIQGGFRC  31
            +C+D++EC+ G  +C + ETC N  G FRC
Sbjct  462  SCEDVNECIKGSQNCRLGETCVNTVGSFRC  491
```

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FBLN1_RNCQDIDECVTGIHNCSIDETCFNIQGGFRC_Mod

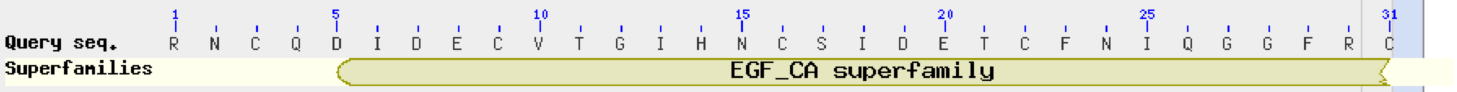
RID	BVDNNF1801R (Expires on 01-21 09:00 am)		
Query ID	lcl|217118	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	31	**Program**	BLASTP 2.2.30+ ▷ Citation

Other reports: ▷ Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

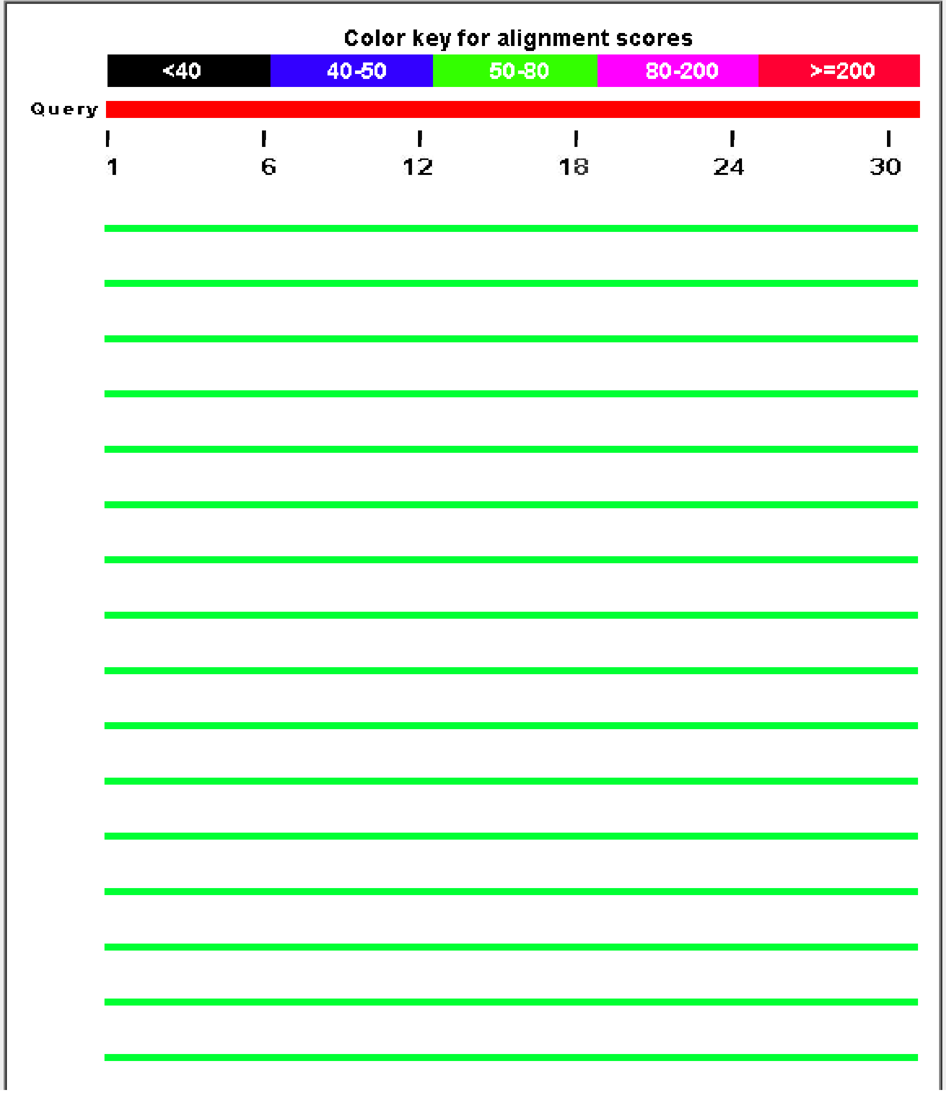
Show Conserved Domains

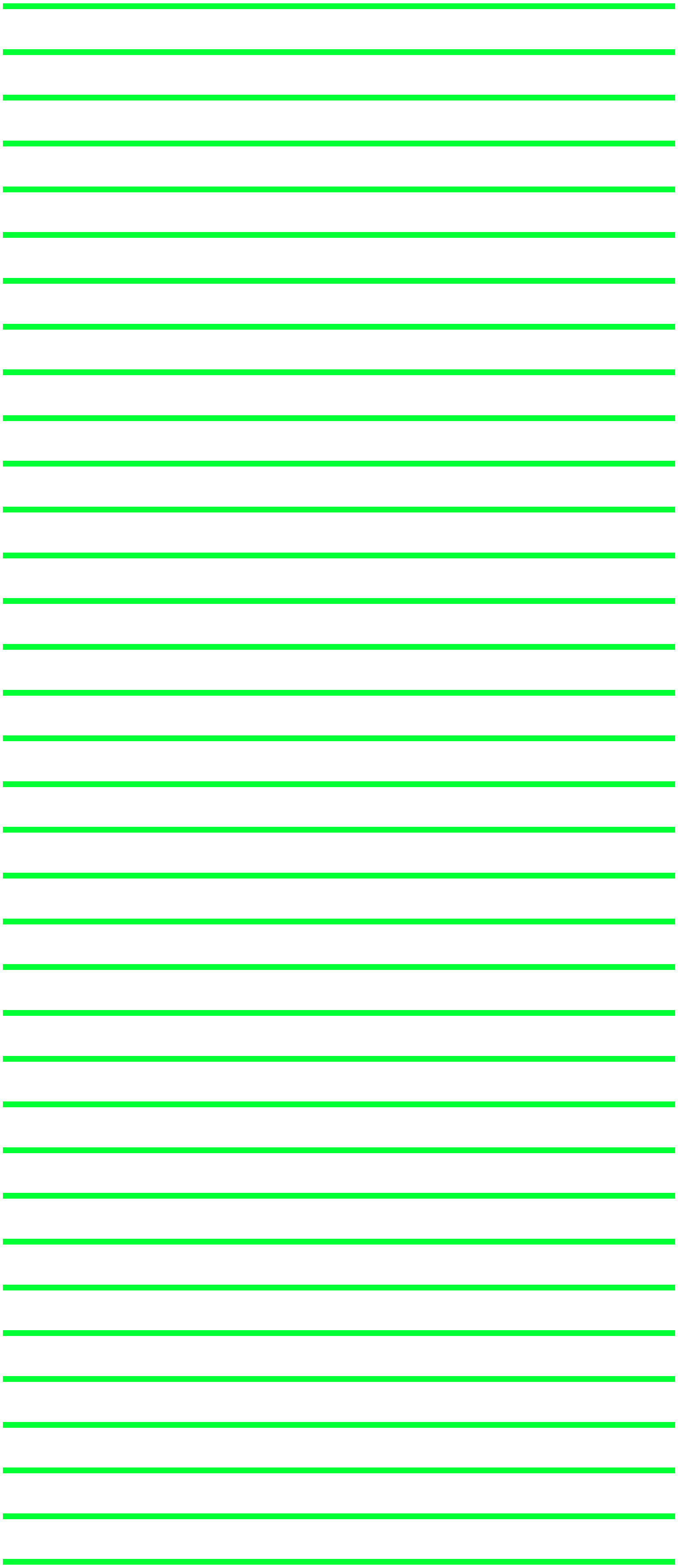
Putative conserved domains have been detected, click on the image below for detailed results.

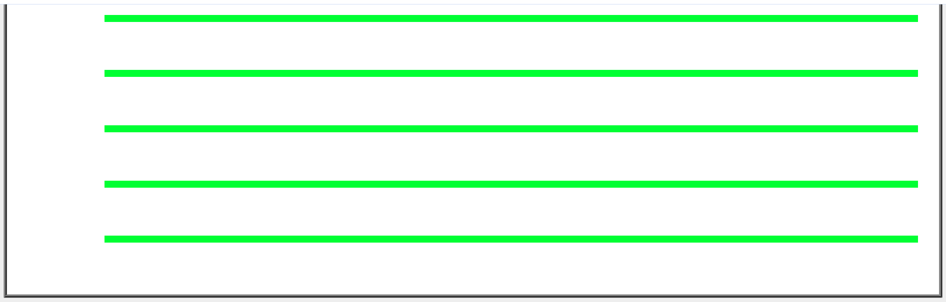


Distribution of 292 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Mus musculus]	64.3	64.3	100%	1e-11	94%	BAE35396.1
☐	PREDICTED: fibulin-1 [Oryctolagus cuniculus]	63.9	63.9	100%	2e-11	90%	XP_008250507.1
☐	PREDICTED: fibulin-1-like [Papio anubis]	65.9	65.9	100%	2e-11	97%	XP_009215764.1
☐	PREDICTED: fibulin-1 [Bubalus bubalis]	66.6	146	100%	2e-11	97%	XP_006063368.1
☐	PREDICTED: fibulin-1 [Ovis aries]	66.2	144	100%	3e-11	97%	XP_004007703.1
☐	fibulin-1 isoform C precursor [Camelus ferus]	66.2	106	100%	3e-11	94%	EPY87041.1
☐	PREDICTED: fibulin-1 [Pongo abelii]	66.2	146	100%	3e-11	97%	XP_009232751.1
☐	PREDICTED: fibulin-1 [Ictidomys tridecemlineatus]	65.9	148	100%	3e-11	97%	XP_005335099.1
☐	PREDICTED: fibulin-1 isoform X4 [Lipotes vexillifer]	65.9	142	100%	3e-11	97%	XP_007453975.1
☐	PREDICTED: fibulin-1 isoform X3 [Lipotes vexillifer]	65.9	142	100%	3e-11	97%	XP_007453974.1
☐	PREDICTED: fibulin-1 isoform X2 [Erinaceus europaeus]	65.9	147	100%	3e-11	97%	XP_007531965.1
☐	PREDICTED: fibulin-1 isoform 2 [Trichechus manatus latirostris]	65.9	147	100%	3e-11	97%	XP_004380068.1
☐	PREDICTED: fibulin-1 isoform 2 [Odobenus rosmarus divergens]	65.9	145	100%	4e-11	97%	XP_004415897.1
☐	fibulin-1 isoform C precursor [Homo sapiens]	65.9	145	100%	4e-11	97%	NP_001987.2
☐	fibulin 1, isoform CRA_f [Homo sapiens]	65.9	145	100%	4e-11	97%	EAW73390.1
☐	PREDICTED: fibulin-1 [Otolemur garnettii]	65.9	149	100%	4e-11	97%	XP_003783160.1
☐	PREDICTED: fibulin-1 isoform X2 [Nannospalax galili]	65.9	147	100%	4e-11	97%	XP_008842913.1
☐	PREDICTED: fibulin-1 isoform X2 [Rhinopithecus roxellana]	65.9	145	100%	4e-11	97%	XP_010365494.1
☐	PREDICTED: fibulin-1 [Mustela putorius furo]	65.9	145	100%	4e-11	97%	XP_004813974.1
☐	PREDICTED: fibulin-1 [Physeter catodon]	65.9	142	100%	4e-11	97%	XP_007128800.1
☐	RecName: Full=Fibulin-1; Short=FIBL-1 [Chlorocebus aethiops]	65.5	144	100%	4e-11	97%	Q8MJJ9.1
☐	PREDICTED: fibulin-1 [Mustela putorius furo]	65.9	145	100%	4e-11	97%	XP_004771346.1
☐	PREDICTED: fibulin-1 isoform X2 [Canis lupus familiaris]	65.9	146	100%	4e-11	97%	XP_005625812.1
☐	PREDICTED: fibulin-1 [Balaenoptera acutorostrata scammoni]	65.5	142	100%	4e-11	97%	XP_007189256.1
☐	PREDICTED: fibulin-1 isoform 2 [Macaca mulatta]	65.9	145	100%	4e-11	97%	XP_001109966.2
☐	unnamed protein product [Homo sapiens]	65.5	145	100%	4e-11	97%	BAG62463.1
☐	PREDICTED: fibulin-1 [Gorilla gorilla gorilla]	65.5	145	100%	4e-11	97%	XP_004063688.1
☐	PREDICTED: fibulin-1 [Macaca fascicularis]	65.5	145	100%	4e-11	97%	XP_005567067.1
☐	PREDICTED: fibulin-1 [Elephantulus edwardii]	65.5	144	100%	4e-11	97%	XP_006888093.1
☐	PREDICTED: fibulin-1 [Nomascus leucogenys]	65.9	144	100%	4e-11	97%	XP_003281320.2

☐	unnamed protein product [Homo sapiens]	65.5	145	100%	4e-11	97%	BAC11705.1
☐	PREDICTED: fibulin-1 [Orcinus orca]	65.5	142	100%	4e-11	97%	XP_004279635.1
☐	PREDICTED: fibulin-1 isoform X1 [Pan paniscus]	65.5	144	100%	4e-11	97%	XP_003812435.1
☐	PREDICTED: fibulin-1-like [Leptonychotes weddellii]	65.5	144	100%	4e-11	97%	XP_006743570.1
☐	PREDICTED: fibulin-1 isoform 1 [Odobenus rosmarus divergens]	65.5	144	100%	4e-11	97%	XP_004415896.1
☐	PREDICTED: fibulin-1 isoform X2 [Lipotes vexillifer]	65.5	141	100%	4e-11	97%	XP_007453973.1
☐	PREDICTED: fibulin-1 isoform 1 [Trichechus manatus latirostris]	65.5	146	100%	5e-11	97%	XP_004380067.1
☐	PREDICTED: fibulin-1 [Loxodonta africana]	65.5	147	100%	5e-11	97%	XP_010598758.1
☐	PREDICTED: fibulin-1 [Pan troglodytes]	65.5	144	100%	5e-11	97%	XP_009436873.1
☐	PREDICTED: fibulin-1 isoform X1 [Erinaceus europaeus]	65.5	146	100%	5e-11	97%	XP_007531964.1
☐	fibulin-1 isoform B precursor [Homo sapiens]	65.5	144	100%	5e-11	97%	NP_006476.2
☐	fibulin 1, isoform CRA_b [Homo sapiens]	65.5	144	100%	5e-11	97%	EAW73386.1
☐	RecName: Full=Fibulin-1; Short=FIBL-1; Flags: Precursor [Homo sapiens]	65.5	144	100%	5e-11	97%	P23142.4
☐	PREDICTED: fibulin-1 isoform X1 [Lipotes vexillifer]	65.5	141	100%	5e-11	97%	XP_007453972.1
☐	PREDICTED: fibulin-1 [Chrysochloris asiatica]	65.5	145	100%	5e-11	97%	XP_006866955.1
☐	PREDICTED: fibulin-1 isoform X1 [Nannospalax galili]	65.5	147	100%	5e-11	97%	XP_008842912.1
☐	fibulin-1 isoform D precursor [Homo sapiens]	65.5	144	100%	5e-11	97%	NP_006477.2
☐	fibulin-1 isoform A precursor [Homo sapiens]	65.1	143	100%	5e-11	97%	NP_006478.2
☐	PREDICTED: fibulin-1 [Tarsius syrichta]	65.5	145	100%	5e-11	97%	XP_008053358.1
☐	PREDICTED: fibulin-1 isoform X1 [Canis lupus familiaris]	65.5	146	100%	5e-11	97%	XP_005625811.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1-like [Galeopterus variegatu	65.1	144	100%	5e-11	97%	XP_008579007.1
☐	PREDICTED: fibulin-1 isoform X3 [Rhinopithecus roxellana]	65.1	144	100%	5e-11	97%	XP_010365573.1
☐	PREDICTED: fibulin-1 [Octodon degus]	65.5	146	100%	5e-11	94%	XP_004642514.1
☐	PREDICTED: fibulin-1 isoform X2 [Ochotona princeps]	65.5	146	100%	5e-11	94%	XP_004589482.1
☐	PREDICTED: fibulin-1 isoform X1 [Rhinopithecus roxellana]	65.5	144	100%	5e-11	97%	XP_010365413.1
☐	PREDICTED: fibulin-1 [Galeopterus variegatus]	64.3	142	100%	6e-11	97%	XP_008562356.1
☐	PREDICTED: fibulin-1 isoform X4 [Rhinopithecus roxellana]	65.1	143	100%	6e-11	97%	XP_010365649.1
☐	PREDICTED: fibulin-1 [Jaculus jaculus]	65.1	149	100%	6e-11	97%	XP_004650445.1
☐	unknown [Homo sapiens]	64.7	142	100%	6e-11	97%	AAG17241.1
☐	PREDICTED: fibulin-1 [Equus caballus]	65.1	145	100%	6e-11	94%	XP_005606874.1
☐	PREDICTED: fibulin-1-like [Echinops telfairi]	65.1	146	100%	6e-11	94%	XP_004700279.1
☐	PREDICTED: fibulin-1 isoform X2 [Chinchilla lanigera]	65.1	144	100%	6e-11	94%	XP_005379549.1
☐	PREDICTED: fibulin-1 isoform X2 [Pan paniscus]	65.1	144	100%	6e-11	97%	XP_008963042.1
☐	PREDICTED: fibulin-1 isoform X2 [Vicugna pacos]	65.1	145	100%	6e-11	94%	XP_006212641.1
☐	PREDICTED: fibulin-1 isoform X2 [Camelus ferus]	65.1	144	100%	6e-11	94%	XP_006176723.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1 [Cavia porcellus]	65.1	146	100%	6e-11	94%	XP_004999606.1
☐	PREDICTED: fibulin-1 isoform X1 [Ochotona princeps]	65.1	145	100%	7e-11	94%	XP_004589481.1
☐	PREDICTED: fibulin-1 [Felis catus]	65.1	146	100%	7e-11	94%	XP_006934231.1
☐	PREDICTED: fibulin-1 [Camelus dromedarius]	65.1	143	100%	8e-11	94%	XP_010981727.1
☐	PREDICTED: fibulin-1 isoform X1 [Chinchilla lanigera]	64.7	144	100%	8e-11	94%	XP_005379548.1
☐	PREDICTED: fibulin-1 isoform X1 [Camelus ferus]	64.7	143	100%	8e-11	94%	XP_006176722.1
☐	PREDICTED: fibulin-1 [Tupaia chinensis]	64.7	141	100%	8e-11	94%	XP_006164720.1
☐	PREDICTED: fibulin-1 [Equus przewalskii]	64.7	144	100%	8e-11	94%	XP_008529127.1
☐	PREDICTED: fibulin-1 isoform X2 [Sorex araneus]	64.7	145	100%	8e-11	90%	XP_004610628.1
☐	PREDICTED: fibulin-1 isoform X1 [Vicugna pacos]	64.7	144	100%	9e-11	94%	XP_006212640.1
☐	PREDICTED: fibulin-1 isoform X1 [Sorex araneus]	64.7	145	100%	1e-10	90%	XP_004610627.1

☐	PREDICTED: fibulin-1 isoform 2 [Ceratotherium simum simum]	64.7	145	100%	1e-10	94%	XP_004438039.1
☐	Fibulin-1 [Tupaia chinensis]	64.7	103	100%	1e-10	94%	ELV12523.1
☐	PREDICTED: fibulin-1 isoform 1 [Ceratotherium simum simum]	64.3	145	100%	1e-10	94%	XP_004438038.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1 [Myotis lucifugus]	63.9	141	100%	2e-10	94%	XP_006104607.1
☐	PREDICTED: fibulin-1 [Orycteropus afer afer]	63.9	143	100%	2e-10	94%	XP_007953835.1
☐	fibulin-1 C [Homo sapiens]	63.9	143	100%	2e-10	94%	CAA37772.1
☐	Fibulin 1 [Homo sapiens]	63.5	143	96%	2e-10	97%	AAH22497.1
☐	fibulin 1 [synthetic construct]	63.5	143	96%	2e-10	97%	ABM84973.1
☐	PREDICTED: fibulin-1 isoform X2 [Chlorocebus sabaeus]	63.5	143	100%	2e-10	94%	XP_007974270.1
☐	PREDICTED: fibulin-1 [Bos mutus]	63.5	141	100%	2e-10	94%	XP_005896425.1
☐	Fibulin-1 [Cricetulus griseus]	63.5	147	100%	2e-10	94%	EGW13789.1
☐	PREDICTED: fibulin-1 [Eptesicus fuscus]	63.5	140	100%	2e-10	94%	XP_008153634.1
☐	PREDICTED: fibulin-1 isoform X2 [Sus scrofa]	63.5	141	100%	2e-10	94%	XP_005663793.1
☐	fibulin-1 isoform D precursor [Homo sapiens]	63.5	142	100%	2e-10	94%	AAK37822.1
☐	fibulin 1 precursor, splice form B - human [Homo sapiens]	63.5	142	100%	2e-10	94%	B36346
☐	PREDICTED: fibulin-1 isoform X2 [Peromyscus maniculatus bairdii]	63.5	147	100%	2e-10	94%	XP_006980340.1
☐	PREDICTED: fibulin-1 [Myotis brandtii]	63.5	140	100%	3e-10	94%	XP_005886100.1
☐	fibulin-1 isoform 2 [Cricetulus griseus]	63.5	147	100%	3e-10	94%	ERE86479.1
☐	unnamed protein product [Mus musculus]	63.5	148	100%	3e-10	94%	BAC39669.1
☐	fibulin-1 A [Homo sapiens]	63.2	142	100%	3e-10	94%	CAA37770.1
☐	TPA: fibulin 1 [Bos taurus]	63.5	141	100%	3e-10	94%	DAA29013.1
☐	fibulin-1 precursor [Bos taurus]	63.5	141	100%	3e-10	94%	NP_001091498.1
☐	PREDICTED: fibulin-1 isoform X2 [Bison bison bison]	63.2	140	100%	3e-10	94%	XP_010835915.1
☐	fibulin-1 isoform 2 [Cricetulus griseus]	63.5	147	100%	3e-10	94%	ERE86478.1

Alignments

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unnamed protein product [Mus musculus]

Sequence ID: dbj|BAE35396.1| **Length:** 228 **Number of Matches:** 1

Range 1: 46 to 76 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
64.3 bits(155)	1e-11	Compositional matrix adjust.	29/31(94%)	30/31(96%)	0/31(0%)

```
Query  1   RNCQDIDECVTGIHNCSIDETCFNIQGGFRC  31
           RNCQDIDECVTGIHNCSI+ETCFNIQG FRC
Sbjct  46  RNCQDIDECVTGIHNCSINETCFNIQGSFRC  76
```

Related Information

Gene - associated gene details

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PREDICTED: fibulin-1, partial [Oryctolagus cuniculus]

Sequence ID: ref|XP_008250507.1| **Length:** 246 **Number of Matches:** 1

Range 1: 64 to 94 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
63.9 bits(154)	2e-11	Compositional matrix adjust.	28/31(90%)	30/31(96%)	0/31(0%)

```
Query  1   RNCQDIDECVTGIHNCSIDETCFNIQGGFRC  31
           RNCQDIDECVTG+HNCSI+ETCFNIQG FRC
Sbjct  64  RNCQDIDECVTGVHNCSINETCFNIQGSFRC  94
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: fibulin-1-like, partial [Papio anubis]

Sequence ID: ref|XP_009215764.1| **Length:** 451 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 269 to 299 GenPept Graphics

Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
65.9 bits(159)	2e-11	Compositional matrix adjust.	30/31(97%)	31/31(100%)	0/31(0%)

```
Query  1    RNCQDIDECVTGIHNCSIDETCFNIQGGFRC  31
            RNCQDIDECVTGIHNCSI+ETCFNIQGGFRC
Sbjct  269  RNCQDIDECVTGIHNCSINETCFNIQGGFRC  299
```

Download GenPept Graphics Sort by: 0 Next Previous Descriptions

PREDICTED: fibulin-1 [Bubalus bubalis]

Sequence ID: ref|XP_006063368.1| **Length:** 944 **Number of Matches:** 3

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 762 to 792 GenPept Graphics

Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
66.6 bits(161)	2e-11	Compositional matrix adjust.	30/31(97%)	31/31(100%)	0/31(0%)

```
Query  1    RNCQDIDECVTGIHNCSIDETCFNIQGGFRC  31
            RNCQDIDECVTGIHNCSI+ETCFNIQGGFRC
Sbjct  762  RNCQDIDECVTGIHNCSINETCFNIQGGFRC  792
```

Range 2: 454 to 483 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Method	Identities	Positives	Gaps
40.0 bits(92)	0.037	Compositional matrix adjust.	15/30(50%)	22/30(73%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHNCSIDETCFNIQGGFRC  31
            +C+D++EC+TG  NC + E+C N  G FRC
Sbjct  454  SCEDVNECITGSQNCRLGESCINTVGSFRC  483
```

Range 3: 500 to 529 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Method	Identities	Positives	Gaps
39.7 bits(91)	0.041	Compositional matrix adjust.	18/30(60%)	21/30(70%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHNCSIDETCFNIQGGFRC  31
            +C+DIDEC +GIHNC   D  C N  G FRC
Sbjct  500  DCKDIDECESGIHNCLPDFICQNTLGSFRC  529
```

Download GenPept Graphics Sort by: 0 Next Previous Descriptions

PREDICTED: fibulin-1 [Ovis aries]

Sequence ID: ref|XP_004007703.1| **Length:** 953 **Number of Matches:** 3

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Range 1: 771 to 801 GenPept Graphics

Next Match Previous Match

Score	Expect	Method	Identities	Positives	Gaps
66.2 bits(160)	3e-11	Compositional matrix adjust.	30/31(97%)	31/31(100%)	0/31(0%)

```
Query  1    RNCQDIDECVTGIHNCSIDETCFNIQGGFRC  31
            RNCQDIDECVTGIHNCSI+ETCFNIQGGFRC
Sbjct  771  RNCQDIDECVTGIHNCSINETCFNIQGGFRC  801
```

Range 2: 508 to 537 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Method	Identities	Positives	Gaps
39.7 bits(91)	0.045	Compositional matrix adjust.	18/30(60%)	21/30(70%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHNCSIDETCFNIQGGFRC  31
            +C+DIDEC +GIHNC   D  C N  G FRC
Sbjct  508  DCKDIDECESGIHNCLPDFICQNTLGSFRC  537
```

Range 3: 462 to 491 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Method	Identities	Positives	Gaps
38.9 bits(89)	0.081	Compositional matrix adjust.	15/30(50%)	21/30(70%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHNCSIDETCFNIQGGFRC  31
            +C+D++EC+ G  NC + ETC N  G FRC
Sbjct  462  SCEDVNECIKGSQNCRLGETCVNTVGSFRC  491
```

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FBLN1_RNCQDIDECVTGIHNCSINETCFNIQGGFRC_NonMod

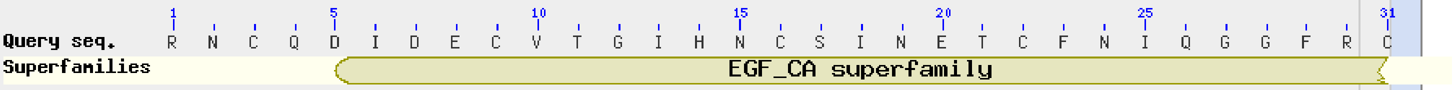
RID	B9E2HR6A01R (Expires on 01-14 13:16 pm)		
Query ID	lcl|199112	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	31		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

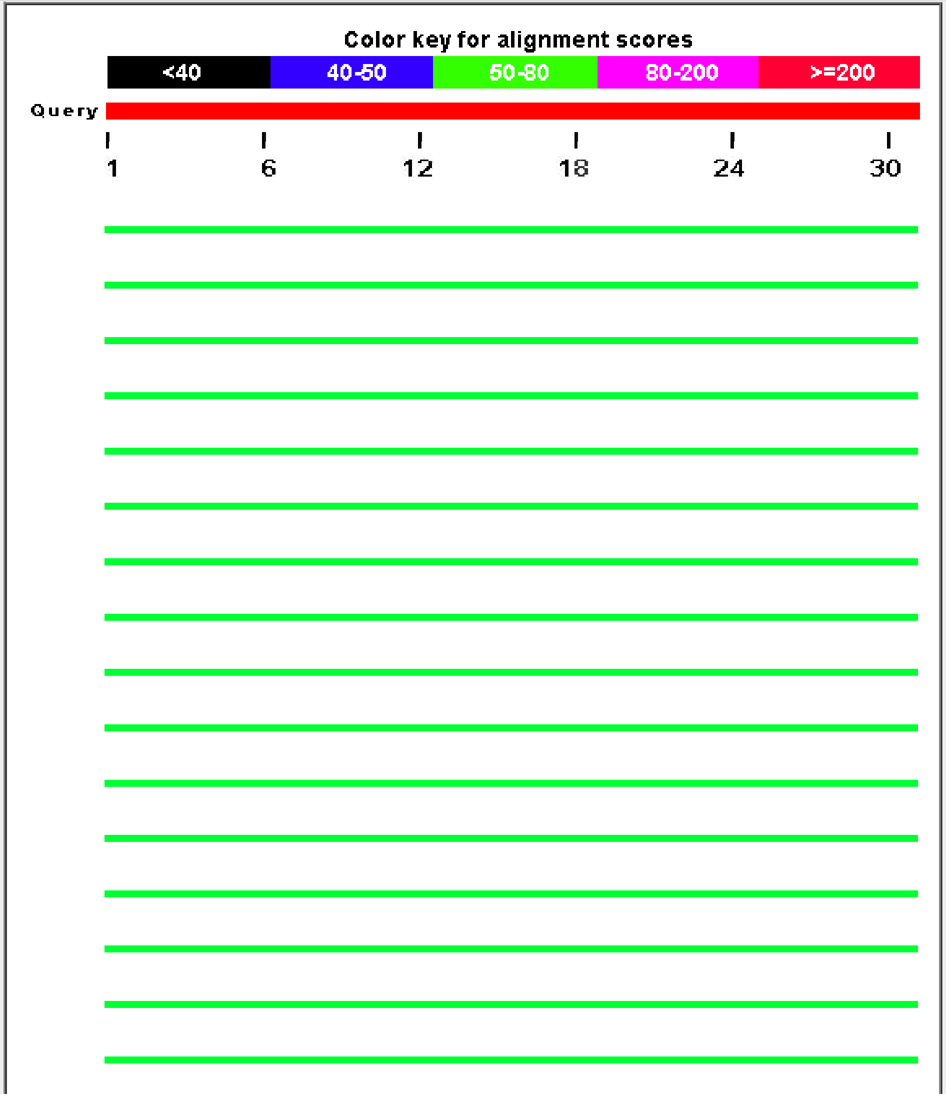
Show Conserved Domains

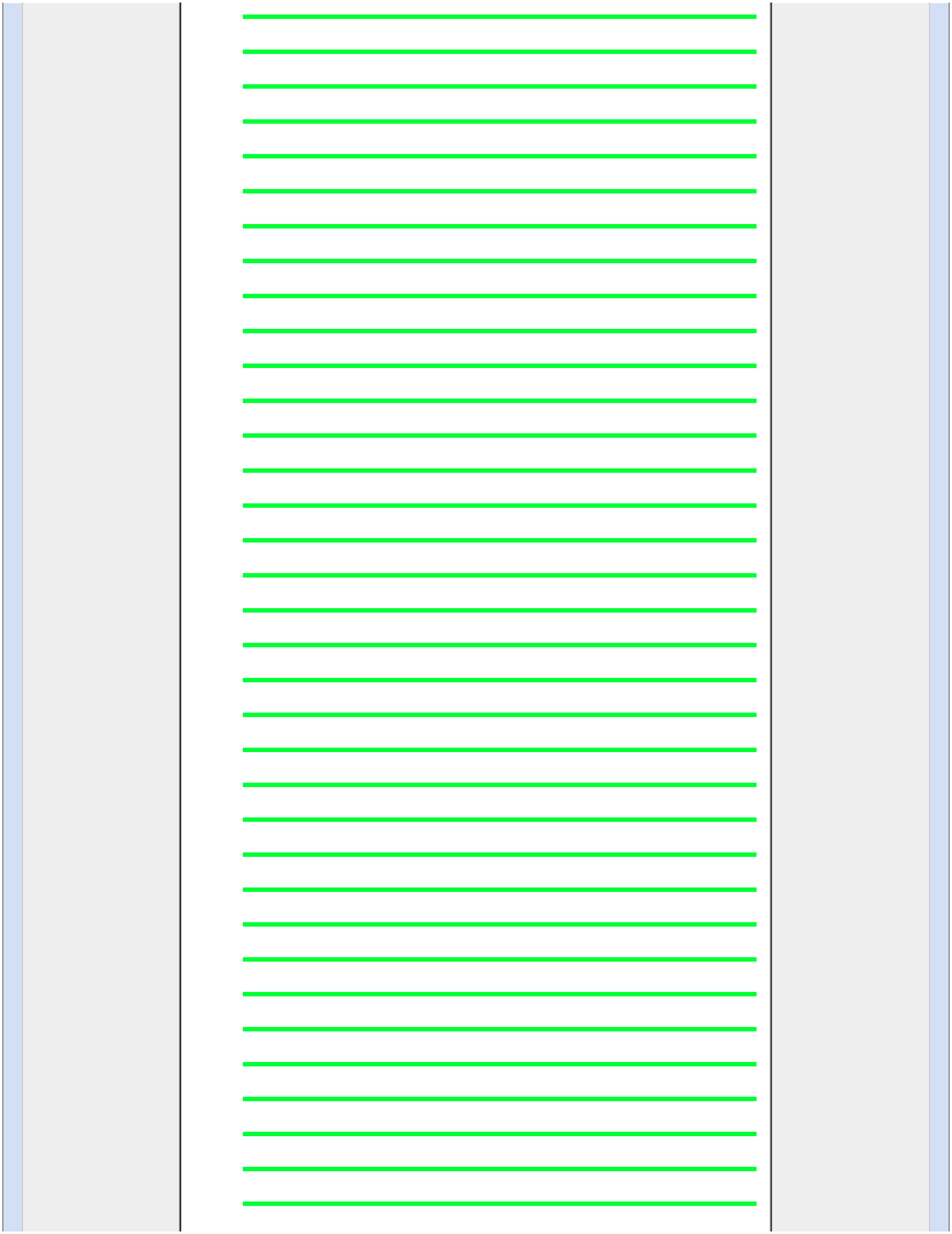
Putative conserved domains have been detected, click on the image below for detailed results.

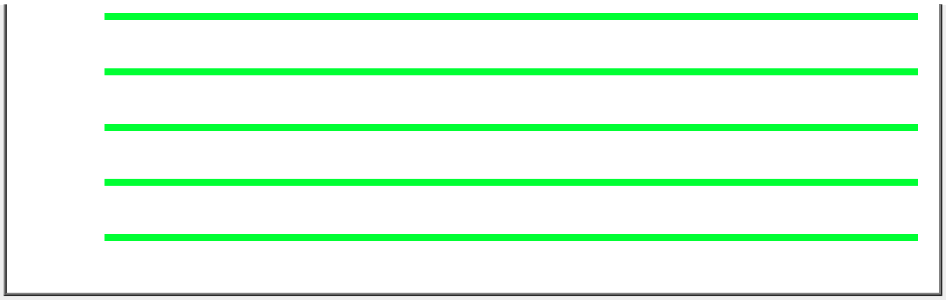


Distribution of 484 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: fibulin-1 [Galeopterus variegatus]	75.1	236	100%	7e-15	100%	gi|667341505|XP_008562356.1
☐	PREDICTED: fibulin-1-like [Papio anubis]	75.1	110	100%	1e-14	100%	gi|685570016|XP_009215764.1
☐	unknown [Homo sapiens]	75.1	235	100%	1e-14	100%	gi|10441928|AAG17241.1
☐	unnamed protein product [Mus musculus]	72.8	72.8	100%	1e-14	97%	gi|74204653|BAE35396.1
☐	PREDICTED: fibulin-1 isoform X4 [Rhinopithecus roxellana]	75.1	233	100%	1e-14	100%	gi|724795561|XP_010365649.1
☐	PREDICTED: fibulin-1 isoform X3 [Rhinopithecus roxellana]	75.1	233	100%	2e-14	100%	gi|724795558|XP_010365573.1
☐	fibulin-1 isoform A precursor [Homo sapiens]	75.1	235	100%	2e-14	100%	gi|34734068|NP_006478.2
☐	PREDICTED: fibulin-1 isoform X2 [Pan paniscus]	75.1	235	100%	2e-14	100%	gi|675717942|XP_008963042.1
☐	fibulin 1, isoform CRA_b [Homo sapiens]	75.1	235	100%	2e-14	100%	gi|119593792|EAW73386.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1-like [Galeopterus	75.1	236	100%	2e-14	100%	gi|667294707|XP_008579007.1
☐	RecName: Full=Fibulin-1; Short=FIBL-1 [Chlorocebus aethiops]	75.1	199	100%	2e-14	100%	gi|30580425|Q8MJJ9.1
☐	fibulin-1 isoform B precursor [Homo sapiens]	75.1	235	100%	2e-14	100%	gi|34734064|NP_006476.2
☐	PREDICTED: fibulin-1-like [Leptonychotes weddellii]	75.1	235	100%	2e-14	100%	gi|585183989|XP_006743570.1
☐	unnamed protein product [Homo sapiens]	75.1	235	100%	2e-14	100%	gi|22761800|BAC11705.1
☐	PREDICTED: fibulin-1 isoform X2 [Rhinopithecus roxellana]	75.1	233	100%	2e-14	100%	gi|724795555|XP_010365494.1
☐	unnamed protein product [Homo sapiens]	75.1	235	100%	2e-14	100%	gi|194374697|BAG62463.1
☐	PREDICTED: fibulin-1 [Macaca fascicularis]	75.1	233	100%	2e-14	100%	gi|544461232|XP_005567067.1
☐	PREDICTED: fibulin-1 [Gorilla gorilla gorilla]	75.1	235	100%	2e-14	100%	gi|426394827|XP_004063688.1
☐	PREDICTED: fibulin-1 isoform X1 [Pan paniscus]	75.1	235	100%	2e-14	100%	gi|397482444|XP_003812435.1
☐	PREDICTED: fibulin-1 [Loxodonta africana]	75.1	269	100%	2e-14	100%	gi|731510789|XP_010598758.1
☐	PREDICTED: fibulin-1 [Elephantulus edwardii]	75.1	235	100%	2e-14	100%	gi|585667023|XP_006888093.1
☐	PREDICTED: fibulin-1 [Tarsius syrichta]	75.1	269	100%	2e-14	100%	gi|640794658|XP_008053358.1
☐	PREDICTED: fibulin-1 [Balaenoptera acutorostrata scammoni]	75.1	197	100%	2e-14	100%	gi|594683418|XP_007189256.1
☐	PREDICTED: fibulin-1 [Physeter catodon]	75.1	232	100%	2e-14	100%	gi|593746998|XP_007128800.1
☐	PREDICTED: fibulin-1 [Orcinus orca]	75.1	232	100%	2e-14	100%	gi|466057370|XP_004279635.1
☐	PREDICTED: fibulin-1 [Ictidomys tridecemlineatus]	75.1	202	100%	2e-14	100%	gi|532098910|XP_005335099.1
☐	PREDICTED: fibulin-1 isoform X1 [Rhinopithecus roxellana]	75.1	233	100%	2e-14	100%	gi|724795552|XP_010365413.1
☐	PREDICTED: fibulin-1 [Jaculus jaculus]	75.1	238	100%	2e-14	100%	gi|507532747|XP_004650445.1
☐	PREDICTED: fibulin-1 isoform X2 [Nannospalax galili]	75.1	236	100%	2e-14	100%	gi|674071544|XP_008842913.1
☐	fibulin-1 isoform C precursor [Homo sapiens]	75.1	235	100%	2e-14	100%	gi|34734062|NP_001987.2

☐	PREDICTED: fibulin-1 isoform X2 [Erinaceus europaeus]	75.1	235	100%	2e-14	100%	gi|617642052|XP_007531965.1
☐	PREDICTED: fibulin-1 isoform 2 [Odobenus rosmarus divergens]	75.1	235	100%	2e-14	100%	gi|472393253|XP_004415897.1
☐	PREDICTED: fibulin-1 isoform 2 [Trichechus manatus latirostris]	75.1	236	100%	2e-14	100%	gi|471390788|XP_004380068.1
☐	PREDICTED: fibulin-1 isoform X4 [Lipotes vexillifer]	75.1	232	100%	2e-14	100%	gi|602683431|XP_007453975.1
☐	PREDICTED: fibulin-1 isoform X3 [Lipotes vexillifer]	75.1	232	100%	2e-14	100%	gi|602683429|XP_007453974.1
☐	PREDICTED: fibulin-1 [Otolemur garnettii]	75.1	237	100%	2e-14	100%	gi|395819580|XP_003783160.1
☐	PREDICTED: fibulin-1 isoform X2 [Canis lupus familiaris]	75.1	237	100%	2e-14	100%	gi|545514461|XP_005625812.1
☐	PREDICTED: fibulin-1 [Oryctolagus cuniculus]	72.4	72.4	100%	2e-14	94%	gi|655897280|XP_008250507.1
☐	fibulin 1, isoform CRA_f [Homo sapiens]	75.1	235	100%	2e-14	100%	gi|119593796|EAW73390.1
☐	PREDICTED: fibulin-1 isoform X1 [Nannospalax galili]	75.1	236	100%	2e-14	100%	gi|674071542|XP_008842912.1
☐	PREDICTED: fibulin-1 [Pan troglodytes]	75.1	235	100%	2e-14	100%	gi|694983727|XP_009436873.1
☐	RecName: Full=Fibulin-1; Short=FIBL-1; Flags: Precursor [Homo sa	75.1	235	100%	2e-14	100%	gi|215274249|P23142.4
☐	fibulin-1 isoform D precursor [Homo sapiens]	75.1	235	100%	2e-14	100%	gi|34734066|NP_006477.2
☐	PREDICTED: fibulin-1 isoform X1 [Erinaceus europaeus]	75.1	235	100%	2e-14	100%	gi|617642049|XP_007531964.1
☐	PREDICTED: fibulin-1 isoform 1 [Odobenus rosmarus divergens]	75.1	235	100%	2e-14	100%	gi|472393251|XP_004415896.1
☐	PREDICTED: fibulin-1 isoform 1 [Trichechus manatus latirostris]	75.1	236	100%	2e-14	100%	gi|471390784|XP_004380067.1
☐	PREDICTED: fibulin-1 isoform X2 [Lipotes vexillifer]	75.1	232	100%	2e-14	100%	gi|602683427|XP_007453973.1
☐	PREDICTED: fibulin-1 isoform X1 [Lipotes vexillifer]	75.1	232	100%	2e-14	100%	gi|602683425|XP_007453972.1
☐	PREDICTED: fibulin-1 isoform X1 [Canis lupus familiaris]	75.1	237	100%	2e-14	100%	gi|545514459|XP_005625811.1
☐	PREDICTED: fibulin-1 [Chrysochloris asiatica]	75.1	234	100%	2e-14	100%	gi|586472756|XP_006866955.1
☐	PREDICTED: fibulin-1 [Nomascus leucogenys]	75.1	235	100%	2e-14	100%	gi|441618218|XP_003281320.2
☐	PREDICTED: fibulin-1 isoform 2 [Macaca mulatta]	75.1	198	100%	2e-14	100%	gi|297261301|XP_001109966.2
☐	PREDICTED: fibulin-1 [Mustela putorius furo]	75.1	269	100%	2e-14	100%	gi|511992630|XP_004813974.1
☐	PREDICTED: fibulin-1 [Equus przewalskii]	74.7	202	100%	2e-14	97%	gi|664743621|XP_008529127.1
☐	PREDICTED: fibulin-1 [Mustela putorius furo]	75.1	269	100%	2e-14	100%	gi|511903702|XP_004771346.1
☐	PREDICTED: fibulin-1 [Pongo abelii]	75.1	235	100%	2e-14	100%	gi|686764893|XP_009232751.1
☐	PREDICTED: fibulin-1 [Bubalus bubalis]	75.1	234	100%	2e-14	100%	gi|594079384|XP_006063368.1
☐	PREDICTED: fibulin-1 [Ovis aries]	75.1	233	100%	2e-14	100%	gi|426227186|XP_004007703.1
☐	PREDICTED: fibulin-1 isoform X2 [Camelus ferus]	74.7	234	100%	2e-14	97%	gi|560900629|XP_006176723.1
☐	PREDICTED: fibulin-1-like [Echinops telfairi]	74.7	236	100%	2e-14	97%	gi|507635833|XP_004700279.1
☐	PREDICTED: fibulin-1 isoform X2 [Vicugna pacos]	74.7	236	100%	2e-14	97%	gi|560980789|XP_006212641.1
☐	PREDICTED: fibulin-1 isoform X1 [Camelus ferus]	74.7	234	100%	3e-14	97%	gi|560900627|XP_006176722.1
☐	PREDICTED: fibulin-1 isoform X1 [Vicugna pacos]	74.7	236	100%	3e-14	97%	gi|560980787|XP_006212640.1
☐	PREDICTED: fibulin-1 isoform X2 [Chinchilla lanigera]	74.7	233	100%	3e-14	97%	gi|533128844|XP_005379549.1
☐	PREDICTED: fibulin-1 isoform X2 [Ochotona princeps]	74.7	235	100%	3e-14	97%	gi|504155089|XP_004589482.1
☐	PREDICTED: fibulin-1 [Tupaia chinensis]	74.7	263	100%	3e-14	97%	gi|562873654|XP_006164720.1
☐	PREDICTED: LOW QUALITY PROTEIN: fibulin-1 [Cavia porcellus]	74.7	235	100%	3e-14	97%	gi|514443922|XP_004999606.1
☐	PREDICTED: fibulin-1 isoform X1 [Chinchilla lanigera]	74.7	233	100%	3e-14	97%	gi|533128842|XP_005379548.1
☐	PREDICTED: fibulin-1 isoform X1 [Ochotona princeps]	74.7	235	100%	3e-14	97%	gi|504155087|XP_004589481.1
☐	PREDICTED: fibulin-1 [Felis catus]	74.7	237	100%	3e-14	97%	gi|586993905|XP_006934231.1
☐	PREDICTED: fibulin-1 [Equus caballus]	74.7	202	100%	3e-14	97%	gi|545206896|XP_005606874.1
☐	PREDICTED: fibulin-1 [Octodon degus]	74.7	267	100%	3e-14	97%	gi|507693081|XP_004642514.1
☐	fibulin-1 isoform C precursor [Camelus ferus]	74.7	191	100%	3e-14	97%	gi|528767382|EPY87041.1
☐	PREDICTED: fibulin-1 isoform X2 [Sorex araneus]	74.3	234	100%	4e-14	94%	gi|505830669|XP_004610628.1
☐	PREDICTED: fibulin-1 isoform X1 [Sorex araneus]	74.3	234	100%	4e-14	94%	gi|505830667|XP_004610627.1
☐	Fibulin-1 [Tupaia chinensis]	74.7	220	100%	4e-14	97%	gi|444519033|ELV12523.1

☐	PREDICTED: fibulin-1 isoform 2 [Ceratotherium simum simum]	73.9	236	100%	5e-14	97%	gi|478527715|XP_004438039.1
☐	PREDICTED: fibulin-1 isoform 1 [Ceratotherium simum simum]	73.9	236	100%	5e-14	97%	gi|478527713|XP_004438038.1
☐	PREDICTED: fibulin-1 [Orycteropus afer afer]	73.2	233	100%	8e-14	97%	gi|634889474|XP_007953835.1
☐	Fibulin 1 [Homo sapiens]	73.2	233	96%	9e-14	100%	gi|18490682|AAH22497.1
☐	fibulin 1 [synthetic construct]	73.2	233	96%	9e-14	100%	gi|123994743|ABM84973.1
☐	PREDICTED: fibulin-1 isoform X3 [Chlorocebus sabaeus]	72.8	231	100%	1e-13	97%	gi|635102866|XP_007974271.1
☐	fibulin-1 A [Homo sapiens]	72.8	233	100%	1e-13	97%	gi|31415|CAA37770.1
☐	fibulin 1 precursor, splice form B - human [Homo sapiens]	72.8	233	100%	1e-13	97%	gi|106017|B36346
☐	Fibulin-1 [Cricetulus griseus]	72.8	202	100%	1e-13	97%	gi|344257685|EGW13789.1
☐	PREDICTED: fibulin-1 [Eptesicus fuscus]	72.8	196	100%	1e-13	97%	gi|641727121|XP_008153634.1
☐	PREDICTED: fibulin-1 isoform X2 [Cricetulus griseus]	72.8	238	100%	1e-13	97%	gi|625255711|XP_007619196.1
☐	PREDICTED: fibulin-1 isoform X4 [Microtus ochrogaster]	72.8	238	100%	1e-13	97%	gi|532022189|XP_005354460.1
☐	PREDICTED: fibulin-1 isoform X3 [Microtus ochrogaster]	72.8	238	100%	1e-13	97%	gi|532022187|XP_005354459.1
☐	PREDICTED: fibulin-1 [Myotis brandtii]	72.8	196	100%	1e-13	97%	gi|554589517|XP_005886100.1
☐	PREDICTED: fibulin-1 isoform X2 [Chlorocebus sabaeus]	72.8	231	100%	1e-13	97%	gi|635102864|XP_007974270.1
☐	fibulin-1 C [Homo sapiens]	72.8	233	100%	1e-13	97%	gi|31419|CAA37772.1
☐	PREDICTED: fibulin-1 isoform X2 [Peromyscus maniculatus bairdii]	72.8	238	100%	1e-13	97%	gi|589935133|XP_006980340.1
☐	PREDICTED: fibulin-1 isoform X1 [Mus musculus]	72.8	239	100%	1e-13	97%	gi|568991352|XP_006520500.1
☐	unnamed protein product [Mus musculus]	72.8	239	100%	1e-13	97%	gi|26352065|BAC39669.1
☐	PREDICTED: fibulin-1 isoform X1 [Rattus norvegicus]	72.8	239	100%	1e-13	97%	gi|564361379|XP_006242223.1
☐	PREDICTED: fibulin-1 isoform X2 [Sus scrofa]	72.8	232	100%	1e-13	97%	gi|545824398|XP_005663793.1
☐	PREDICTED: fibulin-1 [Myotis davidii]	72.8	196	100%	1e-13	97%	gi|584059500|XP_006774235.1
☐	PREDICTED: fibulin-1 isoform X2 [Microtus ochrogaster]	72.8	238	100%	1e-13	97%	gi|532022185|XP_005354458.1
☐	PREDICTED: fibulin-1 isoform X1 [Microtus ochrogaster]	72.8	238	100%	1e-13	97%	gi|532022183|XP_005354457.1

⊟ Alignments

Download ⌄ GenPept Graphics **Sort by:** 0 ▼ Next ▲ Previous ▲ Descriptions

PREDICTED: fibulin-1, partial [Galeopterus variegatus]

Sequence ID: gi|667341505|ref|XP_008562356.1| **Length:** 384 **Number of Matches:** 5

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 339 to 369 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.1 bits(183)	7e-15	31/31(100%)	31/31(100%)	0/31(0%)

```
Query  1    RNCQDIDECVTGIHNCSINETCFNIQGGFRC  31
            RNCQDIDECVTGIHNCSINETCFNIQGGFRC
Sbjct  339  RNCQDIDECVTGIHNCSINETCFNIQGGFRC  369
```

Range 2: 31 to 60 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
47.4 bits(111)	6e-05	16/30(53%)	22/30(73%)	0/30(0%)

```
Query  2   NCQDIDECVTGIHNCSINETCFNIQGGFRC  31
           +C+DI+EC+ G HNC + E+C N  G FRC
Sbjct  31  SCEDINECIMGSHNCRLGESCINTVGSFRC  60
```

Range 3: 77 to 106 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
43.1 bits(100)	0.002	17/30(57%)	21/30(70%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHNCSINETCFNIQGGFRC  31
            +C+DIDEC +GIHNC   +  C  N  G FRC
Sbjct  77   SCKDIDECESGIHNCLPDFICQNTLGSFRC  106
```

Range 4: 123 to 152 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
35.4 bits(80)	0.87	12/30(40%)	19/30(63%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHNCSINETCFNIQGGFRC  31
            NC DI+EC++    C + +TC N +G + C
Sbjct  123  NCIDINECLSISAPCPVGQTCINTEGSYAC  152
```

Range 5: 297 to 325 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
35.0 bits(79)	1.2	17/31(55%)	19/31(61%)	4/31(12%)

```
Query  3    CQDIDECV--TGIHNCSINETCFNIQGGFRC  31
            C+DIDEC   TG H CS    C NI G F+C
Sbjct  297  CEDIDECALPTGGHICSYR--CINIPGSFQC  325
```

Download ⌄ GenPept Graphics **Sort by:** 0 ▼ Next ▲ Previous Descriptions

PREDICTED: fibulin-1-like, partial [Papio anubis]

Sequence ID: gi|685570016|ref|XP_009215764.1| **Length:** 451 **Number of Matches:** 2

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 269 to 299 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.1 bits(183)	1e-14	31/31(100%)	31/31(100%)	0/31(0%)

```
Query  1    RNCQDIDECVTGIHNCSINETCFNIQGGFRC  31
            RNCQDIDECVTGIHNCSINETCFNIQGGFRC
Sbjct  269  RNCQDIDECVTGIHNCSINETCFNIQGGFRC  299
```

Range 2: 227 to 255 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
35.0 bits(79)	1.3	17/31(55%)	19/31(61%)	4/31(12%)

```
Query  3    CQDIDECV--TGIHNCSINETCFNIQGGFRC  31
            C+DIDEC   TG H CS    C NI G F+C
Sbjct  227  CEDIDECALPTGGHICSYR--CINIPGSFQC  255
```

Download ⌄ GenPept Graphics **Sort by:** 0 ▼ Next ▲ Previous Descriptions

unknown [Homo sapiens]

Sequence ID: gi|10441928|gb|AAG17241.1|AF217999_1 **Length:** 495 **Number of Matches:** 5

Related Information

Gene - associated gene details

Range 1: 391 to 421 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.1 bits(183)	1e-14	31/31(100%)	31/31(100%)	0/31(0%)

```
Query  1    RNCQDIDECVTGIHNCSINETCFNIQGGFRC  31
            RNCQDIDECVTGIHNCSINETCFNIQGGFRC
Sbjct  391  RNCQDIDECVTGIHNCSINETCFNIQGGFRC  421
```

Range 2: 83 to 112 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
47.4 bits(111)	8e-05	15/30(50%)	23/30(76%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHNCSINETCFNIQGGFRC  31
            +C+D++EC+TG H+C + E+C N  G FRC
Sbjct  83   SCEDVNECITGSHSCRLGESCINTVGSFRC  112
```

Range 3: 129 to 158 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
43.1 bits(100)	0.002	17/30(57%)	21/30(70%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHNCSINETCFNIQGGFRC  31
            +C+DIDEC +GIHNC  +  C N  G FRC
Sbjct  129  SCKDIDECESGIHNCLPDFICQNTLGSFRC  158
```

Range 4: 175 to 204 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
35.0 bits(79)	1.3	13/30(43%)	18/30(60%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHNCSINETCFNIQGGFRC  31
            NC DI+EC++    C I  TC N +G + C
Sbjct  175  NCIDINECLSISAPCPIGHTCINTEGSYTC  204
```

Range 5: 349 to 377 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
35.0 bits(79)	1.3	17/31(55%)	19/31(61%)	4/31(12%)

```
Query  3    CQDIDECV--TGIHNCSINETCFNIQGGFRC  31
            C+DIDEC   TG H CS    C NI G F+C
Sbjct  349  CEDIDECALPTGGHICSYR--CINIPGSFQC  377
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Mus musculus]

Sequence ID: gi|74204653|dbj|BAE35396.1| **Length:** 228 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 46 to 76 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.8 bits(177)	1e-14	30/31(97%)	30/31(96%)	0/31(0%)

```
Query  1    RNCQDIDECVTGIHNCSINETCFNIQGGFRC  31
            RNCQDIDECVTGIHNCSINETCFNIQG FRC
Sbjct  46   RNCQDIDECVTGIHNCSINETCFNIQGSFRC  76
```

Download GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

PREDICTED: fibulin-1 isoform X4 [Rhinopithecus roxellana]

Sequence ID: gi|724795561|ref|XP_010365649.1| **Length:** 524 **Number of Matches:** 5

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 479 to 509 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.1 bits(183)	1e-14	31/31(100%)	31/31(100%)	0/31(0%)

```
Query  1    RNCQDIDECVTGIHNCSINETCFNIQGGFRC  31
            RNCQDIDECVTGIHNCSINETCFNIQGGFRC
Sbjct  479  RNCQDIDECVTGIHNCSINETCFNIQGGFRC  509
```

Range 2: 171 to 200 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
47.0 bits(110)	1e-04	15/30(50%)	23/30(76%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHNCSINETCFNIQGGFRC  31
            +C+D++EC+TG H+C + E+C N  G FRC
Sbjct  171  SCEDVNECITGSHSCRLGESCVNTVGSFRC  200
```

Range 3: 217 to 246 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
43.1 bits(100)	0.002	17/30(57%)	21/30(70%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHNCSINETCFNIQGGFRC  31
            +C+DIDEC +GIHNC +   C N  G FRC
Sbjct  217  SCKDIDECESGIHNCLPDFICQNTLGSFRC  246
```

Range 4: 437 to 465 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
35.0 bits(79)	1.3	17/31(55%)	19/31(61%)	4/31(12%)

```
Query  3    CQDIDECV--TGIHNCSINETCFNIQGGFRC  31
            C+DIDEC   TG H CS    C NI G F+C
Sbjct  437  CEDIDECALPTGGHICSYR--CINIPGSFQC  465
```

Range 5: 263 to 292 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
33.1 bits(74)	5.9	12/30(40%)	17/30(56%)	0/30(0%)

```
Query  2    NCQDIDECVTGIHNCSINETCFNIQGGFRC  31
            NC DI+EC++    C    TC N +G + C
Sbjct  263  NCIDINECLSISAPCPTGHTCINTEGSYTC  292
```

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Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

FCGBP_RGLCVLSVGADLTTFDGARG_Mod

RID BVDRF04B01R (Expires on 01-21 09:01 am)

Query ID	lcl|244730	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	20		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

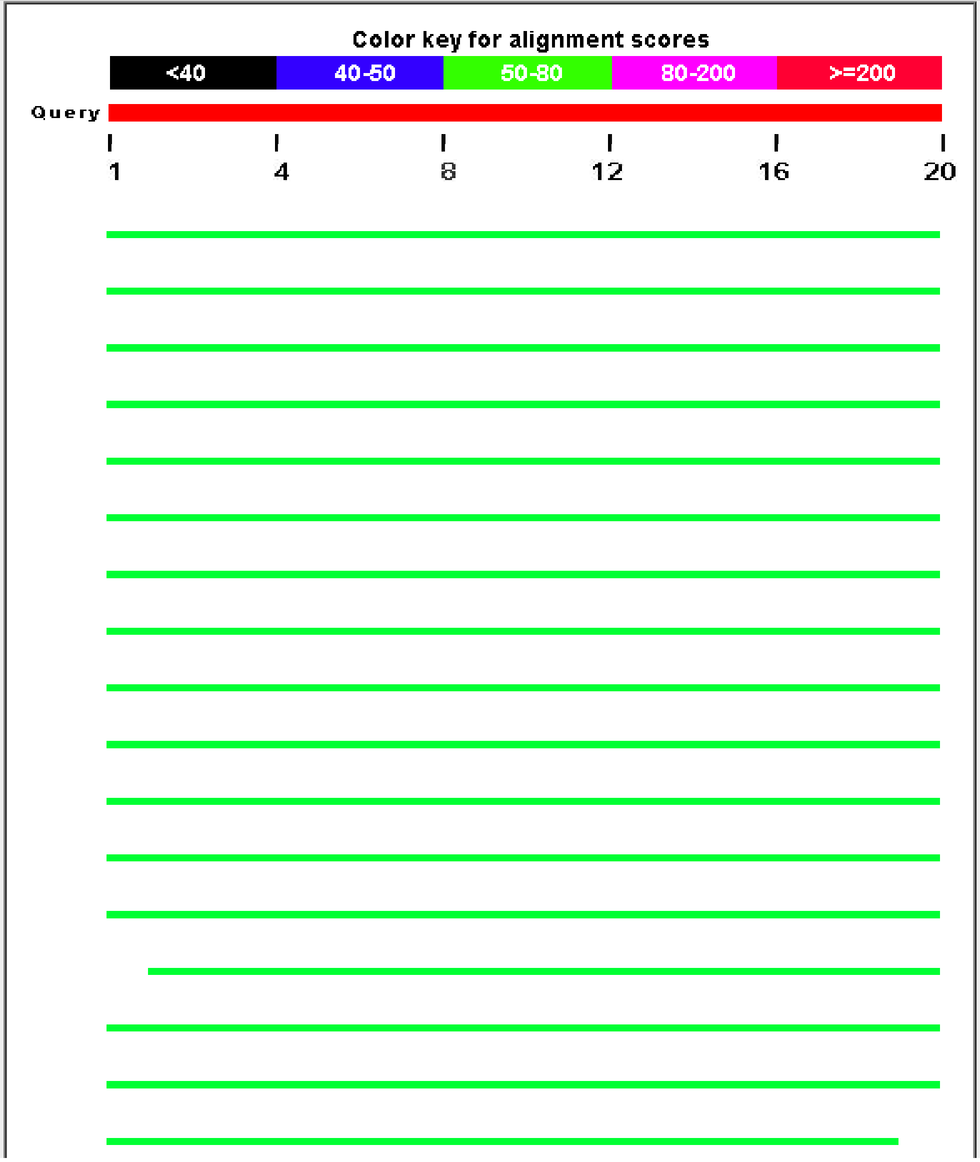
Graphic Summary

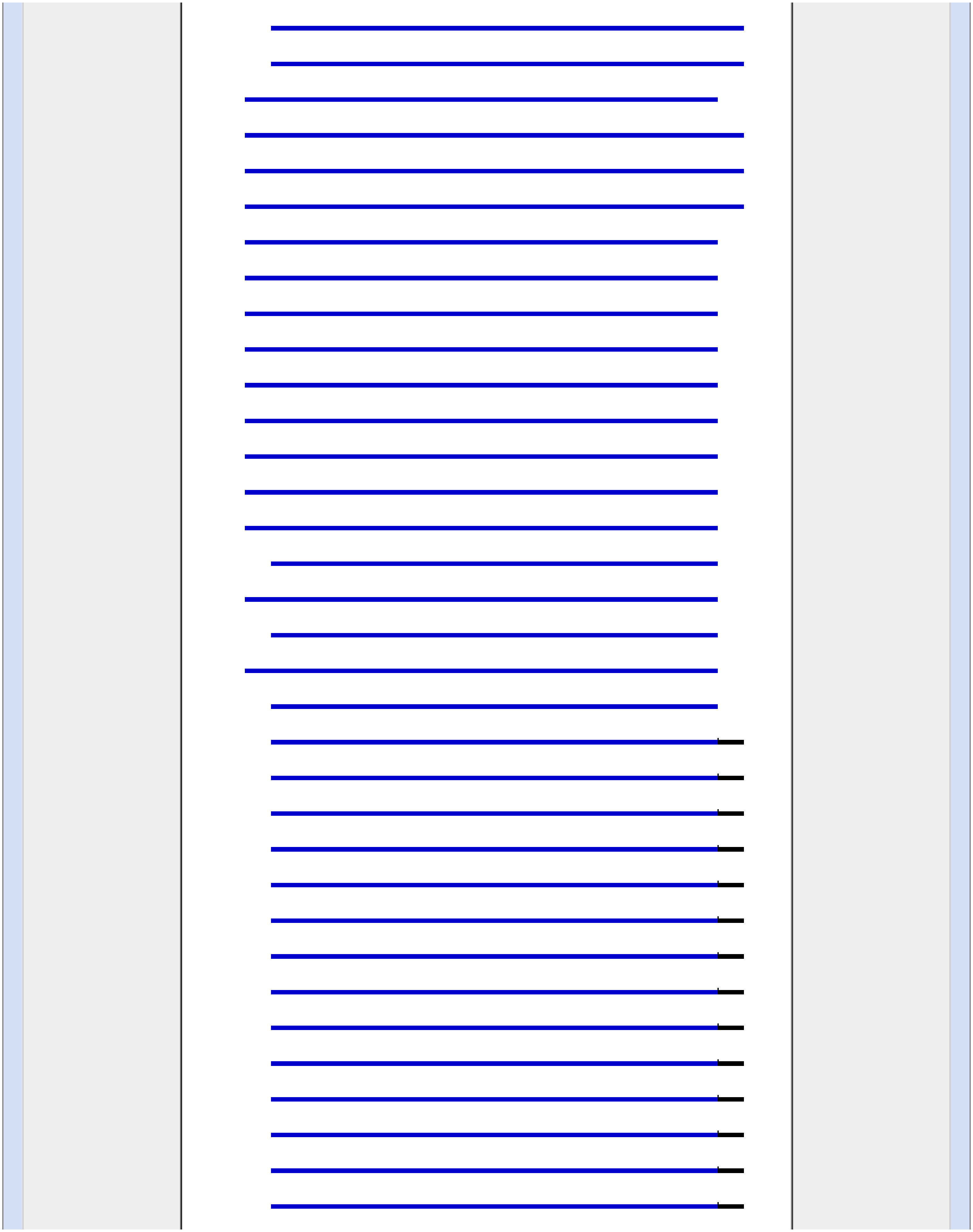
Show Conserved Domains

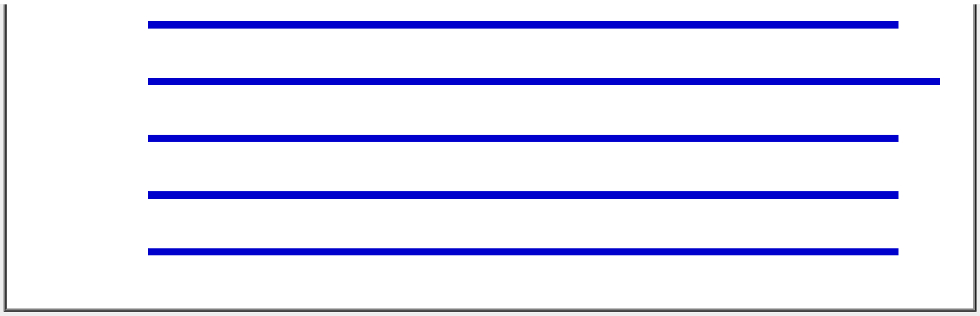
No putative conserved domains have been detected

Distribution of 115 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	IgG Fc binding protein [AA 4671-5405] [Homo sapiens]	60.9	60.9	100%	4e-09	95%	AAD15624.1
☐	Fc fragment of IgG binding protein [Homo sapiens]	60.9	60.9	100%	4e-09	95%	EAW56926.1
☐	PREDICTED: igGFc-binding protein-like [Macaca mulatta]	60.9	60.9	100%	4e-09	95%	XP_001088892.2
☐	PREDICTED: IgGFc-binding protein [Chlorocebus sabaeus]	60.9	60.9	100%	4e-09	95%	XP_007996683.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pan paniscus	60.9	60.9	100%	4e-09	95%	XP_008963216.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Papio anubis	60.9	60.9	100%	4e-09	95%	XP_003915593.1
☐	PREDICTED: IgGFc-binding protein [Nomascus leucogenys]	60.9	60.9	100%	4e-09	95%	XP_003270573.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pongo abelii]	60.9	60.9	100%	4e-09	95%	XP_009230865.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Gorilla gorilla	60.9	60.9	100%	4e-09	95%	XP_004060816.1
☐	PREDICTED: IgGFc-binding protein [Macaca fascicularis]	60.9	60.9	100%	4e-09	95%	XP_005590715.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pan troglody	60.9	60.9	100%	4e-09	95%	XP_009433882.1
☐	IgG Fc binding protein [Homo sapiens]	60.9	60.9	100%	4e-09	95%	BAA19526.1
☐	IgGFc-binding protein precursor [Homo sapiens]	60.9	60.9	100%	4e-09	95%	NP_003881.2
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Rhinopithecu	57.5	57.5	95%	6e-08	95%	XP_010379186.1
☐	PREDICTED: IgGFc-binding protein [Saimiri boliviensis boliviensis]	54.5	54.5	100%	6e-07	90%	XP_010329397.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Callithrix jacc	54.5	54.5	100%	6e-07	90%	XP_008986248.1
☐	PREDICTED: IgGFc-binding protein [Tarsius syrichta]	52.8	52.8	95%	2e-06	89%	XP_008052981.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Equus przew	49.4	49.4	90%	3e-05	89%	XP_008530313.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Equus caball	49.4	49.4	90%	3e-05	89%	XP_005596726.1
☐	PREDICTED: IgGFc-binding protein [Jaculus jaculus]	49.4	49.4	90%	3e-05	89%	XP_004670397.1
☐	PREDICTED: IgGFc-binding protein-like [Tursiops truncatus]	49.0	49.0	95%	4e-05	84%	XP_004313750.1
☐	PREDICTED: IgGFc-binding protein [Lipotes vexillifer]	49.0	49.0	95%	4e-05	84%	XP_007458763.1
☐	PREDICTED: IgGFc-binding protein [Orcinus orca]	49.0	49.0	95%	4e-05	84%	XP_004271425.1
☐	Fcgbp protein [Mus musculus]	46.0	46.0	90%	3e-04	83%	AAH24554.1
☐	Fcgbp protein [Mus musculus]	46.0	46.0	90%	3e-04	83%	AAH24520.1
☐	Fcgbp protein [Mus musculus]	46.0	46.0	90%	3e-04	83%	AAH55475.1
☐	Fcgbp protein [Mus musculus]	46.0	46.0	90%	4e-04	83%	AAH69956.1
☐	Fcgbp protein [Mus musculus]	46.0	46.0	90%	4e-04	83%	AAH92067.1
☐	Fcgbp protein [Mus musculus]	46.0	46.0	90%	4e-04	83%	AAH26653.1

☐	Fcgbp protein [Mus musculus]	46.0	46.0	90%	4e-04	83%	AAH30871.1
☐	mCG145390, isoform CRA_b [Mus musculus]	46.0	46.0	90%	4e-04	83%	EDL24158.1
☐	mCG145390, isoform CRA_a [Mus musculus]	46.0	46.0	90%	4e-04	83%	EDL24157.1
☐	rCG54015 [Rattus norvegicus]	46.0	46.0	85%	4e-04	88%	EDM07917.1
☐	PREDICTED: IgGFc-binding protein-like [Peromyscus maniculatus bairdii]	46.0	46.0	90%	4e-04	83%	XP_006996523.1
☐	PREDICTED: IgGFc-binding protein-like [Nannospalax galili]	46.0	46.0	85%	4e-04	88%	XP_008852263.1
☐	Fc fragment of IgG binding protein precursor [Mus musculus]	46.0	46.0	90%	4e-04	83%	NP_001116075.1
☐	Fc fragment of IgG binding protein precursor [Rattus norvegicus]	46.0	46.0	85%	4e-04	88%	NP_001158129.2
☐	PREDICTED: IgGFc-binding protein isoform X2 [Bubalus bubalis]	46.0	66.6	90%	4e-04	88%	XP_006050099.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Bos taurus]	46.0	66.6	90%	4e-04	88%	XP_010813252.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Bos taurus]	46.0	66.6	90%	4e-04	88%	XP_010798219.1
☐	PREDICTED: zinc finger protein 780B-like isoform X1 [Heterocephalus glaber	46.0	66.6	90%	4e-04	88%	XP_004874222.1
☐	PREDICTED: zinc finger protein 780B [Heterocephalus glaber]	46.0	66.6	90%	4e-04	88%	XP_004878581.1
☐	PREDICTED: IgGFc-binding protein [Bison bison bison]	46.0	66.6	90%	4e-04	88%	XP_010847529.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bubalus bubalis]	46.0	66.6	90%	4e-04	88%	XP_006050098.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bos taurus]	46.0	66.6	90%	4e-04	88%	XP_010813251.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bos taurus]	46.0	66.6	90%	4e-04	88%	XP_010798218.1
☐	PREDICTED: IgGFc-binding protein [Pantholops hodgsonii]	46.0	66.6	90%	4e-04	88%	XP_005963590.1
☐	TPA: Fc fragment of IgG binding protein-like [Bos taurus]	46.0	66.6	90%	4e-04	88%	DAA19876.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ovis aries]	46.0	66.6	90%	4e-04	88%	XP_004015739.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Bos mutus]	46.0	66.6	90%	4e-04	88%	XP_005890645.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Capra hircus	46.0	66.6	90%	4e-04	88%	XP_005692605.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG binding protein [	45.6	45.6	90%	5e-04	83%	XP_005674577.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ursus maritin	45.6	45.6	95%	5e-04	79%	XP_008686987.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Balaenoptera acutorostrata s	45.6	45.6	90%	5e-04	83%	XP_007180031.1
☐	PREDICTED: IgGFc-binding protein [Physeter catodon]	45.6	65.3	90%	5e-04	83%	XP_007122066.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Balaenoptera acutorostrata s	45.6	45.6	90%	5e-04	83%	XP_007180030.1
☐	IgGFc-binding protein [Myotis davidii]	43.1	43.1	85%	0.003	82%	ELK30313.1
☐	PREDICTED: IgGFc-binding protein [Myotis davidii]	43.1	43.1	85%	0.003	82%	XP_006763740.1
☐	RGD1311906 protein [Rattus norvegicus]	42.6	42.6	85%	0.005	82%	AAH99756.1
☐	PREDICTED: IgGFc-binding protein [Fukomys damarensis]	42.6	42.6	85%	0.005	82%	XP_010612839.1
☐	Fc fragment of IgG binding protein-like precursor [Rattus norvegicus]	42.6	42.6	85%	0.005	82%	NP_001158128.1
☐	IgGFc-binding protein [Fukomys damarensis]	42.6	42.6	85%	0.005	82%	KFO19029.1
☐	PREDICTED: IgGFc-binding protein [Octodon degus]	42.6	42.6	85%	0.005	82%	XP_004648069.1
☐	PREDICTED: IgGFc-binding protein-like [Nannospalax galili]	42.2	42.2	90%	0.006	78%	XP_008852264.1
☐	PREDICTED: IgGFc-binding protein-like [Peromyscus maniculatus bairdii]	41.8	41.8	90%	0.009	78%	XP_006996525.1
☐	PREDICTED: IgGFc-binding protein [Pteropus alecto]	41.8	41.8	80%	0.009	81%	XP_006905494.1
☐	IgGFc-binding protein [Pteropus alecto]	41.8	41.8	80%	0.009	81%	ELK18209.1
☐	PREDICTED: IgGFc-binding protein-like [Ailuropoda melanoleuca]	41.4	41.4	95%	0.012	74%	XP_002923768.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG binding protein [	41.4	41.4	95%	0.012	74%	XP_006752469.1
☐	PREDICTED: IgGFc-binding protein [Orycteropus afer afer]	40.1	40.1	95%	0.031	74%	XP_007941342.1
☐	PREDICTED: IgGFc-binding protein [Cavia porcellus]	40.1	40.1	80%	0.031	81%	XP_003462033.1
☐	PREDICTED: IgGFc-binding protein [Galeopterus variegatus]	39.7	39.7	85%	0.042	76%	XP_008580791.1
☐	PREDICTED: IgGFc-binding protein [Tupaia chinensis]	39.2	39.2	100%	0.058	70%	XP_006140449.1
☐	IgGFc-binding protein [Tupaia chinensis]	39.2	39.2	100%	0.058	70%	ELW72413.1

☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Loxodonta af	38.8	38.8	90%	0.079	72%	XP_010598700.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG binding protein [(	38.8	38.8	95%	0.079	68%	XP_004417817.1
☐	PREDICTED: IgGFc-binding protein [Otolemur garnettii]	38.8	38.8	90%	0.079	78%	XP_003802201.1
☐	IgGFc-binding protein [Cricetulus griseus]	38.4	38.4	90%	0.095	72%	ERE59847.1
☐	PREDICTED: IgGFc-binding protein [Mesocricetus auratus]	38.4	38.4	90%	0.11	72%	XP_005086657.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein-like isoform X	38.4	38.4	90%	0.11	72%	XP_007616229.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Chinchilla lanigera]	38.4	38.4	90%	0.11	78%	XP_005414139.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein-like isoform X	38.4	38.4	90%	0.11	72%	XP_007643925.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Chinchilla lanigera]	38.4	38.4	90%	0.11	78%	XP_005414138.1
☐	PREDICTED: IgGFc-binding protein [Elephantulus edwardii]	38.4	38.4	85%	0.11	76%	XP_006901006.1
☐	PREDICTED: IgGFc-binding protein [Ictidomys tridecemlineatus]	38.4	38.4	85%	0.11	76%	XP_005336544.1
☐	PREDICTED: IgGFc-binding protein [Erinaceus europaeus]	37.5	37.5	90%	0.20	72%	XP_007538724.1
☐	PREDICTED: IgGFc-binding protein [Ochotona princeps]	37.1	37.1	85%	0.27	71%	XP_004599764.1
☐	Fc fragment of IgG binding protein [Camelus ferus]	37.1	37.1	85%	0.27	71%	EPY85977.1
☐	PREDICTED: IgGFc-binding protein [Camelus dromedarius]	37.1	37.1	85%	0.27	71%	XP_010983489.1
☐	PREDICTED: IgGFc-binding protein [Camelus bactrianus]	37.1	37.1	85%	0.27	71%	XP_010945545.1
☐	PREDICTED: IgGFc-binding protein [Vicugna pacos]	37.1	37.1	85%	0.27	71%	XP_006215157.1
☐	PREDICTED: IgGFc-binding protein [Camelus ferus]	37.1	37.1	85%	0.27	71%	XP_006178015.1
☐	PREDICTED: IgGFc-binding protein [Microtus ochrogaster]	36.3	36.3	85%	0.50	71%	XP_005371357.1
☐	IgGFc-binding protein [Cricetulus griseus]	35.8	35.8	85%	0.62	71%	ERE60529.1
☐	PREDICTED: IgGFc-binding protein-like isoform X2 [Cricetulus griseus]	35.8	35.8	85%	0.68	71%	XP_007616228.1
☐	PREDICTED: IgGFc-binding protein-like isoform X1 [Cricetulus griseus]	35.8	35.8	85%	0.68	71%	XP_003505295.2
☐	Fc fragment of IgG binding protein-like precursor [Mus musculus]	35.8	35.8	85%	0.68	71%	NP_001158127.1
☐	PREDICTED: IgGFc-binding protein [Panthera tigris altaica]	35.8	35.8	90%	0.68	72%	XP_007087304.1
☐	PREDICTED: IgGFc-binding protein [Echinops telfairi]	35.8	35.8	90%	0.68	72%	XP_004710550.1
☐	PREDICTED: IgGFc-binding protein [Oryctolagus cuniculus]	35.4	35.4	75%	0.93	73%	XP_008249744.1

⊟ Alignments

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IgG Fc binding protein [AA 4671-5405] [Homo sapiens]

Sequence ID: gb|AAD15624.1| **Length:** 735 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 562 to 581 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.9 bits(136)	4e-09	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    RGLCVLSVGADLTTFDGARG  20
            RGLCVLSVGA+LTTFDGARG
Sbjct  562  RGLCVLSVGANLTTFDGARG  581
```

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Fc fragment of IgG binding protein [Homo sapiens]

Sequence ID: gb|EAW56926.1| **Length:** 3004 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 2831 to 2850 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.9 bits(136)	4e-09	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1     RGLCVLSVGADLTTFDGARG  20
             RGLCVLSVGA+LTTFDGARG
Sbjct  2831  RGLCVLSVGANLTTFDGARG  2850
```

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PREDICTED: igGFc-binding protein-like [Macaca mulatta]

Sequence ID: ref|XP_001088892.2| **Length:** 3029 **Number of Matches:** 1

Range 1: 2856 to 2875 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.9 bits(136)	4e-09	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1     RGLCVLSVGADLTTFDGARG  20
             RGLCVLSVGA+LTTFDGARG
Sbjct  2856  RGLCVLSVGANLTTFDGARG  2875
```

Related Information

Gene - associated gene details
UniGene - clustered expressed sequence tags
Map Viewer - aligned genomic context

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PREDICTED: IgGFc-binding protein [Chlorocebus sabaeus]

Sequence ID: ref|XP_007996683.1| **Length:** 3043 **Number of Matches:** 1

Range 1: 2870 to 2889 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.9 bits(136)	4e-09	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1     RGLCVLSVGADLTTFDGARG  20
             RGLCVLSVGA+LTTFDGARG
Sbjct  2870  RGLCVLSVGANLTTFDGARG  2889
```

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pan paniscus]

Sequence ID: ref|XP_008963216.1| **Length:** 3331 **Number of Matches:** 1

Range 1: 3158 to 3177 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.9 bits(136)	4e-09	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1     RGLCVLSVGADLTTFDGARG  20
             RGLCVLSVGA+LTTFDGARG
Sbjct  3158  RGLCVLSVGANLTTFDGARG  3177
```

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

BLAST ®

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▸ NCBI/ BLAST/ blastp suite/ Formatting Results - B951AMP601R

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How to read this page   Blast report description

FCGBP_RGLCVLSVGANLTTFDGARG_NonMod

RID	B951AMP601R (Expires on 01-14 10:42 am)
Query ID	lcl|240446
Description	None
Molecule type	amino acid
Query Length	20

Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ ▷ Citation

Other reports: ▷ Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

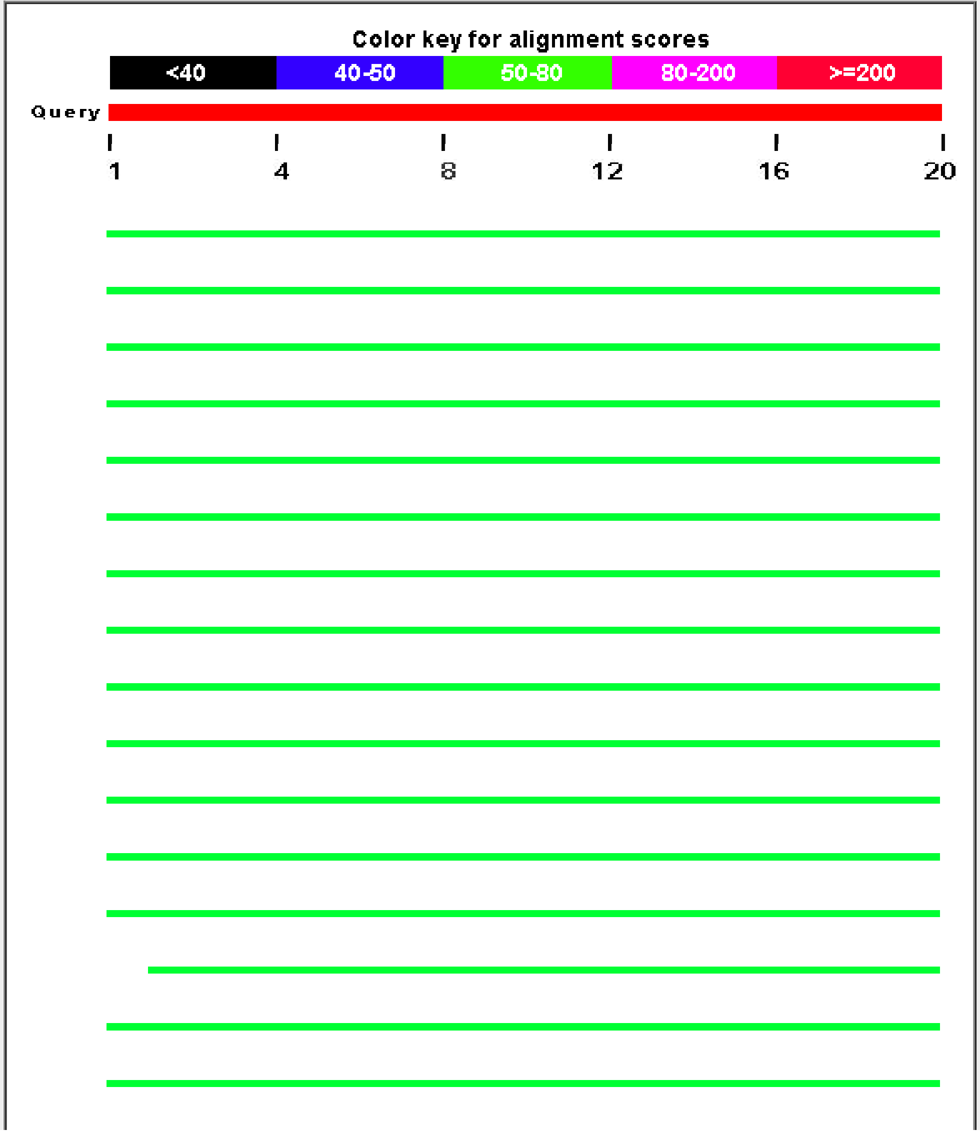
⊟ Graphic Summary

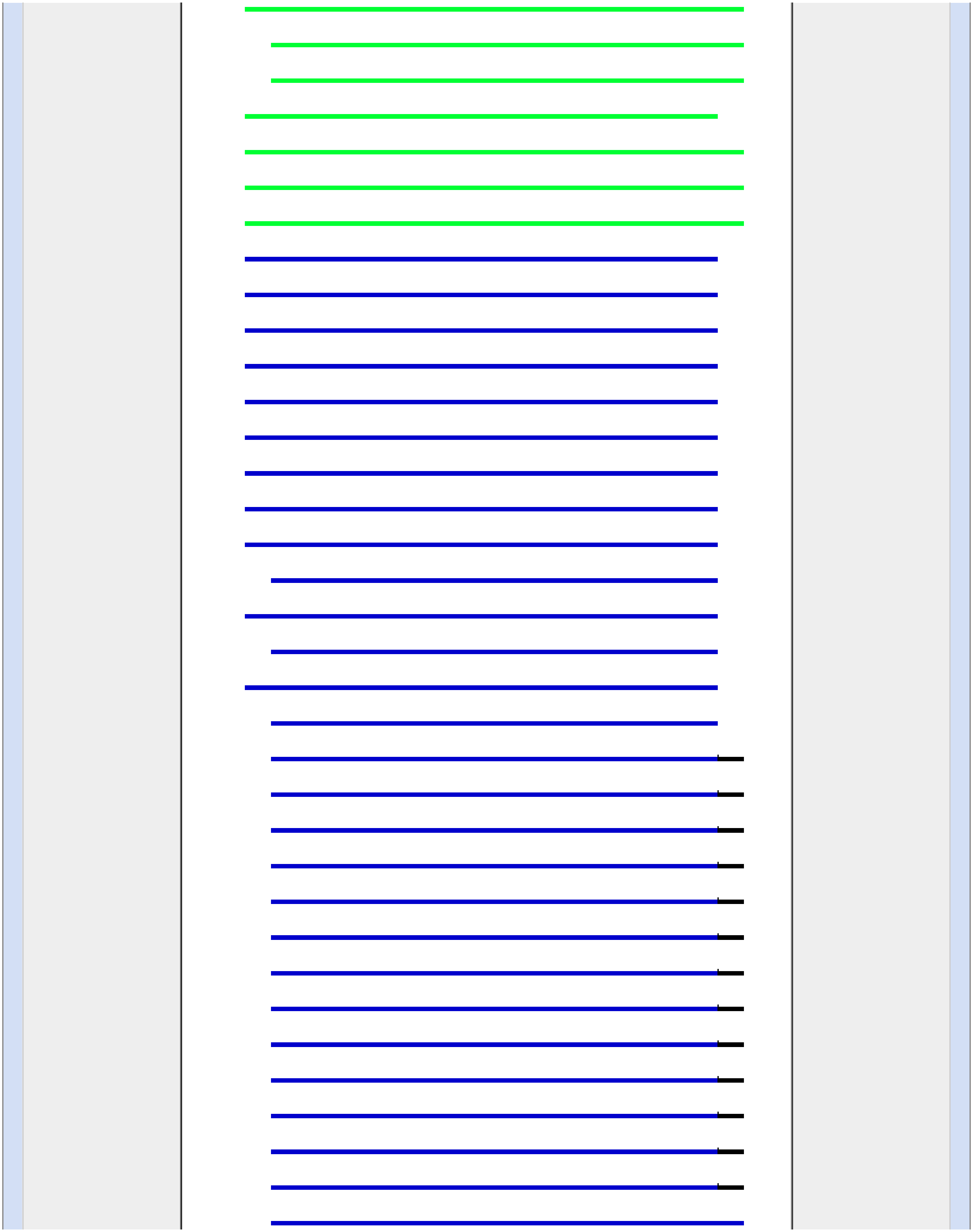
⊟ Show Conserved Domains

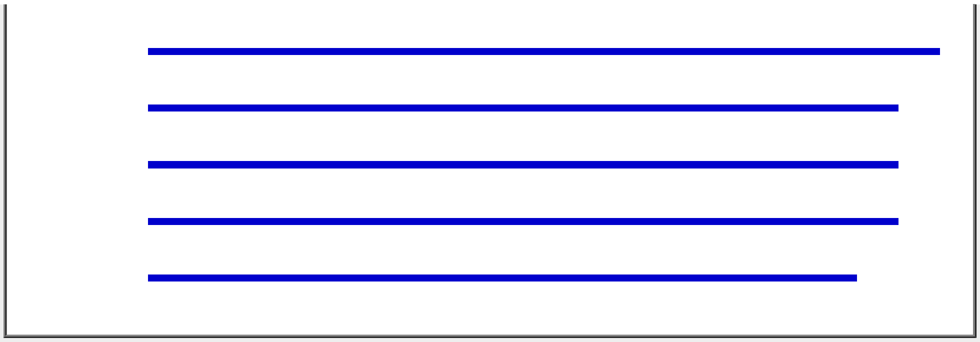
No putative conserved domains have been detected

Distribution of 115 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	IgG Fc binding protein [AA 4671-5405] [Homo sapiens]	63.4	63.4	100%	5e-10	100%	gi|4321127|AAD15624.1
☐	Fc fragment of IgG binding protein [Homo sapiens]	63.4	63.4	100%	5e-10	100%	gi|119577330|EAW56926.1
☐	PREDICTED: igGFc-binding protein-like [Macaca mulatta]	63.4	63.4	100%	5e-10	100%	gi|297277050|XP_001088892.2
☐	PREDICTED: IgGFc-binding protein [Chlorocebus sabaeus]	63.4	63.4	100%	5e-10	100%	gi|635042256|XP_007996683.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pa	63.4	63.4	100%	5e-10	100%	gi|675718714|XP_008963216.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pa	63.4	63.4	100%	5e-10	100%	gi|402905577|XP_003915593.1
☐	PREDICTED: IgGFc-binding protein [Nomascus leucogenys]	63.4	63.4	100%	5e-10	100%	gi|332242810|XP_003270573.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Po	63.4	63.4	100%	5e-10	100%	gi|686758917|XP_009230865.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Go	63.4	63.4	100%	5e-10	100%	gi|426388791|XP_004060816.1
☐	PREDICTED: IgGFc-binding protein [Macaca fascicularis]	63.4	63.4	100%	5e-10	100%	gi|544514342|XP_005590715.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pa	63.4	63.4	100%	5e-10	100%	gi|694975150|XP_009433882.1
☐	IgG Fc binding protein [Homo sapiens]	63.4	63.4	100%	5e-10	100%	gi|1944352|BAA19526.1
☐	IgGFc-binding protein precursor [Homo sapiens]	63.4	63.4	100%	5e-10	100%	gi|154146262|NP_003881.2
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Rh	60.0	60.0	95%	8e-09	100%	gi|724909919|XP_010379186.1
☐	PREDICTED: IgGFc-binding protein [Saimiri boliviensis boliviensis]	57.1	57.1	100%	8e-08	95%	gi|725605545|XP_010329397.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ca	57.1	57.1	100%	8e-08	95%	gi|675761213|XP_008986248.1
☐	PREDICTED: IgGFc-binding protein [Tarsius syrichta]	55.4	55.4	95%	3e-07	95%	gi|640776875|XP_008052981.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Eq	52.0	52.0	90%	4e-06	94%	gi|664745941|XP_008530313.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Eq	52.0	52.0	90%	4e-06	94%	gi|545176771|XP_005596726.1
☐	PREDICTED: IgGFc-binding protein [Jaculus jaculus]	52.0	52.0	90%	4e-06	94%	gi|507573627|XP_004670397.1
☐	PREDICTED: IgGFc-binding protein-like [Tursiops truncatus]	51.5	51.5	95%	5e-06	89%	gi|470605142|XP_004313750.1
☐	PREDICTED: IgGFc-binding protein [Lipotes vexillifer]	51.5	51.5	95%	5e-06	89%	gi|602693350|XP_007458763.1
☐	PREDICTED: IgGFc-binding protein [Orcinus orca]	51.5	51.5	95%	5e-06	89%	gi|466016931|XP_004271425.1
☐	Fcgbp protein [Mus musculus]	48.6	48.6	90%	5e-05	89%	gi|19353631|AAH24554.1
☐	Fcgbp protein [Mus musculus]	48.6	48.6	90%	5e-05	89%	gi|19353600|AAH24520.1
☐	Fcgbp protein [Mus musculus]	48.6	48.6	90%	5e-05	89%	gi|33585463|AAH55475.1
☐	Fcgbp protein [Mus musculus]	48.6	48.6	90%	5e-05	89%	gi|47682932|AAH69956.1
☐	Fcgbp protein [Mus musculus]	48.6	48.6	90%	5e-05	89%	gi|62024652|AAH92067.1
☐							

	Fcgbp protein [Mus musculus]	48.6	48.6	90%	5e-05	89%	gi|20072053|AAH26653.1
☐	Fcgbp protein [Mus musculus]	48.6	48.6	90%	5e-05	89%	gi|21410127|AAH30871.1
☐	mCG145390, isoform CRA_b [Mus musculus]	48.6	48.6	90%	5e-05	89%	gi|148692211|EDL24158.1
☐	mCG145390, isoform CRA_a [Mus musculus]	48.6	48.6	90%	5e-05	89%	gi|148692210|EDL24157.1
☐	rCG54015 [Rattus norvegicus]	48.6	48.6	85%	5e-05	94%	gi|149056486|EDM07917.1
☐	PREDICTED: IgGFc-binding protein-like [Peromyscus maniculatus	48.6	48.6	90%	5e-05	89%	gi|589968051|XP_006996523.1
☐	PREDICTED: IgGFc-binding protein-like [Nannospalax galili]	48.6	48.6	85%	5e-05	94%	gi|674088661|XP_008852263.1
☐	Fc fragment of IgG binding protein precursor [Mus musculus]	48.6	48.6	90%	5e-05	89%	gi|169790797|NP_001116075.1
☐	Fc fragment of IgG binding protein precursor [Rattus norvegicus]	48.6	48.6	85%	5e-05	94%	gi|695917199|NP_001158129.2
☐	PREDICTED: IgGFc-binding protein isoform X2 [Bubalus bubalis]	48.6	69.1	90%	5e-05	94%	gi|594051532|XP_006050099.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bos taurus]	48.6	69.1	90%	5e-05	94%	gi|528991889|XP_002695104.2
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bos taurus]	48.6	69.1	90%	5e-05	94%	gi|528933616|XP_005200216.1
☐	PREDICTED: zinc finger protein 780B-like isoform X1 [Heterocepha	48.6	69.1	90%	5e-05	94%	gi|513026092|XP_004874222.1
☐	PREDICTED: zinc finger protein 780B [Heterocephalus glaber]	48.6	69.1	90%	5e-05	94%	gi|512817473|XP_004878581.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bubalus bubalis]	48.6	69.1	90%	5e-05	94%	gi|594051530|XP_006050098.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Bos taurus]	48.6	69.1	90%	5e-05	94%	gi|528991887|XP_005219168.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Bos taurus]	48.6	69.1	90%	5e-05	94%	gi|528933614|XP_614095.6
☐	PREDICTED: IgGFc-binding protein [Pantholops hodgsonii]	48.6	69.1	90%	5e-05	94%	gi|556735974|XP_005963590.1
☐	TPA: Fc fragment of IgG binding protein-like [Bos taurus]	48.6	69.1	90%	5e-05	94%	gi|296477761|DAA19876.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ov	48.6	69.1	90%	5e-05	94%	gi|426243806|XP_004015739.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Bo	48.6	69.1	90%	5e-05	94%	gi|555957014|XP_005890645.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ca	48.6	69.1	90%	5e-05	94%	gi|548504606|XP_005692605.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG bindin	48.1	48.1	90%	7e-05	89%	gi|545830918|XP_005674577.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Urs	48.1	48.1	95%	7e-05	84%	gi|670991993|XP_008686987.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Balaenoptera acuto	48.1	48.1	90%	7e-05	89%	gi|594663750|XP_007180031.1
☐	PREDICTED: IgGFc-binding protein [Physeter catodon]	48.1	67.9	90%	7e-05	89%	gi|593767123|XP_007122066.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Balaenoptera acuto	48.1	48.1	90%	7e-05	89%	gi|594663748|XP_007180030.1
☐	IgGFc-binding protein [Myotis davidii]	45.6	45.6	85%	5e-04	88%	gi|432102846|ELK30313.1
☐	PREDICTED: IgGFc-binding protein [Myotis davidii]	45.6	45.6	85%	5e-04	88%	gi|584088170|XP_006763740.1
☐	RGD1311906 protein [Rattus norvegicus]	45.2	45.2	85%	7e-04	88%	gi|71681025|AAH99756.1
☐	PREDICTED: IgGFc-binding protein [Fukomys damarensis]	45.2	45.2	85%	7e-04	88%	gi|731289476|XP_010612839.1
☐	Fc fragment of IgG binding protein-like precursor [Rattus norvegicus	45.2	45.2	85%	7e-04	88%	gi|257467627|NP_001158128.1
☐	IgGFc-binding protein [Fukomys damarensis]	45.2	45.2	85%	7e-04	88%	gi|676261951|KFO19029.1
☐	PREDICTED: IgGFc-binding protein [Octodon degus]	45.2	45.2	85%	7e-04	88%	gi|507714064|XP_004648069.1
☐	PREDICTED: IgGFc-binding protein-like [Nannospalax galili]	44.8	44.8	90%	0.001	83%	gi|674088663|XP_008852264.1
☐	PREDICTED: IgGFc-binding protein-like [Peromyscus maniculatus	44.3	44.3	90%	0.001	83%	gi|589968055|XP_006996525.1
☐	PREDICTED: IgGFc-binding protein [Pteropus alecto]	44.3	44.3	80%	0.001	88%	gi|586524140|XP_006905494.1
☐	IgGFc-binding protein [Pteropus alecto]	44.3	44.3	80%	0.001	88%	gi|431920170|ELK18209.1
☐	PREDICTED: IgGFc-binding protein-like [Ailuropoda melanoleuca]	43.9	43.9	95%	0.002	79%	gi|301776693|XP_002923768.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG bindin	43.9	43.9	95%	0.002	79%	gi|585183803|XP_006752469.1
☐	PREDICTED: IgGFc-binding protein [Orycteropus afer afer]	42.6	42.6	95%	0.004	79%	gi|634854573|XP_007941342.1
☐	PREDICTED: IgGFc-binding protein [Cavia porcellus]	42.6	42.6	80%	0.004	88%	gi|348552434|XP_003462033.1
☐	PREDICTED: IgGFc-binding protein [Galeopterus variegatus]	42.2	42.2	85%	0.006	82%	gi|667245485|XP_008580791.1
☐	PREDICTED: IgGFc-binding protein [Tupaia chinensis]	41.8	41.8	100%	0.008	75%	gi|562821062|XP_006140449.1
☐	IgGFc-binding protein [Tupaia chinensis]	41.8	41.8	100%	0.008	75%	gi|444732094|ELW72413.1

☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Lo	41.4	41.4	90%	0.011	78%	gi|731510651|XP_010598700.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG bindin	41.4	41.4	95%	0.011	74%	gi|472353763|XP_004417817.1
☐	PREDICTED: IgGFc-binding protein [Otolemur garnettii]	41.4	41.4	90%	0.011	83%	gi|395859762|XP_003802201.1
☐	IgGFc-binding protein [Cricetulus griseus]	40.9	40.9	90%	0.013	78%	gi|537107439|ERE59847.1
☐	PREDICTED: IgGFc-binding protein [Mesocricetus auratus]	40.9	40.9	90%	0.016	78%	gi|524973628|XP_005086657.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein-like	40.9	40.9	90%	0.016	78%	gi|625249858|XP_007616229.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Chinchilla lanigera]	40.9	40.9	90%	0.016	83%	gi|533203235|XP_005414139.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein-like	40.9	40.9	90%	0.016	78%	gi|625205140|XP_007643925.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Chinchilla lanigera]	40.9	40.9	90%	0.016	83%	gi|533203233|XP_005414138.1
☐	PREDICTED: IgGFc-binding protein [Elephantulus edwardii]	40.9	40.9	85%	0.016	82%	gi|585714650|XP_006901006.1
☐	PREDICTED: IgGFc-binding protein [Ochotona princeps]	39.7	39.7	85%	0.040	76%	gi|504182881|XP_004599764.1
☐	Fc fragment of IgG binding protein [Camelus ferus]	39.7	39.7	85%	0.040	76%	gi|528766318|EPY85977.1
☐	PREDICTED: IgGFc-binding protein [Vicugna pacos]	39.7	39.7	85%	0.040	76%	gi|560985920|XP_006215157.1
☐	PREDICTED: IgGFc-binding protein [Camelus ferus]	39.7	39.7	85%	0.040	76%	gi|560903281|XP_006178015.1
☐	PREDICTED: IgGFc-binding protein [Microtus ochrogaster]	38.8	38.8	85%	0.074	76%	gi|532057309|XP_005371357.1
☐	PREDICTED: IgGFc-binding protein [Erinaceus europaeus]	38.8	58.5	90%	0.074	72%	gi|617664909|XP_007538724.1
☐	IgGFc-binding protein [Cricetulus griseus]	38.4	38.4	85%	0.089	76%	gi|537109414|ERE60529.1
☐	PREDICTED: IgGFc-binding protein-like isoform X2 [Cricetulus gris	38.4	38.4	85%	0.10	76%	gi|625249856|XP_007616228.1
☐	PREDICTED: IgGFc-binding protein-like isoform X1 [Cricetulus gris	38.4	38.4	85%	0.10	76%	gi|625205138|XP_003505295.2
☐	Fc fragment of IgG binding protein-like precursor [Mus musculus]	38.4	38.4	85%	0.10	76%	gi|257467625|NP_001158127.1
☐	PREDICTED: IgGFc-binding protein [Panthera tigris altaica]	38.4	38.4	90%	0.10	78%	gi|591322392|XP_007087304.1
☐	PREDICTED: IgGFc-binding protein [Oryctolagus cuniculus]	38.0	38.0	75%	0.14	80%	gi|655895144|XP_008249744.1
☐	PREDICTED: IgGFc-binding protein [Ictidomys tridecemlineatus]	38.0	38.0	85%	0.14	76%	gi|532101857|XP_005336544.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [My	37.1	37.1	85%	0.26	76%	gi|554548727|XP_005868902.1
☐	PREDICTED: IgGFc-binding protein [Echinops telfairi]	37.1	37.1	90%	0.26	72%	gi|507680836|XP_004710550.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG bindin	37.1	37.1	85%	0.26	76%	gi|558160938|XP_006109819.1
☐	IgGFc-binding protein [Myotis brandtii]	37.1	37.1	85%	0.26	76%	gi|521027545|EPQ09333.1

Alignments

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IgG Fc binding protein [AA 4671-5405] [Homo sapiens]

Sequence ID: gi|4321127|gb|AAD15624.1| **Length:** 735 **Number of Matches:** 1

Range 1: 562 to 581 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.4 bits(142)	5e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    RGLCVLSVGANLTTFDGARG  20
            RGLCVLSVGANLTTFDGARG
Sbjct  562  RGLCVLSVGANLTTFDGARG  581
```

Related Information

Gene - associated gene details

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Fc fragment of IgG binding protein [Homo sapiens]

Sequence ID: gi|119577330|gb|EAW56926.1| **Length:** 3004 **Number of Matches:** 1

Range 1: 2831 to 2850 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.4 bits(142)	5e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1     RGLCVLSVGANLTTFDGARG  20
```

Related Information

Gene - associated gene details

```
                 RGLCVLSVGANLTTFDGARG
Sbjct  2831  RGLCVLSVGANLTTFDGARG  2850
```

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PREDICTED: igGFc-binding protein-like [Macaca mulatta]

Sequence ID: gi|297277050|ref|XP_001088892.2| **Length:** 3029 **Number of Matches:** 1

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Range 1: 2856 to 2875 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.4 bits(142)	5e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1     RGLCVLSVGANLTTFDGARG  20
             RGLCVLSVGANLTTFDGARG
Sbjct  2856  RGLCVLSVGANLTTFDGARG  2875
```

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PREDICTED: IgGFc-binding protein [Chlorocebus sabaeus]

Sequence ID: gi|635042256|ref|XP_007996683.1| **Length:** 3043 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 2870 to 2889 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.4 bits(142)	5e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1     RGLCVLSVGANLTTFDGARG  20
             RGLCVLSVGANLTTFDGARG
Sbjct  2870  RGLCVLSVGANLTTFDGARG  2889
```

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PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pan paniscus]

Sequence ID: gi|675718714|ref|XP_008963216.1| **Length:** 3331 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 3158 to 3177 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.4 bits(142)	5e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1     RGLCVLSVGANLTTFDGARG  20
             RGLCVLSVGANLTTFDGARG
Sbjct  3158  RGLCVLSVGANLTTFDGARG  3177
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVDVH16B01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   Formatting options   Download   How to read this page   Blast report description

FCGBP_RLLISSLSESPASVSILSQADDTSKK_Mod

RID	BVDVH16B01R (Expires on 01-21 09:03 am)		
Query ID	lcl|308726	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	26	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

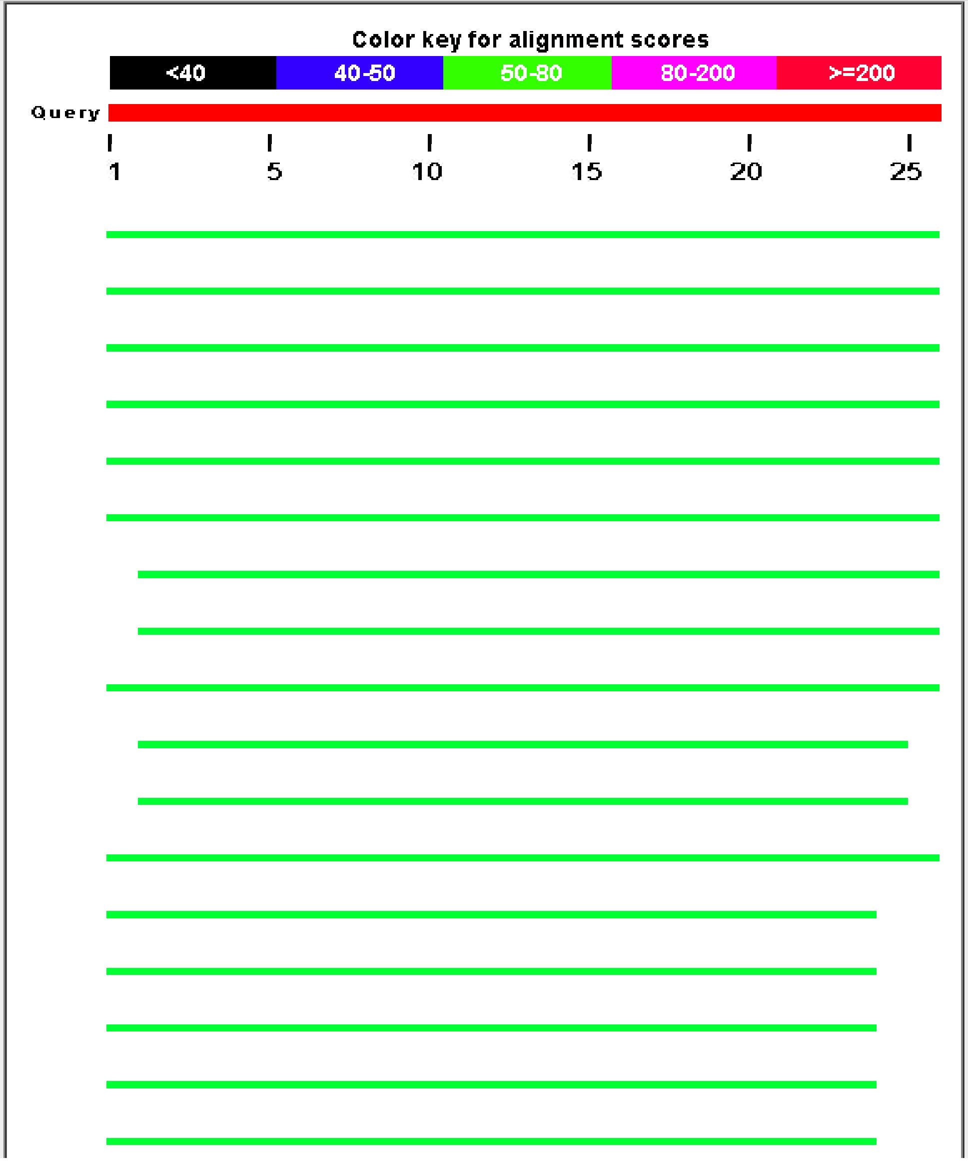
Graphic Summary

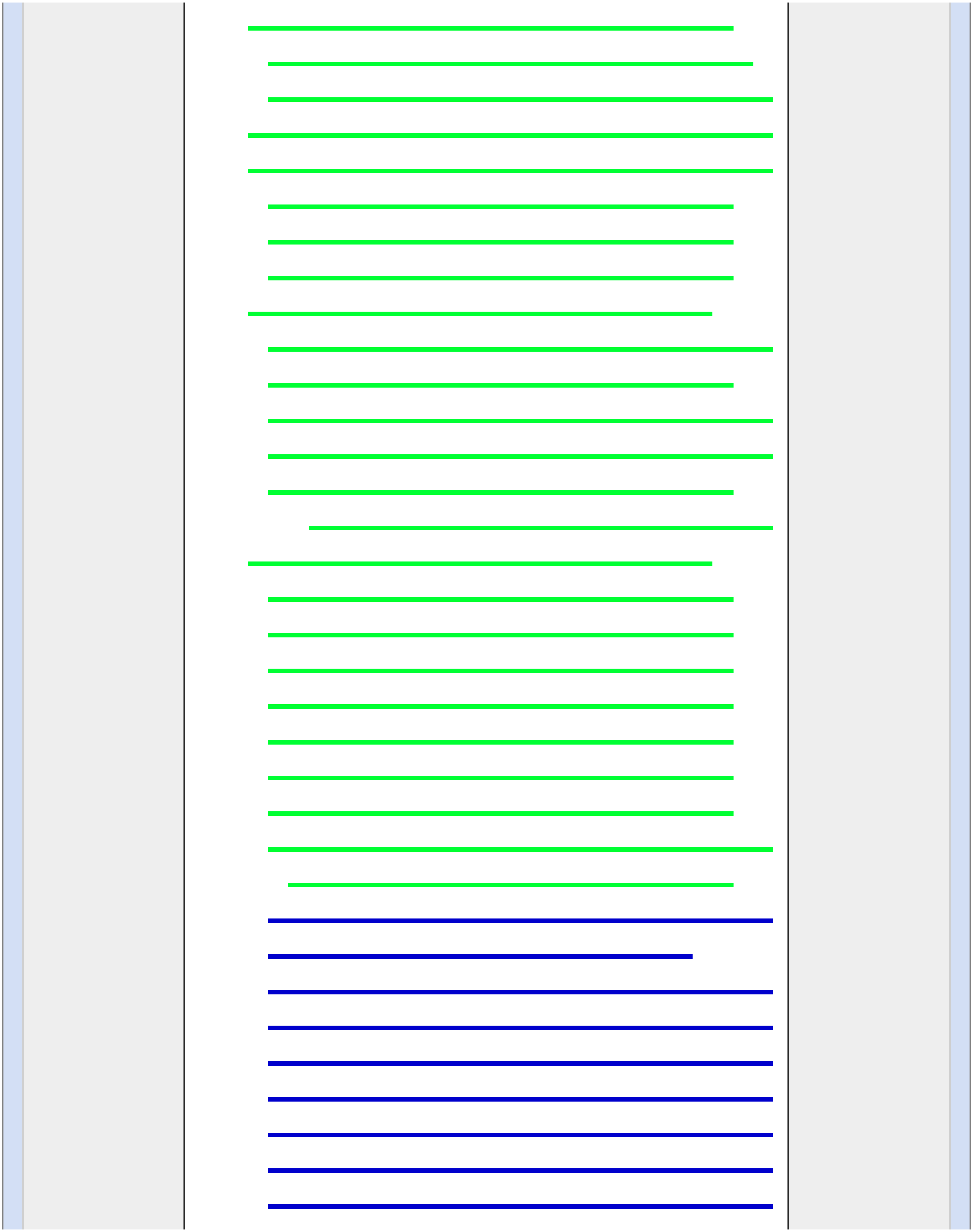
Show Conserved Domains

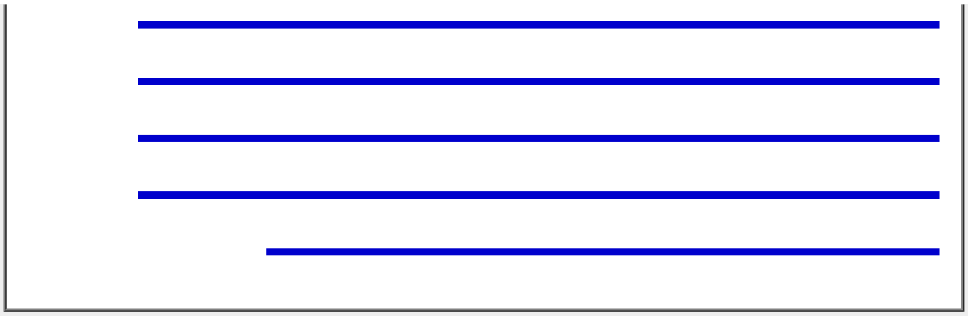
No putative conserved domains have been detected

Distribution of 105 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Fc gamma BP [Homo sapiens]	77.0	77.0	100%	3e-14	96%	AAD39266.1
☐	Fc fragment of IgG binding protein [Homo sapiens]	77.0	77.0	100%	3e-14	96%	EAW56926.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pan paniscus	77.0	77.0	100%	3e-14	96%	XP_008963216.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pan troglody	77.0	77.0	100%	3e-14	96%	XP_009433882.1
☐	IgG Fc binding protein [Homo sapiens]	77.0	77.0	100%	3e-14	96%	BAA19526.1
☐	IgGFc-binding protein precursor [Homo sapiens]	77.0	77.0	100%	3e-14	96%	NP_003881.2
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pongo abelii]	73.6	73.6	96%	4e-13	96%	XP_009230865.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Gorilla gorilla	73.6	73.6	96%	4e-13	96%	XP_004060816.1
☐	PREDICTED: IgGFc-binding protein [Chrysochloris asiatica]	67.7	67.7	100%	5e-11	85%	XP_006871587.1
☐	PREDICTED: IgGFc-binding protein [Cavia porcellus]	67.2	67.2	92%	6e-11	96%	XP_003462033.1
☐	PREDICTED: IgGFc-binding protein [Nomascus leucogenys]	66.4	66.4	92%	1e-10	92%	XP_003270573.1
☐	PREDICTED: IgGFc-binding protein [Tarsius syrichta]	66.0	66.0	100%	2e-10	88%	XP_008052981.1
☐	hypothetical protein EGM_09727 [Macaca fascicularis]	63.4	63.4	92%	1e-09	92%	EHH59582.1
☐	hypothetical protein EGK_10612 [Macaca mulatta]	63.4	63.4	92%	1e-09	92%	EHH30036.1
☐	PREDICTED: igGFc-binding protein-like [Macaca mulatta]	63.4	63.4	92%	1e-09	92%	XP_001088892.2
☐	PREDICTED: IgGFc-binding protein [Chlorocebus sabaeus]	63.4	63.4	92%	1e-09	92%	XP_007996683.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Papio anubis	63.4	63.4	92%	1e-09	92%	XP_003915593.1
☐	PREDICTED: IgGFc-binding protein [Macaca fascicularis]	63.4	63.4	92%	1e-09	92%	XP_005590715.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Rhinopithecu	63.0	63.0	92%	2e-09	92%	XP_010379186.1
☐	IgGFc-binding protein [Fukomys damarensis]	61.7	61.7	96%	4e-09	88%	KFO19029.1
☐	IgGFc-binding protein [Cricetulus griseus]	60.4	60.4	100%	1e-08	81%	EGW06398.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein-like isoform X	60.4	60.4	100%	1e-08	81%	XP_007643925.1
☐	PREDICTED: IgGFc-binding protein [Saimiri boliviensis boliviensis]	59.6	59.6	88%	2e-08	87%	XP_010329397.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Callithrix jacc	59.6	59.6	88%	2e-08	87%	XP_008986248.1
☐	PREDICTED: IgGFc-binding protein [Ceratotherium simum simum]	58.7	58.7	88%	4e-08	87%	XP_004441659.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Loxodonta af	58.7	58.7	88%	4e-08	83%	XP_010598700.1
☐	PREDICTED: IgGFc-binding protein [Felis catus]	58.3	58.3	96%	6e-08	80%	XP_006941331.1
☐	PREDICTED: IgGFc-binding protein [Panthera tigris altaica]	56.6	56.6	88%	2e-07	83%	XP_007087304.1
☐	PREDICTED: IgGFc-binding protein [Echinops telfairi]	56.6	56.6	96%	2e-07	76%	XP_004710550.1

☐	PREDICTED: IgGFc-binding protein [Elephantulus edwardii]	55.8	55.8	96%	4e-07	76%	XP_006901006.1
☐	IgGFc-binding protein [Myotis davidii]	55.4	55.4	88%	6e-07	78%	ELK30312.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Chinchilla lanigera]	54.9	54.9	88%	8e-07	83%	XP_005414138.1
☐	IgGFc-binding protein [Tupaia chinensis]	54.9	54.9	88%	8e-07	83%	ELW72413.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Equus caball	53.7	53.7	88%	2e-06	83%	XP_005596726.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Myotis brand	53.7	53.7	88%	2e-06	78%	XP_005868902.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG binding protein [I	53.7	53.7	88%	2e-06	78%	XP_006109819.1
☐	IgGFc-binding protein [Myotis brandtii]	53.7	53.7	88%	2e-06	78%	EPQ09333.1
☐	PREDICTED: IgGFc-binding protein [Pteropus alecto]	53.2	53.2	88%	3e-06	78%	XP_006905494.1
☐	IgGFc-binding protein [Pteropus alecto]	53.2	53.2	88%	3e-06	78%	ELK18209.1
☐	PREDICTED: IgGFc-binding protein [Galeopterus variegatus]	52.0	52.0	88%	7e-06	83%	XP_008580791.1
☐	PREDICTED: IgGFc-binding protein [Otolemur garnettii]	52.0	52.0	96%	7e-06	80%	XP_003802201.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Eptesicus fus	50.7	50.7	84%	2e-05	78%	XP_008138255.1
☐	PREDICTED: IgGFc-binding protein [Condylura cristata]	49.8	49.8	96%	4e-05	72%	XP_004693946.1
☐	PREDICTED: IgGFc-binding protein [Orycteropus afer afer]	49.8	49.8	80%	4e-05	76%	XP_007941342.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Capra hircus	49.0	49.0	96%	7e-05	72%	XP_005692605.1
☐	IgGFc-binding protein [Heterocephalus glaber]	48.1	48.1	96%	1e-04	76%	EHA99105.1
☐	PREDICTED: IgGFc-binding protein [Lipotes vexillifer]	48.1	48.1	96%	1e-04	72%	XP_007458763.1
☐	PREDICTED: IgGFc-binding protein [Octodon degus]	48.1	48.1	96%	1e-04	76%	XP_004648069.1
☐	PREDICTED: IgGFc-binding protein [Erinaceus europaeus]	48.1	92.9	96%	1e-04	64%	XP_007538724.1
☐	PREDICTED: IgGFc-binding protein [Orcinus orca]	45.6	45.6	96%	8e-04	68%	XP_004271425.1
☐	Fc fragment of IgG binding protein-like protein [Camelus ferus]	45.2	45.2	96%	0.001	64%	EPY85976.1
☐	PREDICTED: IgGFc-binding protein [Camelus dromedarius]	45.2	65.8	96%	0.001	64%	XP_010983489.1
☐	PREDICTED: IgGFc-binding protein [Camelus bactrianus]	45.2	65.8	96%	0.001	64%	XP_010945545.1
☐	PREDICTED: IgGFc-binding protein [Vicugna pacos]	45.2	65.8	96%	0.001	64%	XP_006215157.1
☐	PREDICTED: IgGFc-binding protein [Camelus ferus]	45.2	65.8	96%	0.001	64%	XP_006178015.1
☐	PREDICTED: IgGFc-binding protein [Mesocricetus auratus]	44.8	44.8	80%	0.001	76%	XP_005086657.1
☐	PREDICTED: IgGFc-binding protein [Bison bison bison]	44.8	44.8	96%	0.001	68%	XP_010847529.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bubalus bubalis]	44.8	44.8	96%	0.001	68%	XP_006050098.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bos taurus]	44.8	44.8	96%	0.001	68%	XP_010813251.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bos taurus]	44.8	44.8	96%	0.001	68%	XP_010798218.1
☐	PREDICTED: IgGFc-binding protein [Pantholops hodgsonii]	44.8	44.8	96%	0.001	68%	XP_005963590.1
☐	TPA: Fc fragment of IgG binding protein-like [Bos taurus]	44.8	44.8	96%	0.001	68%	DAA19876.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ovis aries]	44.8	44.8	96%	0.001	68%	XP_004015739.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Bos mutus]	44.8	44.8	96%	0.001	68%	XP_005890645.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Balaenoptera acutorostrata s	43.9	43.9	96%	0.003	68%	XP_007180031.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Balaenoptera acutorostrata s	43.9	43.9	96%	0.003	68%	XP_007180030.1
☐	PREDICTED: IgGFc-binding protein [Physeter catodon]	42.2	42.2	88%	0.009	70%	XP_007122066.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG binding protein [(	40.5	40.5	84%	0.032	68%	XP_004417817.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG binding protein [I	40.5	40.5	84%	0.032	68%	XP_006752469.1
☐	PREDICTED: IgGFc-binding protein [Ictidomys tridecemlineatus]	40.1	40.1	84%	0.043	68%	XP_005336544.1
☐	hypothetical protein PANDA_012964 [Ailuropoda melanoleuca]	39.7	39.7	84%	0.059	68%	EFB16331.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ursus maritin	39.7	39.7	84%	0.059	68%	XP_008686987.1
☐	PREDICTED: IgGFc-binding protein-like [Ailuropoda melanoleuca]	39.7	39.7	84%	0.059	68%	XP_002923768.1
☐	PAS sensor protein [Methanoplanus limicola]	37.5	37.5	73%	0.27	68%	WP_004076509.1

☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Canis lupus f	37.5	37.5	84%	0.28	64%	XP_005616636.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG binding protein [I	35.0	35.0	84%	1.9	64%	XP_004828450.1
☐	Phosphoserine phosphatase 1 [Candidatus Accumulibacter sp. BA-94]	34.1	34.1	65%	3.4	48%	EXI80297.1
☐	Polyketide synthase, enoylreductase [Penicillium expansum]	32.9	32.9	88%	9.5	40%	KGO47706.1
☐	Importin 13, putative [Penicillium digitatum Pd1]	32.9	32.9	80%	9.5	52%	EKV12548.1
☐	RNA pseudouridine synthase superfamily protein [Toxoplasma gondii RUB]	32.9	32.9	76%	9.6	71%	KFG65999.1
☐	RNA pseudouridine synthase superfamily protein [Toxoplasma gondii GT1]	32.9	32.9	76%	9.6	71%	EPR61036.1
☐	RNA pseudouridine synthase superfamily protein [Toxoplasma gondii ME49]	32.9	32.9	76%	9.6	71%	EPT26018.1
☐	RNA pseudouridine synthase superfamily protein [Toxoplasma gondii VAND]	32.9	32.9	76%	9.6	71%	KFH09647.1
☐	PREDICTED: uncharacterized protein LOC104904663 [Beta vulgaris subsp. v	32.5	32.5	76%	13	60%	XP_010691296.1
☐	PTS mannose transporter subunit IIABC [Corynebacterium lubricantis]	32.5	32.5	57%	13	73%	WP_026196293.1
☐	hypothetical protein PDE_00389 [Penicillium oxalicum 114-2]	32.5	32.5	80%	13	62%	EPS25456.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	18	65%	WP_012775806.1
☐	oxidoreductase [Mycobacterium tuberculosis OFXR-6]	32.0	32.0	65%	18	65%	KBJ45988.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	18	65%	WP_010924322.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	18	65%	WP_031674284.1
☐	monooxygenase [Mycobacterium tuberculosis]	32.0	32.0	65%	18	65%	WP_015629755.1
☐	hypothetical protein [Mycobacterium africanum]	32.0	32.0	65%	18	65%	WP_003910233.1
☐	MULTISPECIES: hypothetical protein [Mycobacterium tuberculosis complex]	32.0	32.0	65%	18	65%	WP_003898656.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	18	65%	WP_031652242.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	18	65%	WP_031744179.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	18	65%	WP_031745224.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	18	65%	WP_023641889.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	18	65%	WP_023641782.1
☐	monooxygenase [Mycobacterium tuberculosis]	32.0	32.0	65%	18	65%	WP_015456187.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	18	65%	WP_003912992.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Fc gamma BP, partial [Homo sapiens]

Sequence ID: gb|AAD39266.1|AC007842_1 **Length:** 2843 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 54 to 79 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.0 bits(174)	3e-14	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1   RLLISSLSESPASVSILSQADDTSKK  26
           RLLISSLSESPASVSILSQAD+TSKK
Sbjct  54  RLLISSLSESPASVSILSQADNTSKK  79
```

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Fc fragment of IgG binding protein [Homo sapiens]

Sequence ID: gb|EAW56926.1| **Length:** 3004 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 54 to 79 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.0 bits(174)	3e-14	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1   RLLISSLSESPASVSILSQADDTSKK  26
           RLLISSLSESPASVSILSQAD+TSKK
Sbjct  54  RLLISSLSESPASVSILSQADNTSKK  79
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pan paniscus]

Sequence ID: ref|XP_008963216.1| **Length:** 3331 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 54 to 79 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.0 bits(174)	3e-14	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1   RLLISSLSESPASVSILSQADDTSKK  26
           RLLISSLSESPASVSILSQAD+TSKK
Sbjct  54  RLLISSLSESPASVSILSQADNTSKK  79
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pan troglodytes]

Sequence ID: ref|XP_009433882.1| **Length:** 5257 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 54 to 79 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.0 bits(174)	3e-14	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1   RLLISSLSESPASVSILSQADDTSKK  26
           RLLISSLSESPASVSILSQAD+TSKK
Sbjct  54  RLLISSLSESPASVSILSQADNTSKK  79
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

IgG Fc binding protein [Homo sapiens]

Sequence ID: dbj|BAA19526.1| **Length:** 5405 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 54 to 79 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
77.0 bits(174)	3e-14	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1   RLLISSLSESPASVSILSQADDTSKK  26
           RLLISSLSESPASVSILSQAD+TSKK
Sbjct  54  RLLISSLSESPASVSILSQADNTSKK  79
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download

How to read this page Blast report description

FCGBP_RLLISSLSESPASVSILSQADNTSKK_NonMod

RID	B9E2X3N901R (Expires on 01-14 13:17 pm)
Query ID	lcl|203729
Description	None
Molecule type	amino acid
Query Length	26
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

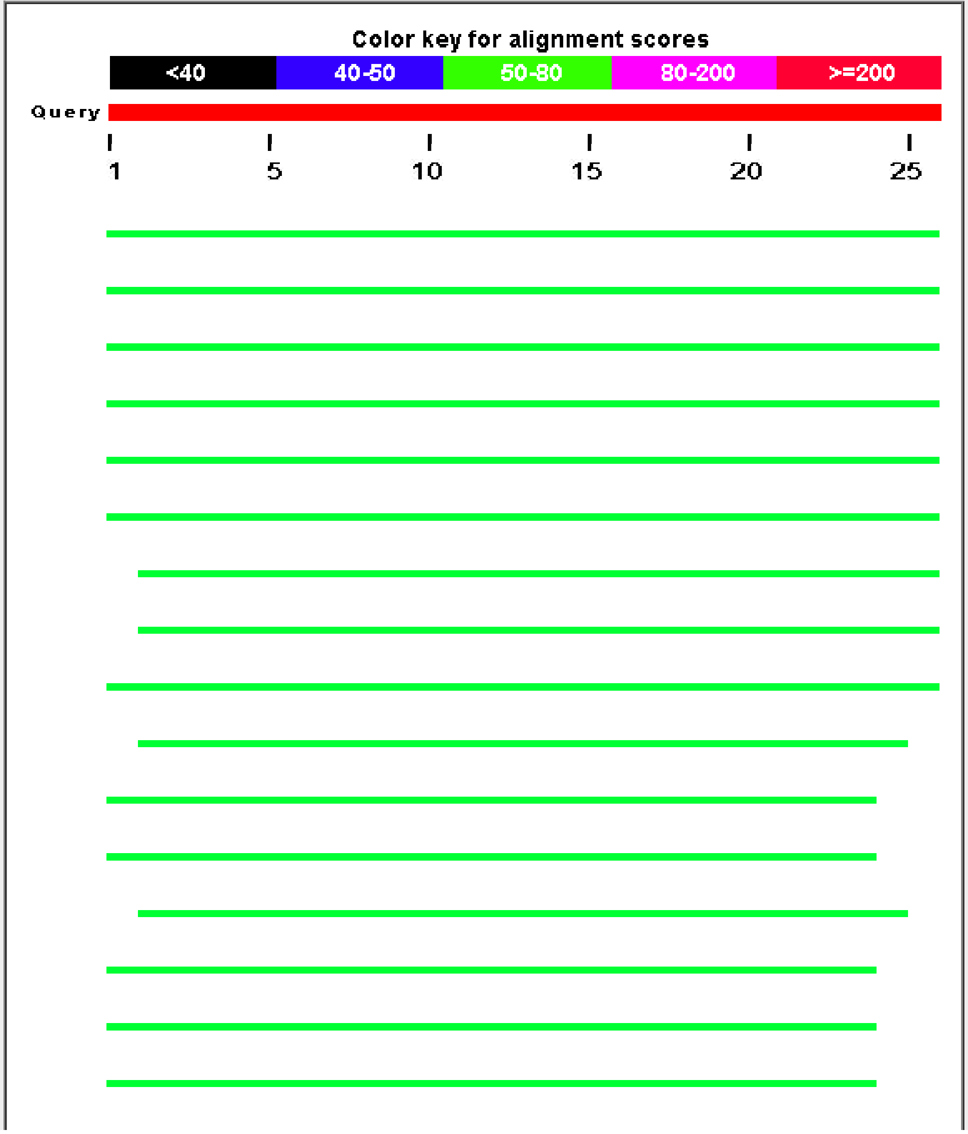
⊟Graphic Summary

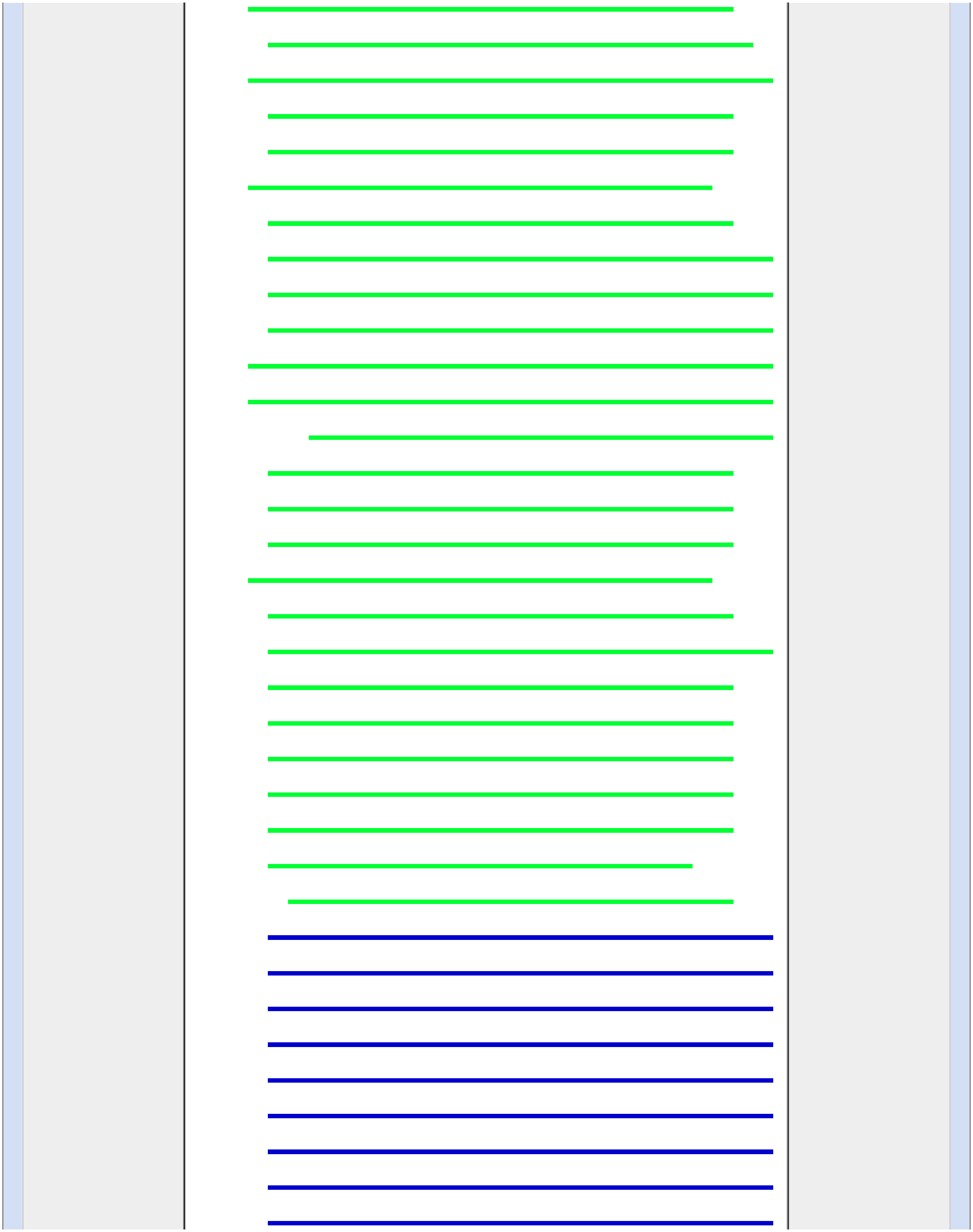
⊟Show Conserved Domains

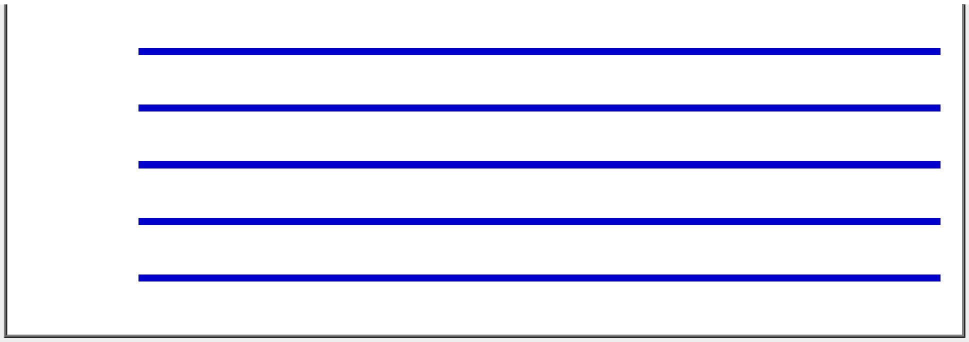
No putative conserved domains have been detected

Distribution of 103 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Fc gamma BP [Homo sapiens]	79.5	79.5	100%	4e-15	100%	gi|5080756|AAD39266.1
☐	Fc fragment of IgG binding protein [Homo sapiens]	79.5	79.5	100%	4e-15	100%	gi|119577330|EAW56926.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pa	79.5	79.5	100%	4e-15	100%	gi|675718714|XP_008963216.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pa	79.5	79.5	100%	4e-15	100%	gi|694975150|XP_009433882.1
☐	IgG Fc binding protein [Homo sapiens]	79.5	79.5	100%	4e-15	100%	gi|1944352|BAA19526.1
☐	IgGFc-binding protein precursor [Homo sapiens]	79.5	79.5	100%	4e-15	100%	gi|154146262|NP_003881.2
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Po	76.1	76.1	96%	6e-14	100%	gi|686758917|XP_009230865.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Go	76.1	76.1	96%	6e-14	100%	gi|426388791|XP_004060816.1
☐	PREDICTED: IgGFc-binding protein [Chrysochloris asiatica]	70.2	70.2	100%	6e-12	88%	gi|586482145|XP_006871587.1
☐	PREDICTED: IgGFc-binding protein [Nomascus leucogenys]	68.9	68.9	92%	2e-11	96%	gi|332242810|XP_003270573.1
☐	hypothetical protein EGM_09727 [Macaca fascicularis]	64.7	64.7	92%	4e-10	92%	gi|355755835|EHH59582.1
☐	hypothetical protein EGK_10612 [Macaca mulatta]	64.7	64.7	92%	4e-10	92%	gi|355703545|EHH30036.1
☐	PREDICTED: IgGFc-binding protein [Cavia porcellus]	64.7	64.7	92%	4e-10	92%	gi|348552434|XP_003462033.1
☐	PREDICTED: igGFc-binding protein-like [Macaca mulatta]	64.7	64.7	92%	4e-10	92%	gi|297277050|XP_001088892.2
☐	PREDICTED: IgGFc-binding protein [Chlorocebus sabaeus]	64.7	64.7	92%	4e-10	92%	gi|635042256|XP_007996683.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pa	64.7	64.7	92%	4e-10	92%	gi|402905577|XP_003915593.1
☐	PREDICTED: IgGFc-binding protein [Macaca fascicularis]	64.7	64.7	92%	4e-10	92%	gi|544514342|XP_005590715.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Rh	64.3	64.3	92%	6e-10	92%	gi|724909919|XP_010379186.1
☐	PREDICTED: IgGFc-binding protein [Tarsius syrichta]	63.4	63.4	100%	1e-09	85%	gi|640776875|XP_008052981.1
☐	PREDICTED: IgGFc-binding protein [Saimiri boliviensis boliviensis]	62.1	62.1	88%	3e-09	91%	gi|725605545|XP_010329397.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ca	62.1	62.1	88%	3e-09	91%	gi|675761213|XP_008986248.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Lo:	61.3	61.3	88%	6e-09	87%	gi|731510651|XP_010598700.1
☐	PREDICTED: IgGFc-binding protein [Ceratotherium simum simum]	60.4	60.4	88%	1e-08	87%	gi|478535060|XP_004441659.1
☐	PREDICTED: IgGFc-binding protein [Echinops telfairi]	59.2	59.2	96%	3e-08	80%	gi|507680836|XP_004710550.1
☐	IgGFc-binding protein [Fukomys damarensis]	59.2	59.2	96%	3e-08	84%	gi|676261951|KFO19029.1
☐	PREDICTED: IgGFc-binding protein [Felis catus]	58.3	58.3	96%	6e-08	80%	gi|587014135|XP_006941331.1
☐	IgGFc-binding protein [Cricetulus griseus]	57.9	57.9	100%	7e-08	77%	gi|344250294|EGW06398.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein-like	57.9	57.9	100%	8e-08	77%	gi|625205140|XP_007643925.1
☐							

	PREDICTED: IgGFc-binding protein isoform X1 [Chinchilla lanigera]	57.5	57.5	88%	1e-07	87%	gi|533203233|XP_005414138.1
☐	PREDICTED: IgGFc-binding protein [Panthera tigris altaica]	56.6	56.6	88%	2e-07	83%	gi|591322392|XP_007087304.1
☐	IgGFc-binding protein [Myotis davidii]	55.4	55.4	88%	5e-07	78%	gi|432102845|ELK30312.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Eq	55.4	55.4	88%	5e-07	83%	gi|545176771|XP_005596726.1
☐	IgGFc-binding protein [Tupaia chinensis]	54.9	54.9	88%	7e-07	83%	gi|444732094|ELW72413.1
☐	PREDICTED: IgGFc-binding protein [Galeopterus variegatus]	54.5	54.5	88%	1e-06	87%	gi|667245485|XP_008580791.1
☐	PREDICTED: IgGFc-binding protein [Elephantulus edwardii]	54.1	54.1	96%	1e-06	76%	gi|585714650|XP_006901006.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [My	53.7	53.7	88%	2e-06	78%	gi|554548727|XP_005868902.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG bindin	53.7	53.7	88%	2e-06	78%	gi|558160938|XP_006109819.1
☐	IgGFc-binding protein [Myotis brandtii]	53.7	53.7	88%	2e-06	78%	gi|521027545|EPQ09333.1
☐	PREDICTED: IgGFc-binding protein [Pteropus alecto]	53.2	53.2	88%	3e-06	78%	gi|586524140|XP_006905494.1
☐	IgGFc-binding protein [Pteropus alecto]	53.2	53.2	88%	3e-06	78%	gi|431920170|ELK18209.1
☐	PREDICTED: IgGFc-binding protein [Orycteropus afer afer]	52.4	52.4	80%	5e-06	81%	gi|634854573|XP_007941342.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ep	50.7	50.7	84%	2e-05	78%	gi|641699510|XP_008138255.1
☐	PREDICTED: IgGFc-binding protein [Condylura cristata]	49.8	49.8	96%	3e-05	72%	gi|507980555|XP_004693946.1
☐	PREDICTED: IgGFc-binding protein [Otolemur garnettii]	49.4	49.4	96%	5e-05	76%	gi|395859762|XP_003802201.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ca	49.0	49.0	96%	6e-05	72%	gi|548504606|XP_005692605.1
☐	IgGFc-binding protein [Heterocephalus glaber]	48.1	48.1	96%	1e-04	76%	gi|351696187|EHA99105.1
☐	PREDICTED: IgGFc-binding protein [Lipotes vexillifer]	48.1	48.1	96%	1e-04	72%	gi|602693350|XP_007458763.1
☐	PREDICTED: IgGFc-binding protein [Orcinus orca]	45.6	45.6	96%	7e-04	68%	gi|466016931|XP_004271425.1
☐	PREDICTED: IgGFc-binding protein [Octodon degus]	45.6	45.6	96%	8e-04	72%	gi|507714064|XP_004648069.1
☐	PREDICTED: IgGFc-binding protein [Erinaceus europaeus]	45.6	87.8	96%	8e-04	60%	gi|617664909|XP_007538724.1
☐	Fc fragment of IgG binding protein-like protein [Camelus ferus]	45.2	45.2	96%	0.001	64%	gi|528766317|EPY85976.1
☐	PREDICTED: IgGFc-binding protein [Vicugna pacos]	45.2	65.8	96%	0.001	64%	gi|560985920|XP_006215157.1
☐	PREDICTED: IgGFc-binding protein [Camelus ferus]	45.2	65.8	96%	0.001	64%	gi|560903281|XP_006178015.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bubalus bubalis]	44.8	44.8	96%	0.001	68%	gi|594051530|XP_006050098.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Bos taurus]	44.8	44.8	96%	0.001	68%	gi|528991887|XP_005219168.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Bos taurus]	44.8	44.8	96%	0.001	68%	gi|528933614|XP_614095.6
☐	PREDICTED: IgGFc-binding protein [Pantholops hodgsonii]	44.8	44.8	96%	0.001	68%	gi|556735974|XP_005963590.1
☐	TPA: Fc fragment of IgG binding protein-like [Bos taurus]	44.8	44.8	96%	0.001	68%	gi|296477761|DAA19876.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ov	44.8	44.8	96%	0.001	68%	gi|426243806|XP_004015739.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Bo	44.8	44.8	96%	0.001	68%	gi|555957014|XP_005890645.1
☐	PREDICTED: IgGFc-binding protein [Mesocricetus auratus]	44.3	44.3	80%	0.002	76%	gi|524973628|XP_005086657.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Balaenoptera acut	43.9	43.9	96%	0.003	68%	gi|594663750|XP_007180031.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Balaenoptera acut	43.9	43.9	96%	0.003	68%	gi|594663748|XP_007180030.1
☐	PREDICTED: IgGFc-binding protein [Physeter catodon]	42.2	42.2	88%	0.009	70%	gi|593767123|XP_007122066.1
☐	PREDICTED: IgGFc-binding protein [Ictidomys tridecemlineatus]	41.4	41.4	84%	0.016	68%	gi|532101857|XP_005336544.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG bindin	40.5	40.5	84%	0.030	68%	gi|472353763|XP_004417817.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG bindin	40.5	40.5	84%	0.030	68%	gi|585183803|XP_006752469.1
☐	hypothetical protein PANDA_012964 [Ailuropoda melanoleuca]	39.7	39.7	84%	0.056	68%	gi|281340747|EFB16331.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Urs	39.7	39.7	84%	0.056	68%	gi|670991993|XP_008686987.1
☐	PREDICTED: IgGFc-binding protein-like [Ailuropoda melanoleuca]	39.7	39.7	84%	0.056	68%	gi|301776693|XP_002923768.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ca	37.5	37.5	84%	0.26	64%	gi|545488517|XP_005616636.1
☐	PAS sensor protein [Methanoplanus limicola]	36.7	36.7	69%	0.48	72%	gi|490177883|WP_004076509.1
☐	hypothetical protein PDE_00389 [Penicillium oxalicum 114-2]	35.0	35.0	80%	1.7	67%	gi|525579206|EPS25456.1

☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG bindin	35.0	35.0	84%	1.8	64%	gi|511913755|XP_004828450.1
☐	Phosphoserine phosphatase 1 [Candidatus Accumulibacter sp. BA-	34.1	34.1	65%	3.2	48%	gi|589608759|EXI80297.1
☐	hypothetical protein [Acinetobacter bereziniae]	34.1	34.1	88%	3.3	63%	gi|491171937|WP_005030304.1
☐	tape measure domain protein [Acinetobacter sp. WC-743]	34.1	34.1	88%	3.3	63%	gi|497269805|WP_009584022.1
☐	hypothetical protein Ecym_1439 [Eremothecium cymbalariae DBVP	33.7	33.7	46%	4.6	92%	gi|363748528|XP_003644482.1
☐	hypothetical protein CAPTEDRAFT_194148 [Capitella teleta]	32.9	32.9	88%	8.8	61%	gi|443689453|ELT91836.1
☐	PTS mannose transporter subunit IIABC [Corynebacterium lubrican	32.5	32.5	57%	12	73%	gi|648504542|WP_026196293.1
☐	RNA pseudouridine synthase superfamily protein [Toxoplasma gon	32.5	32.5	53%	13	86%	gi|672303151|KFG65999.1
☐	RNA pseudouridine synthase superfamily protein [Toxoplasma gon	32.5	32.5	53%	13	86%	gi|523574281|EPR61036.1
☐	RNA pseudouridine synthase superfamily protein [Toxoplasma gon	32.5	32.5	53%	13	86%	gi|527309382|EPT26018.1
☐	RNA pseudouridine synthase superfamily protein [Toxoplasma gon	32.5	32.5	53%	13	86%	gi|672570297|KFH09647.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	17	65%	gi|502378810|WP_012775806.1
☐	oxidoreductase [Mycobacterium tuberculosis OFXR-6]	32.0	32.0	65%	17	65%	gi|623377120|KBJ45988.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	17	65%	gi|499226782|WP_010924322.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	17	65%	gi|685948989|WP_031674284.1
☐	monooxygenase [Mycobacterium tuberculosis]	32.0	32.0	65%	17	65%	gi|505442653|WP_015629755.1
☐	hypothetical protein [Mycobacterium africanum]	32.0	32.0	65%	17	65%	gi|490007392|WP_003910233.1
☐	MULTISPECIES: hypothetical protein [Mycobacterium tuberculosis	32.0	32.0	65%	17	65%	gi|489995617|WP_003898656.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	17	65%	gi|685915310|WP_031652242.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	17	65%	gi|686073968|WP_031744179.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	17	65%	gi|686076415|WP_031745224.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	17	65%	gi|686031688|WP_031722692.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	17	65%	gi|685925501|WP_031660320.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	17	65%	gi|560884160|WP_023641889.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	17	65%	gi|560884051|WP_023641782.1
☐	monooxygenase [Mycobacterium tuberculosis]	32.0	32.0	65%	17	65%	gi|505269085|WP_015456187.1
☐	hypothetical protein [Mycobacterium tuberculosis]	32.0	32.0	65%	17	65%	gi|490010216|WP_003912992.1

⊟ Alignments

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Fc gamma BP, partial [Homo sapiens]

Sequence ID: gi|5080756|gb|AAD39266.1|AC007842_1 **Length:** 2843 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 54 to 79 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	4e-15	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    RLLISSLSESPASVSILSQADNTSKK  26
            RLLISSLSESPASVSILSQADNTSKK
Sbjct  54   RLLISSLSESPASVSILSQADNTSKK  79
```

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Fc fragment of IgG binding protein [Homo sapiens]

Sequence ID: gi|119577330|gb|EAW56926.1| **Length:** 3004 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 54 to 79 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	4e-15	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    RLLISSLSESPASVSILSQADNTSKK  26
```

```
               RLLISSLSESPASVSILSQADNTSKK
Sbjct  54  RLLISSLSESPASVSILSQADNTSKK  79
```

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PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pan paniscus]

Sequence ID: gi|675718714|ref|XP_008963216.1| **Length:** 3331 **Number of Matches:** 1

Range 1: 54 to 79 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	4e-15	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    RLLISSLSESPASVSILSQADNTSKK  26
            RLLISSLSESPASVSILSQADNTSKK
Sbjct  54   RLLISSLSESPASVSILSQADNTSKK  79
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pan troglodytes]

Sequence ID: gi|694975150|ref|XP_009433882.1| **Length:** 5257 **Number of Matches:** 1

Range 1: 54 to 79 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	4e-15	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    RLLISSLSESPASVSILSQADNTSKK  26
            RLLISSLSESPASVSILSQADNTSKK
Sbjct  54   RLLISSLSESPASVSILSQADNTSKK  79
```

Related Information

Gene - associated gene details

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IgG Fc binding protein [Homo sapiens]

Sequence ID: gi|1944352|dbj|BAA19526.1| **Length:** 5405 **Number of Matches:** 1

Range 1: 54 to 79 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	4e-15	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    RLLISSLSESPASVSILSQADNTSKK  26
            RLLISSLSESPASVSILSQADNTSKK
Sbjct  54   RLLISSLSESPASVSILSQADNTSKK  79
```

Related Information

Gene - associated gene details

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVDV1GJT01R

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FCGBP_RYLPVDSSLLTSDCSERC_Mod

RID BVDV1GJT01R (Expires on 01-21 09:03 am)

Query ID	lcl|300122	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	18		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

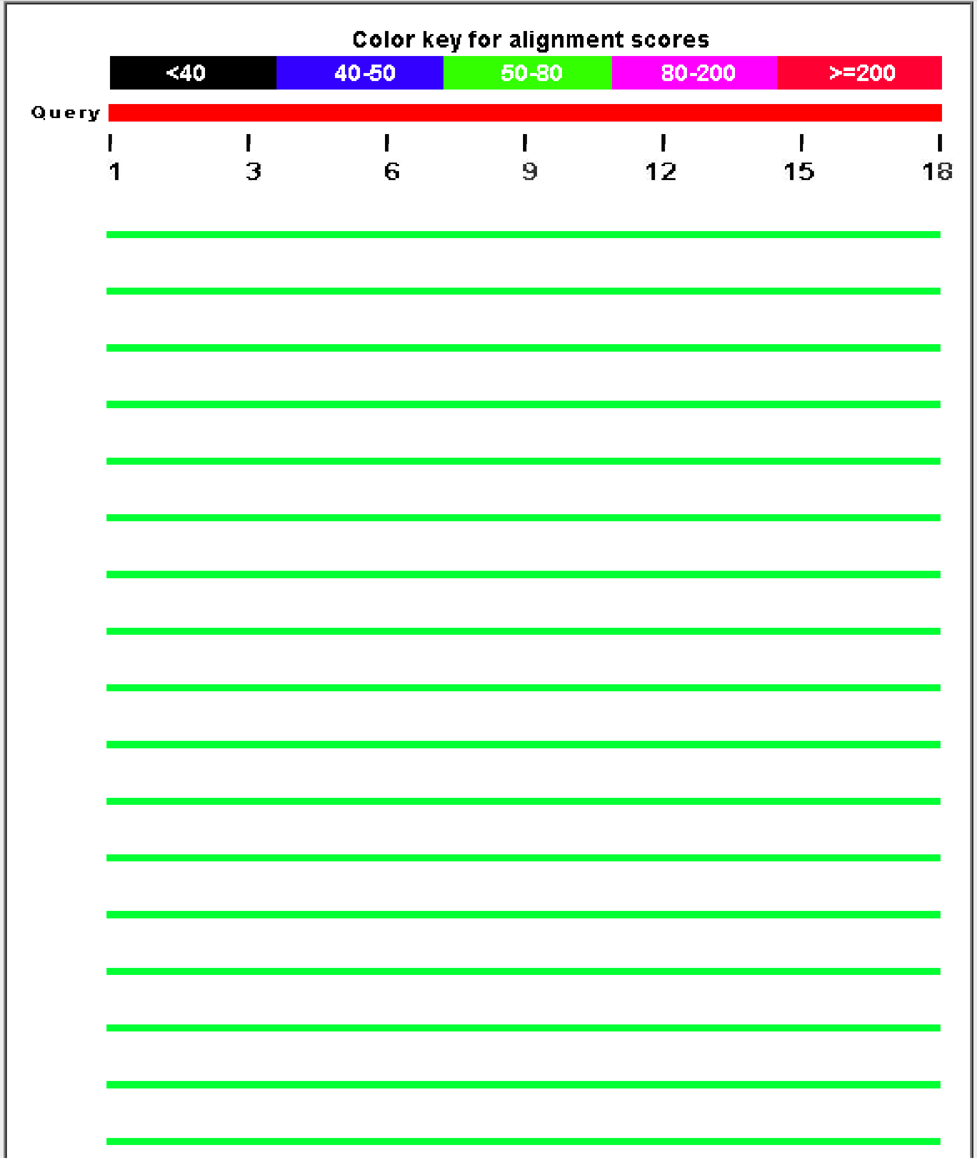
Graphic Summary

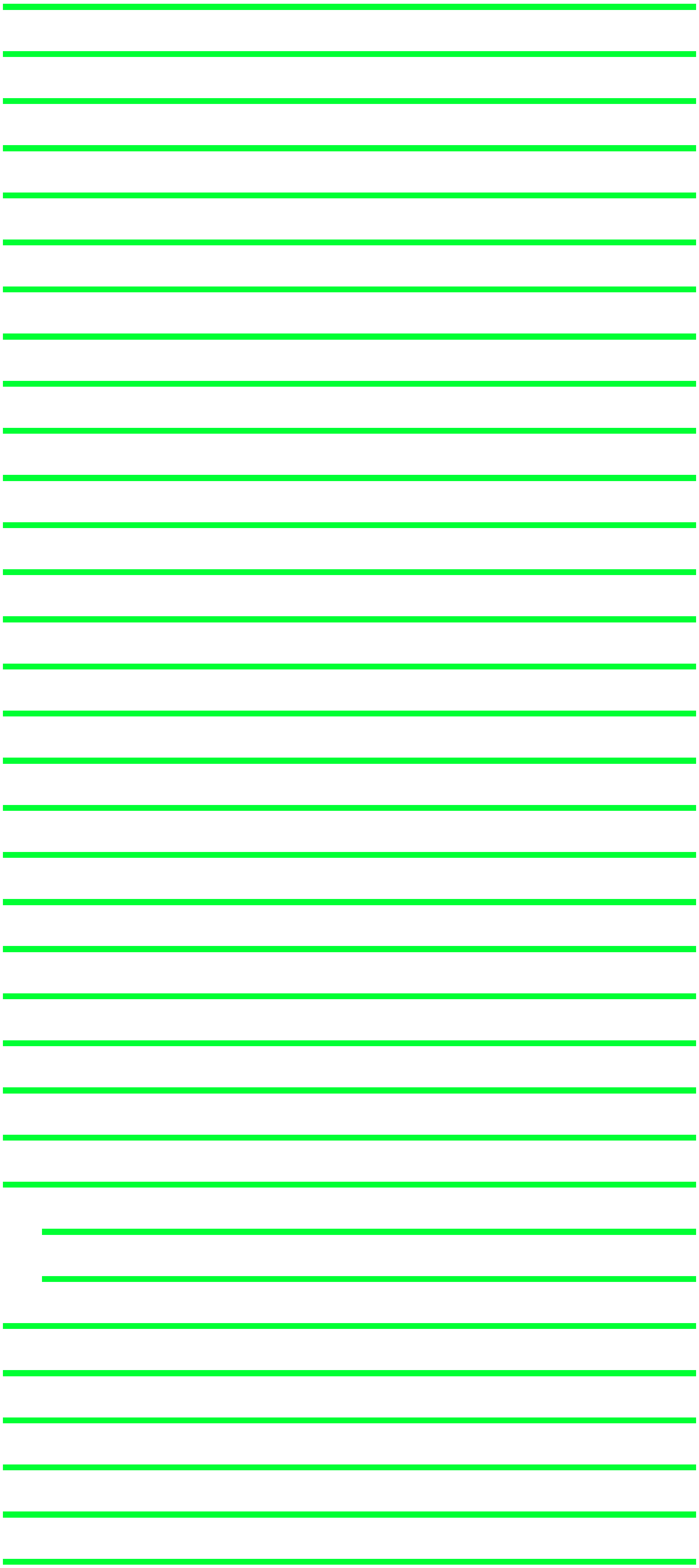
Show Conserved Domains

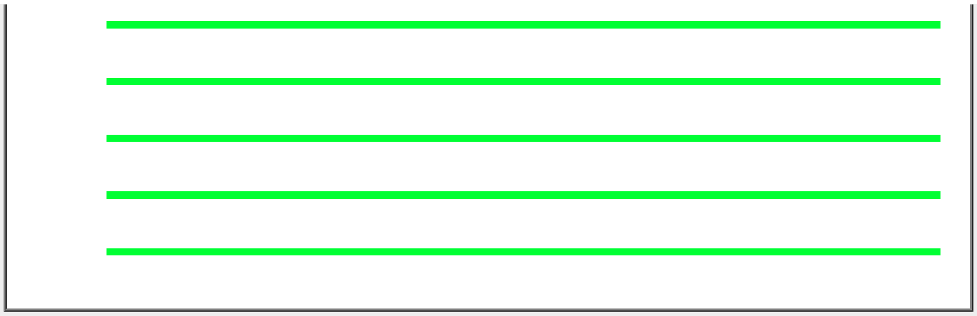
No putative conserved domains have been detected

Distribution of 110 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	IgG Fc binding protein [AA 4671-5405] [Homo sapiens]	58.7	58.7	100%	2e-08	94%	AAD15624.1
☐	PREDICTED: IgGFc-binding protein [Dasypus novemcinctus]	58.7	58.7	100%	2e-08	94%	XP_004474079.1
☐	PREDICTED: IgGFc-binding protein-like [Nannospalax galili]	58.7	58.7	100%	2e-08	94%	XP_008852264.1
☐	PREDICTED: IgGFc-binding protein [Saimiri boliviensis boliviensis]	58.7	58.7	100%	2e-08	94%	XP_010329397.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Loxodonta af	58.7	58.7	100%	2e-08	94%	XP_010598700.1
☐	PREDICTED: IgGFc-binding protein [Orycteropus afer afer]	58.7	58.7	100%	2e-08	94%	XP_007941342.1
☐	PREDICTED: IgGFc-binding protein [Lipotes vexillifer]	58.7	58.7	100%	2e-08	94%	XP_007458763.1
☐	PREDICTED: IgGFc-binding protein [Chrysochloris asiatica]	58.7	58.7	100%	2e-08	94%	XP_006871587.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Balaenoptera acutorostrata s	58.7	58.7	100%	2e-08	94%	XP_007180031.1
☐	Fc fragment of IgG binding protein [Homo sapiens]	58.7	58.7	100%	2e-08	94%	EAW56926.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Balaenoptera acutorostrata s	58.7	58.7	100%	2e-08	94%	XP_007180030.1
☐	PREDICTED: IgGFc-binding protein [Otolemur garnettii]	58.7	58.7	100%	2e-08	94%	XP_003802201.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pan paniscus	58.7	58.7	100%	2e-08	94%	XP_008963216.1
☐	PREDICTED: IgGFc-binding protein [Nomascus leucogenys]	58.7	58.7	100%	2e-08	94%	XP_003270573.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Gorilla gorilla	58.7	58.7	100%	2e-08	94%	XP_004060816.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pan troglody	58.7	58.7	100%	2e-08	94%	XP_009433882.1
☐	IgG Fc binding protein [Homo sapiens]	58.7	58.7	100%	2e-08	94%	BAA19526.1
☐	IgGFc-binding protein precursor [Homo sapiens]	58.7	58.7	100%	2e-08	94%	NP_003881.2
☐	Fc fragment of IgG binding protein [Camelus ferus]	56.2	76.4	100%	1e-07	89%	EPY85977.1
☐	PREDICTED: IgGFc-binding protein [Galeopterus variegatus]	56.2	56.2	100%	1e-07	89%	XP_008580791.1
☐	PREDICTED: IgGFc-binding protein [Camelus dromedarius]	56.2	76.4	100%	1e-07	89%	XP_010983489.1
☐	PREDICTED: IgGFc-binding protein [Camelus bactrianus]	56.2	76.4	100%	1e-07	89%	XP_010945545.1
☐	PREDICTED: IgGFc-binding protein [Vicugna pacos]	56.2	56.2	100%	1e-07	89%	XP_006215157.1
☐	PREDICTED: IgGFc-binding protein [Elephantulus edwardii]	56.2	56.2	100%	1e-07	89%	XP_006901006.1
☐	PREDICTED: IgGFc-binding protein [Camelus ferus]	56.2	76.4	100%	1e-07	89%	XP_006178015.1
☐	PREDICTED: IgGFc-binding protein [Trichechus manatus latirostris]	55.8	55.8	100%	2e-07	89%	XP_004388281.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Equus przew	55.8	55.8	100%	2e-07	89%	XP_008530313.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Bubalus bubalis]	55.8	55.8	100%	2e-07	89%	XP_006050099.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Bos taurus]	55.8	55.8	100%	2e-07	89%	XP_010813252.1

☐	PREDICTED: IgGFc-binding protein isoform X2 [Bos taurus]	55.8	55.8	100%	2e-07	89%	XP_010798219.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Equus caball	55.8	55.8	100%	2e-07	89%	XP_005596726.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Myotis brand	55.8	55.8	100%	2e-07	89%	XP_005868902.1
☐	PREDICTED: IgGFc-binding protein [Bison bison bison]	55.8	55.8	100%	2e-07	89%	XP_010847529.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bubalus bubalis]	55.8	55.8	100%	2e-07	89%	XP_006050098.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bos taurus]	55.8	55.8	100%	2e-07	89%	XP_010813251.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bos taurus]	55.8	55.8	100%	2e-07	89%	XP_010798218.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG binding protein [	55.8	55.8	100%	2e-07	89%	XP_006109819.1
☐	PREDICTED: IgGFc-binding protein [Pantholops hodgsonii]	55.8	55.8	100%	2e-07	89%	XP_005963590.1
☐	TPA: Fc fragment of IgG binding protein-like [Bos taurus]	55.8	55.8	100%	2e-07	89%	DAA19876.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Bos mutus]	55.8	55.8	100%	2e-07	89%	XP_005890645.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Capra hircus	55.8	55.8	100%	2e-07	89%	XP_005692605.1
☐	IgGFc-binding protein [Myotis brandtii]	55.8	55.8	100%	2e-07	89%	EPQ09333.1
☐	PREDICTED: IgGFc-binding protein [Jaculus jaculus]	55.8	55.8	100%	2e-07	89%	XP_004670397.1
☐	PREDICTED: IgGFc-binding protein [Tupaia chinensis]	55.4	55.4	94%	2e-07	94%	XP_006140449.1
☐	IgGFc-binding protein [Tupaia chinensis]	55.4	55.4	94%	2e-07	94%	ELW72413.1
☐	PREDICTED: IgGFc-binding protein-like [Tursiops truncatus]	54.9	54.9	100%	3e-07	89%	XP_004313750.1
☐	PREDICTED: IgGFc-binding protein [Orcinus orca]	54.9	54.9	100%	3e-07	89%	XP_004271425.1
☐	PREDICTED: IgGFc-binding protein [Ictidomys tridecemlineatus]	54.9	54.9	100%	3e-07	89%	XP_005336544.1
☐	PREDICTED: IgGFc-binding protein [Physeter catodon]	54.5	54.5	100%	5e-07	89%	XP_007122066.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pongo abelii]	54.5	54.5	100%	5e-07	89%	XP_009230865.1
☐	PREDICTED: IgGFc-binding protein-like [Nannospalax galili]	53.7	53.7	100%	9e-07	89%	XP_008852263.1
☐	PREDICTED: igGFc-binding protein-like [Macaca mulatta]	53.7	53.7	100%	9e-07	89%	XP_001088892.2
☐	PREDICTED: IgGFc-binding protein [Chlorocebus sabaeus]	53.7	53.7	100%	9e-07	89%	XP_007996683.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Papio anubis	53.7	53.7	100%	9e-07	89%	XP_003915593.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Rhinopithecu	53.7	53.7	100%	9e-07	89%	XP_010379186.1
☐	PREDICTED: IgGFc-binding protein [Macaca fascicularis]	53.7	53.7	100%	9e-07	89%	XP_005590715.1
☐	PREDICTED: IgGFc-binding protein [Pteropus alecto]	53.2	53.2	100%	1e-06	83%	XP_006905494.1
☐	IgGFc-binding protein [Pteropus alecto]	53.2	53.2	100%	1e-06	83%	ELK18209.1
☐	PREDICTED: IgGFc-binding protein [Echinops telfairi]	52.8	52.8	100%	2e-06	83%	XP_004710550.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Callithrix jacc	52.8	52.8	100%	2e-06	83%	XP_008986248.1
☐	IgGFc-binding protein [Myotis davidii]	52.4	52.4	100%	2e-06	83%	ELK30313.1
☐	PREDICTED: IgGFc-binding protein [Myotis davidii]	52.4	52.4	100%	2e-06	83%	XP_006763740.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Eptesicus fus	52.4	52.4	100%	2e-06	83%	XP_008138255.1
☐	PREDICTED: IgGFc-binding protein [Tarsius syrichta]	52.0	52.0	100%	3e-06	83%	XP_008052981.1
☐	PREDICTED: IgGFc-binding protein [Condylura cristata]	51.5	72.5	100%	5e-06	83%	XP_004693946.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ovis aries]	51.5	51.5	94%	5e-06	88%	XP_004015739.1
☐	PREDICTED: IgGFc-binding protein [Erinaceus europaeus]	51.5	51.5	100%	5e-06	83%	XP_007538724.1
☐	9530053A07Rik protein [Mus musculus]	49.8	49.8	94%	1e-05	82%	AAI26888.1
☐	9530053A07Rik protein [Mus musculus]	49.8	49.8	94%	1e-05	82%	AAI26887.1
☐	Fc fragment of IgG binding protein-like precursor [Mus musculus]	49.8	49.8	94%	2e-05	82%	NP_001158127.1
☐	Fcgbp protein [Mus musculus]	47.3	47.3	94%	1e-04	76%	AAH24554.1
☐	Fcgbp protein [Mus musculus]	47.3	47.3	94%	1e-04	76%	AAH24520.1
☐	Fcgbp protein [Mus musculus]	47.3	47.3	94%	1e-04	76%	AAH55475.1
☐	Fcgbp protein [Mus musculus]	47.3	47.3	94%	1e-04	76%	AAH69956.1

☐	Fcgbp protein [Mus musculus]	47.3	47.3	94%	1e-04	76%	AAH92067.1
☐	Fcgbp protein [Mus musculus]	47.3	47.3	94%	1e-04	76%	AAH26653.1
☐	Fcgbp protein [Mus musculus]	47.3	47.3	94%	1e-04	76%	AAH30871.1
☐	mCG145390, isoform CRA_b [Mus musculus]	47.3	47.3	94%	1e-04	76%	EDL24158.1
☐	mCG145390, isoform CRA_a [Mus musculus]	47.3	47.3	94%	1e-04	76%	EDL24157.1
☐	Fc fragment of IgG binding protein precursor [Mus musculus]	47.3	47.3	94%	1e-04	76%	NP_001116075.1
☐	PREDICTED: IgGFc-binding protein [Panthera tigris altaica]	47.3	47.3	94%	1e-04	82%	XP_007087304.1
☐	PREDICTED: IgGFc-binding protein [Felis catus]	47.3	47.3	94%	1e-04	82%	XP_006941331.1
☐	PREDICTED: IgGFc-binding protein [Oryctolagus cuniculus]	46.4	66.6	100%	2e-04	78%	XP_008249744.1
☐	PREDICTED: IgGFc-binding protein [Ochotona princeps]	46.0	67.0	100%	3e-04	72%	XP_004599764.1
☐	hypothetical protein PANDA_012964 [Ailuropoda melanoleuca]	45.6	45.6	94%	4e-04	76%	EFB16331.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ursus maritin	45.6	45.6	94%	4e-04	76%	XP_008686987.1
☐	PREDICTED: IgGFc-binding protein-like [Ailuropoda melanoleuca]	45.6	45.6	94%	4e-04	76%	XP_002923768.1
☐	PREDICTED: IgGFc-binding protein [Cavia porcellus]	44.8	44.8	100%	8e-04	78%	XP_003462033.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Canis lupus f	44.3	44.3	94%	0.001	76%	XP_005616636.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG binding protein [	44.3	44.3	94%	0.001	76%	XP_004828450.1
☐	PREDICTED: IgGFc-binding protein [Sorex araneus]	43.9	43.9	94%	0.002	76%	XP_004620845.1
☐	PREDICTED: IgGFc-binding protein [Microtus ochrogaster]	43.1	64.1	94%	0.003	76%	XP_005371357.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG binding protein [	42.2	42.2	94%	0.005	76%	XP_005674577.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG binding protein [	41.4	41.4	94%	0.010	71%	XP_004417817.1
☐	PREDICTED: IgGFc-binding protein-like [Peromyscus maniculatus bairdii]	40.9	40.9	94%	0.014	71%	XP_006996523.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Chinchilla lanigera]	40.9	61.1	100%	0.014	72%	XP_005414139.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Chinchilla lanigera]	40.9	61.1	100%	0.014	72%	XP_005414138.1
☐	PREDICTED: IgGFc-binding protein [Monodelphis domestica]	40.5	40.5	94%	0.020	71%	XP_007491957.1
☐	PREDICTED: IgGFc-binding protein [Octodon degus]	39.7	39.7	100%	0.037	72%	XP_004648069.1
☐	rCG54015 [Rattus norvegicus]	39.2	39.2	94%	0.050	71%	EDM07917.1

⊟ Alignments

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IgG Fc binding protein [AA 4671-5405] [Homo sapiens]

Sequence ID: gb|AAD15624.1| **Length:** 735 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 511 to 528 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
58.7 bits(131)	2e-08	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    RYLPVDSSLLTSDCSERC  18
            RYLPV+SSLLTSDCSERC
Sbjct  511  RYLPVNSSLLTSDCSERC  528
```

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PREDICTED: IgGFc-binding protein [Dasypus novemcinctus]

Sequence ID: ref|XP_004474079.1| **Length:** 2558 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 2334 to 2351 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
58.7 bits(131)	2e-08	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1     RYLPVDSSLLTSDCSERC  18
             RYLPV+SSLLTSDCSERC
Sbjct  2334  RYLPVNSSLLTSDCSERC  2351
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: IgGFc-binding protein-like [Nannospalax galili]

Sequence ID: ref|XP_008852264.1| **Length:** 2577 **Number of Matches:** 1

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

Range 1: 2355 to 2372 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
58.7 bits(131)	2e-08	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1     RYLPVDSSLLTSDCSERC  18
             RYLPV+SSLLTSDCSERC
Sbjct  2355  RYLPVNSSLLTSDCSERC  2372
```

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PREDICTED: IgGFc-binding protein [Saimiri boliviensis boliviensis]

Sequence ID: ref|XP_010329397.1| **Length:** 2834 **Number of Matches:** 1

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

Range 1: 2610 to 2627 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
58.7 bits(131)	2e-08	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1     RYLPVDSSLLTSDCSERC  18
             RYLPV+SSLLTSDCSERC
Sbjct  2610  RYLPVNSSLLTSDCSERC  2627
```

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PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Loxodonta africana]

Sequence ID: ref|XP_010598700.1| **Length:** 2952 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 2730 to 2747 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
58.7 bits(131)	2e-08	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1     RYLPVDSSLLTSDCSERC  18
             RYLPV+SSLLTSDCSERC
Sbjct  2730  RYLPVNSSLLTSDCSERC  2747
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - B9E60EFB01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | ▷Formatting options | ▷Download

YouTube How to read this page | Blast report description

FCGBP_RYLPVNSSLLTSDCSERC_NonMod

RID B9E60EFB01R (Expires on 01-14 13:18 pm)

Query ID lcl|301508
Description None
Molecule type amino acid
Query Length 18

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

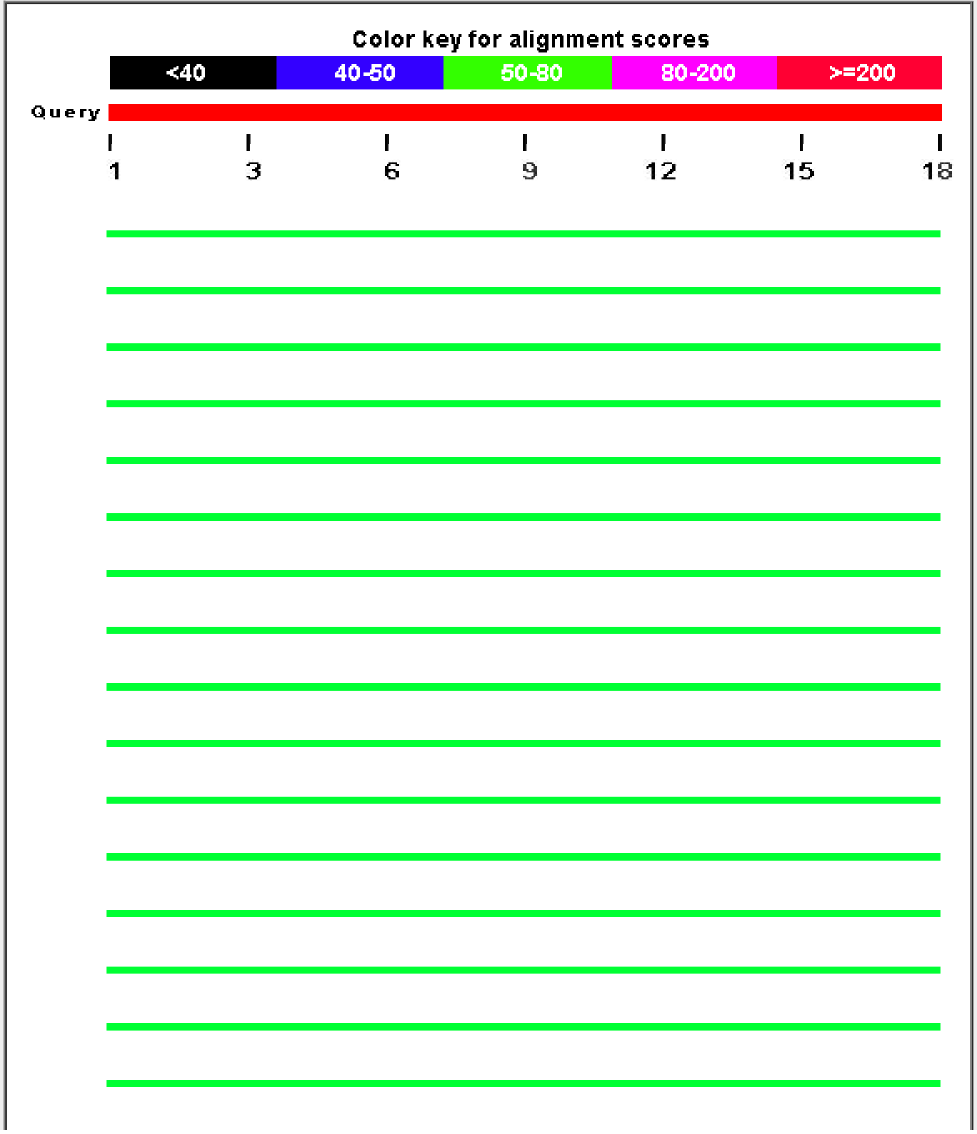
⊟ Graphic Summary

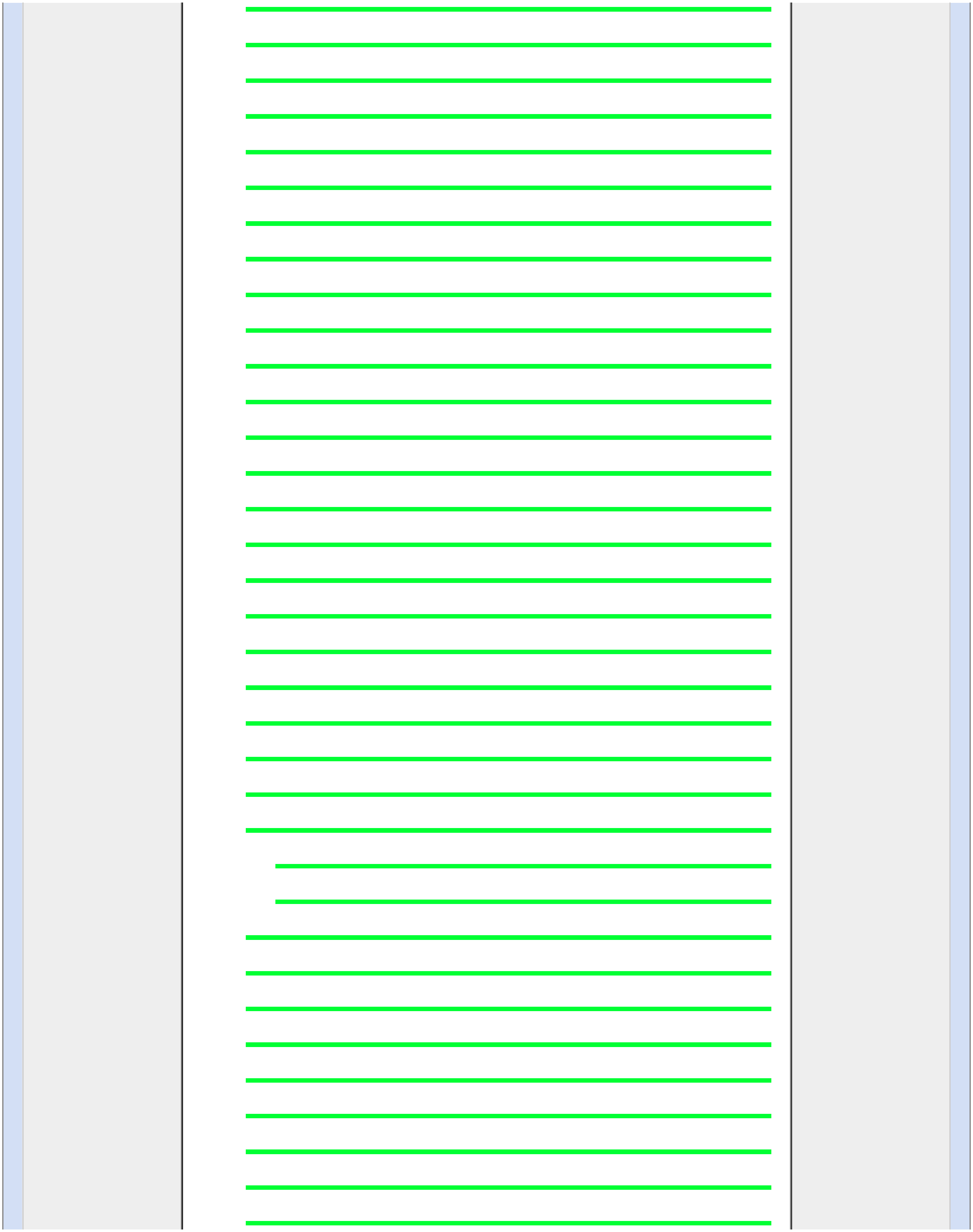
⊟ Show Conserved Domains

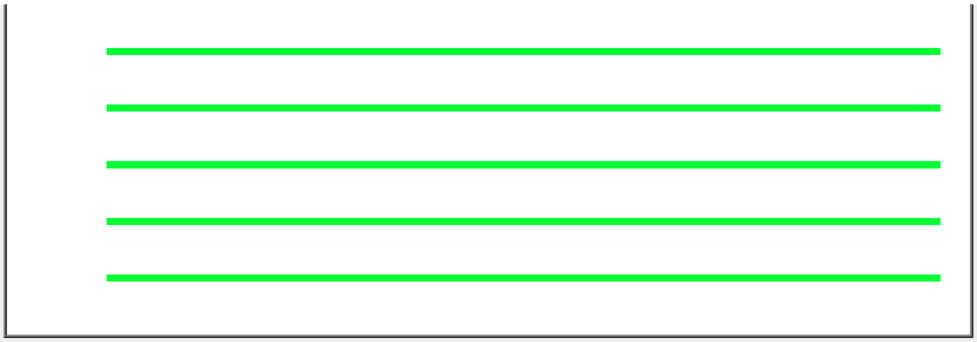
No putative conserved domains have been detected

Distribution of 108 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊖ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	IgG Fc binding protein [AA 4671-5405] [Homo sapiens]	61.3	61.3	100%	2e-09	100%	gi|4321127|AAD15624.1
☐	PREDICTED: IgGFc-binding protein [Dasypus novemcinctus]	61.3	61.3	100%	2e-09	100%	gi|488568912|XP_004474079.1
☐	PREDICTED: IgGFc-binding protein-like [Nannospalax galili]	61.3	61.3	100%	2e-09	100%	gi|674088663|XP_008852264.1
☐	PREDICTED: IgGFc-binding protein [Saimiri boliviensis boliviensis]	61.3	61.3	100%	2e-09	100%	gi|725605545|XP_010329397.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Lo	61.3	61.3	100%	2e-09	100%	gi|731510651|XP_010598700.1
☐	PREDICTED: IgGFc-binding protein [Orycteropus afer afer]	61.3	61.3	100%	2e-09	100%	gi|634854573|XP_007941342.1
☐	PREDICTED: IgGFc-binding protein [Lipotes vexillifer]	61.3	61.3	100%	2e-09	100%	gi|602693350|XP_007458763.1
☐	PREDICTED: IgGFc-binding protein [Chrysochloris asiatica]	61.3	61.3	100%	2e-09	100%	gi|586482145|XP_006871587.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Balaenoptera acut	61.3	61.3	100%	2e-09	100%	gi|594663750|XP_007180031.1
☐	Fc fragment of IgG binding protein [Homo sapiens]	61.3	61.3	100%	2e-09	100%	gi|119577330|EAW56926.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Balaenoptera acut	61.3	61.3	100%	2e-09	100%	gi|594663748|XP_007180030.1
☐	PREDICTED: IgGFc-binding protein [Otolemur garnettii]	61.3	61.3	100%	2e-09	100%	gi|395859762|XP_003802201.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pa	61.3	61.3	100%	2e-09	100%	gi|675718714|XP_008963216.1
☐	PREDICTED: IgGFc-binding protein [Nomascus leucogenys]	61.3	61.3	100%	2e-09	100%	gi|332242810|XP_003270573.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Go	61.3	61.3	100%	2e-09	100%	gi|426388791|XP_004060816.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pa	61.3	61.3	100%	2e-09	100%	gi|694975150|XP_009433882.1
☐	IgG Fc binding protein [Homo sapiens]	61.3	61.3	100%	2e-09	100%	gi|1944352|BAA19526.1
☐	IgGFc-binding protein precursor [Homo sapiens]	61.3	61.3	100%	2e-09	100%	gi|154146262|NP_003881.2
☐	Fc fragment of IgG binding protein [Camelus ferus]	58.7	78.9	100%	2e-08	94%	gi|528766318|EPY85977.1
☐	PREDICTED: IgGFc-binding protein [Galeopterus variegatus]	58.7	58.7	100%	2e-08	94%	gi|667245485|XP_008580791.1
☐	PREDICTED: IgGFc-binding protein [Vicugna pacos]	58.7	58.7	100%	2e-08	94%	gi|560985920|XP_006215157.1
☐	PREDICTED: IgGFc-binding protein [Elephantulus edwardii]	58.7	58.7	100%	2e-08	94%	gi|585714650|XP_006901006.1
☐	PREDICTED: IgGFc-binding protein [Camelus ferus]	58.7	78.9	100%	2e-08	94%	gi|560903281|XP_006178015.1
☐	PREDICTED: IgGFc-binding protein [Trichechus manatus latirostris	58.3	58.3	100%	2e-08	94%	gi|471413470|XP_004388281.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Eq	58.3	58.3	100%	2e-08	94%	gi|664745941|XP_008530313.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Bubalus bubalis]	58.3	58.3	100%	2e-08	94%	gi|594051532|XP_006050099.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bos taurus]	58.3	58.3	100%	2e-08	94%	gi|528991889|XP_002695104.2
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bos taurus]	58.3	58.3	100%	2e-08	94%	gi|528933616|XP_005200216.1
☐							

	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Eq	58.3	58.3	100%	2e-08	94%	gi|545176771|XP_005596726.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [My	58.3	58.3	100%	2e-08	94%	gi|554548727|XP_005868902.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Bubalus bubalis]	58.3	58.3	100%	2e-08	94%	gi|594051530|XP_006050098.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Bos taurus]	58.3	58.3	100%	2e-08	94%	gi|528991887|XP_005219168.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Bos taurus]	58.3	58.3	100%	2e-08	94%	gi|528933614|XP_614095.6
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG bindin	58.3	58.3	100%	2e-08	94%	gi|558160938|XP_006109819.1
☐	PREDICTED: IgGFc-binding protein [Pantholops hodgsonii]	58.3	58.3	100%	2e-08	94%	gi|556735974|XP_005963590.1
☐	TPA: Fc fragment of IgG binding protein-like [Bos taurus]	58.3	58.3	100%	2e-08	94%	gi|296477761|DAA19876.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Bo	58.3	58.3	100%	2e-08	94%	gi|555957014|XP_005890645.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ca	58.3	58.3	100%	2e-08	94%	gi|548504606|XP_005692605.1
☐	IgGFc-binding protein [Myotis brandtii]	58.3	58.3	100%	2e-08	94%	gi|521027545|EPQ09333.1
☐	PREDICTED: IgGFc-binding protein [Jaculus jaculus]	58.3	58.3	100%	2e-08	94%	gi|507573627|XP_004670397.1
☐	PREDICTED: IgGFc-binding protein [Tupaia chinensis]	57.9	57.9	94%	3e-08	100%	gi|562821062|XP_006140449.1
☐	IgGFc-binding protein [Tupaia chinensis]	57.9	57.9	94%	3e-08	100%	gi|444732094|ELW72413.1
☐	PREDICTED: IgGFc-binding protein-like [Tursiops truncatus]	57.5	57.5	100%	4e-08	94%	gi|470605142|XP_004313750.1
☐	PREDICTED: IgGFc-binding protein [Orcinus orca]	57.5	57.5	100%	4e-08	94%	gi|466016931|XP_004271425.1
☐	PREDICTED: IgGFc-binding protein [Ictidomys tridecemlineatus]	57.5	57.5	100%	4e-08	94%	gi|532101857|XP_005336544.1
☐	PREDICTED: IgGFc-binding protein [Physeter catodon]	57.1	57.1	100%	6e-08	94%	gi|593767123|XP_007122066.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Po	57.1	57.1	100%	6e-08	94%	gi|686758917|XP_009230865.1
☐	PREDICTED: IgGFc-binding protein-like [Nannospalax galili]	56.2	56.2	100%	1e-07	94%	gi|674088661|XP_008852263.1
☐	PREDICTED: igGFc-binding protein-like [Macaca mulatta]	56.2	56.2	100%	1e-07	94%	gi|297277050|XP_001088892.2
☐	PREDICTED: IgGFc-binding protein [Chlorocebus sabaeus]	56.2	56.2	100%	1e-07	94%	gi|635042256|XP_007996683.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Pa	56.2	56.2	100%	1e-07	94%	gi|402905577|XP_003915593.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Rh	56.2	56.2	100%	1e-07	94%	gi|724909919|XP_010379186.1
☐	PREDICTED: IgGFc-binding protein [Macaca fascicularis]	56.2	56.2	100%	1e-07	94%	gi|544514342|XP_005590715.1
☐	PREDICTED: IgGFc-binding protein [Pteropus alecto]	55.8	55.8	100%	2e-07	89%	gi|586524140|XP_006905494.1
☐	IgGFc-binding protein [Pteropus alecto]	55.8	55.8	100%	2e-07	89%	gi|431920170|ELK18209.1
☐	PREDICTED: IgGFc-binding protein [Echinops telfairi]	55.4	55.4	100%	2e-07	89%	gi|507680836|XP_004710550.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ca	55.4	55.4	100%	2e-07	89%	gi|675761213|XP_008986248.1
☐	IgGFc-binding protein [Myotis davidii]	54.9	54.9	100%	3e-07	89%	gi|432102846|ELK30313.1
☐	PREDICTED: IgGFc-binding protein [Myotis davidii]	54.9	54.9	100%	3e-07	89%	gi|584088170|XP_006763740.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ep	54.9	54.9	100%	3e-07	89%	gi|641699510|XP_008138255.1
☐	PREDICTED: IgGFc-binding protein [Tarsius syrichta]	54.5	54.5	100%	4e-07	89%	gi|640776875|XP_008052981.1
☐	PREDICTED: IgGFc-binding protein [Condylura cristata]	54.1	75.1	100%	6e-07	89%	gi|507980555|XP_004693946.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ov	54.1	54.1	94%	6e-07	94%	gi|426243806|XP_004015739.1
☐	PREDICTED: IgGFc-binding protein [Erinaceus europaeus]	54.1	54.1	100%	6e-07	89%	gi|617664909|XP_007538724.1
☐	Fcgbp protein [Mus musculus]	49.8	49.8	94%	1e-05	82%	gi|19353631|AAH24554.1
☐	Fcgbp protein [Mus musculus]	49.8	49.8	94%	1e-05	82%	gi|19353600|AAH24520.1
☐	Fcgbp protein [Mus musculus]	49.8	49.8	94%	1e-05	82%	gi|33585463|AAH55475.1
☐	Fcgbp protein [Mus musculus]	49.8	49.8	94%	1e-05	82%	gi|47682932|AAH69956.1
☐	Fcgbp protein [Mus musculus]	49.8	49.8	94%	1e-05	82%	gi|62024652|AAH92067.1
☐	Fcgbp protein [Mus musculus]	49.8	49.8	94%	1e-05	82%	gi|20072053|AAH26653.1
☐	Fcgbp protein [Mus musculus]	49.8	49.8	94%	2e-05	82%	gi|21410127|AAH30871.1
☐	mCG145390, isoform CRA_b [Mus musculus]	49.8	49.8	94%	2e-05	82%	gi|148692211|EDL24158.1
☐	mCG145390, isoform CRA_a [Mus musculus]	49.8	49.8	94%	2e-05	82%	gi|148692210|EDL24157.1

☐	Fc fragment of IgG binding protein precursor [Mus musculus]	49.8	49.8	94%	2e-05	82%	gi|169790797|NP_001116075.1
☐	PREDICTED: IgGFc-binding protein [Panthera tigris altaica]	49.8	49.8	94%	2e-05	88%	gi|591322392|XP_007087304.1
☐	PREDICTED: IgGFc-binding protein [Felis catus]	49.8	49.8	94%	2e-05	88%	gi|587014135|XP_006941331.1
☐	PREDICTED: IgGFc-binding protein [Oryctolagus cuniculus]	49.0	69.1	100%	3e-05	83%	gi|655895144|XP_008249744.1
☐	PREDICTED: IgGFc-binding protein [Ochotona princeps]	48.6	69.6	100%	4e-05	78%	gi|504182881|XP_004599764.1
☐	hypothetical protein PANDA_012964 [Ailuropoda melanoleuca]	48.1	48.1	94%	6e-05	82%	gi|281340747|EFB16331.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ur	48.1	48.1	94%	6e-05	82%	gi|670991993|XP_008686987.1
☐	PREDICTED: IgGFc-binding protein-like [Ailuropoda melanoleuca]	48.1	48.1	94%	6e-05	82%	gi|301776693|XP_002923768.1
☐	9530053A07Rik protein [Mus musculus]	47.3	47.3	94%	9e-05	76%	gi|119850932|AAI26888.1
☐	9530053A07Rik protein [Mus musculus]	47.3	47.3	94%	9e-05	76%	gi|119850803|AAI26887.1
☐	Fc fragment of IgG binding protein-like precursor [Mus musculus]	47.3	47.3	94%	1e-04	76%	gi|257467625|NP_001158127.1
☐	PREDICTED: IgGFc-binding protein [Cavia porcellus]	47.3	47.3	100%	1e-04	83%	gi|348552434|XP_003462033.1
☐	PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Ca	46.9	46.9	94%	2e-04	82%	gi|545488517|XP_005616636.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG bindin	46.9	46.9	94%	2e-04	82%	gi|511913755|XP_004828450.1
☐	PREDICTED: IgGFc-binding protein [Sorex araneus]	46.4	46.4	94%	2e-04	82%	gi|505854851|XP_004620845.1
☐	PREDICTED: IgGFc-binding protein [Microtus ochrogaster]	45.6	66.6	94%	4e-04	82%	gi|532057309|XP_005371357.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG bindin	44.8	44.8	94%	8e-04	82%	gi|545830918|XP_005674577.1
☐	PREDICTED: LOW QUALITY PROTEIN: Fc fragment of IgG bindin	43.9	43.9	94%	0.001	76%	gi|472353763|XP_004417817.1
☐	PREDICTED: IgGFc-binding protein-like [Peromyscus maniculatus	43.5	43.5	94%	0.002	76%	gi|589968051|XP_006996523.1
☐	PREDICTED: IgGFc-binding protein isoform X2 [Chinchilla lanigera]	43.5	63.6	100%	0.002	78%	gi|533203235|XP_005414139.1
☐	PREDICTED: IgGFc-binding protein isoform X1 [Chinchilla lanigera]	43.5	63.6	100%	0.002	78%	gi|533203233|XP_005414138.1
☐	PREDICTED: IgGFc-binding protein [Monodelphis domestica]	43.1	43.1	94%	0.003	76%	gi|612025837|XP_007491957.1
☐	PREDICTED: IgGFc-binding protein [Octodon degus]	42.2	42.2	100%	0.005	78%	gi|507714064|XP_004648069.1
☐	rCG54015 [Rattus norvegicus]	41.8	41.8	94%	0.007	76%	gi|149056486|EDM07917.1
☐	RGD1311906 protein [Rattus norvegicus]	41.8	41.8	94%	0.007	76%	gi|71681025|AAH99756.1
☐	Fc fragment of IgG binding protein-like precursor [Rattus norvegicus	41.8	41.8	94%	0.007	76%	gi|257467627|NP_001158128.1
☐	Fc fragment of IgG binding protein precursor [Rattus norvegicus]	41.8	41.8	94%	0.007	76%	gi|695917199|NP_001158129.2

⊟ Alignments

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IgG Fc binding protein [AA 4671-5405] [Homo sapiens]

Sequence ID: gi|4321127|gb|AAD15624.1| **Length:** 735 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 511 to 528 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    RYLPVNSSLLTSDCSERC  18
            RYLPVNSSLLTSDCSERC
Sbjct  511  RYLPVNSSLLTSDCSERC  528
```

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PREDICTED: IgGFc-binding protein [Dasypus novemcinctus]

Sequence ID: gi|488568912|ref|XP_004474079.1| **Length:** 2558 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 2334 to 2351 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1     RYLPVNSSLLTSDCSERC  18
```

```
                 RYLPVNSSLLTSDCSERC
Sbjct  2334  RYLPVNSSLLTSDCSERC  2351
```

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PREDICTED: IgGFc-binding protein-like [Nannospalax galili]

Sequence ID: gi|674088663|ref|XP_008852264.1| **Length:** 2577 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 2355 to 2372 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1     RYLPVNSSLLTSDCSERC  18
             RYLPVNSSLLTSDCSERC
Sbjct  2355  RYLPVNSSLLTSDCSERC  2372
```

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PREDICTED: IgGFc-binding protein [Saimiri boliviensis boliviensis]

Sequence ID: gi|725605545|ref|XP_010329397.1| **Length:** 2834 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 2610 to 2627 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1     RYLPVNSSLLTSDCSERC  18
             RYLPVNSSLLTSDCSERC
Sbjct  2610  RYLPVNSSLLTSDCSERC  2627
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: LOW QUALITY PROTEIN: IgGFc-binding protein [Loxodonta africana]

Sequence ID: gi|731510651|ref|XP_010598700.1| **Length:** 2952 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 2730 to 2747 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1     RYLPVNSSLLTSDCSERC  18
             RYLPVNSSLLTSDCSERC
Sbjct  2730  RYLPVNSSLLTSDCSERC  2747
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

FLT4_KLVIQNADVSAMYKC_Mod

RID BVDWU9V801R (Expires on 01-21 09:04 am)

Query ID lcl|327098
Description None
Molecule type amino acid
Query Length 15

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

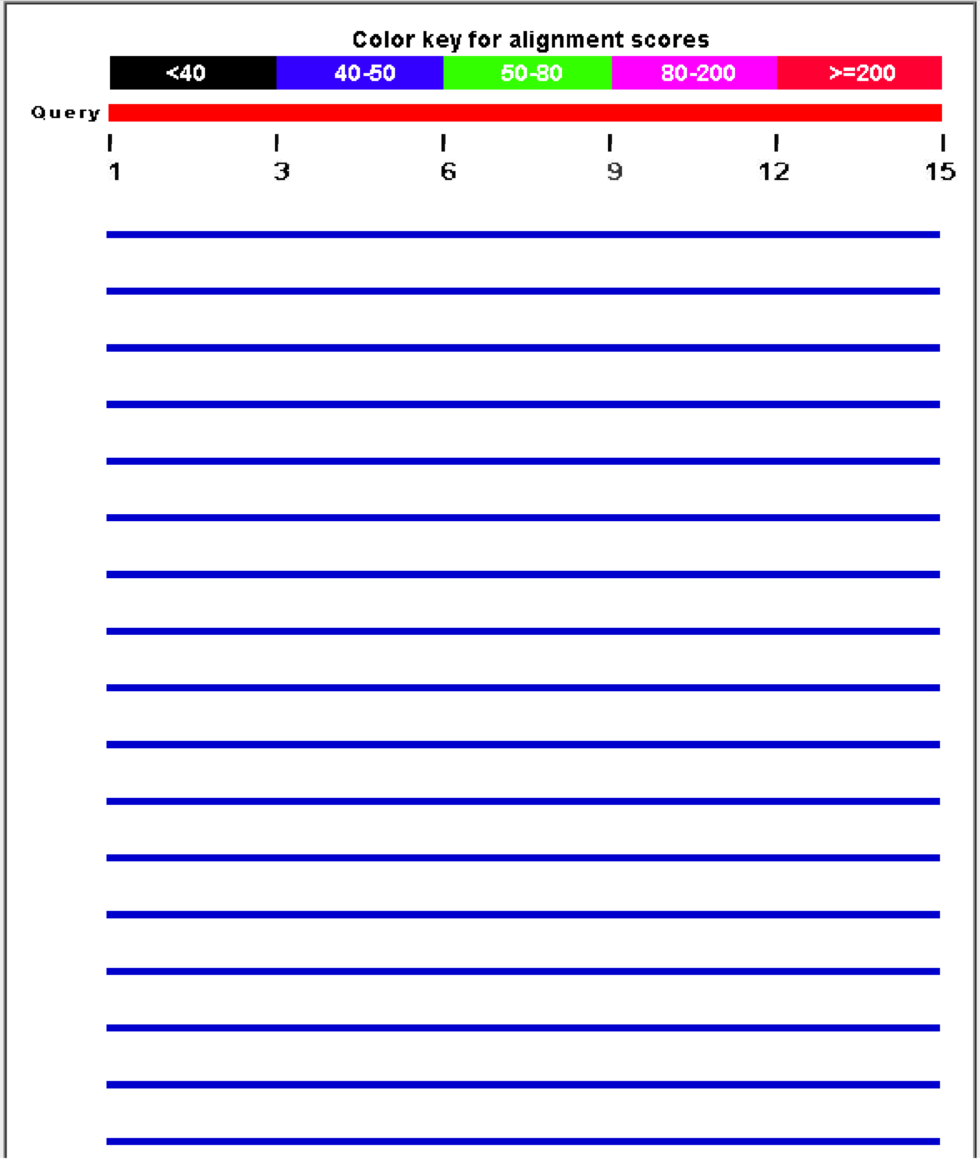
Graphic Summary

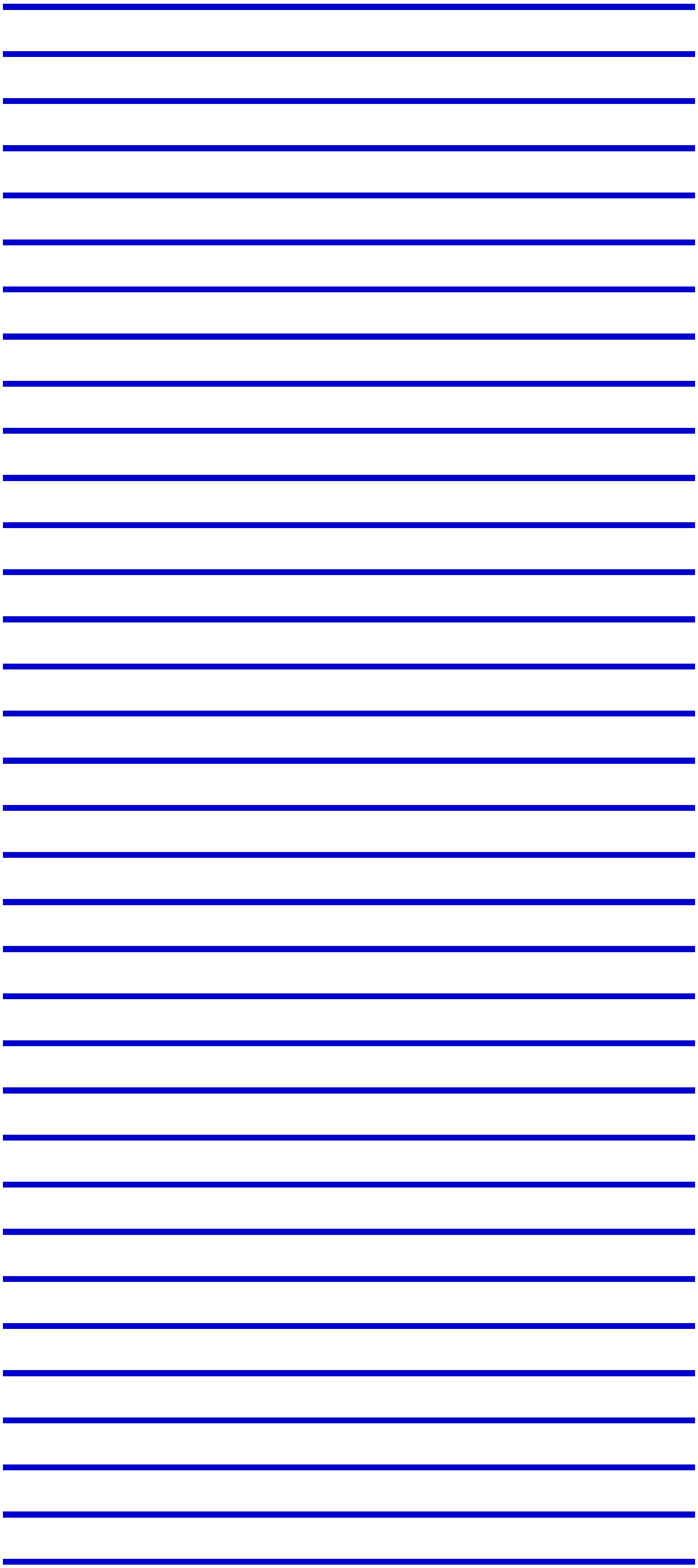
Show Conserved Domains

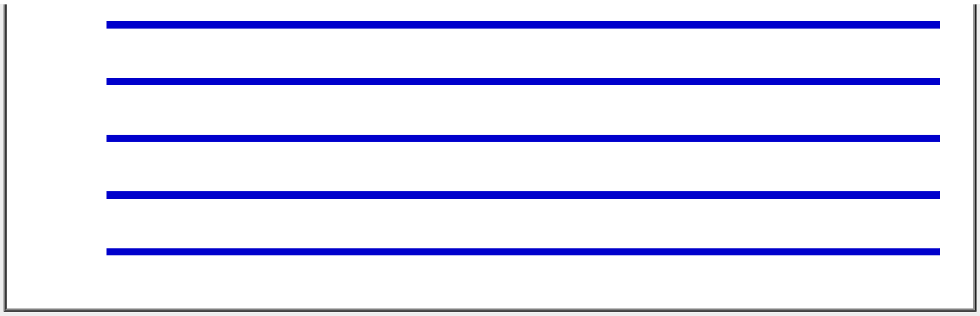
No putative conserved domains have been detected

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of Vegfr-3 Extracellular Domains D4-5 [Homo sapi	49.8	49.8	100%	9e-06	93%	4BSJ_A
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Pongo abelii]	49.8	49.8	100%	1e-05	93%	XP_009239654.1
☐	Vascular endothelial growth factor receptor 3 precursor variant [Homo sapiens	49.8	49.8	100%	1e-05	93%	BAD92874.1
☐	soluble VEGFR3 variant 1 [Homo sapiens]	49.8	49.8	100%	1e-05	93%	ACF47600.1
☐	PREDICTED: vascular endothelial growth factor receptor 3-like [Leptonychote	49.8	49.8	100%	1e-05	93%	XP_006746634.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X3 [Rhino	49.8	49.8	100%	1e-05	93%	XP_010373329.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X7 [Pan tr	49.8	49.8	100%	1e-05	93%	XP_009448613.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X2 [Rhino	49.8	49.8	100%	1e-05	93%	XP_010373327.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial growth factor re	49.8	49.8	100%	1e-05	93%	XP_008987571.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X3 [Chloro	49.8	49.8	100%	1e-05	93%	XP_008013748.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X2 [Saimir	49.8	49.8	100%	1e-05	93%	XP_010330147.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial growth factor re	49.8	49.8	100%	1e-05	93%	XP_002816373.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X2 [Chloro	49.8	49.8	100%	1e-05	93%	XP_008013747.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X6 [Pan tr	49.8	49.8	100%	1e-05	93%	XP_009448612.1
☐	unnamed protein product [Homo sapiens]	49.8	49.8	100%	1e-05	93%	CAA49505.1
☐	vascular endothelial growth factor receptor 3 isoform 2 precursor [Homo sapie	49.8	49.8	100%	1e-05	93%	NP_002011.2
☐	unnamed protein product [Homo sapiens]	49.8	49.8	100%	1e-05	93%	BAF84368.1
☐	VEGFR3 short form [Homo sapiens]	49.8	49.8	100%	1e-05	93%	AAO89504.1
☐	FTL4 [Homo sapiens]	49.8	49.8	100%	1e-05	93%	CAA48290.1
☐	hypothetical protein PANDA_017671 [Ailuropoda melanoleuca]	49.8	49.8	100%	1e-05	93%	EFB13501.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X5 [Pan tr	49.8	49.8	100%	1e-05	93%	XP_009448611.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X4 [Pan tr	49.8	49.8	100%	1e-05	93%	XP_009448610.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X1 [Rhino	49.8	49.8	100%	1e-05	93%	XP_010373326.1
☐	PREDICTED: vascular endothelial growth factor receptor 3-like [Macaca mula	49.8	49.8	100%	1e-05	93%	XP_001107118.2
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Gorilla gorilla gori	49.8	49.8	100%	1e-05	93%	XP_004043215.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X3 [Muste	49.8	49.8	100%	1e-05	93%	XP_004759037.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Ochotona princep	49.8	49.8	100%	1e-05	93%	XP_004599097.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X1 [Chloro	49.8	49.8	100%	1e-05	93%	XP_008013746.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Macaca fascicula	49.8	49.8	100%	1e-05	93%	XP_005558869.1

☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X1 [Saimir	49.8	49.8	100%	1e-05	93%	XP_003944009.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial growth factor re	49.8	49.8	100%	1e-05	93%	XP_003900691.1
☐	VEGFR3 long form [Homo sapiens]	49.8	49.8	100%	1e-05	93%	AAO89505.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform 2 [Nomasc	49.8	49.8	100%	1e-05	93%	XP_003279615.2
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X3 [Pan tr	49.8	49.8	100%	1e-05	93%	XP_518160.4
☐	vascular endothelial growth factor receptor 3 isoform 1 precursor [Homo sapie	49.8	49.8	100%	1e-05	93%	NP_891555.2
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X2 [Muste	49.8	49.8	100%	1e-05	93%	XP_004759036.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X1 [Muste	49.8	49.8	100%	1e-05	93%	XP_004759035.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X2 [Pan tr	49.8	49.8	100%	1e-05	93%	XP_009448609.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Ursus maritimus]	49.8	49.8	100%	1e-05	93%	XP_008707769.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial growth factor re	49.8	49.8	100%	1e-05	93%	XP_008955193.1
☐	PREDICTED: vascular endothelial growth factor receptor 3-like [Ailuropoda m	49.8	49.8	100%	1e-05	93%	XP_002927834.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X1 [Pan tr	49.8	49.8	100%	1e-05	93%	XP_009448608.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Odobenus rosmar	49.8	49.8	100%	1e-05	93%	XP_004412739.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Erinaceus europa	49.8	49.8	100%	1e-05	93%	XP_007527230.1
☐	PREDICTED: vascular endothelial growth factor receptor 3-like [Tarsius syrich	47.3	47.3	100%	8e-05	87%	XP_008072035.1
☐	rCG35022, isoform CRA_a [Rattus norvegicus]	47.3	47.3	100%	8e-05	87%	EDM04224.1
☐	Vascular endothelial growth factor receptor 3 [Pteropus alecto]	47.3	47.3	100%	8e-05	87%	ELK03188.1
☐	PREDICTED: vascular endothelial growth factor receptor 3-like [Myotis lucifug	47.3	47.3	100%	8e-05	87%	XP_006108959.1
☐	rCG35022, isoform CRA_c [Rattus norvegicus]	47.3	47.3	100%	8e-05	87%	EDM04226.1
☐	receptor tyrosine kinase VEGFR-3kt [Rattus norvegicus]	47.3	47.3	100%	8e-05	87%	AAL13270.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial growth factor re	47.3	47.3	100%	8e-05	87%	XP_010592785.1
☐	vascular endothelial growth factor receptor [Cricetulus griseus]	47.3	47.3	100%	8e-05	87%	ERE67633.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X4 [Panth	47.3	47.3	100%	8e-05	87%	XP_007083127.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X4 [Felis c	47.3	47.3	100%	8e-05	87%	XP_006927563.1
☐	Vascular endothelial growth factor receptor 3 [Cricetulus griseus]	47.3	47.3	100%	8e-05	87%	EGW02874.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Myotis brandtii]	47.3	47.3	100%	8e-05	87%	XP_005865016.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Myotis davidii]	47.3	47.3	100%	8e-05	87%	XP_006775477.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Pteropus alecto]	47.3	47.3	100%	8e-05	87%	XP_006923300.1
☐	FMS-like tyrosine kinase 4 [Mus musculus]	47.3	47.3	100%	8e-05	87%	EDL33745.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial growth factor re	47.3	47.3	100%	8e-05	87%	XP_007644094.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X3 [Felis c	47.3	47.3	100%	8e-05	87%	XP_006927562.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Camelus ferus]	47.3	47.3	100%	8e-05	87%	XP_006175816.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X3 [Panth	47.3	47.3	100%	8e-05	87%	XP_007083126.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X2 [Panth	47.3	47.3	100%	8e-05	87%	XP_007083125.1
☐	fms-related tyrosine kinase 4 isoform 1-like protein [Camelus ferus]	47.3	47.3	100%	8e-05	87%	EPY87675.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X1 [Panth	47.3	47.3	100%	8e-05	87%	XP_007083124.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Camelus dromeda	47.3	47.3	100%	8e-05	87%	XP_010991945.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial growth factor re	47.3	47.3	100%	8e-05	87%	XP_002721370.2
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X2 [Came	47.3	47.3	100%	8e-05	87%	XP_010944438.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X2 [Fukom	47.3	47.3	100%	8e-05	87%	XP_010622027.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X1 [Fukom	47.3	47.3	100%	8e-05	87%	XP_010622026.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X1 [Came	47.3	47.3	100%	8e-05	87%	XP_010944437.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Orycteropus afer	47.3	67.4	100%	8e-05	87%	XP_007951628.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Jaculus jaculus]	47.3	47.3	100%	8e-05	87%	XP_004666583.1

☐	PREDICTED: vascular endothelial growth factor receptor 3 [Orcinus orca]	47.3	47.3	100%	8e-05	87%	XP_004284117.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Nannospalax gali	47.3	47.3	100%	8e-05	87%	XP_008850448.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Eptesicus fuscus]	47.3	47.3	100%	8e-05	87%	XP_008156907.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Echinops telfairi]	47.3	47.3	100%	8e-05	87%	XP_004697235.1
☐	PREDICTED: vascular endothelial growth factor receptor 3-like [Tursiops trun	47.3	47.3	100%	8e-05	87%	XP_004322923.1
☐	rCG35022, isoform CRA_b [Rattus norvegicus]	47.3	47.3	100%	8e-05	87%	EDM04225.1
☐	vascular endothelial growth factor receptor 3 precursor [Rattus norvegicus]	47.3	47.3	100%	8e-05	87%	NP_446104.1
☐	vascular endothelial growth factor receptor 3 precursor [Mus musculus]	47.3	47.3	100%	8e-05	87%	NP_032055.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Ictidomys tridecer	47.3	47.3	100%	8e-05	87%	XP_005339388.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X2 [Felis c	47.3	47.3	100%	8e-05	87%	XP_006927561.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X1 [Felis c	47.3	47.3	100%	8e-05	87%	XP_006927560.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Canis lupus famili	47.3	47.3	100%	8e-05	87%	XP_005626341.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X4 [Balaer	47.3	47.3	100%	8e-05	87%	XP_007169893.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X3 [Balaer	47.3	47.3	100%	8e-05	87%	XP_007169892.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X2 [Balaer	47.3	47.3	100%	8e-05	87%	XP_007169891.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform X1 [Balaer	47.3	47.3	100%	8e-05	87%	XP_007169890.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Galeopterus varie	47.3	47.3	100%	8e-05	87%	XP_008570738.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Mesocricetus aura	47.3	47.3	100%	8e-05	87%	XP_005072029.1
☐	Vascular endothelial growth factor receptor 3 [Fukomys damarensis]	47.3	47.3	100%	8e-05	87%	KFO33406.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Microtus ochrogas	47.3	47.3	100%	8e-05	87%	XP_005350374.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Cavia porcellus]	47.3	47.3	100%	8e-05	87%	XP_003461142.2
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Otolemur garnetti	47.3	47.3	100%	8e-05	87%	XP_003799229.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Sus scrofa]	47.3	47.3	100%	8e-05	87%	XP_005661495.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Ceratotherium sin	47.3	47.3	100%	8e-05	87%	XP_004428735.1
☐	PREDICTED: vascular endothelial growth factor receptor 3-like [Physeter catc	47.3	47.3	100%	8e-05	87%	XP_007123800.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial growth factor re	47.3	47.3	100%	8e-05	87%	XP_006199176.1

⊟ Alignments

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Chain A, Crystal Structure Of Vegfr-3 Extracellular Domains D4-5

Sequence ID: pdb|4BSJ|A **Length:** 232 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 193 to 207 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	9e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    KLVIQNADVSAMYKC  15
            KLVIQNA+VSAMYKC
Sbjct  193  KLVIQNANVSAMYKC  207
```

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PREDICTED: vascular endothelial growth factor receptor 3, partial [Pongo abelii]

Sequence ID: ref|XP_009239654.1| **Length:** 440 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 408 to 422 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	1e-05	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    KLVIQNADVSAMYKC  15
            KLVIQNA+VSAMYKC
Sbjct  408  KLVIQNANVSAMYKC  422
```

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Vascular endothelial growth factor receptor 3 precursor variant [Homo sapiens]

Sequence ID: dbj|BAD92874.1| **Length:** 649 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 218 to 232 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	1e-05	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    KLVIQNADVSAMYKC  15
            KLVIQNA+VSAMYKC
Sbjct  218  KLVIQNANVSAMYKC  232
```

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soluble VEGFR3 variant 1 [Homo sapiens]

Sequence ID: gb|ACF47600.1| **Length:** 765 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 520 to 534 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	1e-05	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    KLVIQNADVSAMYKC  15
            KLVIQNA+VSAMYKC
Sbjct  520  KLVIQNANVSAMYKC  534
```

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PREDICTED: vascular endothelial growth factor receptor 3-like [Leptonychotes weddellii]

Sequence ID: ref|XP_006746634.1| **Length:** 968 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 126 to 140 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	1e-05	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    KLVIQNADVSAMYKC  15
            KLVIQNA+VSAMYKC
Sbjct  126  KLVIQNANVSAMYKC  140
```

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NCBI/ BLAST/ blastp suite/ **Formatting Results - B9E3NW7301R**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download

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FLT4_KLVIQNANVSAMYKC_NonMod

RID B9E3NW7301R (Expires on 01-14 13:17 pm)

Query ID lcl|282674
Description None
Molecule type amino acid
Query Length 15

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

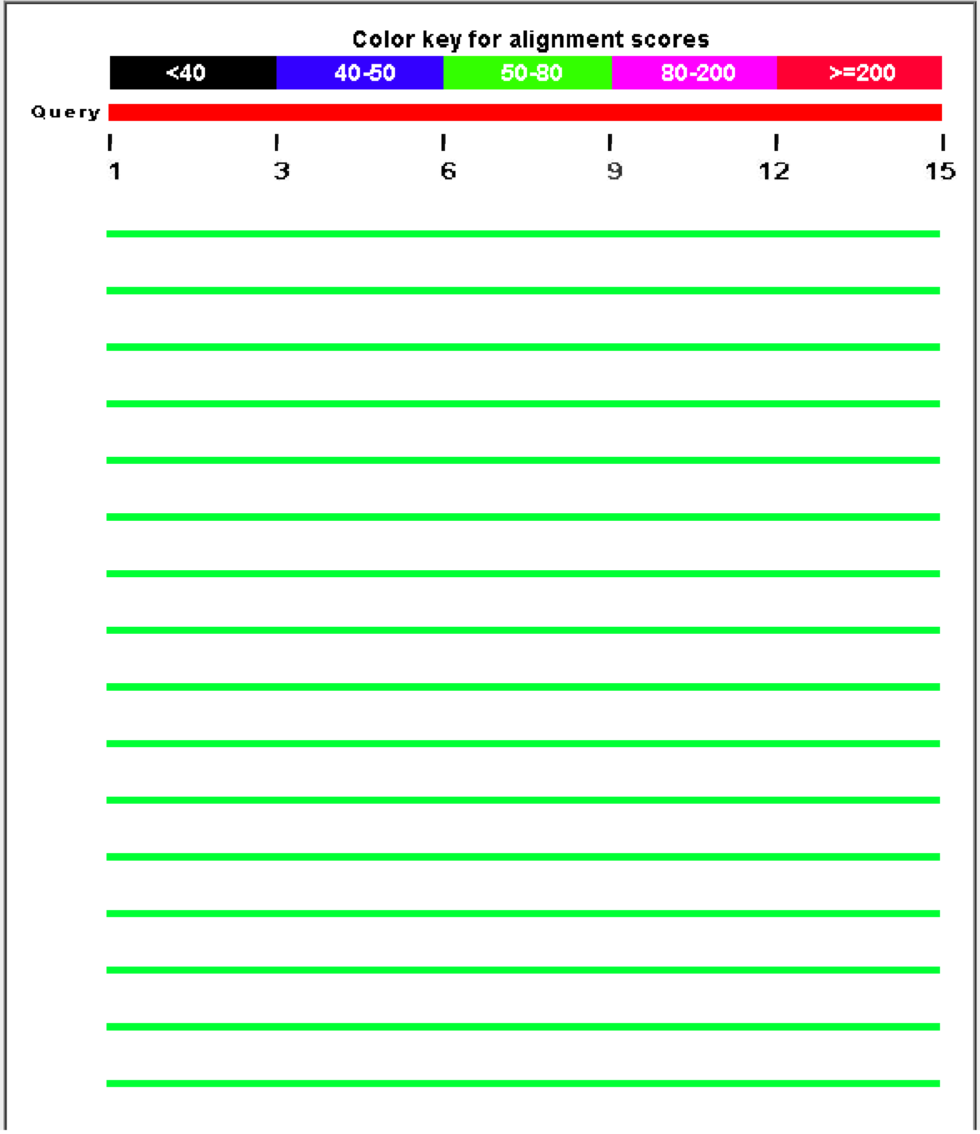
Graphic Summary

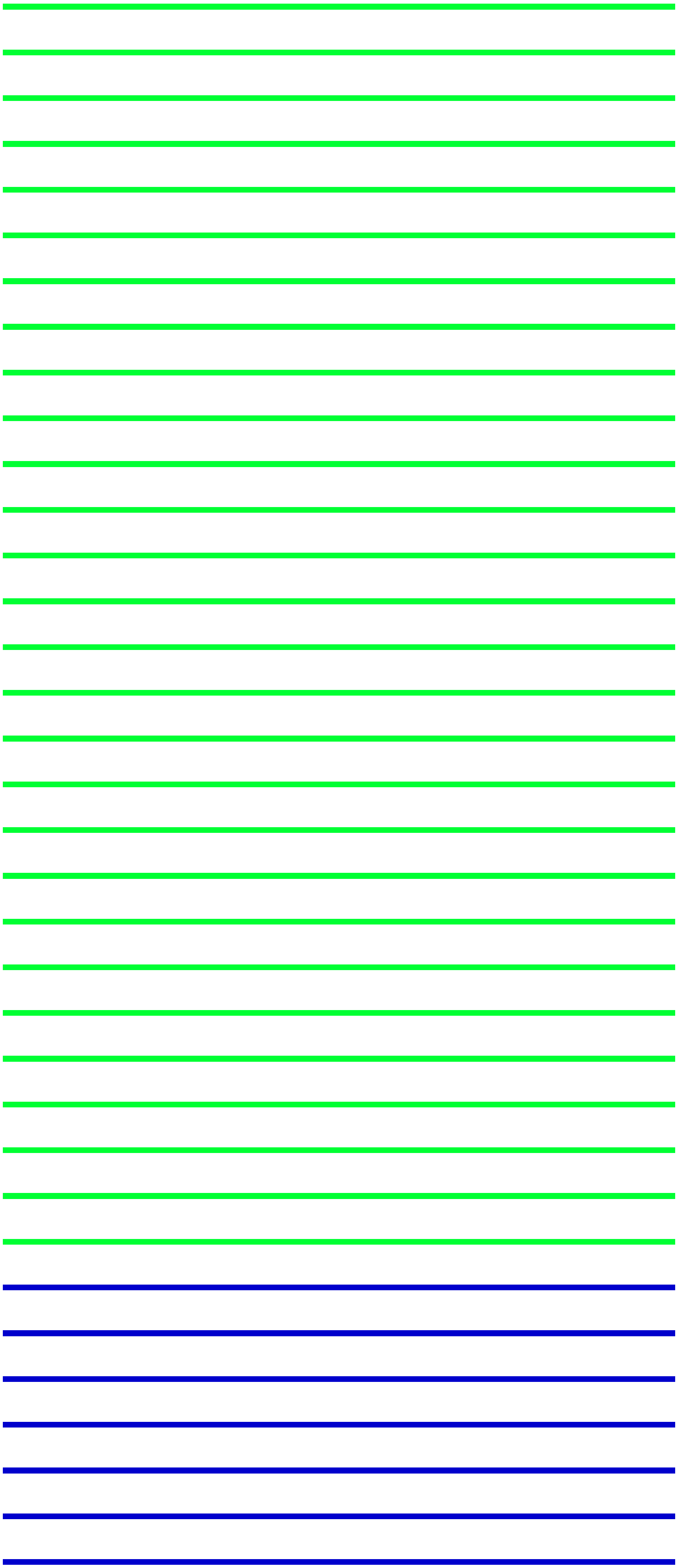
Show Conserved Domains

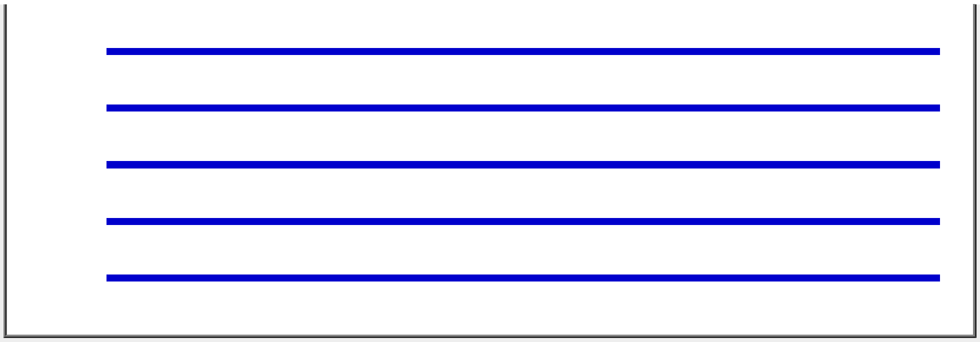
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of Vegfr-3 Extracellular Domains D4-5 [	52.4	52.4	100%	1e-06	100%	gi|528081982|4BSJ_A
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Pongo	52.4	52.4	100%	1e-06	100%	gi|686720607|XP_009239654.1
☐	Vascular endothelial growth factor receptor 3 precursor variant [Ho	52.4	52.4	100%	1e-06	100%	gi|62088854|BAD92874.1
☐	soluble VEGFR3 variant 1 [Homo sapiens]	52.4	52.4	100%	1e-06	100%	gi|194318424|ACF47600.1
☐	PREDICTED: vascular endothelial growth factor receptor 3-like [Le	52.4	52.4	100%	1e-06	100%	gi|585190706|XP_006746634.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|724882613|XP_010373329.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|694914105|XP_009448613.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|724882610|XP_010373327.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial grow	52.4	52.4	100%	1e-06	100%	gi|675644040|XP_008987571.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|635125862|XP_008013748.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|725607374|XP_010330147.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial grow	52.4	52.4	100%	1e-06	100%	gi|297676933|XP_002816373.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|635125860|XP_008013747.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|694914102|XP_009448612.1
☐	unnamed protein product [Homo sapiens]	52.4	52.4	100%	1e-06	100%	gi|297050|CAA49505.1
☐	vascular endothelial growth factor receptor 3 isoform 2 precursor [H	52.4	52.4	100%	1e-06	100%	gi|103472027|NP_002011.2
☐	unnamed protein product [Homo sapiens]	52.4	52.4	100%	1e-06	100%	gi|158256790|BAF84368.1
☐	VEGFR3 short form [Homo sapiens]	52.4	52.4	100%	1e-06	100%	gi|29691195|AAO89504.1
☐	FTL4 [Homo sapiens]	52.4	52.4	100%	1e-06	100%	gi|388522|CAA48290.1
☐	hypothetical protein PANDA_017671 [Ailuropoda melanoleuca]	52.4	52.4	100%	1e-06	100%	gi|281337917|EFB13501.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|694914100|XP_009448611.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|694914098|XP_009448610.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|724882607|XP_010373326.1
☐	PREDICTED: vascular endothelial growth factor receptor 3-like [Ma	52.4	52.4	100%	1e-06	100%	gi|297295921|XP_001107118.2
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Gorilla	52.4	52.4	100%	1e-06	100%	gi|426351351|XP_004043215.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|511878159|XP_004759037.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Ochoto	52.4	52.4	100%	1e-06	100%	gi|504181140|XP_004599097.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|635125858|XP_008013746.1
☐							

	PREDICTED: vascular endothelial growth factor receptor 3 [Macac	52.4	52.4	100%	1e-06	100%	gi|544441629|XP_005558869.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|403307013|XP_003944009.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial grow	52.4	52.4	100%	1e-06	100%	gi|402873672|XP_003900691.1
☐	VEGFR3 long form [Homo sapiens]	52.4	52.4	100%	1e-06	100%	gi|29691197|AAO89505.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|441595610|XP_003279615.2
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|410040129|XP_518160.4
☐	vascular endothelial growth factor receptor 3 isoform 1 precursor [H	52.4	52.4	100%	1e-06	100%	gi|104294888|NP_891555.2
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|511878157|XP_004759036.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|511878155|XP_004759035.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|694914096|XP_009448609.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Ursus	52.4	52.4	100%	1e-06	100%	gi|671033898|XP_008707769.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial grow	52.4	52.4	100%	1e-06	100%	gi|675687833|XP_008955193.1
☐	PREDICTED: vascular endothelial growth factor receptor 3-like [Ail	52.4	52.4	100%	1e-06	100%	gi|301784839|XP_002927834.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	52.4	52.4	100%	1e-06	100%	gi|694914094|XP_009448608.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Odobe	52.4	52.4	100%	1e-06	100%	gi|472386779|XP_004412739.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Erinac	52.4	52.4	100%	1e-06	100%	gi|617620255|XP_007527230.1
☐	PREDICTED: vascular endothelial growth factor receptor 3-like [Ta	49.8	49.8	100%	1e-05	93%	gi|640780561|XP_008072035.1
☐	rCG35022, isoform CRA_a [Rattus norvegicus]	49.8	49.8	100%	1e-05	93%	gi|149052407|EDM04224.1
☐	Vascular endothelial growth factor receptor 3 [Pteropus alecto]	49.8	49.8	100%	1e-05	93%	gi|431892755|ELK03188.1
☐	PREDICTED: vascular endothelial growth factor receptor 3-like [My	49.8	49.8	100%	1e-05	93%	gi|558217352|XP_006108959.1
☐	rCG35022, isoform CRA_c [Rattus norvegicus]	49.8	49.8	100%	1e-05	93%	gi|149052409|EDM04226.1
☐	receptor tyrosine kinase VEGFR-3kt [Rattus norvegicus]	49.8	49.8	100%	1e-05	93%	gi|16033530|AAL13270.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial grow	49.8	49.8	100%	1e-05	93%	gi|731455917|XP_010592785.1
☐	vascular endothelial growth factor receptor [Cricetulus griseus]	49.8	49.8	100%	1e-05	93%	gi|537140755|ERE67633.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|591313353|XP_007083127.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|586974127|XP_006927563.1
☐	Vascular endothelial growth factor receptor 3 [Cricetulus griseus]	49.8	49.8	100%	1e-05	93%	gi|344246770|EGW02874.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Myotis	49.8	49.8	100%	1e-05	93%	gi|554540751|XP_005865016.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Myotis	49.8	49.8	100%	1e-05	93%	gi|584062112|XP_006775477.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Pterop	49.8	49.8	100%	1e-05	93%	gi|586536882|XP_006923300.1
☐	FMS-like tyrosine kinase 4 [Mus musculus]	49.8	49.8	100%	1e-05	93%	gi|148701798|EDL33745.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial grow	49.8	49.8	100%	1e-05	93%	gi|625205554|XP_007644094.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|586974125|XP_006927562.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Camel	49.8	49.8	100%	1e-05	93%	gi|560898747|XP_006175816.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|591313351|XP_007083126.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|591313349|XP_007083125.1
☐	fms-related tyrosine kinase 4 isoform 1-like protein [Camelus ferus]	49.8	49.8	100%	1e-05	93%	gi|528768016|EPY87675.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|591313347|XP_007083124.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial grow	49.8	49.8	100%	1e-05	93%	gi|655883932|XP_002721370.2
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|731215213|XP_010622027.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|731215211|XP_010622026.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Orycte	49.8	49.8	100%	1e-05	93%	gi|634883366|XP_007951628.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Jaculus	49.8	49.8	100%	1e-05	93%	gi|507565865|XP_004666583.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Orcinus	49.8	49.8	100%	1e-05	93%	gi|466079414|XP_004284117.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Nanno	49.8	49.8	100%	1e-05	93%	gi|674085341|XP_008850448.1

☐	PREDICTED: vascular endothelial growth factor receptor 3 [Eptesic	49.8	49.8	100%	1e-05	93%	gi|641733026|XP_008156907.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Echino	49.8	49.8	100%	1e-05	93%	gi|507623209|XP_004697235.1
☐	PREDICTED: vascular endothelial growth factor receptor 3-like [Tu	49.8	49.8	100%	1e-05	93%	gi|470634767|XP_004322923.1
☐	rCG35022, isoform CRA_b [Rattus norvegicus]	49.8	49.8	100%	1e-05	93%	gi|149052408|EDM04225.1
☐	vascular endothelial growth factor receptor 3 precursor [Rattus norv	49.8	49.8	100%	1e-05	93%	gi|16758466|NP_446104.1
☐	vascular endothelial growth factor receptor 3 precursor [Mus muscu	49.8	49.8	100%	1e-05	93%	gi|6679813|NP_032055.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Ictidom	49.8	49.8	100%	1e-05	93%	gi|532109344|XP_005339388.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|586974123|XP_006927561.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|586974121|XP_006927560.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Canis l	49.8	49.8	100%	1e-05	93%	gi|545516115|XP_005626341.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|594632793|XP_007169893.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|594632791|XP_007169892.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|594632789|XP_007169891.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|594632787|XP_007169890.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Galeop	49.8	49.8	100%	1e-05	93%	gi|667270562|XP_008570738.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Mesocr	49.8	49.8	100%	1e-05	93%	gi|524939685|XP_005072029.1
☐	Vascular endothelial growth factor receptor 3 [Fukomys damarensis	49.8	49.8	100%	1e-05	93%	gi|676279442|KFO33406.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Microtu	49.8	49.8	100%	1e-05	93%	gi|532013185|XP_005350374.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Cavia p	49.8	49.8	100%	1e-05	93%	gi|514443259|XP_003461142.2
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Otolem	49.8	49.8	100%	1e-05	93%	gi|395853466|XP_003799229.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Sus scr	49.8	49.8	100%	1e-05	93%	gi|545811050|XP_005661495.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Cerato	49.8	49.8	100%	1e-05	93%	gi|478508908|XP_004428735.1
☐	PREDICTED: vascular endothelial growth factor receptor 3-like [Ph	49.8	49.8	100%	1e-05	93%	gi|593770855|XP_007123800.1
☐	PREDICTED: LOW QUALITY PROTEIN: vascular endothelial grow	49.8	49.8	100%	1e-05	93%	gi|560953322|XP_006199176.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 isoform	49.8	49.8	100%	1e-05	93%	gi|625276407|XP_007629826.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Triche	49.8	49.8	100%	1e-05	93%	gi|471411380|XP_004387243.1
☐	PREDICTED: vascular endothelial growth factor receptor 3 [Condyl	49.8	49.8	100%	1e-05	93%	gi|507979923|XP_004693728.1

⊟ Alignments

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Chain A, Crystal Structure Of Vegfr-3 Extracellular Domains D4-5

Sequence ID: gi|528081982|pdb|4BSJ|A **Length:** 232 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 193 to 207 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	1e-06	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KLVIQNANVSAMYKC  15
            KLVIQNANVSAMYKC
Sbjct  193  KLVIQNANVSAMYKC  207
```

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PREDICTED: vascular endothelial growth factor receptor 3, partial [Pongo abelii]

Sequence ID: gi|686720607|ref|XP_009239654.1| **Length:** 440 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 408 to 422 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	1e-06	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KLVIQNANVSAMYKC  15
```

```
           KLVIQNANVSAMYKC
Sbjct  408  KLVIQNANVSAMYKC  422
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Vascular endothelial growth factor receptor 3 precursor variant [Homo sapiens]

Sequence ID: gi|62088854|dbj|BAD92874.1| **Length:** 649 **Number of Matches:** 1

Range 1: 218 to 232 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	1e-06	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KLVIQNANVSAMYKC  15
           KLVIQNANVSAMYKC
Sbjct  218  KLVIQNANVSAMYKC  232
```

Related Information

Gene - associated gene details

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soluble VEGFR3 variant 1 [Homo sapiens]

Sequence ID: gi|194318424|gb|ACF47600.1| **Length:** 765 **Number of Matches:** 1

Range 1: 520 to 534 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	1e-06	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KLVIQNANVSAMYKC  15
           KLVIQNANVSAMYKC
Sbjct  520  KLVIQNANVSAMYKC  534
```

Related Information

Gene - associated gene details

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: vascular endothelial growth factor receptor 3-like [Leptonychotes weddellii]

Sequence ID: gi|585190706|ref|XP_006746634.1| **Length:** 968 **Number of Matches:** 1

Range 1: 126 to 140 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	1e-06	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KLVIQNANVSAMYKC  15
           KLVIQNANVSAMYKC
Sbjct  126  KLVIQNANVSAMYKC  140
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

GOLM1_KAVLVNDITTGERL_Mod

RID BVDXS4GB01R (Expires on 01-21 09:04 am)

Query ID	lcl|335339	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	14		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

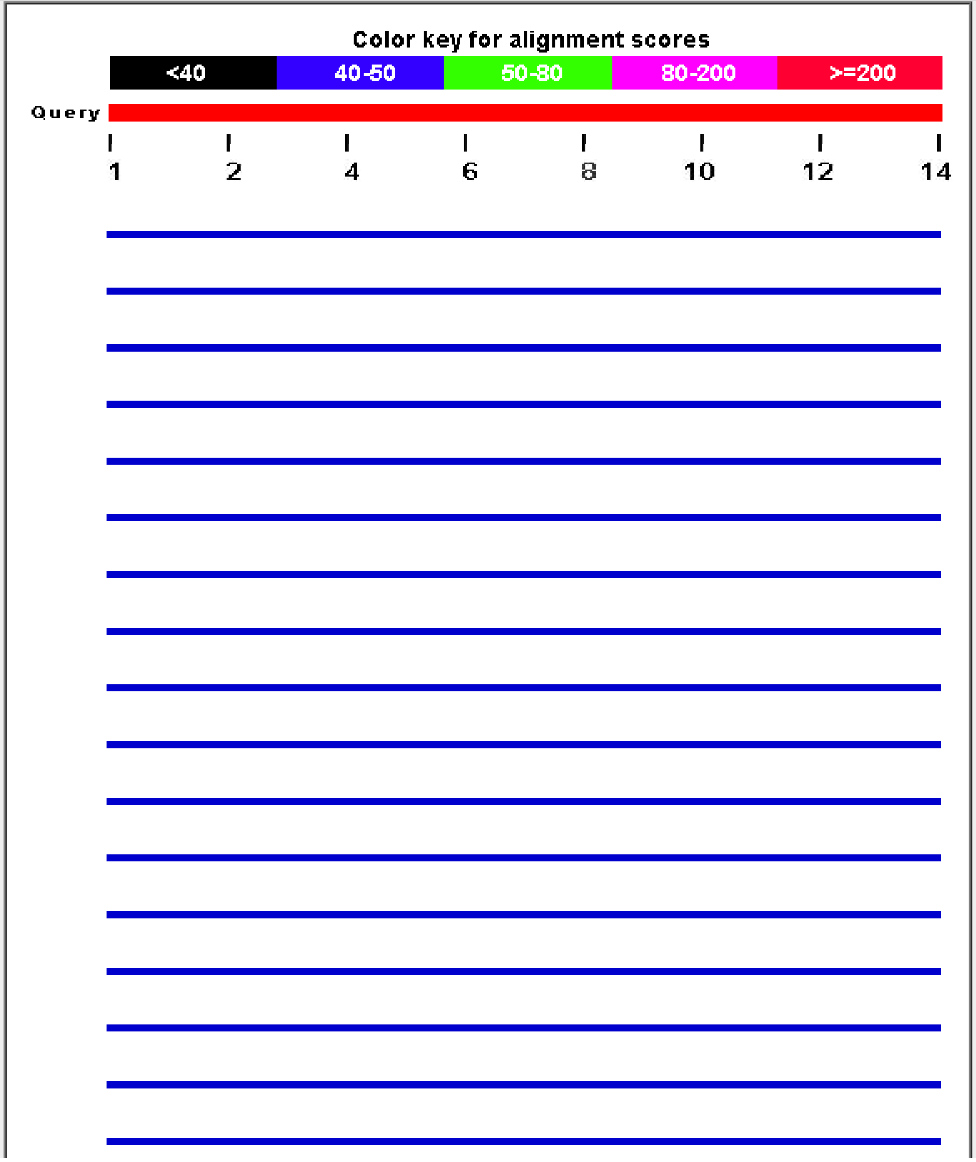
Graphic Summary

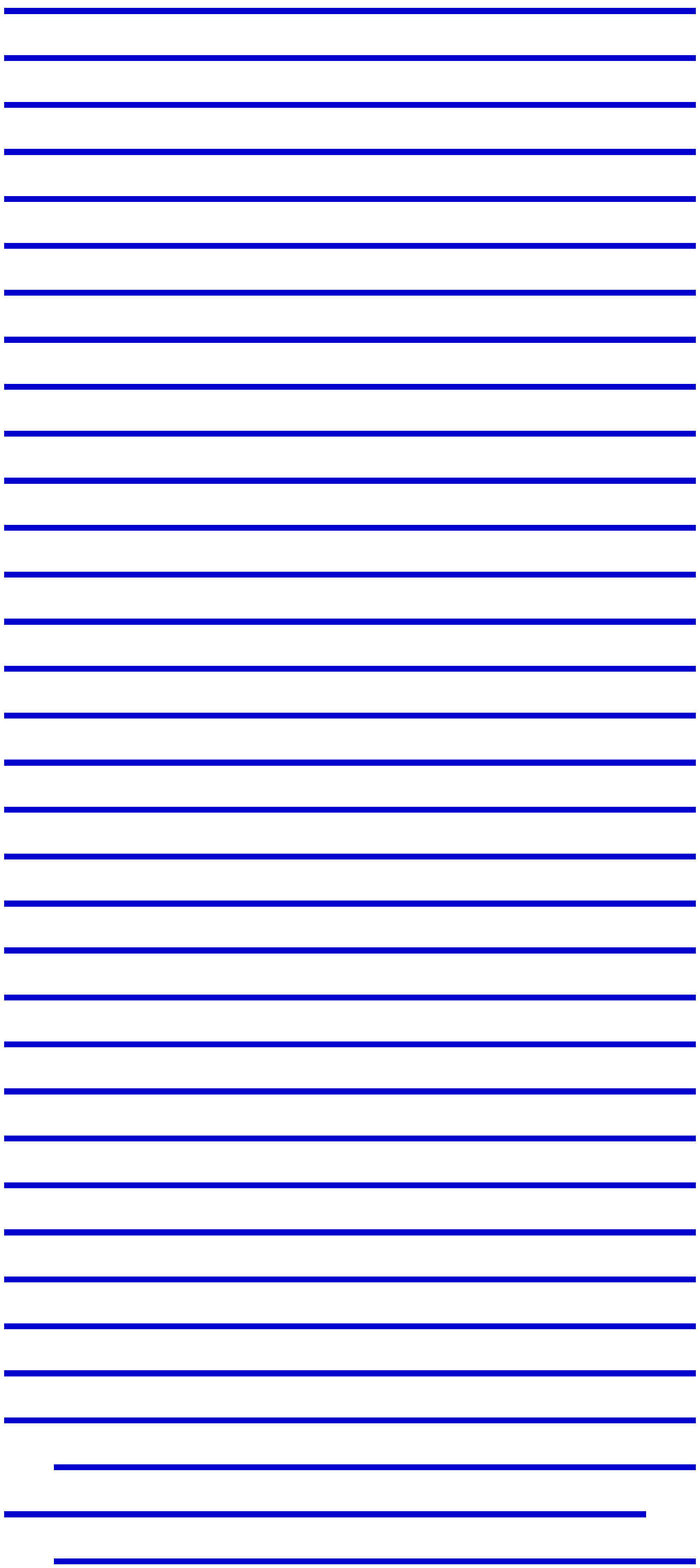
Show Conserved Domains

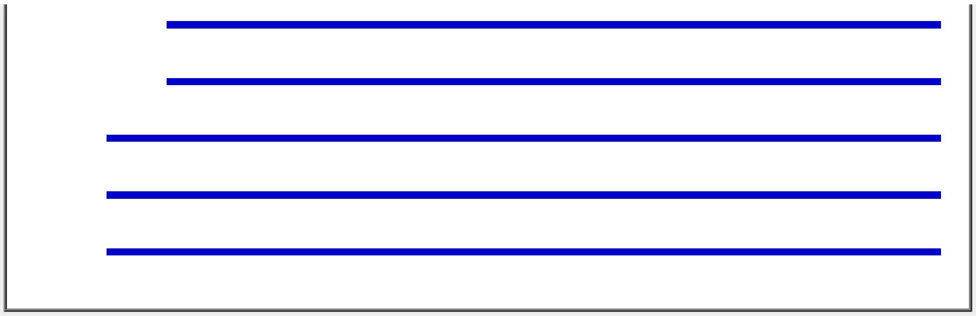
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: uncharacterized protein LOC104673793 [Rhinopithecus roxella	43.5	43.5	100%	0.001	93%	XP_010376237.1
☐	PREDICTED: Golgi membrane protein 1 [Camelus ferus]	43.5	43.5	100%	0.001	93%	XP_006187389.1
☐	PREDICTED: Golgi membrane protein 1 [Camelus dromedarius]	43.5	43.5	100%	0.001	93%	XP_010973186.1
☐	PREDICTED: Golgi membrane protein 1 [Ursus maritimus]	43.5	43.5	100%	0.001	93%	XP_008694047.1
☐	PREDICTED: Golgi membrane protein 1 isoform X5 [Pan paniscus]	43.5	43.5	100%	0.001	93%	XP_008959606.1
☐	PREDICTED: Golgi membrane protein 1 isoform X4 [Pan paniscus]	43.5	43.5	100%	0.001	93%	XP_008959605.1
☐	PREDICTED: Golgi membrane protein 1 isoform X5 [Bubalus bubalis]	43.5	43.5	100%	0.001	93%	XP_006066905.1
☐	PREDICTED: Golgi membrane protein 1 isoform X3 [Bos taurus]	43.5	43.5	100%	0.001	93%	XP_010806444.1
☐	PREDICTED: Golgi membrane protein 1 isoform X3 [Tarsius syrichta]	43.5	43.5	100%	0.001	93%	XP_008069750.1
☐	PREDICTED: Golgi membrane protein 1 isoform X4 [Bubalus bubalis]	43.5	43.5	100%	0.001	93%	XP_006066904.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Bos taurus]	43.5	43.5	100%	0.001	93%	XP_010806443.1
☐	PREDICTED: Golgi membrane protein 1 isoform X3 [Pan paniscus]	43.5	43.5	100%	0.001	93%	XP_008959604.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Tarsius syrichta]	43.5	43.5	100%	0.001	93%	XP_008069749.1
☐	PREDICTED: Golgi membrane protein 1 [Chrysochloris asiatica]	43.5	43.5	100%	0.001	93%	XP_006877790.1
☐	PREDICTED: Golgi membrane protein 1 isoform 2 [Nomascus leucogenys]	43.5	43.5	100%	0.001	93%	XP_004087075.1
☐	golgi membrane protein GP73 [Homo sapiens]	43.5	43.5	100%	0.001	93%	AAF44663.1
☐	GOLPH2 [Homo sapiens]	43.5	43.5	100%	0.001	93%	CAG33482.1
☐	PREDICTED: Golgi membrane protein 1 [Camelus bactrianus]	43.5	43.5	100%	0.001	93%	XP_010965740.1
☐	Golgi membrane protein 1 [Homo sapiens]	43.5	43.5	100%	0.001	93%	NP_057632.2
☐	PREDICTED: Golgi membrane protein 1 [Pantholops hodgsonii]	43.5	43.5	100%	0.001	93%	XP_005971557.1
☐	PREDICTED: Golgi membrane protein 1 [Ceratotherium simum simum]	43.5	43.5	100%	0.001	93%	XP_004440862.1
☐	PREDICTED: Golgi membrane protein 1 [Callithrix jacchus]	43.5	43.5	100%	0.001	93%	XP_002742818.2
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Tarsius syrichta]	43.5	43.5	100%	0.001	93%	XP_008069747.1
☐	PREDICTED: Golgi membrane protein 1 [Odobenus rosmarus divergens]	43.5	43.5	100%	0.001	93%	XP_004407641.1
☐	PREDICTED: Golgi membrane protein 1 [Chlorocebus sabaeus]	43.5	43.5	100%	0.001	93%	XP_007967835.1
☐	PREDICTED: Golgi membrane protein 1 [Papio anubis]	43.5	43.5	100%	0.001	93%	XP_003911922.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Pan paniscus]	43.5	43.5	100%	0.001	93%	XP_003809220.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Bubalus bubalis]	43.5	43.5	100%	0.001	93%	XP_006066901.1
☐	PREDICTED: Golgi membrane protein 1 [Bos mutus]	43.5	43.5	100%	0.001	93%	XP_005900661.1

☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Capra hircus]	43.5	43.5	100%	0.001	93%	XP_005684184.1
☐	PREDICTED: Golgi membrane protein 1 [Ovis aries]	43.5	43.5	100%	0.001	93%	XP_004004148.1
☐	Golgi membrane protein 1 [Bos taurus]	43.5	43.5	100%	0.001	93%	NP_001179392.1
☐	PREDICTED: Golgi membrane protein 1 [Orycteropus afer afer]	43.5	43.5	100%	0.001	93%	XP_007937219.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Canis lupus familiaris]	43.5	43.5	100%	0.001	93%	XP_005615865.1
☐	PREDICTED: LOW QUALITY PROTEIN: Golgi membrane protein 1 [Myotis d	43.5	43.5	100%	0.001	93%	XP_006759551.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Canis lupus familiaris]	43.5	43.5	100%	0.001	93%	XP_533506.4
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Capra hircus]	43.5	43.5	100%	0.001	93%	XP_005684183.1
☐	PREDICTED: Golgi membrane protein 1 [Sus scrofa]	43.5	43.5	100%	0.001	93%	XP_005656864.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Saimiri boliviensis bolivie	43.5	43.5	100%	0.001	93%	XP_010350172.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Saimiri boliviensis bolivie	43.5	43.5	100%	0.001	93%	XP_010350171.1
☐	PREDICTED: Golgi membrane protein 1 [Vicugna pacos]	43.5	43.5	100%	0.001	93%	XP_006209334.1
☐	PREDICTED: LOW QUALITY PROTEIN: Golgi membrane protein 1 [Myotis lu	43.5	43.5	100%	0.001	93%	XP_006102193.1
☐	PREDICTED: Golgi membrane protein 1-like [Ailuropoda melanoleuca]	43.5	43.5	100%	0.001	93%	XP_002915059.1
☐	PREDICTED: Golgi membrane protein 1 [Pan troglodytes]	43.5	43.5	100%	0.001	93%	XP_520104.5
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Pan paniscus]	43.5	43.5	100%	0.001	93%	XP_008959602.1
☐	PREDICTED: LOW QUALITY PROTEIN: Golgi membrane protein 1 [Myotis b	43.5	43.5	100%	0.001	93%	XP_005868323.1
☐	PREDICTED: Golgi membrane protein 1 [Bison bison bison]	43.5	43.5	100%	0.001	93%	XP_010838473.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Cricetulus griseus]	41.4	41.4	100%	0.006	86%	XP_007614235.1
☐	PREDICTED: Golgi membrane protein 1 [Pongo abelii]	40.5	40.5	92%	0.012	92%	XP_003777442.1
☐	PREDICTED: Golgi membrane protein 1 [Echinops telfairi]	40.5	40.5	92%	0.012	92%	XP_004716038.1
☐	Golgi membrane protein 1 [Bos mutus]	40.5	40.5	92%	0.012	92%	ELR52897.1
☐	Golgi membrane protein 1 [Myotis davidii]	40.5	40.5	92%	0.012	92%	ELK33482.1
☐	Cytosolic carboxypeptidase 1 [Myotis brandtii]	40.5	40.5	92%	0.013	92%	EPQ09014.1
☐	PREDICTED: Golgi membrane protein 1 [Oryctolagus cuniculus]	40.1	40.1	100%	0.017	86%	XP_008255630.1
☐	PREDICTED: Golgi membrane protein 1 [Panthera tigris altaica]	40.1	40.1	100%	0.017	86%	XP_007091183.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Physeter catodon]	40.1	40.1	100%	0.017	86%	XP_007118655.1
☐	Golgi membrane protein 1 [Mus musculus]	40.1	40.1	100%	0.017	86%	NP_001030294.1
☐	Golgi membrane protein 1 [Mus musculus]	40.1	40.1	100%	0.017	86%	AAH11152.1
☐	unnamed protein product [Mus musculus]	40.1	40.1	100%	0.017	86%	BAE21897.1
☐	unnamed protein product [Mus musculus]	40.1	40.1	100%	0.017	86%	BAE39697.1
☐	Golgi membrane protein 1 [Mus musculus]	40.1	40.1	100%	0.017	86%	AAH98486.1
☐	PREDICTED: Golgi membrane protein 1 [Eptesicus fuscus]	40.1	40.1	100%	0.017	86%	XP_008140237.1
☐	PREDICTED: Golgi membrane protein 1 [Ictidomys tridecemlineatus]	40.1	40.1	100%	0.017	86%	XP_005337493.1
☐	PREDICTED: LOW QUALITY PROTEIN: Golgi membrane protein 1 [Equus p	40.1	40.1	100%	0.017	86%	XP_008536302.1
☐	PREDICTED: Golgi membrane protein 1 [Otolemur garnettii]	40.1	40.1	100%	0.017	86%	XP_003783039.1
☐	PREDICTED: Golgi membrane protein 1 [Equus caballus]	40.1	40.1	100%	0.017	86%	XP_001495688.3
☐	PREDICTED: Golgi membrane protein 1 [Tupaia chinensis]	40.1	40.1	100%	0.017	86%	XP_006139911.1
☐	PREDICTED: Golgi membrane protein 1 [Lipotes vexillifer]	40.1	40.1	100%	0.017	86%	XP_007456171.1
☐	PREDICTED: Golgi membrane protein 1 isoform X3 [Balaenoptera acutorostra	40.1	40.1	100%	0.017	86%	XP_007177015.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Physeter catodon]	40.1	40.1	100%	0.017	86%	XP_007118654.1
☐	PREDICTED: Golgi membrane protein 1 [Tursiops truncatus]	40.1	40.1	100%	0.017	86%	XP_004317452.1
☐	PREDICTED: Golgi membrane protein 1 [Orcinus orca]	40.1	40.1	100%	0.017	86%	XP_004283095.1
☐	PREDICTED: Golgi membrane protein 1 [Felis catus]	40.1	40.1	100%	0.017	86%	XP_003995502.1
☐	PREDICTED: Golgi membrane protein 1 [Nannospalax galili]	40.1	40.1	100%	0.017	86%	XP_008831327.1

☐	PREDICTED: Golgi membrane protein 1 isoform X4 [Rattus norvegicus]	40.1	40.1	100%	0.017	86%	XP_001056825.3
☐	PREDICTED: Golgi membrane protein 1 isoform X3 [Rattus norvegicus]	40.1	40.1	100%	0.017	86%	XP_006253609.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Rattus norvegicus]	40.1	40.1	100%	0.017	86%	XP_006253608.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Rattus norvegicus]	40.1	40.1	100%	0.017	86%	XP_006222393.1
☐	PREDICTED: Golgi membrane protein 1 [Callithrix jacchus]	39.7	39.7	100%	0.023	86%	XP_009001845.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Cricetulus griseus]	38.4	38.4	92%	0.061	85%	XP_003512118.1
☐	Golgi membrane protein 1 [Cricetulus griseus]	38.4	38.4	92%	0.061	85%	EGW03539.1
☐	PREDICTED: Golgi membrane protein 1 [Condylura cristata]	37.1	37.1	100%	0.16	79%	XP_004678038.1
☐	PREDICTED: Golgi membrane protein 1 isoform 3 [Dasypus novemcinctus]	37.1	37.1	100%	0.16	79%	XP_004461590.1
☐	PREDICTED: Golgi membrane protein 1 [Pteropus alecto]	37.1	37.1	100%	0.16	79%	XP_006916141.1
☐	PREDICTED: Golgi membrane protein 1 [Trichechus manatus latirostris]	37.1	37.1	100%	0.16	79%	XP_004381373.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Balaenoptera acutorostra	37.1	37.1	92%	0.16	85%	XP_007177014.1
☐	PREDICTED: Golgi membrane protein 1 isoform 2 [Dasypus novemcinctus]	37.1	37.1	100%	0.16	79%	XP_004461589.1
☐	PREDICTED: Golgi membrane protein 1 isoform 1 [Dasypus novemcinctus]	37.1	37.1	100%	0.16	79%	XP_004461588.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Balaenoptera acutorostra	37.1	37.1	92%	0.16	85%	XP_007177013.1
☐	Golgi membrane protein 1 [Pteropus alecto]	37.1	37.1	100%	0.16	79%	ELK09097.1
☐	Golgi membrane protein 1 [Tupaia chinensis]	37.1	37.1	92%	0.17	85%	ELW72919.1
☐	PREDICTED: Golgi membrane protein 1 [Peromyscus maniculatus bairdii]	36.7	36.7	100%	0.22	79%	XP_006981757.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Mustela putorius furo]	36.7	36.7	100%	0.22	79%	XP_004816631.1
☐	PREDICTED: Golgi membrane protein 1 isoform X3 [Mustela putorius furo]	36.7	36.7	100%	0.22	79%	XP_004774167.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Mustela putorius furo]	36.7	36.7	100%	0.22	79%	XP_004774166.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Mustela putorius furo]	36.7	36.7	100%	0.22	79%	XP_004774165.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Chinchilla lanigera]	36.3	36.3	100%	0.30	79%	XP_005387979.1
☐	PREDICTED: Golgi membrane protein 1 [Octodon degus]	36.3	36.3	100%	0.30	79%	XP_004639443.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Chinchilla lanigera]	36.3	36.3	100%	0.30	79%	XP_005387978.1
☐	PREDICTED: Golgi membrane protein 1 [Microtus ochrogaster]	34.6	34.6	100%	1.1	71%	XP_005355363.1

⊟ Alignments

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PREDICTED: uncharacterized protein LOC104673793, partial [Rhinopithecus roxellana]

Sequence ID: ref|XP_010376237.1| **Length:** 292 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 247 to 260 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
43.5 bits(95)	0.001	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KAVLVNDITTGERL  14
            KAVLVN+ITTGERL
Sbjct  247  KAVLVNNITTGERL  260
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: Golgi membrane protein 1 [Camelus ferus]

Sequence ID: ref|XP_006187389.1| **Length:** 313 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 103 to 116 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
43.5 bits(95)	0.001	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KAVLVNDITTGERL  14
            KAVLVN+ITTGERL
Sbjct  103  KAVLVNNITTGERL  116
```

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PREDICTED: Golgi membrane protein 1 [Camelus dromedarius]

Sequence ID: ref|XP_010973186.1| **Length:** 322 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 103 to 116 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
43.5 bits(95)	0.001	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KAVLVNDITTGERL  14
            KAVLVN+ITTGERL
Sbjct  103  KAVLVNNITTGERL  116
```

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PREDICTED: Golgi membrane protein 1 [Ursus maritimus]

Sequence ID: ref|XP_008694047.1| **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 103 to 116 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
43.5 bits(95)	0.001	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KAVLVNDITTGERL  14
            KAVLVN+ITTGERL
Sbjct  103  KAVLVNNITTGERL  116
```

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PREDICTED: Golgi membrane protein 1 isoform X5 [Pan paniscus]

Sequence ID: ref|XP_008959606.1| **Length:** 382 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 103 to 116 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
43.5 bits(95)	0.001	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KAVLVNDITTGERL  14
            KAVLVN+ITTGERL
Sbjct  103  KAVLVNNITTGERL  116
```

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Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

GOLM1_KAVLVNNITTGERL_NonMod

RID B9E6EREC01R (Expires on 01-14 13:18 pm)

Query ID lcl|305648
Description None
Molecule type amino acid
Query Length 14

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

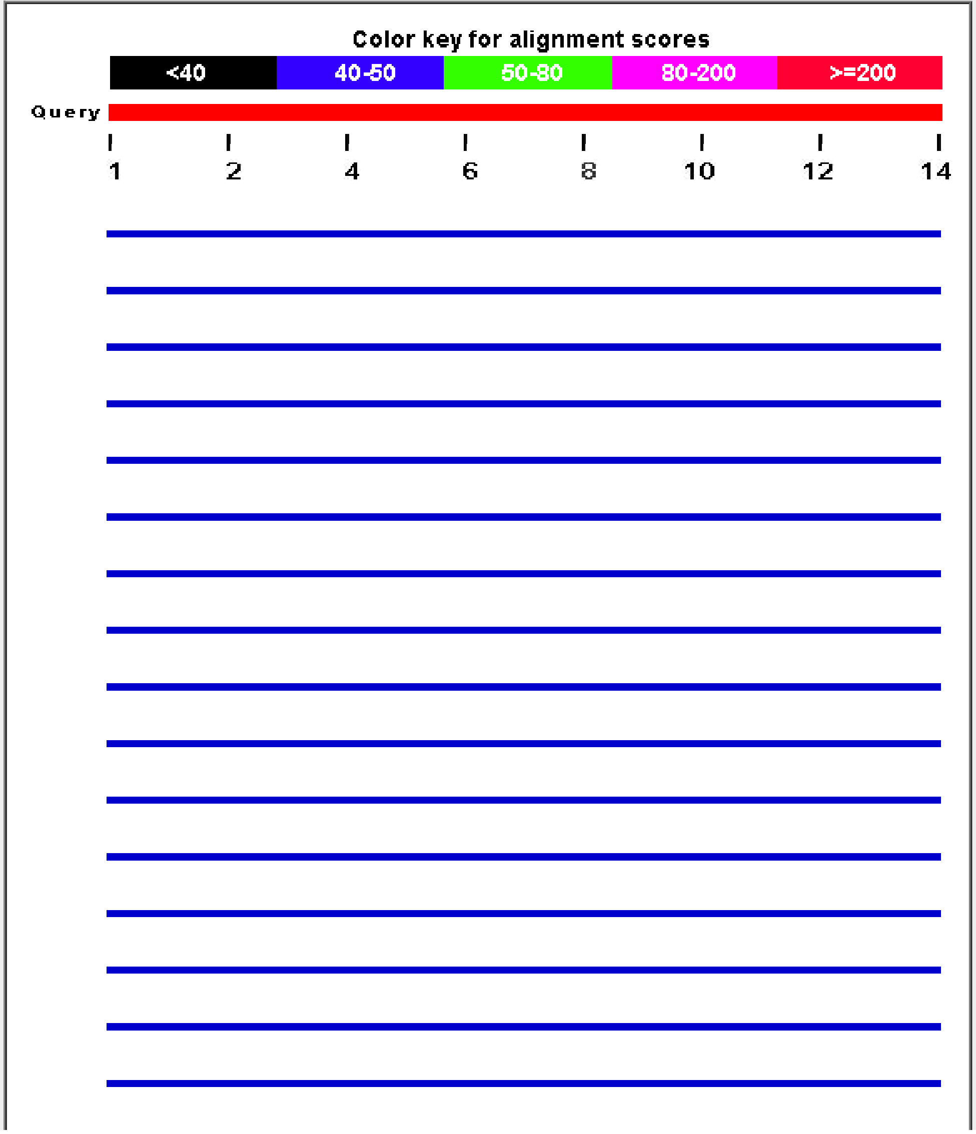
Graphic Summary

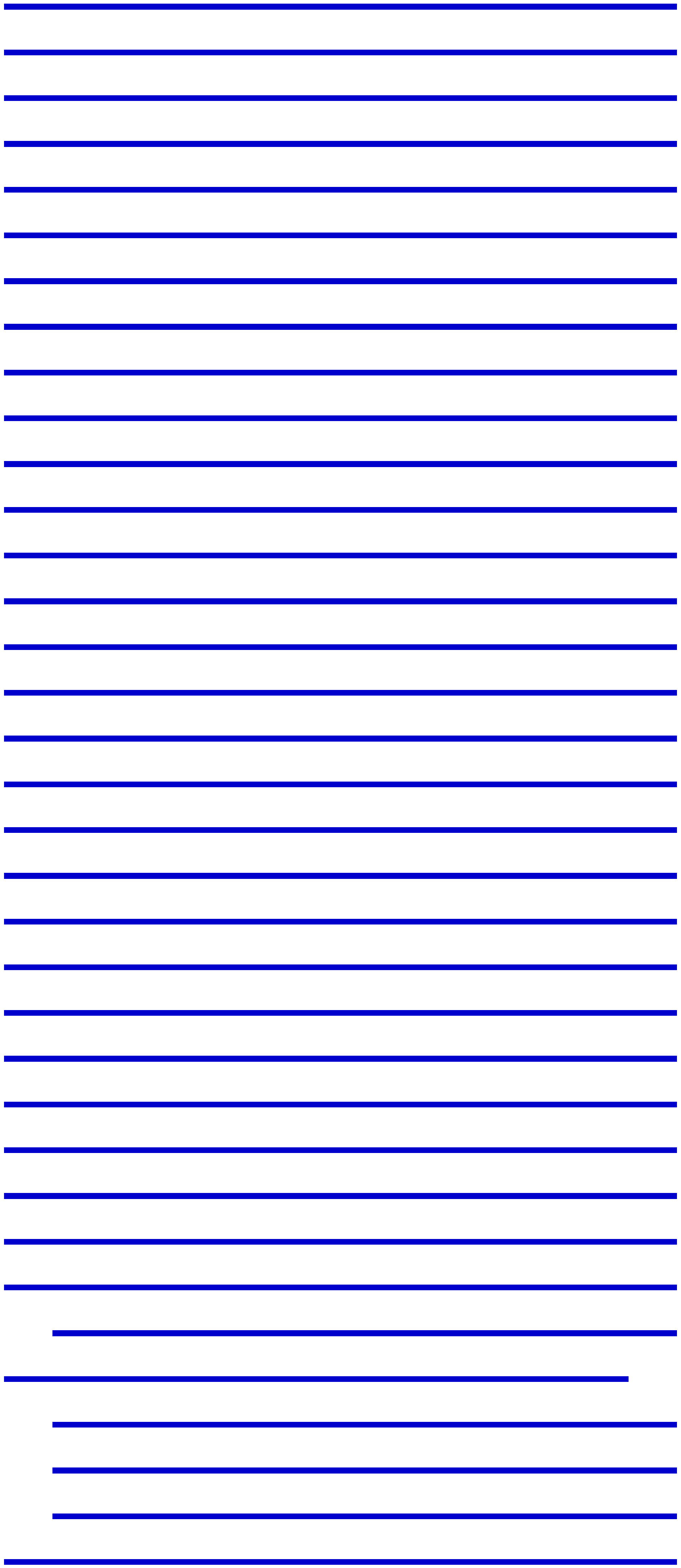
Show Conserved Domains

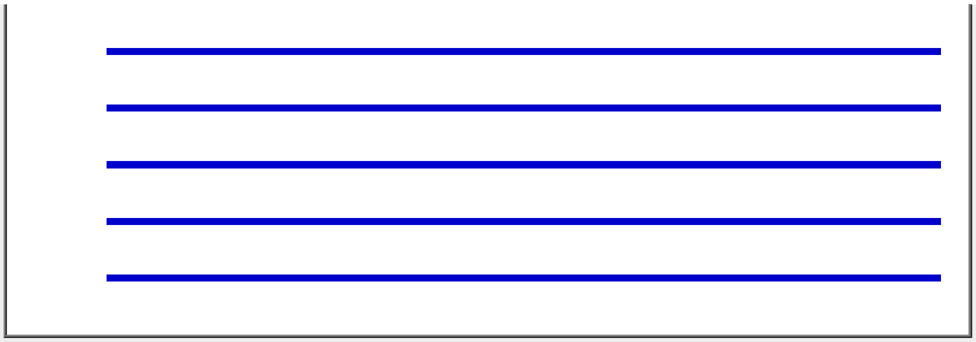
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: uncharacterized protein LOC104673793 [Rhinopithec	46.0	46.0	100%	2e-04	100%	gi|724801945|XP_010376237.1
☐	PREDICTED: Golgi membrane protein 1 [Camelus ferus]	46.0	46.0	100%	2e-04	100%	gi|560922380|XP_006187389.1
☐	PREDICTED: Golgi membrane protein 1 [Ursus maritimus]	46.0	46.0	100%	2e-04	100%	gi|671006359|XP_008694047.1
☐	PREDICTED: Golgi membrane protein 1 isoform X5 [Pan paniscus]	46.0	46.0	100%	2e-04	100%	gi|675701076|XP_008959606.1
☐	PREDICTED: Golgi membrane protein 1 isoform X4 [Pan paniscus]	46.0	46.0	100%	2e-04	100%	gi|675701074|XP_008959605.1
☐	PREDICTED: Golgi membrane protein 1 isoform X5 [Bubalus bubal	46.0	46.0	100%	2e-04	100%	gi|594086823|XP_006066905.1
☐	PREDICTED: Golgi membrane protein 1 isoform X5 [Bos taurus]	46.0	46.0	100%	2e-04	100%	gi|528959493|XP_005210451.1
☐	PREDICTED: Golgi membrane protein 1 isoform X3 [Tarsius syricht	46.0	46.0	100%	2e-04	100%	gi|640825296|XP_008069750.1
☐	PREDICTED: Golgi membrane protein 1 isoform X4 [Bubalus bubal	46.0	46.0	100%	2e-04	100%	gi|594086821|XP_006066904.1
☐	PREDICTED: Golgi membrane protein 1 isoform X4 [Bos taurus]	46.0	46.0	100%	2e-04	100%	gi|528959491|XP_005210450.1
☐	PREDICTED: Golgi membrane protein 1 isoform X3 [Pan paniscus]	46.0	46.0	100%	2e-04	100%	gi|675701072|XP_008959604.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Tarsius syricht	46.0	46.0	100%	2e-04	100%	gi|640825294|XP_008069749.1
☐	PREDICTED: Golgi membrane protein 1 [Chrysochloris asiatica]	46.0	46.0	100%	2e-04	100%	gi|586494692|XP_006877790.1
☐	PREDICTED: Golgi membrane protein 1 isoform 2 [Nomascus leuc	46.0	46.0	100%	2e-04	100%	gi|441593338|XP_004087075.1
☐	golgi membrane protein GP73 [Homo sapiens]	46.0	46.0	100%	2e-04	100%	gi|7271867|AAF44663.1
☐	GOLPH2 [Homo sapiens]	46.0	46.0	100%	2e-04	100%	gi|48146519|CAG33482.1
☐	Golgi membrane protein 1 [Homo sapiens]	46.0	46.0	100%	2e-04	100%	gi|29550838|NP_057632.2
☐	PREDICTED: Golgi membrane protein 1 [Pantholops hodgsonii]	46.0	46.0	100%	2e-04	100%	gi|556752330|XP_005971557.1
☐	PREDICTED: Golgi membrane protein 1 [Ceratotherium simum sim	46.0	46.0	100%	2e-04	100%	gi|478533440|XP_004440862.1
☐	PREDICTED: Golgi membrane protein 1 [Callithrix jacchus]	46.0	46.0	100%	2e-04	100%	gi|675637249|XP_002742818.2
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Tarsius syricht	46.0	46.0	100%	2e-04	100%	gi|640825292|XP_008069747.1
☐	PREDICTED: Golgi membrane protein 1 [Odobenus rosmarus diver	46.0	46.0	100%	2e-04	100%	gi|472376412|XP_004407641.1
☐	PREDICTED: Golgi membrane protein 1 [Chlorocebus sabaeus]	46.0	46.0	100%	2e-04	100%	gi|635074424|XP_007967835.1
☐	PREDICTED: Golgi membrane protein 1 [Papio anubis]	46.0	46.0	100%	2e-04	100%	gi|402897779|XP_003911922.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Pan paniscus]	46.0	46.0	100%	2e-04	100%	gi|397475597|XP_003809220.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Bubalus bubal	46.0	46.0	100%	2e-04	100%	gi|594086815|XP_006066901.1
☐	PREDICTED: Golgi membrane protein 1 [Bos mutus]	46.0	46.0	100%	2e-04	100%	gi|555977415|XP_005900661.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Capra hircus]	46.0	46.0	100%	2e-04	100%	gi|548477923|XP_005684184.1
☐							

	PREDICTED: Golgi membrane protein 1 [Ovis aries]	46.0	46.0	100%	2e-04	100%	gi|426219885|XP_004004148.1
☐	Golgi membrane protein 1 [Bos taurus]	46.0	46.0	100%	2e-04	100%	gi|300794576|NP_001179392.1
☐	PREDICTED: Golgi membrane protein 1 [Orycteropus afer afer]	46.0	46.0	100%	2e-04	100%	gi|634822876|XP_007937219.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Canis lupus fa	46.0	46.0	100%	2e-04	100%	gi|545486427|XP_005615865.1
☐	PREDICTED: LOW QUALITY PROTEIN: Golgi membrane protein 1	46.0	46.0	100%	2e-04	100%	gi|584078847|XP_006759551.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Canis lupus fa	46.0	46.0	100%	2e-04	100%	gi|545486425|XP_533506.4
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Capra hircus]	46.0	46.0	100%	2e-04	100%	gi|548477921|XP_005684183.1
☐	PREDICTED: Golgi membrane protein 1 [Sus scrofa]	46.0	46.0	100%	2e-04	100%	gi|545852940|XP_005656864.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Saimiri bolivie	46.0	46.0	100%	2e-04	100%	gi|725600181|XP_010350172.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Saimiri bolivie	46.0	46.0	100%	2e-04	100%	gi|725600179|XP_010350171.1
☐	PREDICTED: Golgi membrane protein 1 [Vicugna pacos]	46.0	46.0	100%	2e-04	100%	gi|560974024|XP_006209334.1
☐	PREDICTED: LOW QUALITY PROTEIN: Golgi membrane protein 1	46.0	46.0	100%	2e-04	100%	gi|558185268|XP_006102193.1
☐	PREDICTED: Golgi membrane protein 1-like [Ailuropoda melanoleu	46.0	46.0	100%	2e-04	100%	gi|301758432|XP_002915059.1
☐	PREDICTED: Golgi membrane protein 1 [Pan troglodytes]	46.0	46.0	100%	2e-04	100%	gi|694930481|XP_520104.5
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Pan paniscus]	46.0	46.0	100%	2e-04	100%	gi|675701065|XP_008959602.1
☐	PREDICTED: LOW QUALITY PROTEIN: Golgi membrane protein 1	46.0	46.0	100%	2e-04	100%	gi|554547544|XP_005868323.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Cricetulus gris	43.9	43.9	100%	8e-04	93%	gi|625245956|XP_007614235.1
☐	PREDICTED: Golgi membrane protein 1 [Pongo abelii]	43.1	43.1	92%	0.002	100%	gi|395740598|XP_003777442.1
☐	PREDICTED: Golgi membrane protein 1 [Echinops telfairi]	43.1	43.1	92%	0.002	100%	gi|507704042|XP_004716038.1
☐	Golgi membrane protein 1 [Bos mutus]	43.1	43.1	92%	0.002	100%	gi|440902052|ELR52897.1
☐	Golgi membrane protein 1 [Myotis davidii]	43.1	43.1	92%	0.002	100%	gi|432109012|ELK33482.1
☐	Cytosolic carboxypeptidase 1 [Myotis brandtii]	43.1	43.1	92%	0.002	100%	gi|521027226|EPQ09014.1
☐	PREDICTED: Golgi membrane protein 1 [Oryctolagus cuniculus]	42.6	42.6	100%	0.002	93%	gi|655600783|XP_008255630.1
☐	PREDICTED: Golgi membrane protein 1 [Panthera tigris altaica]	42.6	42.6	100%	0.002	93%	gi|591330699|XP_007091183.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Physeter catod	42.6	42.6	100%	0.002	93%	gi|593759817|XP_007118655.1
☐	Golgi membrane protein 1 [Mus musculus]	42.6	42.6	100%	0.002	93%	gi|78190500|NP_001030294.1
☐	Golgi membrane protein 1 [Mus musculus]	42.6	42.6	100%	0.002	93%	gi|15029858|AAH11152.1
☐	unnamed protein product [Mus musculus]	42.6	42.6	100%	0.002	93%	gi|74228820|BAE21897.1
☐	unnamed protein product [Mus musculus]	42.6	42.6	100%	0.002	93%	gi|74198427|BAE39697.1
☐	Golgi membrane protein 1 [Mus musculus]	42.6	42.6	100%	0.002	93%	gi|68534689|AAH98486.1
☐	PREDICTED: Golgi membrane protein 1 [Eptesicus fuscus]	42.6	42.6	100%	0.002	93%	gi|641703059|XP_008140237.1
☐	PREDICTED: Golgi membrane protein 1 [Ictidomys tridecemlineatu	42.6	42.6	100%	0.002	93%	gi|532103791|XP_005337493.1
☐	PREDICTED: LOW QUALITY PROTEIN: Golgi membrane protein 1	42.6	42.6	100%	0.002	93%	gi|664757550|XP_008536302.1
☐	PREDICTED: Golgi membrane protein 1 [Otolemur garnettii]	42.6	42.6	100%	0.002	93%	gi|395819314|XP_003783039.1
☐	PREDICTED: Golgi membrane protein 1 [Equus caballus]	42.6	42.6	100%	0.002	93%	gi|338719632|XP_001495688.3
☐	PREDICTED: Golgi membrane protein 1 [Tupaia chinensis]	42.6	42.6	100%	0.002	93%	gi|562819874|XP_006139911.1
☐	PREDICTED: Golgi membrane protein 1 [Lipotes vexillifer]	42.6	42.6	100%	0.002	93%	gi|602687893|XP_007456171.1
☐	PREDICTED: Golgi membrane protein 1 isoform X3 [Balaenoptera a	42.6	42.6	100%	0.002	93%	gi|594657336|XP_007177015.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Physeter catod	42.6	42.6	100%	0.002	93%	gi|593759815|XP_007118654.1
☐	PREDICTED: Golgi membrane protein 1 [Tursiops truncatus]	42.6	42.6	100%	0.002	93%	gi|470617224|XP_004317452.1
☐	PREDICTED: Golgi membrane protein 1 [Orcinus orca]	42.6	42.6	100%	0.002	93%	gi|466074240|XP_004283095.1
☐	PREDICTED: Golgi membrane protein 1 [Felis catus]	42.6	42.6	100%	0.002	93%	gi|410978237|XP_003995502.1
☐	PREDICTED: Golgi membrane protein 1 [Nannospalax galili]	42.6	42.6	100%	0.002	93%	gi|674050240|XP_008831327.1
☐	PREDICTED: Golgi membrane protein 1 isoform X4 [Rattus norveg	42.6	42.6	100%	0.002	93%	gi|564390273|XP_001056825.3
☐	PREDICTED: Golgi membrane protein 1 isoform X3 [Rattus norveg	42.6	42.6	100%	0.002	93%	gi|564390271|XP_006253609.1

☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Rattus norveg	42.6	42.6	100%	0.002	93%	gi|564390269|XP_006253608.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Rattus norveg	42.6	42.6	100%	0.002	93%	gi|564319421|XP_006222393.1
☐	PREDICTED: Golgi membrane protein 1 [Callithrix jacchus]	42.2	42.2	100%	0.003	93%	gi|675678184|XP_009001845.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Cricetulus gris	40.9	40.9	92%	0.008	92%	gi|354500055|XP_003512118.1
☐	Golgi membrane protein 1 [Cricetulus griseus]	40.9	40.9	92%	0.008	92%	gi|344247435|EGW03539.1
☐	PREDICTED: Golgi membrane protein 1 [Condylura cristata]	39.7	39.7	100%	0.022	86%	gi|507933604|XP_004678038.1
☐	PREDICTED: Golgi membrane protein 1 isoform 3 [Dasypus novem	39.7	39.7	100%	0.022	86%	gi|488539956|XP_004461590.1
☐	PREDICTED: Golgi membrane protein 1 [Pteropus alecto]	39.7	39.7	100%	0.022	86%	gi|586565826|XP_006916141.1
☐	PREDICTED: Golgi membrane protein 1 [Trichechus manatus latirc	39.7	39.7	100%	0.022	86%	gi|471395002|XP_004381373.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Balaenoptera a	39.7	39.7	92%	0.022	92%	gi|594657334|XP_007177014.1
☐	PREDICTED: Golgi membrane protein 1 isoform 2 [Dasypus novem	39.7	39.7	100%	0.022	86%	gi|488539954|XP_004461589.1
☐	PREDICTED: Golgi membrane protein 1 isoform 1 [Dasypus novem	39.7	39.7	100%	0.022	86%	gi|488539952|XP_004461588.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Balaenoptera a	39.7	39.7	92%	0.022	92%	gi|594657332|XP_007177013.1
☐	Golgi membrane protein 1 [Pteropus alecto]	39.7	39.7	100%	0.022	86%	gi|431902882|ELK09097.1
☐	Golgi membrane protein 1 [Tupaia chinensis]	39.7	39.7	92%	0.023	92%	gi|444732635|ELW72919.1
☐	PREDICTED: Golgi membrane protein 1 [Peromyscus maniculatus	39.2	39.2	100%	0.030	86%	gi|589938004|XP_006981757.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Mustela putori	39.2	39.2	100%	0.030	86%	gi|511998126|XP_004816631.1
☐	PREDICTED: Golgi membrane protein 1 isoform X3 [Mustela putori	39.2	39.2	100%	0.031	86%	gi|511909490|XP_004774167.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Mustela putori	39.2	39.2	100%	0.031	86%	gi|511909488|XP_004774166.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Mustela putori	39.2	39.2	100%	0.031	86%	gi|511909486|XP_004774165.1
☐	PREDICTED: Golgi membrane protein 1 isoform X2 [Chinchilla lani	38.8	38.8	100%	0.042	86%	gi|533147122|XP_005387979.1
☐	PREDICTED: Golgi membrane protein 1 [Octodon degus]	38.8	38.8	100%	0.042	86%	gi|507681012|XP_004639443.1
☐	PREDICTED: Golgi membrane protein 1 isoform X1 [Chinchilla lani	38.8	38.8	100%	0.042	86%	gi|533147120|XP_005387978.1
☐	PREDICTED: Golgi membrane protein 1 [Microtus ochrogaster]	37.1	37.1	100%	0.15	79%	gi|532024082|XP_005355363.1
☐	PREDICTED: Golgi membrane protein 1-like [Elephantulus edwardi	36.3	36.3	100%	0.29	86%	gi|585714388|XP_006900934.1
☐	PREDICTED: Golgi membrane protein 1 [Loxodonta africana]	36.3	36.3	100%	0.29	79%	gi|344271969|XP_003407809.1
☐	Golgi membrane protein 1 [Chelonia mydas]	35.8	35.8	92%	0.37	85%	gi|465964601|EMP30393.1

⊟ Alignments

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PREDICTED: uncharacterized protein LOC104673793, partial [Rhinopithecus roxellana]

Sequence ID: gi|724801945|ref|XP_010376237.1| **Length:** 292 **Number of Matches:** 1

Range 1: 247 to 260 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.0 bits(101)	2e-04	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KAVLVNNITTGERL  14
            KAVLVNNITTGERL
Sbjct  247  KAVLVNNITTGERL  260
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: Golgi membrane protein 1 [Camelus ferus]

Sequence ID: gi|560922380|ref|XP_006187389.1| **Length:** 313 **Number of Matches:** 1

Range 1: 103 to 116 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.0 bits(101)	2e-04	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KAVLVNNITTGERL  14
```

Related Information

Gene - associated gene details

```
                KAVLVNNITTGERL
Sbjct  103  KAVLVNNITTGERL  116
```

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PREDICTED: Golgi membrane protein 1 [Ursus maritimus]

Sequence ID: gi|671006359|ref|XP_008694047.1| **Length:** 373 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 103 to 116 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.0 bits(101)	2e-04	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KAVLVNNITTGERL  14
            KAVLVNNITTGERL
Sbjct  103  KAVLVNNITTGERL  116
```

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PREDICTED: Golgi membrane protein 1 isoform X5 [Pan paniscus]

Sequence ID: gi|675701076|ref|XP_008959606.1| **Length:** 382 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 103 to 116 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.0 bits(101)	2e-04	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KAVLVNNITTGERL  14
            KAVLVNNITTGERL
Sbjct  103  KAVLVNNITTGERL  116
```

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PREDICTED: Golgi membrane protein 1 isoform X4 [Pan paniscus]

Sequence ID: gi|675701074|ref|XP_008959605.1| **Length:** 383 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 103 to 116 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.0 bits(101)	2e-04	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KAVLVNNITTGERL  14
            KAVLVNNITTGERL
Sbjct  103  KAVLVNNITTGERL  116
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVDYR8U601R

Your search parameters were adjusted to search for a short input sequence.

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GPLD1_KEKLNVEAADWTVRG_Mod

RID BVDYR8U601R (Expires on 01-21 09:05 am)

Query ID	lcl|192983	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	15		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

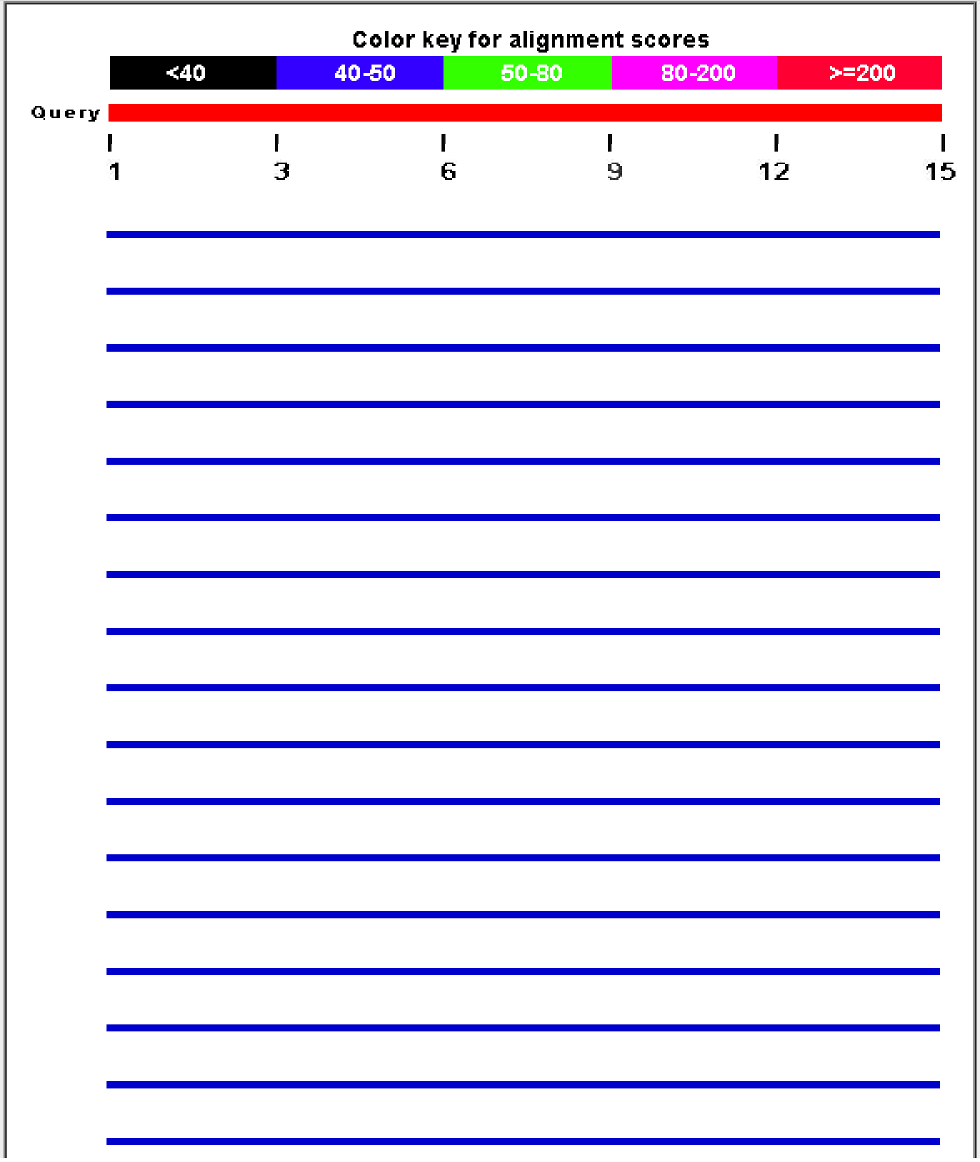
Graphic Summary

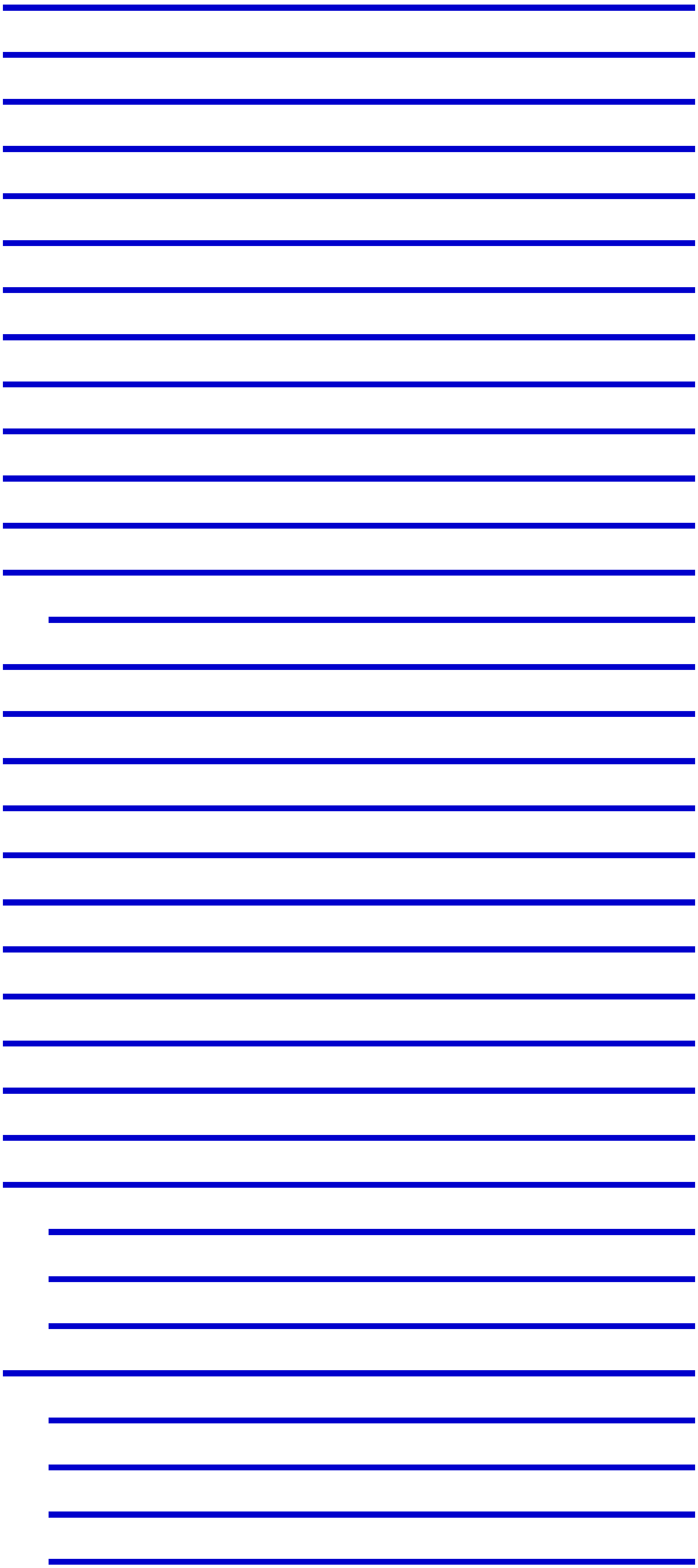
Show Conserved Domains

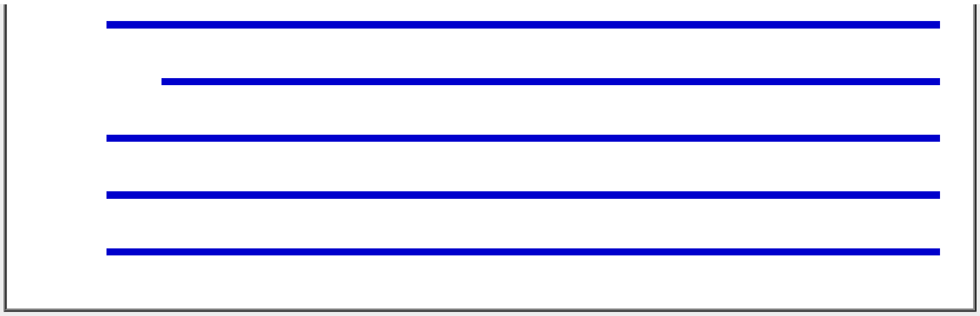
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	48.6	48.6	100%	3e-05	93%	CAC14844.1
☐	Unknown (protein for IMAGE:3354070) [Homo sapiens]	48.6	48.6	100%	3e-05	93%	AAH07614.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_009202774.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_008975042.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_005553977.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_005249075.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_009202773.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_007971742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-like [Maca	48.6	48.6	100%	3e-05	93%	XP_002803682.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pongo ab	48.6	48.6	100%	3e-05	93%	XP_009239742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_007971741.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_007971740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_007971746.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 2	48.6	48.6	100%	3e-05	93%	XP_004043389.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 1	48.6	48.6	100%	3e-05	93%	XP_004043388.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	48.6	48.6	100%	3e-05	93%	CAC87068.1
☐	phospholipase D [Homo sapiens]	48.6	48.6	100%	3e-05	93%	AAA36445.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_003823243.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Homo sapien	48.6	48.6	100%	3e-05	93%	NP_001494.2
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Homo sapier	48.6	48.6	100%	3e-05	93%	AAG16627.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Rhinopith	48.6	48.6	100%	3e-05	93%	XP_010363586.1
☐	phospholipase D [Homo sapiens]	48.6	48.6	100%	3e-05	93%	AAA36444.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_005553976.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_003897171.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pan trogl	48.6	48.6	100%	3e-05	93%	XP_518268.4
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_009202772.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_008975041.1
☐	hypothetical protein EGM_13271 [Macaca fascicularis]	48.6	48.6	100%	3e-05	93%	EHH52757.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_c [Homo	48.6	48.6	100%	3e-05	93%	EAW55450.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.6	48.6	100%	3e-05	93%	XP_005553975.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Saimiri bo	48.1	48.1	93%	4e-05	100%	XP_003927350.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Callithrix	47.7	47.7	100%	6e-05	93%	XP_002746229.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Orycterop	45.2	45.2	100%	4e-04	93%	XP_007948002.1
☐	hypothetical protein EGK_21153 [Macaca mulatta]	44.8	44.8	100%	6e-04	87%	EHH25414.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Condylura	44.3	44.3	100%	8e-04	87%	XP_004693375.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Sus scrof	44.3	44.3	100%	8e-04	87%	XP_001925944.5
☐	Phosphatidylinositol-glycan-specific phospholipase D [Pteropus alecto]	43.9	43.9	100%	0.001	87%	ELK05805.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	43.9	43.9	100%	0.001	87%	XP_006919597.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Leptonyc	43.9	43.9	100%	0.001	87%	XP_006739372.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Nomascu	43.9	43.9	100%	0.001	87%	XP_003263611.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Trichechu	41.8	41.8	100%	0.005	87%	XP_004384046.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Loxodont	41.8	41.8	100%	0.005	87%	XP_003416488.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Odobenu	41.4	41.4	100%	0.008	80%	XP_004406584.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	93%	0.010	86%	XP_006051268.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Capra hir	40.9	40.9	93%	0.010	86%	XP_005696842.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ovis aries	40.9	40.9	93%	0.010	86%	XP_004019154.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Panthera	40.9	40.9	100%	0.010	80%	XP_007074479.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	93%	0.010	86%	XP_006051267.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	93%	0.010	86%	XP_006051266.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	93%	0.010	86%	XP_006051265.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	93%	0.010	86%	XP_006051264.1
☐	hypothetical protein CB1_000595062 [Camelus ferus]	40.5	40.5	100%	0.014	80%	EPY83136.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Eptesicus	40.5	40.5	93%	0.014	86%	XP_008145534.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	40.5	40.5	100%	0.014	80%	XP_006182298.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Camelus	40.5	40.5	100%	0.014	80%	XP_010944080.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	40.5	40.5	100%	0.014	80%	XP_010978426.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Vicugna	40.5	40.5	100%	0.014	80%	XP_006198740.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	40.1	40.1	93%	0.020	86%	XP_005863221.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	39.7	39.7	100%	0.027	80%	XP_008511735.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	39.7	39.7	100%	0.027	80%	XP_008511734.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Equus ca	39.7	39.7	100%	0.027	80%	XP_001497586.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	39.7	39.7	100%	0.027	80%	XP_008511732.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	39.7	39.7	100%	0.027	80%	XP_008511731.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	39.7	39.7	100%	0.027	80%	XP_008511730.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Myotis brandtii]	39.2	39.2	86%	0.037	92%	EPQ05831.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	39.2	39.2	100%	0.038	80%	XP_004761311.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Physeter	39.2	39.2	100%	0.038	80%	XP_007116306.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Orcinus	39.2	39.2	100%	0.038	80%	XP_004273574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	39.2	39.2	100%	0.038	80%	XP_007197201.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	39.2	39.2	100%	0.038	80%	XP_007197200.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	39.2	39.2	100%	0.038	80%	XP_004761310.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Tursiops	39.2	39.2	100%	0.038	80%	XP_004313968.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ochotona	38.4	38.4	100%	0.071	80%	XP_004593176.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ceratothe	38.4	38.4	100%	0.071	80%	XP_004432133.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X2	38.0	38.0	100%	0.098	80%	XP_007454575.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X1	38.0	38.0	100%	0.098	80%	XP_007454574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Elephantu	38.0	38.0	100%	0.098	80%	XP_006888712.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	37.5	37.5	93%	0.13	79%	XP_005903212.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Bos mutus]	37.5	37.5	93%	0.13	79%	ELR50996.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X2	37.5	37.5	93%	0.13	79%	XP_010841812.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Bos taurus]	37.5	37.5	93%	0.13	79%	NP_777241.1
☐	TPA: phosphatidylinositol-glycan-specific phospholipase D [Bos taurus]	37.5	37.5	93%	0.13	79%	DAA16116.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X1	37.5	37.5	93%	0.13	79%	XP_010841810.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3	37.5	37.5	93%	0.13	79%	XP_005223795.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X2	37.5	37.5	93%	0.13	79%	XP_005223794.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X1	37.5	37.5	93%	0.13	79%	XP_010816770.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Erinaceus	37.1	37.1	100%	0.18	73%	XP_007526005.1
☐	hypothetical protein PANDA_003876 [Ailuropoda melanoleuca]	36.7	36.7	93%	0.25	79%	EFB28343.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3	36.7	36.7	93%	0.25	86%	XP_005640137.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoformX1	36.7	36.7	93%	0.25	86%	XP_535902.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-like [Ailuro	36.7	36.7	93%	0.25	79%	XP_002915859.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X2	36.7	36.7	93%	0.25	86%	XP_005640136.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pantholo	36.3	36.3	93%	0.35	79%	XP_005973908.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Galeopte	36.3	36.3	100%	0.35	73%	XP_008578807.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Chinchilla	35.8	35.8	80%	0.48	92%	XP_005403486.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Tarsius s	35.0	35.0	100%	0.89	73%	XP_008048656.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Jaculus ja	34.6	34.6	80%	1.2	83%	XP_004669997.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ictidomys	34.6	34.6	93%	1.2	79%	XP_005337080.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	34.6	34.6	100%	1.2	73%	XP_003788429.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Chrysoch	32.9	32.9	93%	4.2	71%	XP_006878008.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

glycosylphosphatidylinositol phospholipase D [Homo sapiens]

Sequence ID: emb|CAC14844.1| **Length:** 457 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 176 to 190 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.6 bits(107)	3e-05	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    KEKLNVEAADWTVRG  15
            KEKLNVEAA+WTVRG
Sbjct  176  KEKLNVEAANWTVRG  190
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Unknown (protein for IMAGE:3354070), partial [Homo sapiens]

Sequence ID: gb|AAH07614.1| **Length:** 575 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 294 to 308 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.6 bits(107)	3e-05	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    KEKLNVEAADWTVRG  15
            KEKLNVEAA+WTVRG
Sbjct  294  KEKLNVEAANWTVRG  308
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X4 [Papio anubis]

Sequence ID: ref|XP_009202774.1| **Length:** 677 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 396 to 410 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.6 bits(107)	3e-05	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    KEKLNVEAADWTVRG  15
            KEKLNVEAA+WTVRG
Sbjct  396  KEKLNVEAANWTVRG  410
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Pan paniscus]

Sequence ID: ref|XP_008975042.1| **Length:** 677 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 396 to 410 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.6 bits(107)	3e-05	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    KEKLNVEAADWTVRG  15
            KEKLNVEAA+WTVRG
Sbjct  396  KEKLNVEAANWTVRG  410
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Macaca fascicularis]

Sequence ID: ref|XP_005553977.1| **Length:** 677 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 396 to 410 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.6 bits(107)	3e-05	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    KEKLNVEAADWTVRG  15
            KEKLNVEAA+WTVRG
Sbjct  396  KEKLNVEAANWTVRG  410
```

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - B9FCV9F301R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download

How to read this page   Blast report description

GPLD1_KEKLNVEAANWTVRG_NonMod

RID	B9FCV9F301R (Expires on 01-14 13:39 pm)		
Query ID	lcl|253118	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	15		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

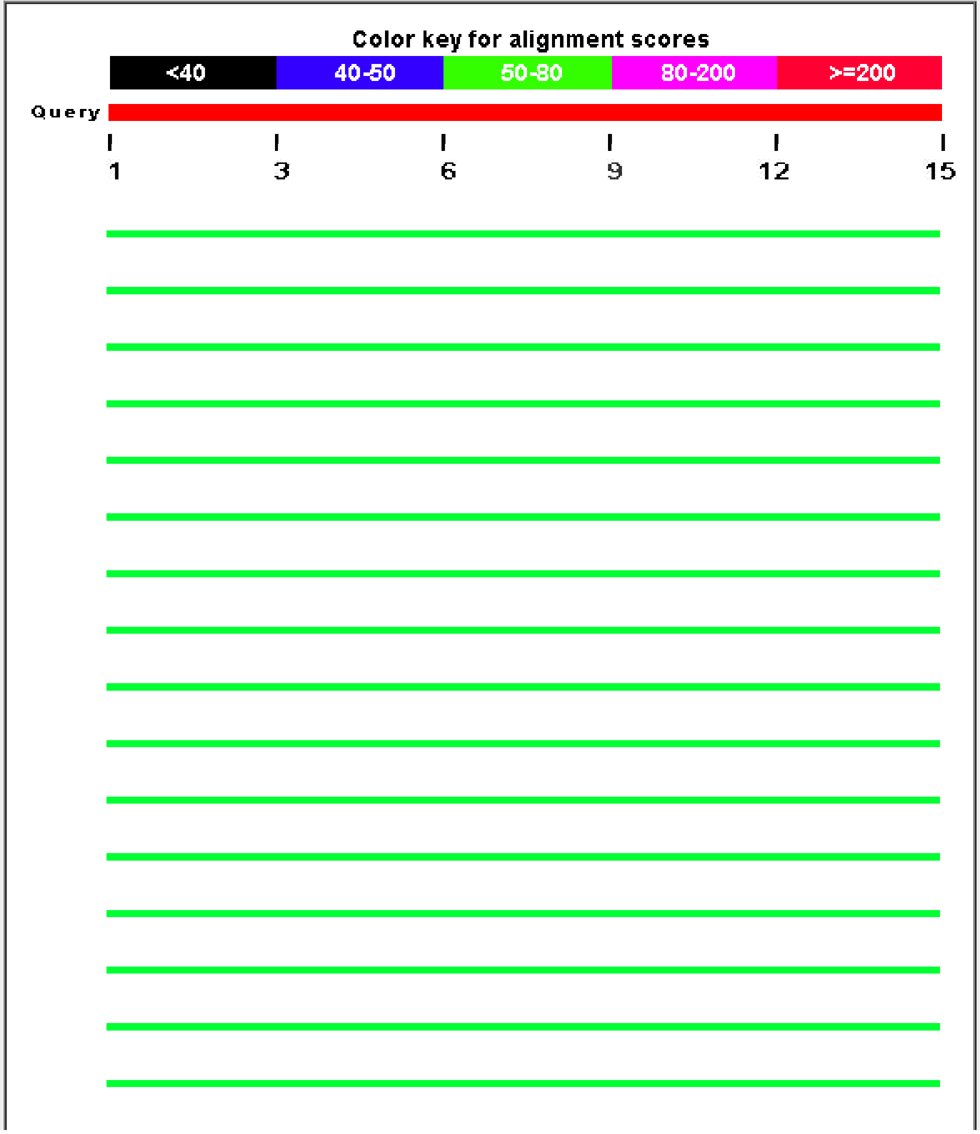
Graphic Summary

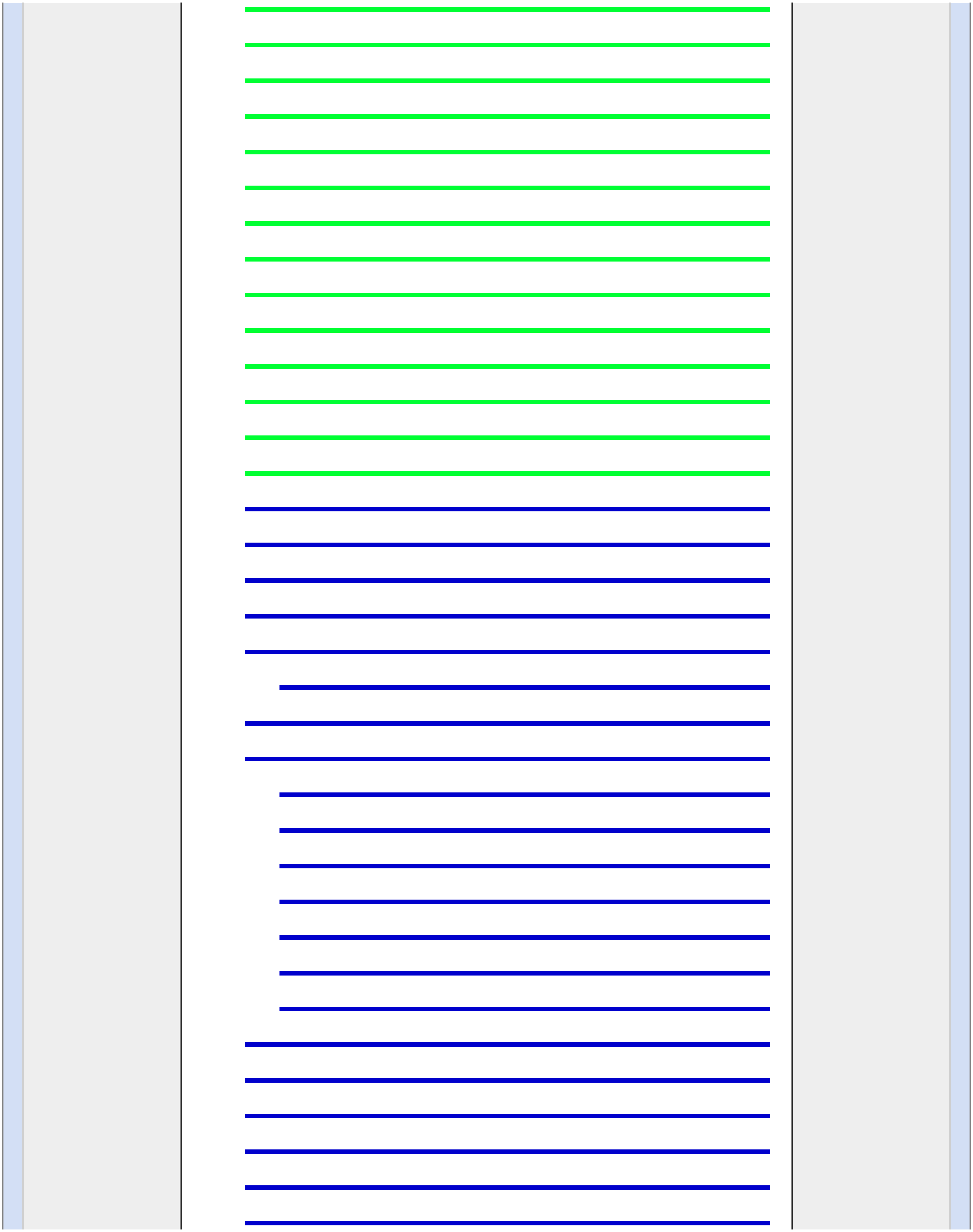
Show Conserved Domains

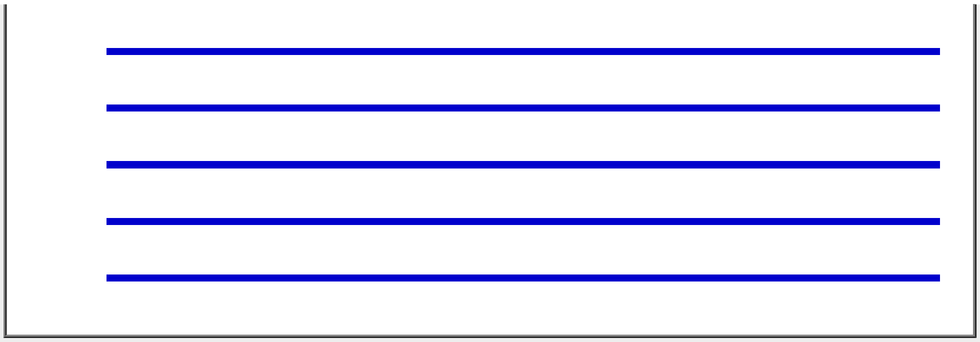
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	51.1	51.1	100%	4e-06	100%	gi|11122875|CAC14844.1
☐	Unknown (protein for IMAGE:3354070) [Homo sapiens]	51.1	51.1	100%	4e-06	100%	gi|14043248|AAH07614.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|685535046|XP_009202774.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|675773160|XP_008975042.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|544429971|XP_005553977.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|530381810|XP_005249075.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|685535044|XP_009202773.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|635096985|XP_007971742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|297290177|XP_002803682.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|686720936|XP_009239742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|635096983|XP_007971741.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|635096981|XP_007971740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|635096993|XP_007971746.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|426351748|XP_004043389.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|426351746|XP_004043388.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	51.1	51.1	100%	4e-06	100%	gi|20269065|CAC87068.1
☐	phospholipase D [Homo sapiens]	51.1	51.1	100%	4e-06	100%	gi|388765|AAA36445.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|397505380|XP_003823243.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Ho	51.1	51.1	100%	4e-06	100%	gi|29171717|NP_001494.2
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Hc	51.1	51.1	100%	4e-06	100%	gi|14195001|AAG16627.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|724798150|XP_010363586.1
☐	phospholipase D [Homo sapiens]	51.1	51.1	100%	4e-06	100%	gi|388763|AAA36444.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|544429969|XP_005553976.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|402865969|XP_003897171.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|410040317|XP_518268.4
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|685535041|XP_009202772.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|675773152|XP_008975041.1
☐	hypothetical protein EGM_13271 [Macaca fascicularis]	51.1	51.1	100%	4e-06	100%	gi|355748274|EHH52757.1
☐							

	glycosylphosphatidylinositol specific phospholipase D1, isoform CR	51.1	51.1	100%	4e-06	100%	gi|119575854|EAW55450.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	4e-06	100%	gi|544429967|XP_005553975.1
☐	hypothetical protein EGK_21153 [Macaca mulatta]	47.3	47.3	100%	7e-05	93%	gi|355569342|EHH25414.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	46.9	46.9	100%	1e-04	93%	gi|507979038|XP_004693375.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	46.9	46.9	100%	1e-04	93%	gi|545837650|XP_001925944.5
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	46.4	46.4	100%	1e-04	93%	gi|585175123|XP_006739372.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	46.4	46.4	100%	1e-04	93%	gi|332228866|XP_003263611.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	45.6	93%	3e-04	93%	gi|403270800|XP_003927350.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.2	45.2	100%	4e-04	87%	gi|675650934|XP_002746229.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.9	43.9	100%	0.001	87%	gi|472374241|XP_004406584.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	93%	0.001	93%	gi|594053987|XP_006051268.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	93%	0.001	93%	gi|548518368|XP_005696842.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	93%	0.001	93%	gi|426250866|XP_004019154.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	93%	0.001	93%	gi|594053985|XP_006051267.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	93%	0.001	93%	gi|594053983|XP_006051266.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	93%	0.001	93%	gi|594053981|XP_006051265.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	93%	0.001	93%	gi|594053979|XP_006051264.1
☐	hypothetical protein CB1_000595062 [Camelus ferus]	43.1	43.1	100%	0.002	87%	gi|528763477|EPY83136.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	43.1	43.1	100%	0.002	87%	gi|560912019|XP_006182298.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.1	43.1	100%	0.002	87%	gi|560952422|XP_006198740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	42.6	42.6	100%	0.003	87%	gi|634873155|XP_007948002.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	42.2	42.2	100%	0.004	87%	gi|664709546|XP_008511735.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	42.2	42.2	100%	0.004	87%	gi|664709544|XP_008511734.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	42.2	42.2	100%	0.004	87%	gi|149732005|XP_001497586.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	42.2	42.2	100%	0.004	87%	gi|664709542|XP_008511732.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	42.2	42.2	100%	0.004	87%	gi|664709540|XP_008511731.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	42.2	42.2	100%	0.004	87%	gi|664709538|XP_008511730.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	41.8	41.8	100%	0.005	87%	gi|511882880|XP_004761311.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	41.8	41.8	100%	0.005	87%	gi|593754864|XP_007116306.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	41.8	41.8	100%	0.005	87%	gi|466027702|XP_004273574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	41.8	41.8	100%	0.005	87%	gi|594700264|XP_007197201.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	41.8	41.8	100%	0.005	87%	gi|594700262|XP_007197200.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	41.8	41.8	100%	0.005	87%	gi|511882878|XP_004761310.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	41.8	41.8	100%	0.005	87%	gi|470605744|XP_004313968.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Pteropus ale	41.4	41.4	100%	0.007	80%	gi|431896393|ELK05805.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	41.4	41.4	100%	0.007	80%	gi|586529361|XP_006919597.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.9	40.9	100%	0.010	87%	gi|478515788|XP_004432133.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	40.1	40.1	93%	0.019	86%	gi|555982613|XP_005903212.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Bos mutus]	40.1	40.1	93%	0.019	86%	gi|440899735|ELR50996.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Bo	40.1	40.1	93%	0.019	86%	gi|27807363|NP_777241.1
☐	TPA: phosphatidylinositol-glycan-specific phospholipase D [Bos tau	40.1	40.1	93%	0.019	86%	gi|296474001|DAA16116.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.1	40.1	93%	0.019	86%	gi|529003874|XP_005223795.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.1	40.1	93%	0.019	86%	gi|529003872|XP_005223794.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.1	40.1	93%	0.019	86%	gi|529003870|XP_005223793.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	39.7	39.7	100%	0.026	80%	gi|617615072|XP_007526005.1

☐	hypothetical protein PANDA_003876 [Ailuropoda melanoleuca]	39.2	39.2	93%	0.035	86%	gi|281352759|EFB28343.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	39.2	39.2	100%	0.035	80%	gi|471403600|XP_004384046.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	39.2	39.2	100%	0.035	80%	gi|344289516|XP_003416488.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-	39.2	39.2	93%	0.035	86%	gi|301760102|XP_002915859.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	38.8	38.8	93%	0.049	86%	gi|556757122|XP_005973908.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	38.8	38.8	100%	0.049	80%	gi|667294118|XP_008578807.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	38.4	38.4	100%	0.067	73%	gi|591294474|XP_007074479.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	38.0	38.0	93%	0.092	79%	gi|641712629|XP_008145534.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.5	37.5	93%	0.13	86%	gi|545554532|XP_005640137.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.5	37.5	93%	0.13	86%	gi|74003954|XP_535902.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.5	37.5	93%	0.13	86%	gi|545554529|XP_005640136.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	37.5	37.5	93%	0.13	79%	gi|554537051|XP_005863221.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Myotis brand	36.7	36.7	86%	0.24	85%	gi|521024043|EPQ05831.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.8	35.8	100%	0.45	73%	gi|504166674|XP_004593176.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.4	35.4	100%	0.61	73%	gi|602684652|XP_007454575.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.4	35.4	100%	0.61	73%	gi|602684650|XP_007454574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.4	35.4	93%	0.61	79%	gi|586495128|XP_006878008.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.4	35.4	100%	0.61	73%	gi|585669334|XP_006888712.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	34.6	34.6	93%	1.1	79%	gi|671000878|XP_008691294.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	33.3	33.3	80%	2.9	83%	gi|533180623|XP_005403486.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.9	32.9	100%	4.0	67%	gi|612008081|XP_007487938.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.9	32.9	100%	4.0	67%	gi|612008079|XP_001375600.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.9	32.9	100%	4.0	67%	gi|612008077|XP_007487937.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.5	32.5	100%	5.4	67%	gi|640776034|XP_008048656.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.0	32.0	80%	7.4	75%	gi|507572817|XP_004669997.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.0	32.0	93%	7.4	71%	gi|532102948|XP_005337080.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	32.0	32.0	100%	7.4	67%	gi|395830643|XP_003788429.1

Alignments

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glycosylphosphatidylinositol phospholipase D [Homo sapiens]

Sequence ID: gi|11122875|emb|CAC14844.1| **Length:** 457 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 176 to 190 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.1 bits(113)	4e-06	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KEKLNVEAANWTVRG  15
            KEKLNVEAANWTVRG
Sbjct  176  KEKLNVEAANWTVRG  190
```

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Unknown (protein for IMAGE:3354070), partial [Homo sapiens]

Sequence ID: gi|14043248|gb|AAH07614.1| **Length:** 575 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 294 to 308 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.1 bits(113)	4e-06	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KEKLNVEAANWTVRG  15
```

```
                KEKLNVEAANWTVRG
Sbjct  294  KEKLNVEAANWTVRG  308
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X4 [Papio anubis]

Sequence ID: gi|685535046|ref|XP_009202774.1| **Length:** 677 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 396 to 410 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.1 bits(113)	4e-06	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KEKLNVEAANWTVRG  15
            KEKLNVEAANWTVRG
Sbjct  396  KEKLNVEAANWTVRG  410
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Pan paniscus]

Sequence ID: gi|675773160|ref|XP_008975042.1| **Length:** 677 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 396 to 410 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.1 bits(113)	4e-06	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KEKLNVEAANWTVRG  15
            KEKLNVEAANWTVRG
Sbjct  396  KEKLNVEAANWTVRG  410
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Macaca fascicularis]

Sequence ID: gi|544429971|ref|XP_005553977.1| **Length:** 677 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 396 to 410 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.1 bits(113)	4e-06	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KEKLNVEAANWTVRG  15
            KEKLNVEAANWTVRG
Sbjct  396  KEKLNVEAANWTVRG  410
```

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BVE0ZZZ001R**

Your search parameters were adjusted to search for a short input sequence.

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GPLD1_KFHDVSESTHWTPFLDASVHYIRE_Mod

RID BVE0ZZZ001R (Expires on 01-21 09:06 am)

Query ID lcl|216296
Description None
Molecule type amino acid
Query Length 24

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

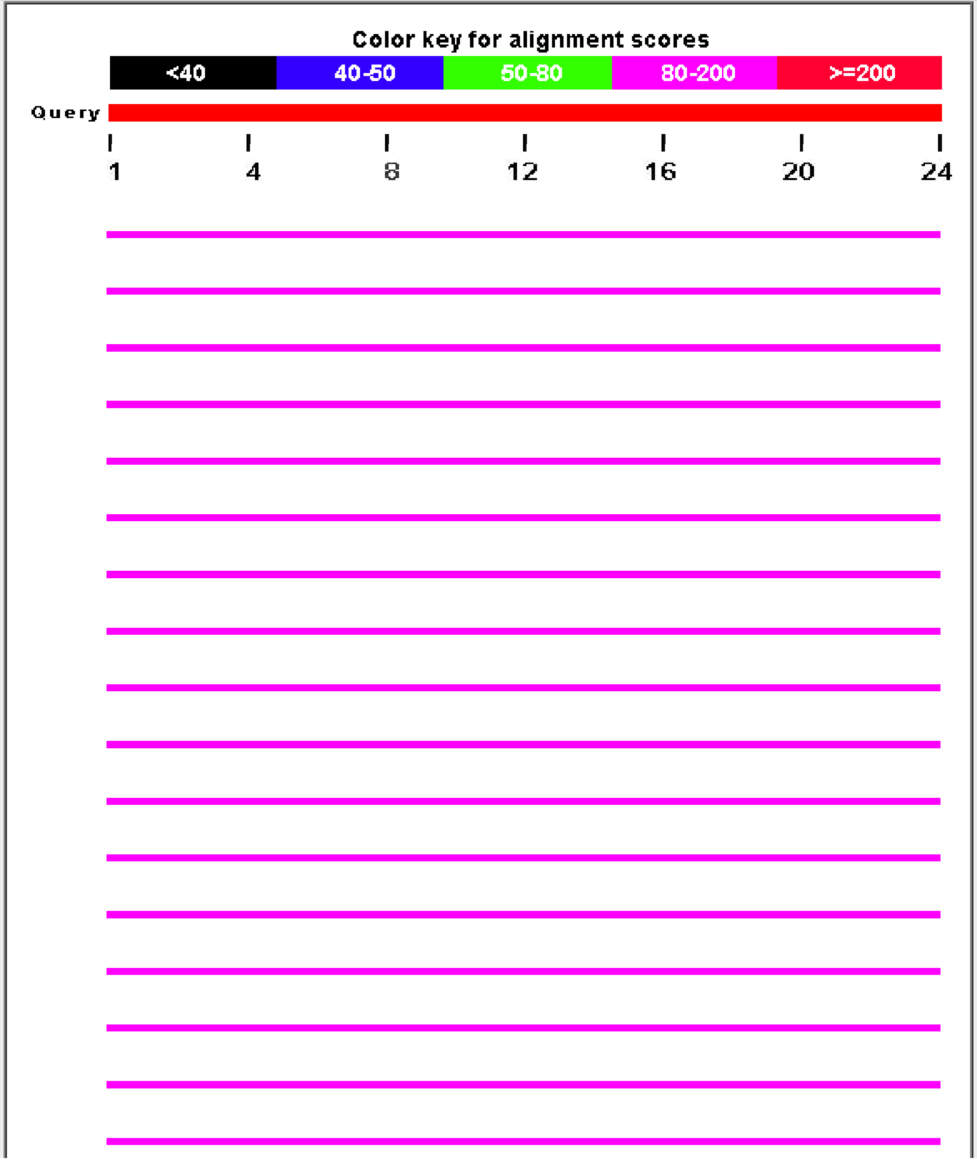
Graphic Summary

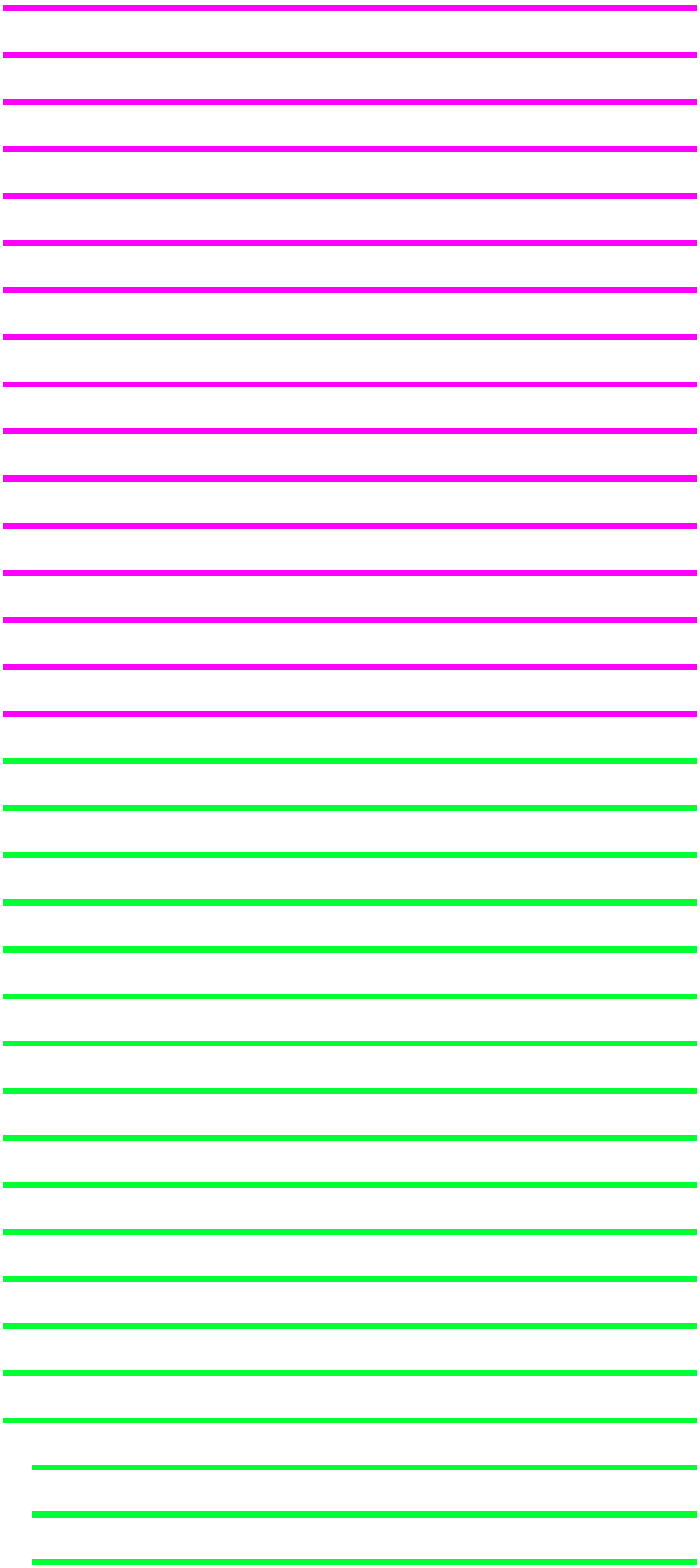
Show Conserved Domains

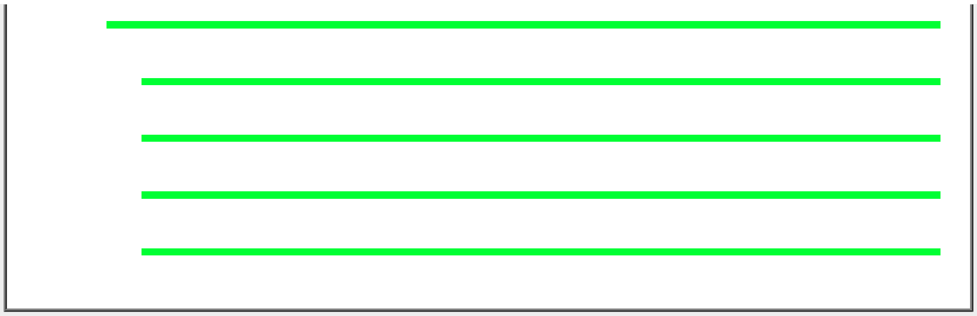
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Glycosylphosphatidylinositol specific phospholipase D1, isoform 2 precursor [	81.2	81.2	100%	5e-16	96%	AAI12002.1
☐	Glycosylphosphatidylinositol specific phospholipase D1 [Homo sapiens]	81.2	81.2	100%	5e-16	96%	AAH20748.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_b [Hom	81.2	81.2	100%	5e-16	96%	EAW55449.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-like [Maca	81.2	81.2	100%	8e-16	96%	XP_002803682.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_007971741.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_010621250.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_007971740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_008511734.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_010621248.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_004761311.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_007971746.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 2	81.2	81.2	100%	8e-16	96%	XP_004043389.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 1	81.2	81.2	100%	8e-16	96%	XP_004043388.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	81.2	81.2	100%	8e-16	96%	CAC87068.1
☐	phospholipase D [Homo sapiens]	81.2	81.2	100%	8e-16	96%	AAA36445.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Saimiri b	81.2	81.2	100%	8e-16	96%	XP_003927350.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Homo sapien	81.2	81.2	100%	8e-16	96%	NP_001494.2
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Homo sapie	81.2	81.2	100%	8e-16	96%	AAG16627.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Rhinopith	81.2	81.2	100%	8e-16	96%	XP_010363586.1
☐	phospholipase D [Homo sapiens]	81.2	81.2	100%	8e-16	96%	AAA36444.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_005553976.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_003897171.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Equus ca	81.2	81.2	100%	8e-16	96%	XP_001497586.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_008511732.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_008511731.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_009202772.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_004761310.1
☐	hypothetical protein EGK_21153 [Macaca mulatta]	81.2	81.2	100%	8e-16	96%	EHH25414.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_c [Hom	81.2	81.2	100%	8e-16	96%	EAW55450.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Nomascu	81.2	81.2	100%	8e-16	96%	XP_003263611.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_005553975.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Fukomys damarensis]	81.2	81.2	100%	8e-16	96%	KFO33840.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	81.2	81.2	100%	8e-16	96%	XP_008511730.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Octodon	79.1	79.1	100%	4e-15	92%	XP_004640232.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	79.1	79.1	100%	4e-15	92%	XP_005003342.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	79.1	79.1	100%	4e-15	92%	XP_003468912.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	79.1	79.1	100%	4e-15	92%	XP_004462113.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Galeopte	79.1	79.1	100%	4e-15	92%	XP_008578807.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Tarsius s	79.1	79.1	100%	4e-15	92%	XP_008048656.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Condylur	79.1	79.1	100%	4e-15	92%	XP_004693375.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Erinaceu	79.1	79.1	100%	4e-15	92%	XP_007526005.1
☐	hypothetical protein EGM_13271 [Macaca fascicularis]	79.1	79.1	100%	4e-15	92%	EHH52757.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Chinchilla	79.1	79.1	100%	4e-15	92%	XP_005403486.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Heterocephalus glaber]	78.7	78.7	100%	6e-15	92%	EHB09593.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	78.7	78.7	100%	6e-15	92%	XP_004847665.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	78.7	78.7	100%	6e-15	92%	XP_004847664.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	78.7	78.7	100%	6e-15	92%	XP_004847663.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Heteroce	78.7	78.7	100%	6e-15	92%	XP_004895023.1
☐	hypothetical protein CB1_000595062 [Camelus ferus]	78.3	78.3	95%	8e-15	96%	EPY83136.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ursus ma	78.3	78.3	95%	8e-15	96%	XP_008691294.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	78.3	78.3	95%	8e-15	96%	XP_004614021.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pongo ab	78.3	78.3	100%	8e-15	92%	XP_009239742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Felis catu	78.3	78.3	95%	8e-15	96%	XP_003985826.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	78.3	78.3	95%	8e-15	96%	XP_005640137.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	78.3	78.3	95%	8e-15	96%	XP_006182298.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Camelus	78.3	78.3	95%	8e-15	96%	XP_010944080.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoformX1	78.3	78.3	95%	8e-15	96%	XP_535902.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ictidomys	78.3	78.3	100%	8e-15	92%	XP_005337080.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Panthera	78.3	78.3	95%	8e-15	96%	XP_007074479.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	78.3	78.3	100%	8e-15	92%	XP_003823243.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	78.3	78.3	95%	8e-15	96%	XP_010978426.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ceratothe	78.3	78.3	95%	8e-15	96%	XP_004432133.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	78.3	78.3	95%	8e-15	96%	XP_005640136.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pan trogl	78.3	78.3	100%	8e-15	92%	XP_518268.4
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	78.3	78.3	100%	8e-15	92%	XP_008975041.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	76.6	76.6	100%	3e-14	88%	XP_008769857.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Rattus norve	76.6	76.6	100%	3e-14	88%	NP_001093982.1
☐	RecName: Full=Phosphatidylinositol-glycan-specific phospholipase D; Short=	76.6	76.6	100%	3e-14	88%	Q8R2H5.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	76.6	76.6	100%	3e-14	88%	XP_006145185.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Tupaia chinensis]	76.6	76.6	100%	3e-14	88%	ELW68777.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Pteropus alecto]	76.1	76.1	95%	4e-14	91%	ELK05805.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	76.1	76.1	95%	4e-14	91%	XP_006919597.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Leptonyc	76.1	76.1	95%	4e-14	91%	XP_006739372.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Odobenu	76.1	76.1	95%	4e-14	91%	XP_004406584.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Myotis da	75.7	75.7	95%	6e-14	91%	XP_006763163.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Jaculus ja	75.3	75.3	100%	8e-14	88%	XP_004669997.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Nannospa	75.3	75.3	100%	8e-14	88%	XP_008845321.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Vicugna p	75.3	75.3	95%	8e-14	96%	XP_006198740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	74.9	74.9	100%	1e-13	88%	XP_008260728.1
☐	hypothetical protein PANDA_003876 [Ailuropoda melanoleuca]	74.9	74.9	95%	1e-13	91%	EFB28343.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	74.9	74.9	91%	1e-13	95%	XP_005903212.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Bos mutus]	74.9	74.9	91%	1e-13	95%	ELR50996.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	74.9	74.9	100%	1e-13	88%	XP_008260723.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	74.9	74.9	91%	1e-13	95%	XP_010841812.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	74.9	74.9	91%	1e-13	95%	XP_006051268.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Panthol	74.9	74.9	91%	1e-13	95%	XP_005973908.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Capra hir	74.9	74.9	91%	1e-13	95%	XP_005696842.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ochotona	74.9	74.9	100%	1e-13	88%	XP_004593176.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Bos taurus]	74.9	74.9	91%	1e-13	95%	NP_777241.1
☐	TPA: phosphatidylinositol-glycan-specific phospholipase D [Bos taurus]	74.9	74.9	91%	1e-13	95%	DAA16116.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-like [Ailur	74.9	74.9	95%	1e-13	91%	XP_002915859.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	74.9	74.9	91%	1e-13	95%	XP_010841810.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	74.9	74.9	91%	1e-13	95%	XP_005223795.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	74.9	74.9	91%	1e-13	95%	XP_006051267.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	74.9	74.9	91%	1e-13	95%	XP_005223794.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	74.9	74.9	91%	1e-13	95%	XP_006051266.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	74.9	74.9	91%	1e-13	95%	XP_006051265.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	74.9	74.9	91%	1e-13	95%	XP_006051264.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	74.9	74.9	91%	1e-13	95%	XP_010816770.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Sus scrof	74.4	74.4	95%	2e-13	91%	XP_001925944.5

⊟ Alignments

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Glycosylphosphatidylinositol specific phospholipase D1, isoform 2 precursor [Homo sapiens]

Sequence ID: gb|AAI12002.1| **Length:** 176 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 79 to 102 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.2 bits(184)	5e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    KFHDVSESTHWTPFLDASVHYIRE  24
            KFHDVSESTHWTPFL+ASVHYIRE
Sbjct  79   KFHDVSESTHWTPFLNASVHYIRE  102
```

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Glycosylphosphatidylinositol specific phospholipase D1 [Homo sapiens]

Sequence ID: gb|AAH20748.1| **Length:** 176 **Number of Matches:** 1

▷ See 3 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins

Range 1: 79 to 102 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.2 bits(184)	5e-16	23/24(96%)	24/24(100%)	0/24(0%)

identical to the subject

```
Query  1    KFHDVSESTHWTPFLDASVHYIRE  24
            KFHDVSESTHWTPFL+ASVHYIRE
Sbjct  79   KFHDVSESTHWTPFLNASVHYIRE  102
```

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glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_b [Homo sapiens]

Sequence ID: gb|EAW55449.1| **Length:** 186 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 89 to 112 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.2 bits(184)	5e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    KFHDVSESTHWTPFLDASVHYIRE  24
            KFHDVSESTHWTPFL+ASVHYIRE
Sbjct  89   KFHDVSESTHWTPFLNASVHYIRE  112
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-like [Macaca mulatta]

Sequence ID: ref|XP_002803682.1| **Length:** 734 **Number of Matches:** 1

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Range 1: 66 to 89 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.2 bits(184)	8e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1   KFHDVSESTHWTPFLDASVHYIRE  24
           KFHDVSESTHWTPFL+ASVHYIRE
Sbjct  66  KFHDVSESTHWTPFLNASVHYIRE  89
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X2 [Chlorocebus sabaeus]

Sequence ID: ref|XP_007971741.1| **Length:** 772 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 50 to 73 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.2 bits(184)	8e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1   KFHDVSESTHWTPFLDASVHYIRE  24
           KFHDVSESTHWTPFL+ASVHYIRE
Sbjct  50  KFHDVSESTHWTPFLNASVHYIRE  73
```

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - B9ED1FSV01R

Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

GPLD1_KFHDVSESTHWTPFLNASVHYIRE_NonMod

RID B9ED1FSV01R (Expires on 01-14 13:22 pm)

Query ID	lcl|377669	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	24		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

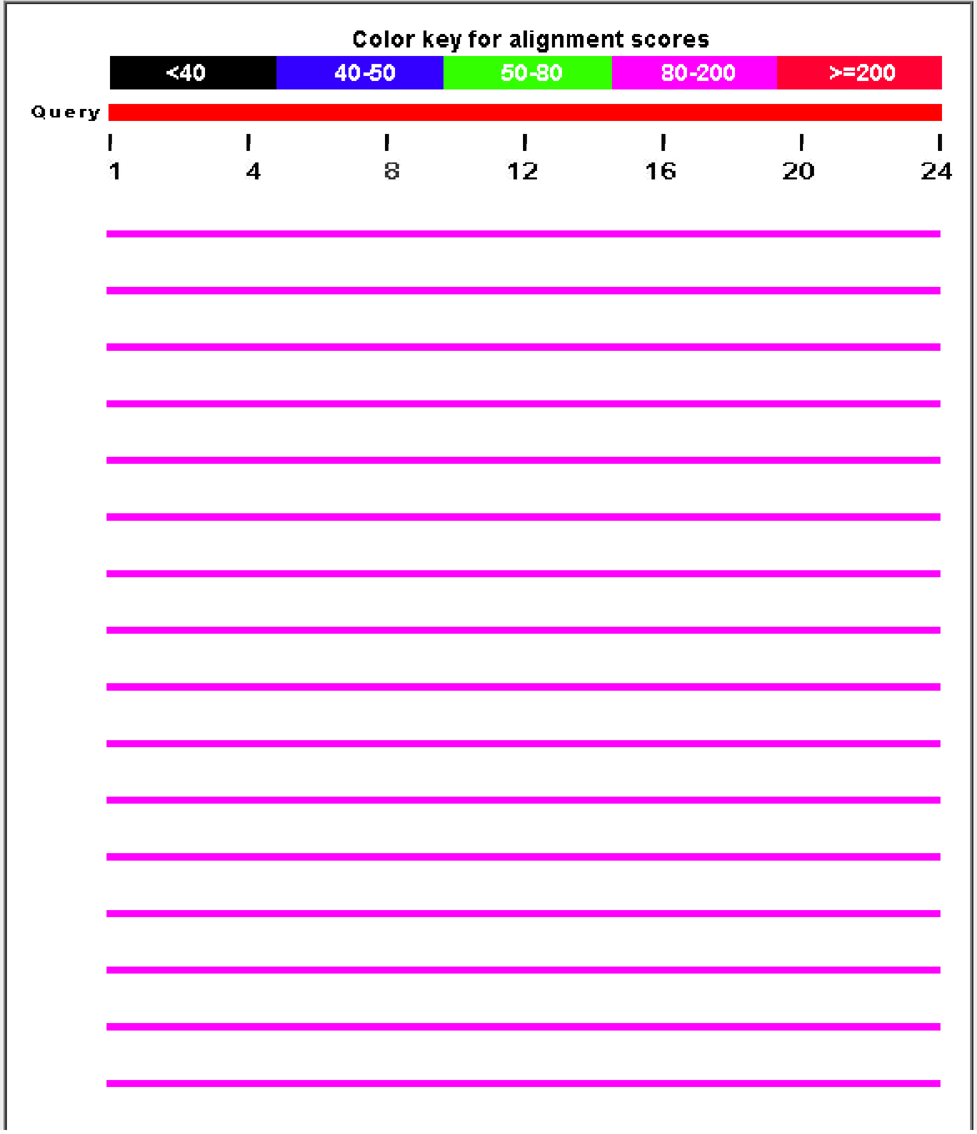
Graphic Summary

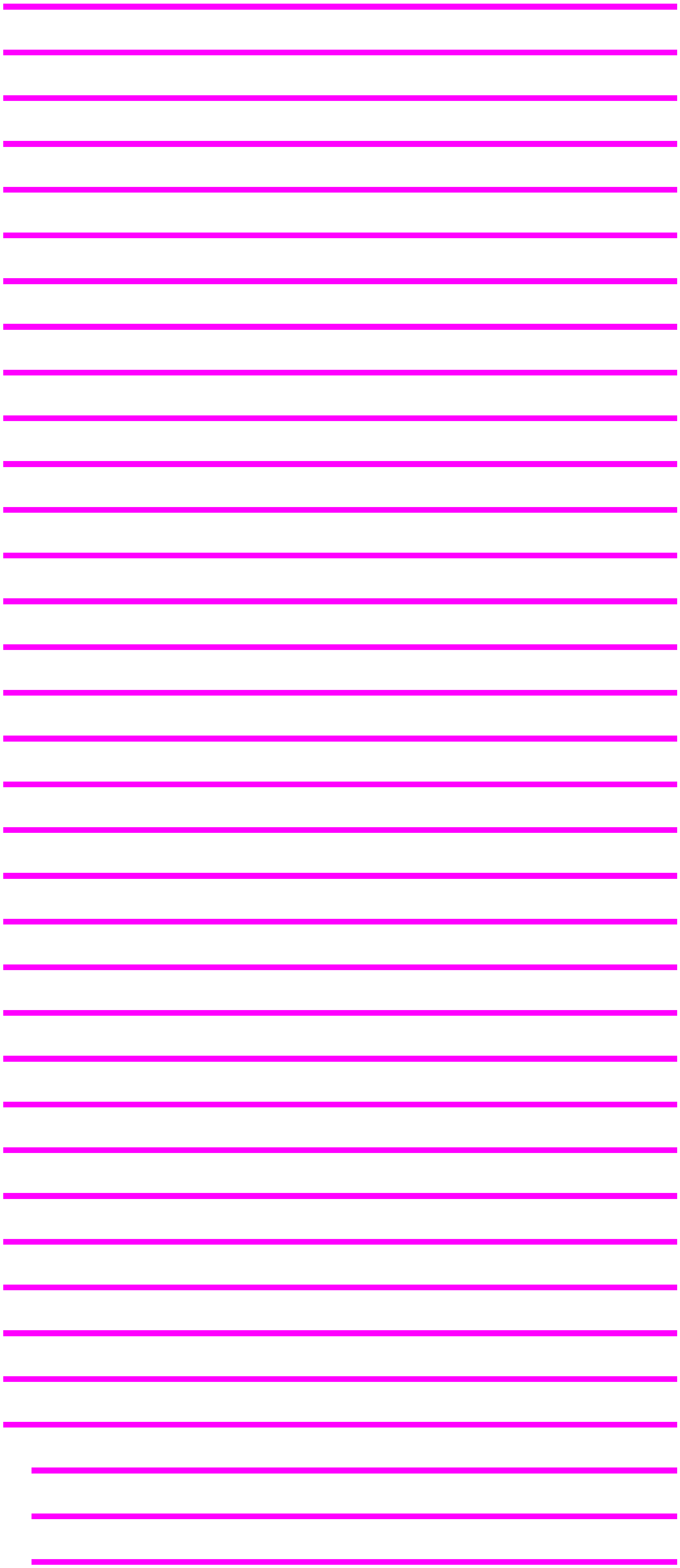
Show Conserved Domains

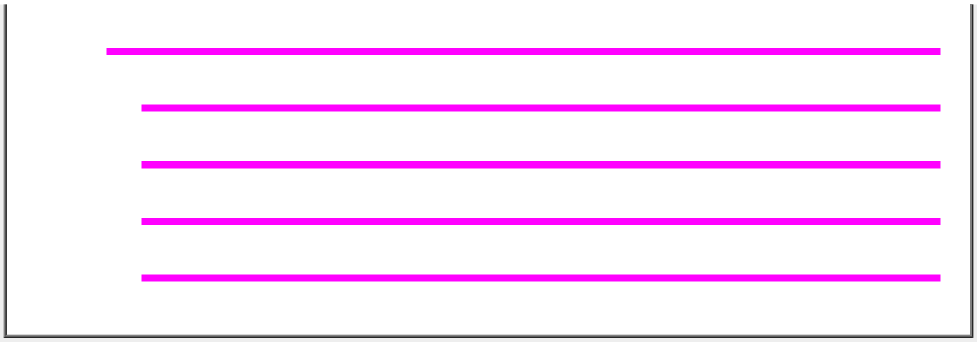
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Glycosylphosphatidylinositol specific phospholipase D1, isoform 2 p	83.8	83.8	100%	6e-17	100%	gi|85567090|AAI12002.1
☐	Glycosylphosphatidylinositol specific phospholipase D1 [Homo sapi	83.8	83.8	100%	6e-17	100%	gi|18088448|AAH20748.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CR	83.8	83.8	100%	6e-17	100%	gi|119575853|EAW55449.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|297290177|XP_002803682.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|635096983|XP_007971741.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|731213592|XP_010621250.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|635096981|XP_007971740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|664709544|XP_008511734.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|731213588|XP_010621248.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|511882880|XP_004761311.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|635096993|XP_007971746.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|426351748|XP_004043389.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|426351746|XP_004043388.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	83.8	83.8	100%	1e-16	100%	gi|20269065|CAC87068.1
☐	phospholipase D [Homo sapiens]	83.8	83.8	100%	1e-16	100%	gi|388765|AAA36445.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|403270800|XP_003927350.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Ho	83.8	83.8	100%	1e-16	100%	gi|29171717|NP_001494.2
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Hc	83.8	83.8	100%	1e-16	100%	gi|14195001|AAG16627.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|724798150|XP_010363586.1
☐	phospholipase D [Homo sapiens]	83.8	83.8	100%	1e-16	100%	gi|388763|AAA36444.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|544429969|XP_005553976.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|402865969|XP_003897171.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|149732005|XP_001497586.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|664709542|XP_008511732.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|664709540|XP_008511731.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|685535041|XP_009202772.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|511882878|XP_004761310.1
☐	hypothetical protein EGK_21153 [Macaca mulatta]	83.8	83.8	100%	1e-16	100%	gi|355569342|EHH25414.1
☐							

	glycosylphosphatidylinositol specific phospholipase D1, isoform CR.	83.8	83.8	100%	1e-16	100%	gi|119575854|EAW55450.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|332228866|XP_003263611.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|544429967|XP_005553975.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Fukomys dar	83.8	83.8	100%	1e-16	100%	gi|676279913|KFO33840.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	83.8	83.8	100%	1e-16	100%	gi|664709538|XP_008511730.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	81.7	81.7	100%	5e-16	96%	gi|507684247|XP_004640232.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	81.7	81.7	100%	5e-16	96%	gi|514459231|XP_005003342.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	81.7	81.7	100%	5e-16	96%	gi|348566244|XP_003468912.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	81.7	81.7	100%	5e-16	96%	gi|488541031|XP_004462113.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	81.7	81.7	100%	5e-16	96%	gi|667294118|XP_008578807.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	81.7	81.7	100%	5e-16	96%	gi|640776034|XP_008048656.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	81.7	81.7	100%	5e-16	96%	gi|507979038|XP_004693375.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	81.7	81.7	100%	5e-16	96%	gi|617615072|XP_007526005.1
☐	hypothetical protein EGM_13271 [Macaca fascicularis]	81.7	81.7	100%	5e-16	96%	gi|355748274|EHH52757.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	81.7	81.7	100%	5e-16	96%	gi|533180623|XP_005403486.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Heterocepha	81.2	81.2	100%	7e-16	96%	gi|351706674|EHB09593.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	81.2	81.2	100%	7e-16	96%	gi|512971060|XP_004847665.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	81.2	81.2	100%	7e-16	96%	gi|512971057|XP_004847664.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	81.2	81.2	100%	7e-16	96%	gi|512971055|XP_004847663.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	81.2	81.2	100%	7e-16	96%	gi|512880679|XP_004895023.1
☐	hypothetical protein CB1_000595062 [Camelus ferus]	80.8	80.8	95%	1e-15	100%	gi|528763477|EPY83136.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	80.8	80.8	95%	1e-15	100%	gi|671000878|XP_008691294.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	80.8	80.8	95%	1e-15	100%	gi|505841011|XP_004614021.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	80.8	80.8	100%	1e-15	96%	gi|686720936|XP_009239742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	80.8	80.8	95%	1e-15	100%	gi|410958439|XP_003985826.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	80.8	80.8	95%	1e-15	100%	gi|545554532|XP_005640137.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	80.8	80.8	95%	1e-15	100%	gi|560912019|XP_006182298.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	80.8	80.8	95%	1e-15	100%	gi|74003954|XP_535902.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	80.8	80.8	100%	1e-15	96%	gi|532102948|XP_005337080.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	80.8	80.8	95%	1e-15	100%	gi|591294474|XP_007074479.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	80.8	80.8	100%	1e-15	96%	gi|397505380|XP_003823243.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	80.8	80.8	95%	1e-15	100%	gi|478515788|XP_004432133.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	80.8	80.8	95%	1e-15	100%	gi|545554529|XP_005640136.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	80.8	80.8	100%	1e-15	96%	gi|410040317|XP_518268.4
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	80.8	80.8	100%	1e-15	96%	gi|675773152|XP_008975041.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	79.1	79.1	100%	4e-15	92%	gi|672081759|XP_008769857.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Rat	79.1	79.1	100%	4e-15	92%	gi|213688382|NP_001093982.1
☐	RecName: Full=Phosphatidylinositol-glycan-specific phospholipase	79.1	79.1	100%	4e-15	92%	gi|81871416|Q8R2H5.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	79.1	79.1	100%	4e-15	92%	gi|562831414|XP_006145185.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Tupaia chine	79.1	79.1	100%	4e-15	92%	gi|444728318|ELW68777.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Pteropus ale	78.7	78.7	95%	5e-15	96%	gi|431896393|ELK05805.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	78.7	78.7	95%	5e-15	96%	gi|586529361|XP_006919597.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	78.7	78.7	95%	5e-15	96%	gi|585175123|XP_006739372.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	78.7	78.7	95%	5e-15	96%	gi|472374241|XP_004406584.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	78.3	78.3	95%	7e-15	96%	gi|584086909|XP_006763163.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.8	77.8	100%	1e-14	92%	gi|507572817|XP_004669997.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.8	77.8	100%	1e-14	92%	gi|674075950|XP_008845321.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.4	77.4	100%	1e-14	92%	gi|655839984|XP_008260728.1
☐	hypothetical protein PANDA_003876 [Ailuropoda melanoleuca]	77.4	77.4	95%	1e-14	96%	gi|281352759|EFB28343.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	77.4	77.4	91%	1e-14	100%	gi|555982613|XP_005903212.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Bos mutus]	77.4	77.4	91%	1e-14	100%	gi|440899735|ELR50996.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.4	77.4	100%	1e-14	92%	gi|655839976|XP_008260723.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.4	77.4	91%	1e-14	100%	gi|594053987|XP_006051268.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.4	77.4	91%	1e-14	100%	gi|556757122|XP_005973908.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.4	77.4	91%	1e-14	100%	gi|548518368|XP_005696842.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.4	77.4	100%	1e-14	92%	gi|504166674|XP_004593176.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Bos	77.4	77.4	91%	1e-14	100%	gi|27807363|NP_777241.1
☐	TPA: phosphatidylinositol-glycan-specific phospholipase D [Bos tau	77.4	77.4	91%	1e-14	100%	gi|296474001|DAA16116.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.4	77.4	95%	1e-14	96%	gi|301760102|XP_002915859.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.4	77.4	91%	1e-14	100%	gi|529003874|XP_005223795.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.4	77.4	91%	1e-14	100%	gi|594053985|XP_006051267.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.4	77.4	91%	1e-14	100%	gi|529003872|XP_005223794.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.4	77.4	91%	1e-14	100%	gi|594053983|XP_006051266.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.4	77.4	91%	1e-14	100%	gi|594053981|XP_006051265.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.4	77.4	91%	1e-14	100%	gi|529003870|XP_005223793.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.4	77.4	91%	1e-14	100%	gi|594053979|XP_006051264.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	77.0	77.0	95%	2e-14	96%	gi|545837650|XP_001925944.5
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	76.6	76.6	95%	3e-14	96%	gi|560952422|XP_006198740.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	76.6	76.6	100%	3e-14	92%	gi|395830643|XP_003788429.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	76.1	76.1	95%	4e-14	91%	gi|466027702|XP_004273574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	76.1	76.1	100%	4e-14	88%	gi|634873155|XP_007948002.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	76.1	76.1	100%	4e-14	88%	gi|471403600|XP_004384046.1

⊟ Alignments

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Glycosylphosphatidylinositol specific phospholipase D1, isoform 2 precursor [Homo sapiens]

Sequence ID: gi|85567090|gb|AAI12002.1| **Length:** 176 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 79 to 102 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
83.8 bits(190)	6e-17	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KFHDVSESTHWTPFLNASVHYIRE  24
            KFHDVSESTHWTPFLNASVHYIRE
Sbjct  79   KFHDVSESTHWTPFLNASVHYIRE  102
```

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Glycosylphosphatidylinositol specific phospholipase D1 [Homo sapiens]

Sequence ID: gi|18088448|gb|AAH20748.1| **Length:** 176 **Number of Matches:** 1

▸ See 3 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 79 to 102 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
83.8 bits(190)	6e-17	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KFHDVSESTHWTPFLNASVHYIRE  24
            KFHDVSESTHWTPFLNASVHYIRE
Sbjct  79   KFHDVSESTHWTPFLNASVHYIRE  102
```

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glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_b [Homo sapiens]

Sequence ID: gi|119575853|gb|EAW55449.1| **Length:** 186 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 89 to 112 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
83.8 bits(190)	6e-17	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KFHDVSESTHWTPFLNASVHYIRE  24
            KFHDVSESTHWTPFLNASVHYIRE
Sbjct  89   KFHDVSESTHWTPFLNASVHYIRE  112
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-like [Macaca mulatta]

Sequence ID: gi|297290177|ref|XP_002803682.1| **Length:** 734 **Number of Matches:** 1

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Range 1: 66 to 89 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
83.8 bits(190)	1e-16	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1   KFHDVSESTHWTPFLNASVHYIRE  24
           KFHDVSESTHWTPFLNASVHYIRE
Sbjct  66  KFHDVSESTHWTPFLNASVHYIRE  89
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X2 [Chlorocebus sabaeus]

Sequence ID: gi|635096983|ref|XP_007971741.1| **Length:** 772 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 50 to 73 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
83.8 bits(190)	1e-16	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1   KFHDVSESTHWTPFLNASVHYIRE  24
           KFHDVSESTHWTPFLNASVHYIRE
Sbjct  50  KFHDVSESTHWTPFLNASVHYIRE  73
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BVE3BK8T01R**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download YouTube How to read this page Blast report description

GPLD1_KLGTSLSSGHVLMDGTLKQ_Mod

RID BVE3BK8T01R (Expires on 01-21 09:07 am)

Query ID lcl|250205
Description None
Molecule type amino acid
Query Length 19

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

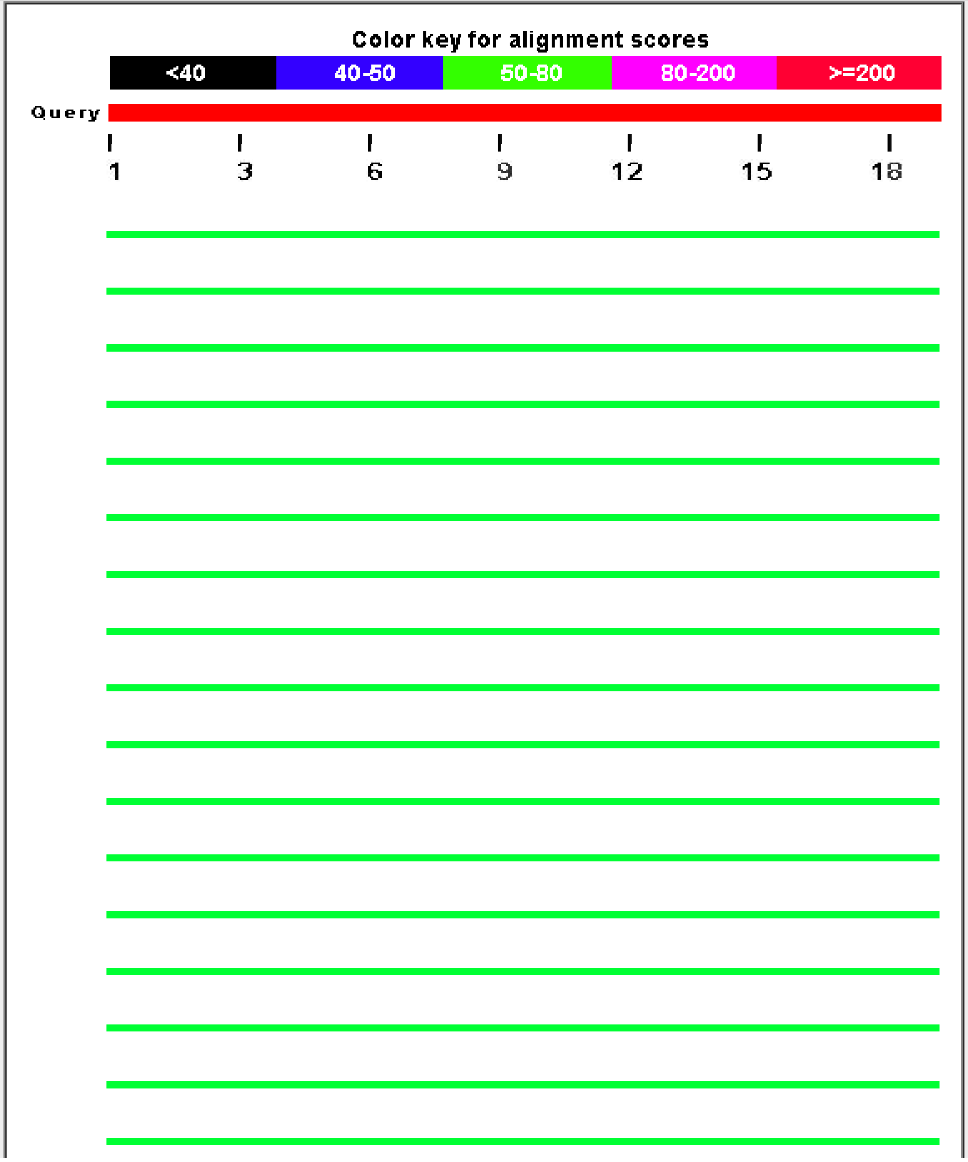
⊟Graphic Summary

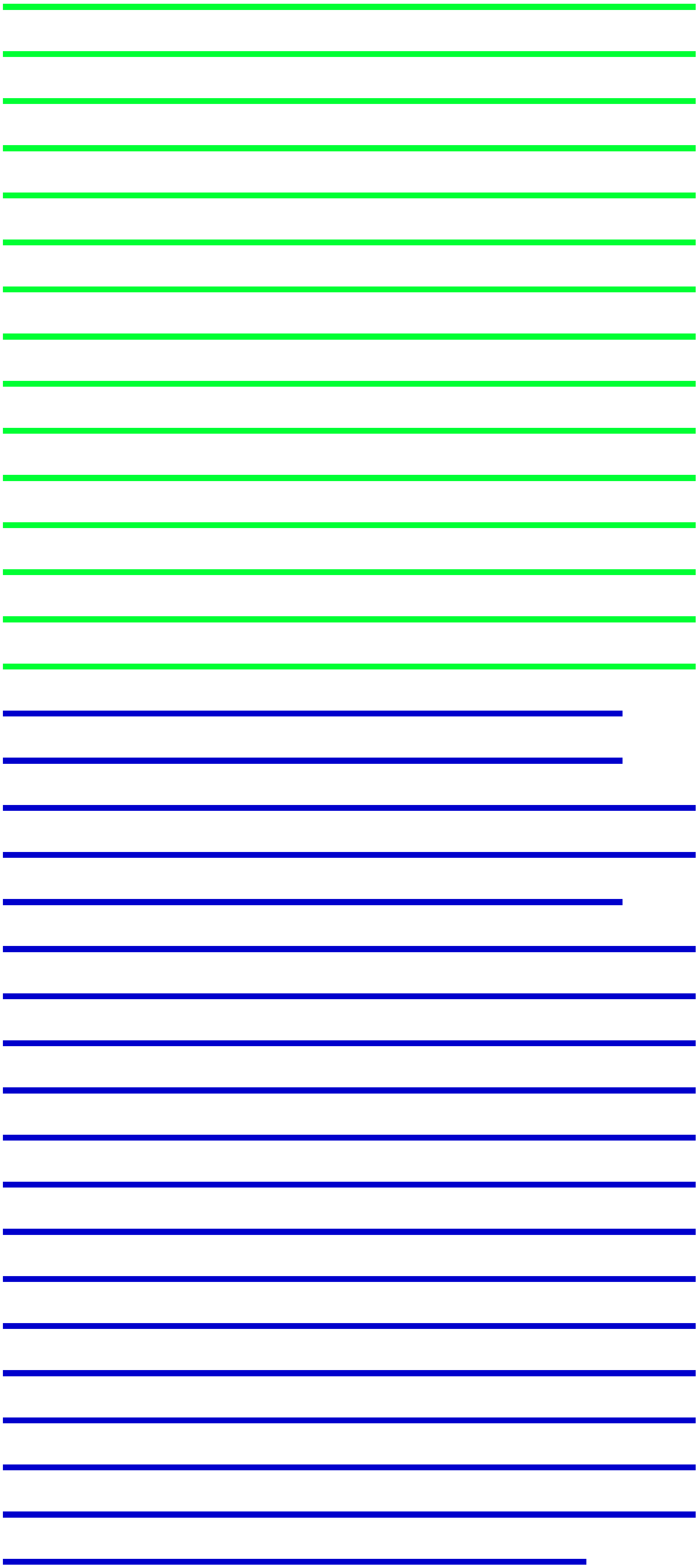
⊟Show Conserved Domains

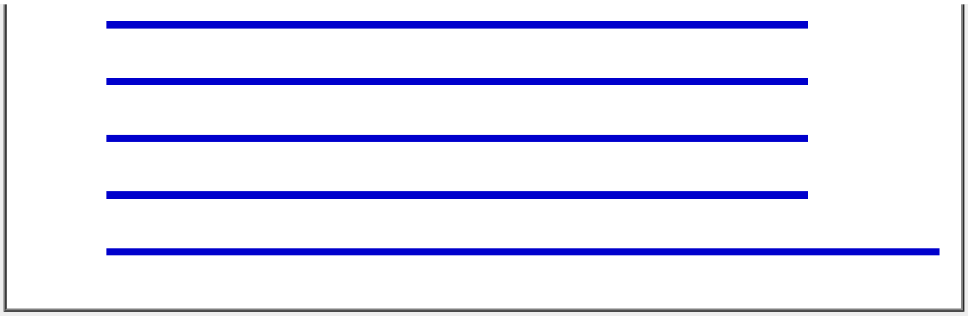
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	57.9	57.9	100%	3e-08	95%	CAC14844.1
☐	Unknown (protein for IMAGE:3354070) [Homo sapiens]	57.9	57.9	100%	3e-08	95%	AAH07614.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	57.9	57.9	100%	3e-08	95%	XP_005249075.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	57.9	57.9	100%	4e-08	95%	CAC87068.1
☐	phospholipase D [Homo sapiens]	57.9	57.9	100%	4e-08	95%	AAA36445.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Homo sapien	57.9	57.9	100%	4e-08	95%	NP_001494.2
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Homo sapier	57.9	57.9	100%	4e-08	95%	AAG16627.2
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_c [Homo	57.9	57.9	100%	4e-08	95%	EAW55450.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	53.7	100%	9e-07	89%	XP_009202774.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	53.7	100%	9e-07	89%	XP_005553977.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	53.7	100%	9e-07	89%	XP_009202773.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	53.7	100%	9e-07	89%	XP_007971742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-like [Maca	53.7	53.7	100%	9e-07	89%	XP_002803682.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pongo ab	53.7	53.7	100%	9e-07	89%	XP_009239742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	53.7	100%	9e-07	89%	XP_007971741.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	53.7	100%	9e-07	89%	XP_007971740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	53.7	100%	9e-07	89%	XP_007971746.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Tarsius s	53.7	53.7	100%	9e-07	89%	XP_008048656.1
☐	phospholipase D [Homo sapiens]	53.7	53.7	100%	9e-07	89%	AAA36444.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	53.7	100%	9e-07	89%	XP_005553976.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	53.7	100%	9e-07	89%	XP_003897171.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	53.7	100%	1e-06	89%	XP_009202772.1
☐	hypothetical protein EGM_13271 [Macaca fascicularis]	53.7	53.7	100%	1e-06	89%	EHH52757.1
☐	hypothetical protein EGK_21153 [Macaca mulatta]	53.7	53.7	100%	1e-06	89%	EHH25414.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Nomascu	53.7	53.7	100%	1e-06	89%	XP_003263611.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	53.7	100%	1e-06	89%	XP_005553975.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	51.1	51.1	100%	7e-06	84%	XP_004847666.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Heterocephalus glaber]	51.1	51.1	100%	7e-06	84%	EHB09593.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	51.1	51.1	100%	7e-06	84%	XP_004847665.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	51.1	51.1	100%	7e-06	84%	XP_004847664.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	51.1	51.1	100%	7e-06	84%	XP_004847663.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Heteroce	51.1	51.1	100%	7e-06	84%	XP_004895023.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	49.0	49.0	89%	3e-05	88%	XP_010621250.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	49.0	49.0	89%	3e-05	88%	XP_010621248.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	49.0	49.0	100%	3e-05	84%	XP_007454575.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	49.0	49.0	100%	3e-05	84%	XP_007454574.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Fukomys damarensis]	49.0	49.0	89%	3e-05	88%	KFO33840.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Chinchilla	49.0	49.0	100%	3e-05	79%	XP_005403486.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Callithrix	49.0	49.0	100%	3e-05	84%	XP_002746229.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Rhinopith	48.6	48.6	100%	5e-05	84%	XP_010363586.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.1	48.1	100%	6e-05	79%	XP_008975042.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.1	48.1	100%	7e-05	79%	XP_005003342.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.1	48.1	100%	7e-05	79%	XP_003468912.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 2	48.1	48.1	100%	7e-05	79%	XP_004043389.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 1	48.1	48.1	100%	7e-05	79%	XP_004043388.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.1	48.1	100%	7e-05	79%	XP_003823243.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pan trogl	48.1	48.1	100%	7e-05	79%	XP_518268.4
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	48.1	48.1	100%	7e-05	79%	XP_008975041.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Galeopte	46.9	46.9	100%	2e-04	79%	XP_008578807.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Loxodont	46.9	46.9	100%	2e-04	79%	XP_003416488.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Physeter	46.0	46.0	84%	3e-04	88%	XP_007116306.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Orcinus c	46.0	46.0	84%	3e-04	88%	XP_004273574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	46.0	46.0	84%	3e-04	88%	XP_007197201.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	46.0	46.0	84%	3e-04	88%	XP_007197200.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Tursiops	46.0	46.0	84%	3e-04	88%	XP_004313968.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Saimiri bo	45.2	45.2	100%	6e-04	79%	XP_003927350.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Felis catu	43.9	43.9	100%	0.002	79%	XP_003985826.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Panthera	43.9	43.9	100%	0.002	79%	XP_007074479.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	43.1	43.1	100%	0.003	79%	XP_007627730.1
☐	phosphatidylinositol-glycan-specific phospholipase D-like protein [Cricetulus g	43.1	43.1	100%	0.003	79%	ERE77282.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Cricetulus griseus]	43.1	43.1	100%	0.003	79%	EGV94314.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	43.1	43.1	100%	0.003	79%	XP_004761311.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Leptonyc	43.1	43.1	100%	0.003	79%	XP_006739372.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Peromys	43.1	43.1	100%	0.003	79%	XP_006977193.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Microtus	43.1	43.1	100%	0.003	79%	XP_005355039.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	43.1	43.1	100%	0.003	79%	XP_003502241.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	43.1	43.1	100%	0.003	79%	XP_004761310.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Mesocric	43.1	43.1	100%	0.003	79%	XP_005066341.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Orycterop	42.2	42.2	100%	0.006	74%	XP_007948002.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Trichechu	42.2	42.2	100%	0.006	74%	XP_004384046.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	41.8	41.8	100%	0.008	74%	XP_008260728.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	41.8	41.8	100%	0.008	74%	XP_008260723.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Echinops	41.4	41.4	78%	0.011	87%	XP_004712567.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Odobenu	41.4	41.4	100%	0.011	74%	XP_004406584.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Octodon	40.9	40.9	89%	0.015	76%	XP_004640232.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Eptesicus	40.9	40.9	84%	0.015	81%	XP_008145534.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	40.9	40.9	84%	0.015	81%	XP_005903212.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Bos mutus]	40.9	40.9	84%	0.015	81%	ELR50996.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	84%	0.015	81%	XP_010841812.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Nannosp	40.9	40.9	89%	0.015	82%	XP_008845321.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	84%	0.015	81%	XP_006051268.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Bos taurus]	40.9	40.9	84%	0.015	81%	NP_777241.1
☐	TPA: phosphatidylinositol-glycan-specific phospholipase D [Bos taurus]	40.9	40.9	84%	0.015	81%	DAA16116.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	84%	0.015	81%	XP_006919597.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	84%	0.015	81%	XP_010841810.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	84%	0.015	81%	XP_005223795.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	84%	0.015	81%	XP_006051267.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	84%	0.015	81%	XP_005223794.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	84%	0.015	81%	XP_006051266.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Sus scrof	40.9	40.9	84%	0.015	81%	XP_001925944.5
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	84%	0.015	81%	XP_006051265.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	84%	0.015	81%	XP_006051264.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.9	40.9	84%	0.015	81%	XP_010816770.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.5	40.5	100%	0.021	74%	XP_005640137.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoformX1	40.5	40.5	100%	0.021	74%	XP_535902.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Elephant	40.5	40.5	100%	0.021	68%	XP_006888712.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	40.5	40.5	100%	0.021	74%	XP_005640136.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ursus ma	40.1	40.1	84%	0.028	81%	XP_008691294.1
☐	hypothetical protein PANDA_003876 [Ailuropoda melanoleuca]	40.1	40.1	84%	0.028	81%	EFB28343.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	40.1	40.1	100%	0.028	74%	XP_004462113.1

⊟ Alignments

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glycosylphosphatidylinositol phospholipase D [Homo sapiens]

Sequence ID: emb|CAC14844.1| **Length:** 457 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 263 to 281 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.9 bits(129)	3e-08	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLGTSLSSGHVLMDGTLKQ  19
            KLGTSLSSGHVLM+GTLKQ
Sbjct  263  KLGTSLSSGHVLMNGTLKQ  281
```

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Unknown (protein for IMAGE:3354070), partial [Homo sapiens]

Sequence ID: gb|AAH07614.1| **Length:** 575 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 381 to 399 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.9 bits(129)	3e-08	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLGTSLSSGHVLMDGTLKQ  19
            KLGTSLSSGHVLM+GTLKQ
Sbjct  381  KLGTSLSSGHVLMNGTLKQ  399
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Homo sapiens]

Sequence ID: ref|XP_005249075.1| **Length:** 677 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 483 to 501 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.9 bits(129)	3e-08	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLGTSLSSGHVLMDGTLKQ  19
            KLGTSLSSGHVLM+GTLKQ
Sbjct  483  KLGTSLSSGHVLMNGTLKQ  501
```

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glycosylphosphatidylinositol phospholipase D [Homo sapiens]

Sequence ID: emb|CAC87068.1| **Length:** 840 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 646 to 664 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.9 bits(129)	4e-08	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLGTSLSSGHVLMDGTLKQ  19
            KLGTSLSSGHVLM+GTLKQ
Sbjct  646  KLGTSLSSGHVLMNGTLKQ  664
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

phospholipase D [Homo sapiens]

Sequence ID: gb|AAA36445.1| **Length:** 840 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 646 to 664 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.9 bits(129)	4e-08	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KLGTSLSSGHVLMDGTLKQ  19
            KLGTSLSSGHVLM+GTLKQ
Sbjct  646  KLGTSLSSGHVLMNGTLKQ  664
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - B9E7AZE601R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download

How to read this page | Blast report description

GPLD1_KLGTSLSSGHVLMNGTLKQ_NonMod

RID B9E7AZE601R (Expires on 01-14 13:19 pm)

Query ID	lcl|316949	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	19		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

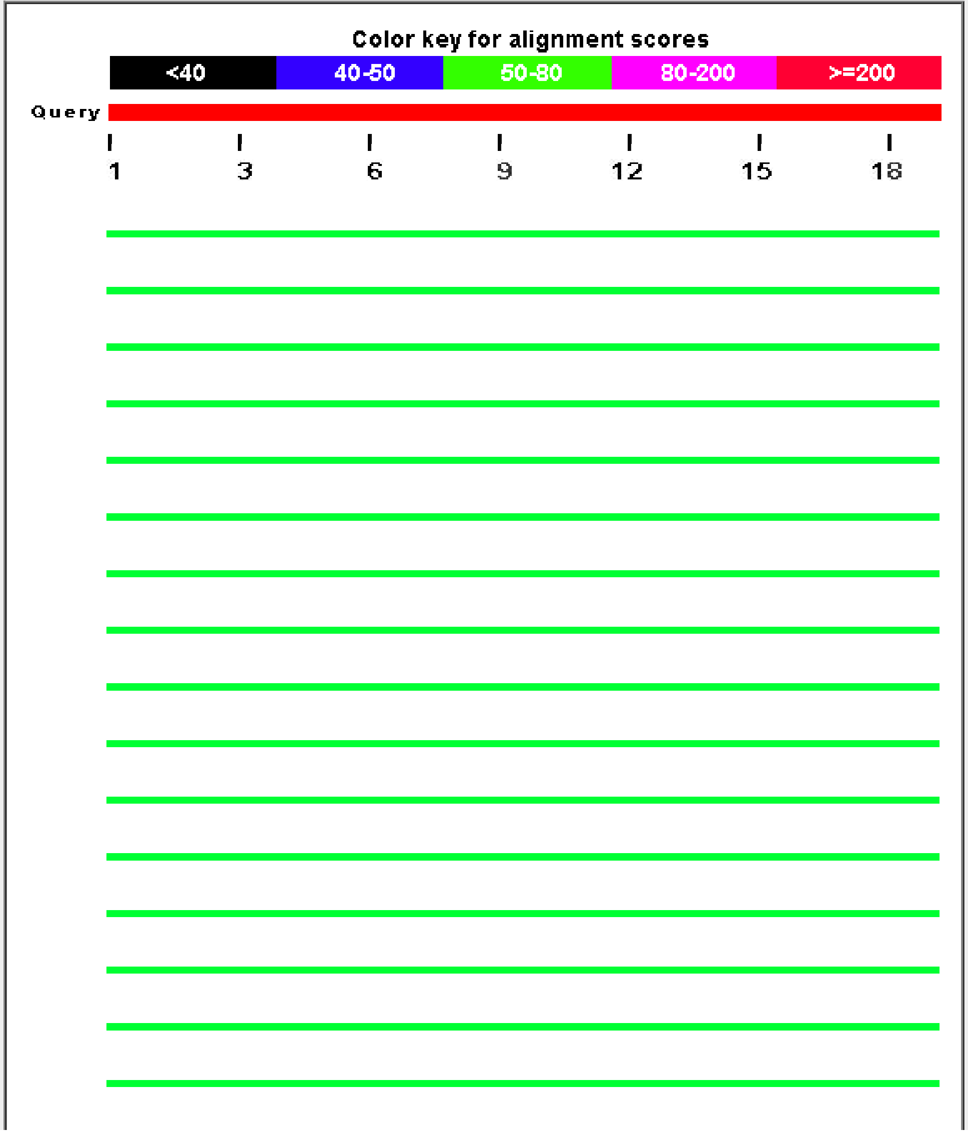
Graphic Summary

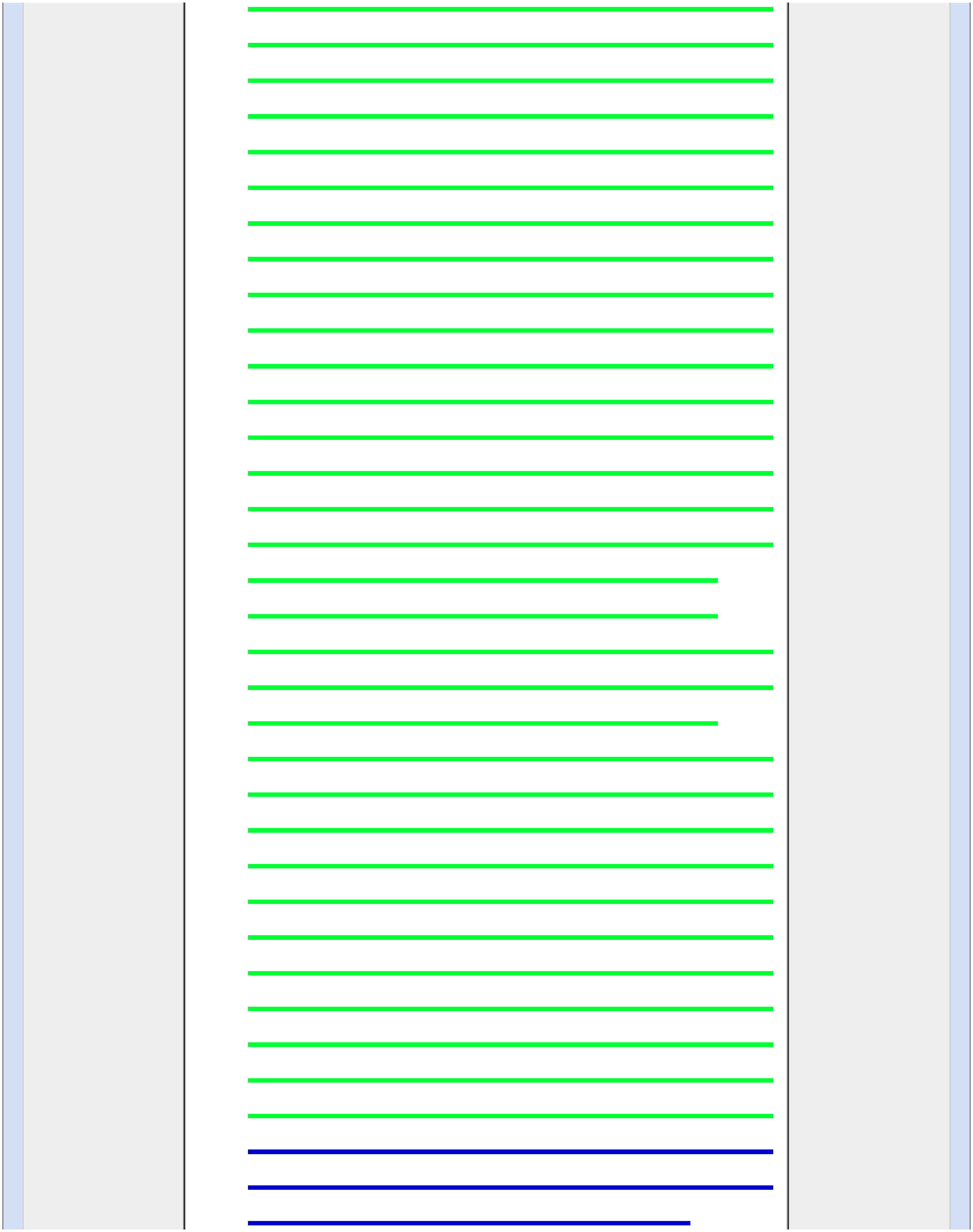
Show Conserved Domains

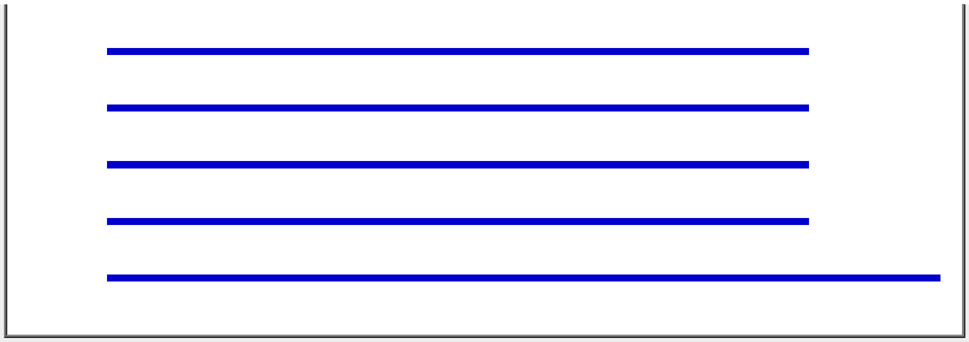
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	60.4	60.4	100%	4e-09	100%	gi|11122875|CAC14844.1
☐	Unknown (protein for IMAGE:3354070) [Homo sapiens]	60.4	60.4	100%	4e-09	100%	gi|14043248|AAH07614.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	60.4	60.4	100%	4e-09	100%	gi|530381810|XP_005249075.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	60.4	60.4	100%	5e-09	100%	gi|20269065|CAC87068.1
☐	phospholipase D [Homo sapiens]	60.4	60.4	100%	5e-09	100%	gi|388765|AAA36445.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Ho	60.4	60.4	100%	5e-09	100%	gi|29171717|NP_001494.2
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Ho	60.4	60.4	100%	5e-09	100%	gi|14195001|AAG16627.2
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CR	60.4	60.4	100%	5e-09	100%	gi|119575854|EAW55450.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|685535046|XP_009202774.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|544429971|XP_005553977.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|685535044|XP_009202773.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|635096985|XP_007971742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|297290177|XP_002803682.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|686720936|XP_009239742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|635096983|XP_007971741.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|635096981|XP_007971740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|635096993|XP_007971746.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|640776034|XP_008048656.1
☐	phospholipase D [Homo sapiens]	56.2	56.2	100%	1e-07	95%	gi|388763|AAA36444.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|544429969|XP_005553976.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|402865969|XP_003897171.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|685535041|XP_009202772.1
☐	hypothetical protein EGM_13271 [Macaca fascicularis]	56.2	56.2	100%	1e-07	95%	gi|355748274|EHH52757.1
☐	hypothetical protein EGK_21153 [Macaca mulatta]	56.2	56.2	100%	1e-07	95%	gi|355569342|EHH25414.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|332228866|XP_003263611.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	95%	gi|544429967|XP_005553975.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	53.7	53.7	100%	9e-07	89%	gi|512971062|XP_004847666.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Heterocepha	53.7	53.7	100%	9e-07	89%	gi|351706674|EHB09593.1
☐							

	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	53.7	53.7	100%	9e-07	89%	gi|512971060|XP_004847665.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	53.7	53.7	100%	9e-07	89%	gi|512971057|XP_004847664.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	53.7	53.7	100%	9e-07	89%	gi|512971055|XP_004847663.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	53.7	53.7	100%	9e-07	89%	gi|512880679|XP_004895023.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.5	51.5	89%	5e-06	94%	gi|731213592|XP_010621250.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.5	51.5	89%	5e-06	94%	gi|731213588|XP_010621248.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.5	51.5	100%	5e-06	89%	gi|602684652|XP_007454575.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.5	51.5	100%	5e-06	89%	gi|602684650|XP_007454574.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Fukomys dar	51.5	51.5	89%	5e-06	94%	gi|676279913|KFO33840.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.5	51.5	100%	5e-06	84%	gi|533180623|XP_005403486.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.5	51.5	100%	5e-06	89%	gi|675650934|XP_002746229.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.1	51.1	100%	6e-06	89%	gi|724798150|XP_010363586.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	50.7	50.7	100%	9e-06	84%	gi|675773160|XP_008975042.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	50.7	50.7	100%	9e-06	84%	gi|514459231|XP_005003342.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	50.7	50.7	100%	9e-06	84%	gi|348566244|XP_003468912.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	50.7	50.7	100%	9e-06	84%	gi|426351748|XP_004043389.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	50.7	50.7	100%	9e-06	84%	gi|426351746|XP_004043388.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	50.7	50.7	100%	9e-06	84%	gi|397505380|XP_003823243.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	50.7	50.7	100%	9e-06	84%	gi|410040317|XP_518268.4
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	50.7	50.7	100%	9e-06	84%	gi|675773152|XP_008975041.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	49.4	49.4	100%	2e-05	84%	gi|667294118|XP_008578807.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	49.4	49.4	100%	2e-05	84%	gi|344289516|XP_003416488.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.6	48.6	84%	4e-05	94%	gi|593754864|XP_007116306.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.6	48.6	84%	4e-05	94%	gi|466027702|XP_004273574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.6	48.6	84%	4e-05	94%	gi|594700264|XP_007197201.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.6	48.6	84%	4e-05	94%	gi|594700262|XP_007197200.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.6	48.6	84%	4e-05	94%	gi|470605744|XP_004313968.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	47.7	47.7	100%	9e-05	84%	gi|403270800|XP_003927350.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	46.4	46.4	100%	2e-04	84%	gi|410958439|XP_003985826.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	46.4	46.4	100%	2e-04	84%	gi|591294474|XP_007074479.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	45.6	100%	4e-04	84%	gi|625272320|XP_007627730.1
☐	phosphatidylinositol-glycan-specific phospholipase D-like protein [C	45.6	45.6	100%	4e-04	84%	gi|537192249|ERE77282.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Cricetulus gri	45.6	45.6	100%	4e-04	84%	gi|344238211|EGV94314.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	45.6	100%	4e-04	84%	gi|511882880|XP_004761311.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	45.6	100%	4e-04	84%	gi|585175123|XP_006739372.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	45.6	100%	4e-04	84%	gi|589928750|XP_006977193.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	45.6	100%	4e-04	84%	gi|532023384|XP_005355039.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	45.6	100%	4e-04	84%	gi|354480090|XP_003502241.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	45.6	100%	4e-04	84%	gi|511882878|XP_004761310.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	45.6	100%	4e-04	84%	gi|524924187|XP_005066341.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	8e-04	79%	gi|634873155|XP_007948002.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	8e-04	79%	gi|471403600|XP_004384046.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.3	44.3	100%	0.001	79%	gi|655839984|XP_008260728.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.3	44.3	100%	0.001	79%	gi|655839976|XP_008260723.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.9	43.9	78%	0.002	93%	gi|507689072|XP_004712567.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.9	43.9	100%	0.002	79%	gi|472374241|XP_004406584.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	89%	0.002	82%	gi|507684247|XP_004640232.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	84%	0.002	88%	gi|641712629|XP_008145534.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	43.5	43.5	84%	0.002	88%	gi|555982613|XP_005903212.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Bos mutus]	43.5	43.5	84%	0.002	88%	gi|440899735|ELR50996.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	89%	0.002	88%	gi|674075950|XP_008845321.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	84%	0.002	88%	gi|594053987|XP_006051268.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Bos	43.5	43.5	84%	0.002	88%	gi|27807363|NP_777241.1
☐	TPA: phosphatidylinositol-glycan-specific phospholipase D [Bos tau	43.5	43.5	84%	0.002	88%	gi|296474001|DAA16116.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	84%	0.002	88%	gi|586529361|XP_006919597.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	84%	0.002	88%	gi|529003874|XP_005223795.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	84%	0.002	88%	gi|594053985|XP_006051267.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	84%	0.002	88%	gi|529003872|XP_005223794.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	84%	0.002	88%	gi|594053983|XP_006051266.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	84%	0.002	88%	gi|545837650|XP_001925944.5
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	84%	0.002	88%	gi|594053981|XP_006051265.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	84%	0.002	88%	gi|529003870|XP_005223793.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.5	43.5	84%	0.002	88%	gi|594053979|XP_006051264.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.1	43.1	100%	0.003	79%	gi|545554532|XP_005640137.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.1	43.1	100%	0.003	79%	gi|74003954|XP_535902.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.1	43.1	100%	0.003	74%	gi|585669334|XP_006888712.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	43.1	43.1	100%	0.003	79%	gi|545554529|XP_005640136.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	42.6	42.6	84%	0.004	88%	gi|671000878|XP_008691294.1
☐	hypothetical protein PANDA_003876 [Ailuropoda melanoleuca]	42.6	42.6	84%	0.004	88%	gi|281352759|EFB28343.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	42.6	42.6	100%	0.004	79%	gi|488541031|XP_004462113.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-	42.6	42.6	84%	0.004	88%	gi|301760102|XP_002915859.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	42.2	42.2	100%	0.005	79%	gi|586495128|XP_006878008.1

⊖ Alignments

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glycosylphosphatidylinositol phospholipase D [Homo sapiens]

Sequence ID: gi|11122875|emb|CAC14844.1| **Length:** 457 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 263 to 281 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	4e-09	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLGTSLSSGHVLMNGTLKQ  19
            KLGTSLSSGHVLMNGTLKQ
Sbjct  263  KLGTSLSSGHVLMNGTLKQ  281
```

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Unknown (protein for IMAGE:3354070), partial [Homo sapiens]

Sequence ID: gi|14043248|gb|AAH07614.1| **Length:** 575 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 381 to 399 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	4e-09	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLGTSLSSGHVLMNGTLKQ  19
```

```
               KLGTSLSSGHVLMNGTLKQ
Sbjct  381  KLGTSLSSGHVLMNGTLKQ  399
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Homo sapiens]

Sequence ID: gi|530381810|ref|XP_005249075.1| **Length:** 677 **Number of Matches:** 1

Range 1: 483 to 501 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	4e-09	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLGTSLSSGHVLMNGTLKQ  19
            KLGTSLSSGHVLMNGTLKQ
Sbjct  483  KLGTSLSSGHVLMNGTLKQ  501
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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glycosylphosphatidylinositol phospholipase D [Homo sapiens]

Sequence ID: gi|20269065|emb|CAC87068.1| **Length:** 840 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 646 to 664 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	5e-09	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLGTSLSSGHVLMNGTLKQ  19
            KLGTSLSSGHVLMNGTLKQ
Sbjct  646  KLGTSLSSGHVLMNGTLKQ  664
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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phospholipase D [Homo sapiens]

Sequence ID: gi|388765|gb|AAA36445.1| **Length:** 840 **Number of Matches:** 1

Range 1: 646 to 664 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	5e-09	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KLGTSLSSGHVLMNGTLKQ  19
            KLGTSLSSGHVLMNGTLKQ
Sbjct  646  KLGTSLSSGHVLMNGTLKQ  664
```

Related Information

Gene - associated gene details

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVE4BZK901R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download How to read this page Blast report description

GPLD1_KLNVEAADWTVRG_Mod

RID BVE4BZK901R (Expires on 01-21 09:08 am)

Query ID	lcl|263726	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	13	**Program**	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

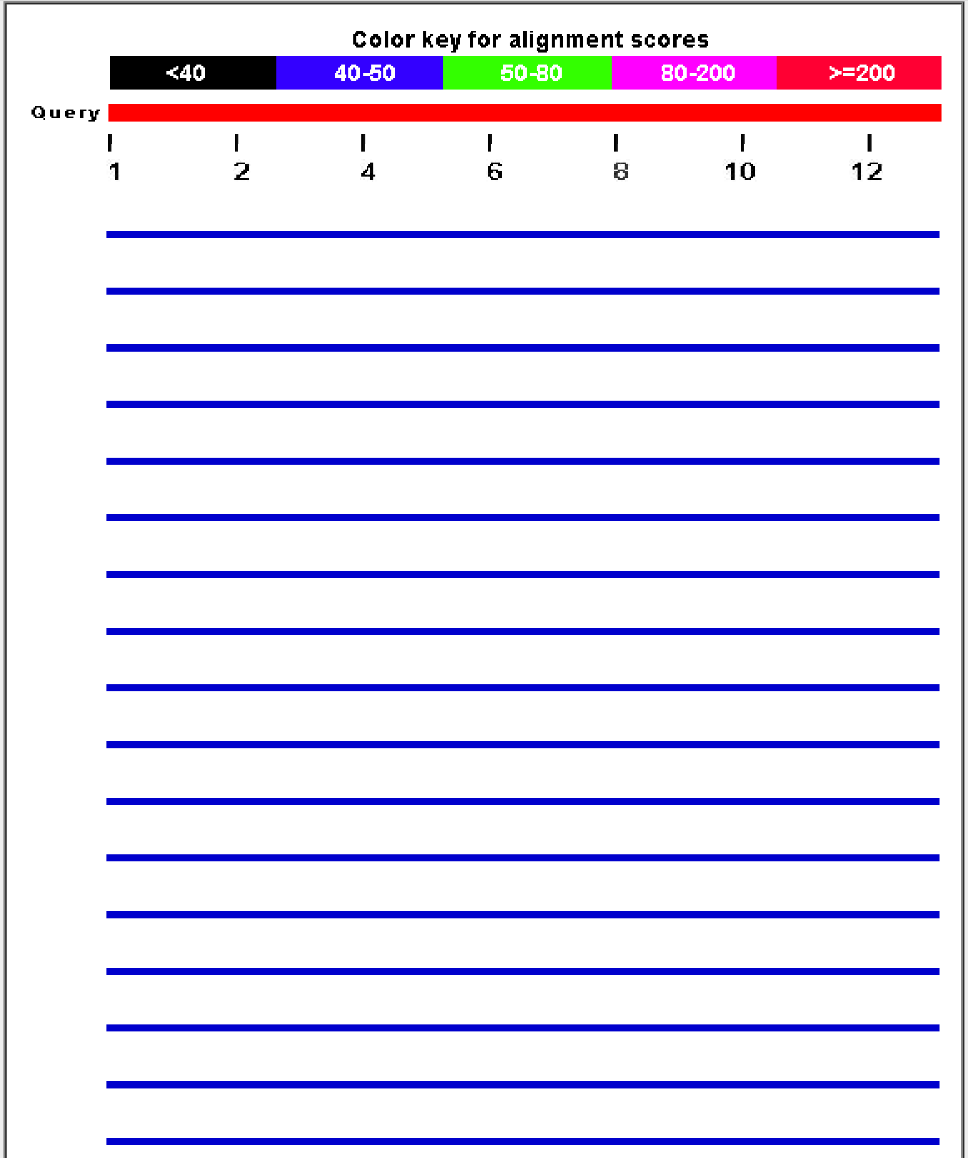
Graphic Summary

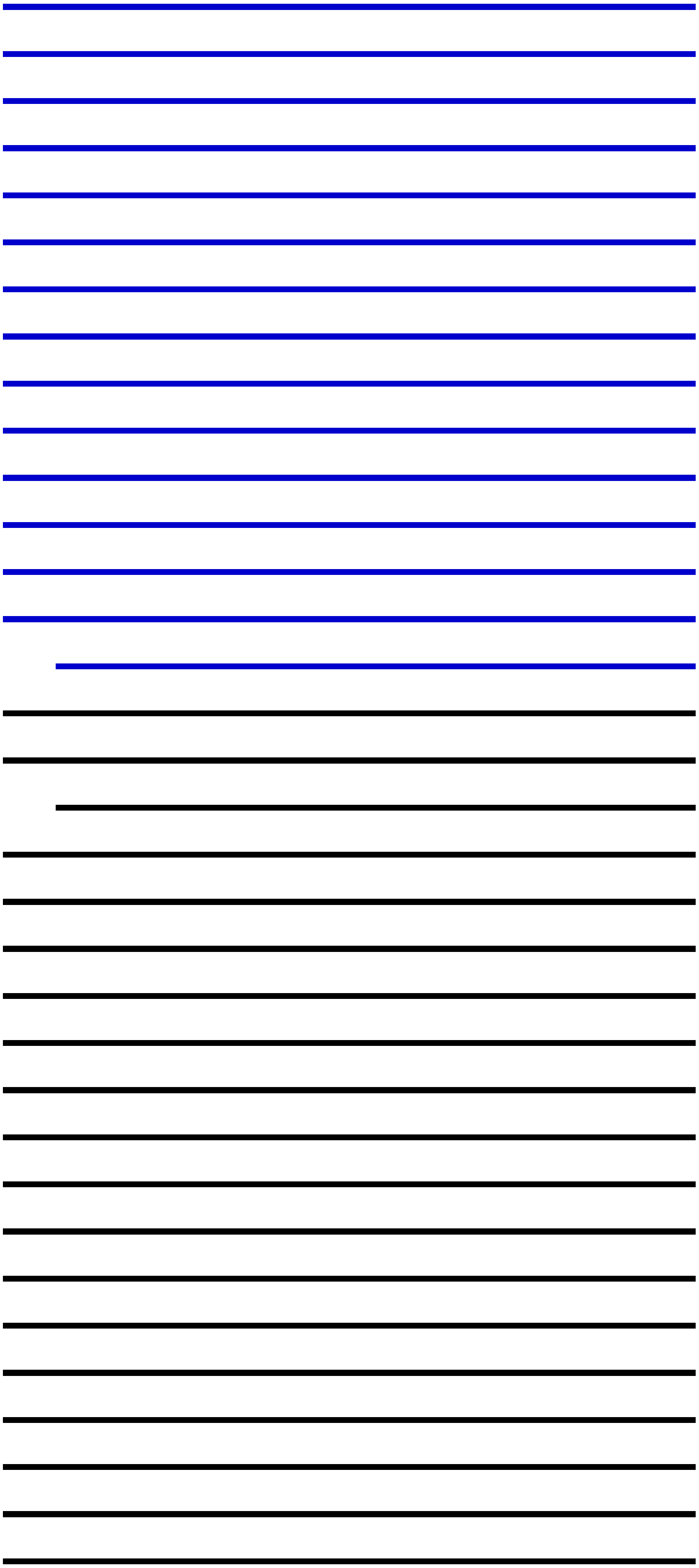
Show Conserved Domains

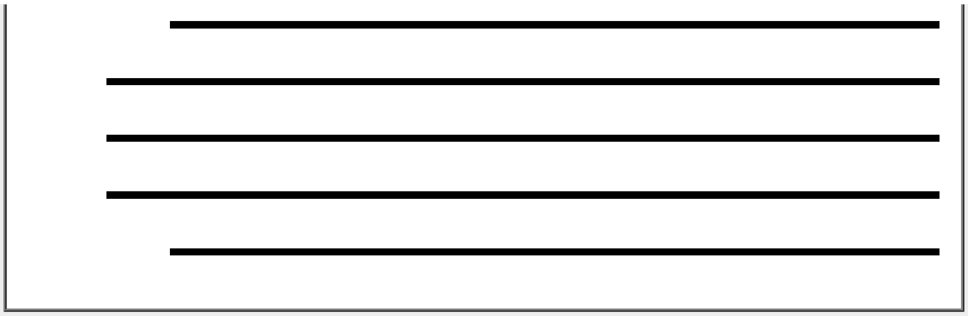
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Saimiri bo	44.8	44.8	100%	4e-04	100%	XP_003927350.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	42.2	42.2	100%	0.003	92%	CAC14844.1
☐	Unknown (protein for IMAGE:3354070) [Homo sapiens]	42.2	42.2	100%	0.003	92%	AAH07614.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X4	42.2	42.2	100%	0.003	92%	XP_009202774.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3	42.2	42.2	100%	0.003	92%	XP_008975042.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3	42.2	42.2	100%	0.003	92%	XP_005553977.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3	42.2	42.2	100%	0.003	92%	XP_005249075.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3	42.2	42.2	100%	0.003	92%	XP_009202773.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3	42.2	42.2	100%	0.003	92%	XP_007971742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-like [Maca	42.2	42.2	100%	0.003	92%	XP_002803682.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pongo ab	42.2	42.2	100%	0.003	92%	XP_009239742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X2	42.2	42.2	100%	0.003	92%	XP_007971741.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X1	42.2	42.2	100%	0.003	92%	XP_007971740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X4	42.2	42.2	100%	0.003	92%	XP_007971746.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 2	42.2	42.2	100%	0.003	92%	XP_004043389.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 1	42.2	42.2	100%	0.003	92%	XP_004043388.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	42.2	42.2	100%	0.003	92%	CAC87068.1
☐	phospholipase D [Homo sapiens]	42.2	42.2	100%	0.003	92%	AAA36445.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X2	42.2	42.2	100%	0.003	92%	XP_003823243.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Homo sapien	42.2	42.2	100%	0.003	92%	NP_001494.2
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Homo sapier	42.2	42.2	100%	0.003	92%	AAG16627.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Rhinopith	42.2	42.2	100%	0.003	92%	XP_010363586.1
☐	phospholipase D [Homo sapiens]	42.2	42.2	100%	0.003	92%	AAA36444.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X2	42.2	42.2	100%	0.003	92%	XP_005553976.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X2	42.2	42.2	100%	0.003	92%	XP_003897171.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pan trogl	42.2	42.2	100%	0.003	92%	XP_518268.4
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X1	42.2	42.2	100%	0.003	92%	XP_009202772.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X1	42.2	42.2	100%	0.003	92%	XP_008975041.1
☐	hypothetical protein EGM_13271 [Macaca fascicularis]	42.2	42.2	100%	0.003	92%	EHH52757.1

☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_c [Hom	42.2	42.2	100%	0.003	92%	EAW55450.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	42.2	42.2	100%	0.003	92%	XP_005553975.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Callithrix	41.8	41.8	92%	0.004	100%	XP_002746229.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Eptesicus	39.7	39.7	100%	0.022	92%	XP_008145534.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Myotis brandtii]	39.2	39.2	100%	0.030	92%	EPQ05831.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Condylur	39.2	39.2	92%	0.030	92%	XP_004693375.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	39.2	39.2	100%	0.030	92%	XP_005863221.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Orycterop	38.8	38.8	100%	0.042	92%	XP_007948002.1
☐	hypothetical protein EGK_21153 [Macaca mulatta]	38.4	38.4	100%	0.058	85%	EHH25414.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Sus scrof	38.0	38.0	100%	0.080	85%	XP_001925944.5
☐	Phosphatidylinositol-glycan-specific phospholipase D [Pteropus alecto]	37.5	37.5	100%	0.11	85%	ELK05805.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	37.5	37.5	100%	0.11	85%	XP_006051268.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Capra hir	37.5	37.5	100%	0.11	85%	XP_005696842.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ovis arie	37.5	37.5	100%	0.11	85%	XP_004019154.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	37.5	37.5	100%	0.11	85%	XP_006919597.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Leptonyc	37.5	37.5	100%	0.11	85%	XP_006739372.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	37.5	37.5	100%	0.11	85%	XP_006051267.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	37.5	37.5	100%	0.11	85%	XP_006051266.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Nomascu	37.5	37.5	100%	0.11	85%	XP_003263611.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	37.5	37.5	100%	0.11	85%	XP_006051265.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	37.5	37.5	100%	0.11	85%	XP_006051264.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ochoton	37.1	37.1	100%	0.15	85%	XP_004593176.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Chinchill	35.8	35.8	92%	0.40	92%	XP_005403486.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Trichechu	35.4	35.4	100%	0.54	85%	XP_004384046.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Loxodont	35.4	35.4	100%	0.54	85%	XP_003416488.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Odobenu	35.0	35.0	100%	0.75	77%	XP_004406584.1
☐	hypothetical protein CB1_000595062 [Camelus ferus]	34.6	34.6	92%	1.0	83%	EPY83136.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	34.6	34.6	92%	1.0	83%	XP_008511735.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Jaculus j	34.6	34.6	92%	1.0	83%	XP_004669997.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	34.6	34.6	92%	1.0	83%	XP_006182298.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Camelus	34.6	34.6	92%	1.0	83%	XP_010944080.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	34.6	34.6	92%	1.0	83%	XP_008511734.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	34.6	34.6	92%	1.0	83%	XP_004761311.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Physeter	34.6	34.6	92%	1.0	83%	XP_007116306.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Panthol	34.6	34.6	92%	1.0	83%	XP_005973908.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Orcinus	34.6	34.6	92%	1.0	83%	XP_004273574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Panthera	34.6	34.6	92%	1.0	83%	XP_007074479.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	34.6	34.6	92%	1.0	83%	XP_010978426.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Equus ca	34.6	34.6	92%	1.0	83%	XP_001497586.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Vicugna	34.6	34.6	92%	1.0	83%	XP_006198740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	34.6	34.6	92%	1.0	83%	XP_007197201.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	34.6	34.6	92%	1.0	83%	XP_008511732.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	34.6	34.6	92%	1.0	83%	XP_008511731.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	34.6	34.6	92%	1.0	83%	XP_007197200.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	34.6	34.6	92%	1.0	83%	XP_004761310.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Tursiops	34.6	34.6	92%	1.0	83%	XP_004313968.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	34.6	34.6	92%	1.0	83%	XP_008511730.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	34.1	34.1	100%	1.4	77%	XP_005903212.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Bos mutus]	34.1	34.1	100%	1.4	77%	ELR50996.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	34.1	34.1	100%	1.4	77%	XP_010841812.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Bos taurus]	34.1	34.1	100%	1.4	77%	NP_777241.1
☐	TPA: phosphatidylinositol-glycan-specific phospholipase D [Bos taurus]	34.1	34.1	100%	1.4	77%	DAA16116.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	34.1	34.1	100%	1.4	77%	XP_010841810.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	34.1	34.1	100%	1.4	77%	XP_005223795.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	34.1	34.1	100%	1.4	77%	XP_005223794.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	34.1	34.1	100%	1.4	77%	XP_010816770.1
☐	hypothetical protein PANDA_003876 [Ailuropoda melanoleuca]	33.3	33.3	100%	2.6	77%	EFB28343.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	33.3	33.3	100%	2.6	85%	XP_005640137.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoformX1	33.3	33.3	100%	2.6	85%	XP_535902.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	33.3	33.3	92%	2.6	83%	XP_007454575.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	33.3	33.3	92%	2.6	83%	XP_007454574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-like [Ailur	33.3	33.3	100%	2.6	77%	XP_002915859.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ceratothe	33.3	33.3	92%	2.6	83%	XP_004432133.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	33.3	33.3	100%	2.6	85%	XP_005640136.1
☐	Alpha-glucan water dikinase, chloroplastic [Auxenochlorella protothecoides]	32.9	32.9	69%	3.6	100%	KFM28490.1
☐	hypothetical protein [Haloferax prahovense]	32.5	32.5	92%	4.8	77%	WP_008095608.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Octodon	32.5	32.5	92%	4.9	83%	XP_004640232.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	32.5	32.5	92%	4.9	83%	XP_010621250.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	32.5	32.5	92%	4.9	83%	XP_010621248.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ictidomys	32.5	32.5	92%	4.9	83%	XP_005337080.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	32.5	32.5	100%	4.9	77%	XP_003788429.1

⊟ Alignments

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Saimiri boliviensis boliviensis]

Sequence ID: ref|XP_003927350.1| **Length:** 840 **Number of Matches:** 1

Range 1: 561 to 573 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.8 bits(98)	4e-04	13/13(100%)	13/13(100%)	0/13(0%)

```
Query  1    KLNVEAADWTVRG  13
            KLNVEAADWTVRG
Sbjct  561  KLNVEAADWTVRG  573
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

glycosylphosphatidylinositol phospholipase D [Homo sapiens]

Sequence ID: emb|CAC14844.1| **Length:** 457 **Number of Matches:** 1

Range 1: 178 to 190 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
42.2 bits(92)	0.003	12/13(92%)	13/13(100%)	0/13(0%)

Related Information

Gene - associated gene details

```
Query  1    KLNVEAADWTVRG  13
            KLNVEAA+WTVRG
Sbjct  178  KLNVEAANWTVRG  190
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Unknown (protein for IMAGE:3354070), partial [Homo sapiens]

Sequence ID: gb|AAH07614.1| **Length:** 575 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 296 to 308 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
42.2 bits(92)	0.003	12/13(92%)	13/13(100%)	0/13(0%)

```
Query  1    KLNVEAADWTVRG  13
            KLNVEAA+WTVRG
Sbjct  296  KLNVEAANWTVRG  308
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X4 [Papio anubis]

Sequence ID: ref|XP_009202774.1| **Length:** 677 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 398 to 410 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
42.2 bits(92)	0.003	12/13(92%)	13/13(100%)	0/13(0%)

```
Query  1    KLNVEAADWTVRG  13
            KLNVEAA+WTVRG
Sbjct  398  KLNVEAANWTVRG  410
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Pan paniscus]

Sequence ID: ref|XP_008975042.1| **Length:** 677 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 398 to 410 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
42.2 bits(92)	0.003	12/13(92%)	13/13(100%)	0/13(0%)

```
Query  1    KLNVEAADWTVRG  13
            KLNVEAA+WTVRG
Sbjct  398  KLNVEAANWTVRG  410
```

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NCBI/ BLAST/ blastp suite/ **Formatting Results - B9E7U9DD01R**

Your search parameters were adjusted to search for a short input sequence.

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GPLD1_KLNVEAANWTVRG_NonMod

RID B9E7U9DD01R (Expires on 01-14 13:19 pm)

Query ID	lcl|321260	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	13		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

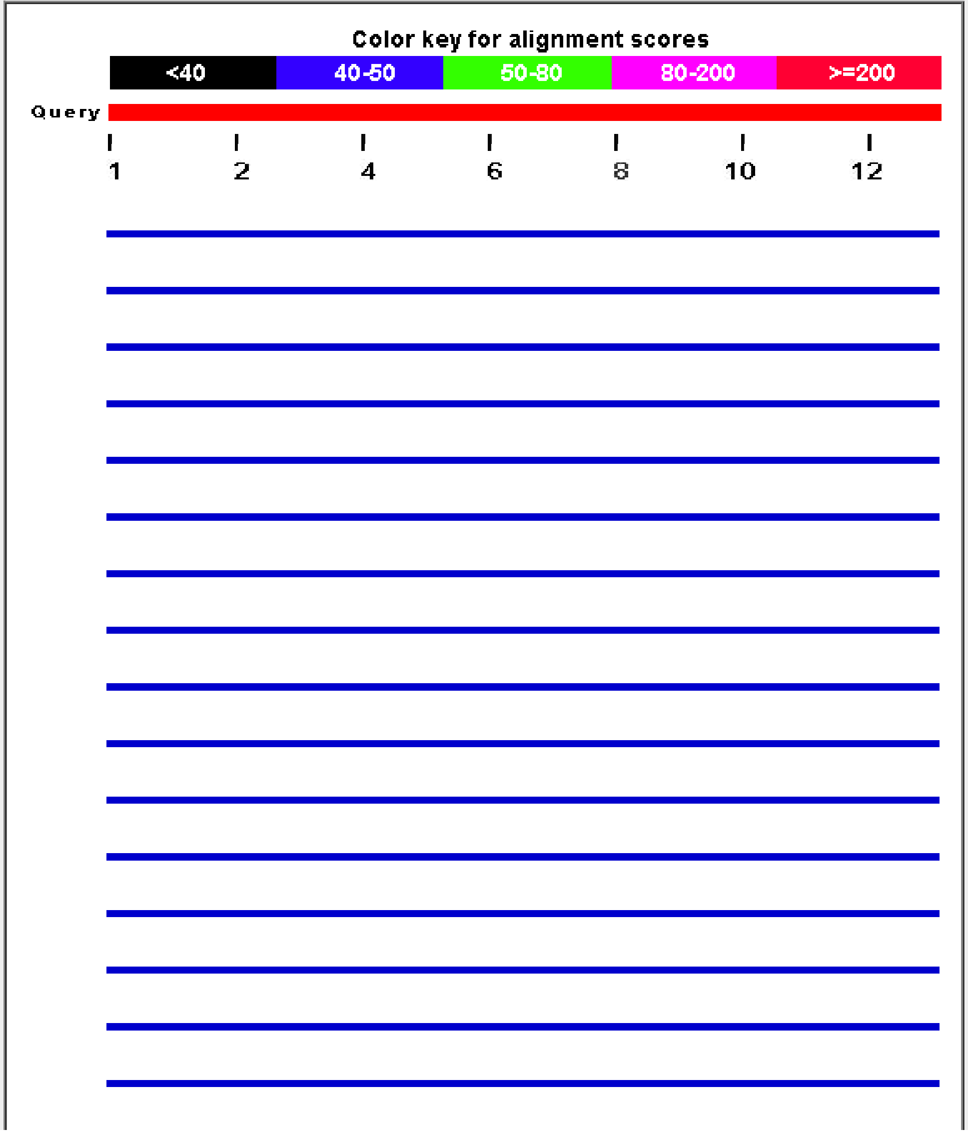
Graphic Summary

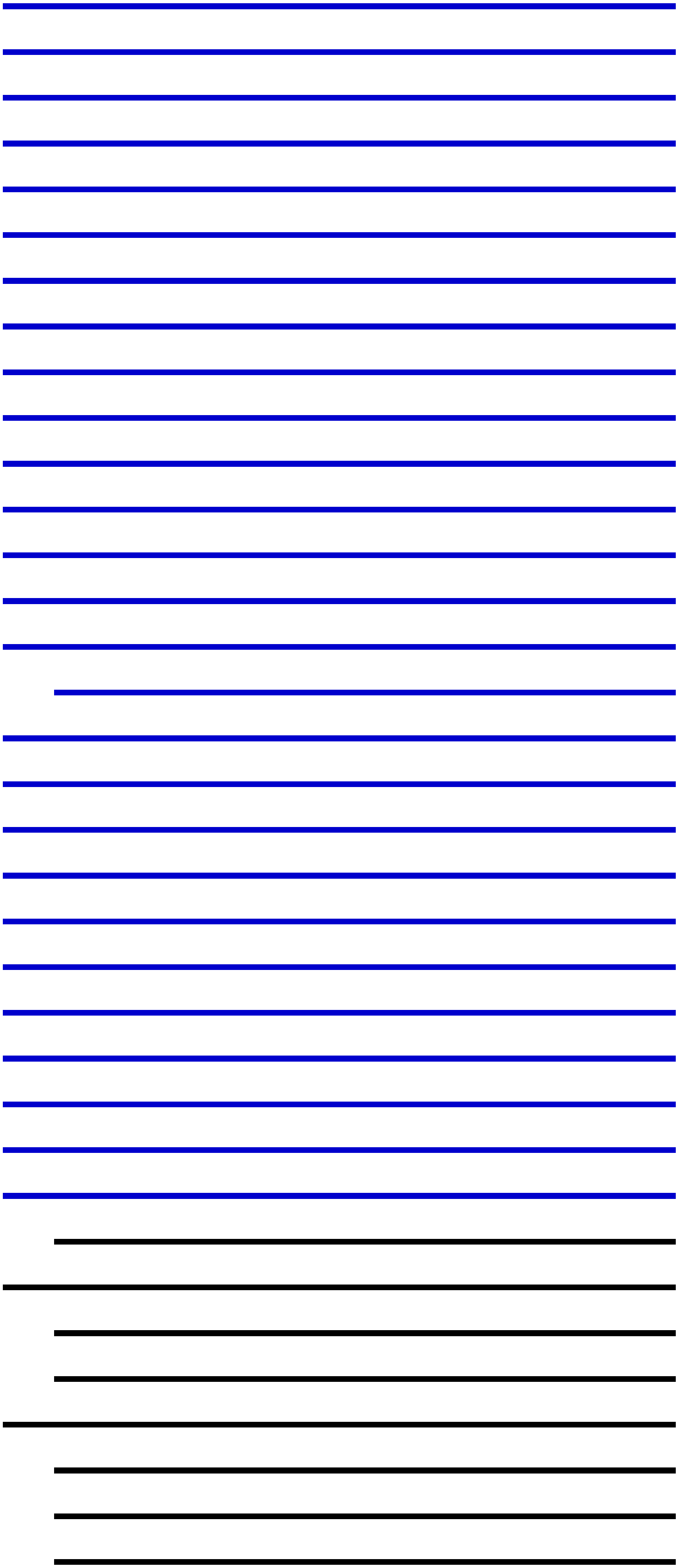
Show Conserved Domains

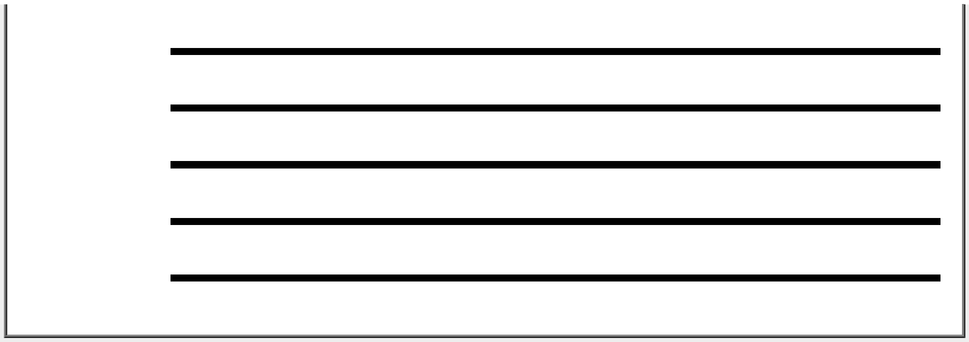
No putative conserved domains have been detected

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	44.8	44.8	100%	4e-04	100%	gi|11122875|CAC14844.1
☐	Unknown (protein for IMAGE:3354070) [Homo sapiens]	44.8	44.8	100%	4e-04	100%	gi|14043248|AAH07614.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|685535046|XP_009202774.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|675773160|XP_008975042.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|544429971|XP_005553977.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|530381810|XP_005249075.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|685535044|XP_009202773.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|635096985|XP_007971742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|297290177|XP_002803682.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|686720936|XP_009239742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|635096983|XP_007971741.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|635096981|XP_007971740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|635096993|XP_007971746.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|426351748|XP_004043389.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|426351746|XP_004043388.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	44.8	44.8	100%	4e-04	100%	gi|20269065|CAC87068.1
☐	phospholipase D [Homo sapiens]	44.8	44.8	100%	4e-04	100%	gi|388765|AAA36445.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|397505380|XP_003823243.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Ho	44.8	44.8	100%	4e-04	100%	gi|29171717|NP_001494.2
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Hc	44.8	44.8	100%	4e-04	100%	gi|14195001|AAG16627.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|724798150|XP_010363586.1
☐	phospholipase D [Homo sapiens]	44.8	44.8	100%	4e-04	100%	gi|388763|AAA36444.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|544429969|XP_005553976.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|402865969|XP_003897171.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|410040317|XP_518268.4
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|685535041|XP_009202772.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|675773152|XP_008975041.1
☐	hypothetical protein EGM_13271 [Macaca fascicularis]	44.8	44.8	100%	4e-04	100%	gi|355748274|EHH52757.1
☐							

	glycosylphosphatidylinositol specific phospholipase D1, isoform CR	44.8	44.8	100%	4e-04	100%	gi|119575854|EAW55450.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	44.8	44.8	100%	4e-04	100%	gi|544429967|XP_005553975.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	42.2	42.2	100%	0.003	92%	gi|403270800|XP_003927350.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	41.8	41.8	92%	0.004	100%	gi|507979038|XP_004693375.1
☐	hypothetical protein EGK_21153 [Macaca mulatta]	40.9	40.9	100%	0.008	92%	gi|355569342|EHH25414.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.5	40.5	100%	0.011	92%	gi|545837650|XP_001925944.5
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.1	40.1	100%	0.015	92%	gi|594053987|XP_006051268.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.1	40.1	100%	0.015	92%	gi|548518368|XP_005696842.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.1	40.1	100%	0.015	92%	gi|426250866|XP_004019154.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.1	40.1	100%	0.015	92%	gi|585175123|XP_006739372.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.1	40.1	100%	0.015	92%	gi|594053985|XP_006051267.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.1	40.1	100%	0.015	92%	gi|594053983|XP_006051266.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.1	40.1	100%	0.015	92%	gi|332228866|XP_003263611.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.1	40.1	100%	0.015	92%	gi|594053981|XP_006051265.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.1	40.1	100%	0.015	92%	gi|594053979|XP_006051264.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	39.2	39.2	92%	0.029	92%	gi|675650934|XP_002746229.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.5	37.5	100%	0.10	85%	gi|472374241|XP_004406584.1
☐	hypothetical protein CB1_000595062 [Camelus ferus]	37.1	37.1	92%	0.14	92%	gi|528763477|EPY83136.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|664709546|XP_008511735.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	100%	0.14	85%	gi|641712629|XP_008145534.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	37.1	37.1	92%	0.14	92%	gi|560912019|XP_006182298.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|664709544|XP_008511734.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|511882880|XP_004761311.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|593754864|XP_007116306.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|556757122|XP_005973908.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|466027702|XP_004273574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|149732005|XP_001497586.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|560952422|XP_006198740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|594700264|XP_007197201.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|664709542|XP_008511732.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|664709540|XP_008511731.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|594700262|XP_007197200.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|511882878|XP_004761310.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|470605744|XP_004313968.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.1	37.1	92%	0.14	92%	gi|664709538|XP_008511730.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Myotis brand	36.7	36.7	100%	0.20	85%	gi|521024043|EPQ05831.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	36.7	36.7	100%	0.20	85%	gi|555982613|XP_005903212.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Bos mutus]	36.7	36.7	100%	0.20	85%	gi|440899735|ELR50996.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Bos	36.7	36.7	100%	0.20	85%	gi|27807363|NP_777241.1
☐	TPA: phosphatidylinositol-glycan-specific phospholipase D [Bos tau	36.7	36.7	100%	0.20	85%	gi|296474001|DAA16116.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	36.7	36.7	100%	0.20	85%	gi|529003874|XP_005223795.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	36.7	36.7	100%	0.20	85%	gi|529003872|XP_005223794.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	36.7	36.7	100%	0.20	85%	gi|529003870|XP_005223793.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	36.7	36.7	100%	0.20	85%	gi|554537051|XP_005863221.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	36.3	36.3	100%	0.27	85%	gi|634873155|XP_007948002.1

☐	hypothetical protein PANDA_003876 [Ailuropoda melanoleuca]	35.8	35.8	100%	0.37	85%	gi|281352759|EFB28343.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-	35.8	35.8	100%	0.37	85%	gi|301760102|XP_002915859.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.8	35.8	92%	0.37	92%	gi|478515788|XP_004432133.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Pteropus ale	35.0	35.0	100%	0.70	77%	gi|431896393|ELK05805.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.0	35.0	100%	0.70	77%	gi|586529361|XP_006919597.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	34.6	34.6	100%	0.96	77%	gi|504166674|XP_004593176.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	34.1	34.1	100%	1.3	85%	gi|545554532|XP_005640137.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	34.1	34.1	100%	1.3	85%	gi|74003954|XP_535902.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	34.1	34.1	100%	1.3	85%	gi|545554529|XP_005640136.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	33.3	33.3	100%	2.5	77%	gi|617615072|XP_007526005.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	33.3	33.3	92%	2.5	83%	gi|533180623|XP_005403486.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.9	32.9	92%	3.4	83%	gi|671000878|XP_008691294.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.9	32.9	92%	3.4	83%	gi|667294118|XP_008578807.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.9	32.9	100%	3.4	77%	gi|471403600|XP_004384046.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.9	32.9	100%	3.4	77%	gi|344289516|XP_003416488.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.0	32.0	92%	6.4	75%	gi|507572817|XP_004669997.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.0	32.0	100%	6.4	77%	gi|586495128|XP_006878008.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.0	32.0	92%	6.4	75%	gi|591294474|XP_007074479.1
☐	hypothetical protein [Corynebacterium mastitidis]	31.6	31.6	84%	8.5	91%	gi|516827401|WP_018118945.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	30.8	30.8	92%	16	75%	gi|602684652|XP_007454575.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	30.8	30.8	92%	16	75%	gi|602684650|XP_007454574.1
☐	abortive infection protein [Leptolyngbya sp. PCC 7376]	30.3	50.1	92%	22	75%	gi|504946464|WP_015133566.1
☐	PTS mannitol transporter subunit IIBC [Tepidanaerobacter acetatox	30.3	30.3	69%	22	89%	gi|503544991|WP_013779067.1
☐	phosphoenolpyruvate-dependent sugar phosphotransferase system	30.3	30.3	69%	22	89%	gi|505108599|WP_015295701.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	30.3	30.3	92%	22	75%	gi|612008081|XP_007487938.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	30.3	30.3	92%	22	75%	gi|612008079|XP_001375600.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	30.3	30.3	92%	22	75%	gi|612008077|XP_007487937.1

⊟ Alignments

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVE5DH9K01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

GPLD1_KNDFHRDLTTSLTESVDRN_Mod

RID BVE5DH9K01R (Expires on 01-21 09:08 am)

Query ID	lcl|280655	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	19		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

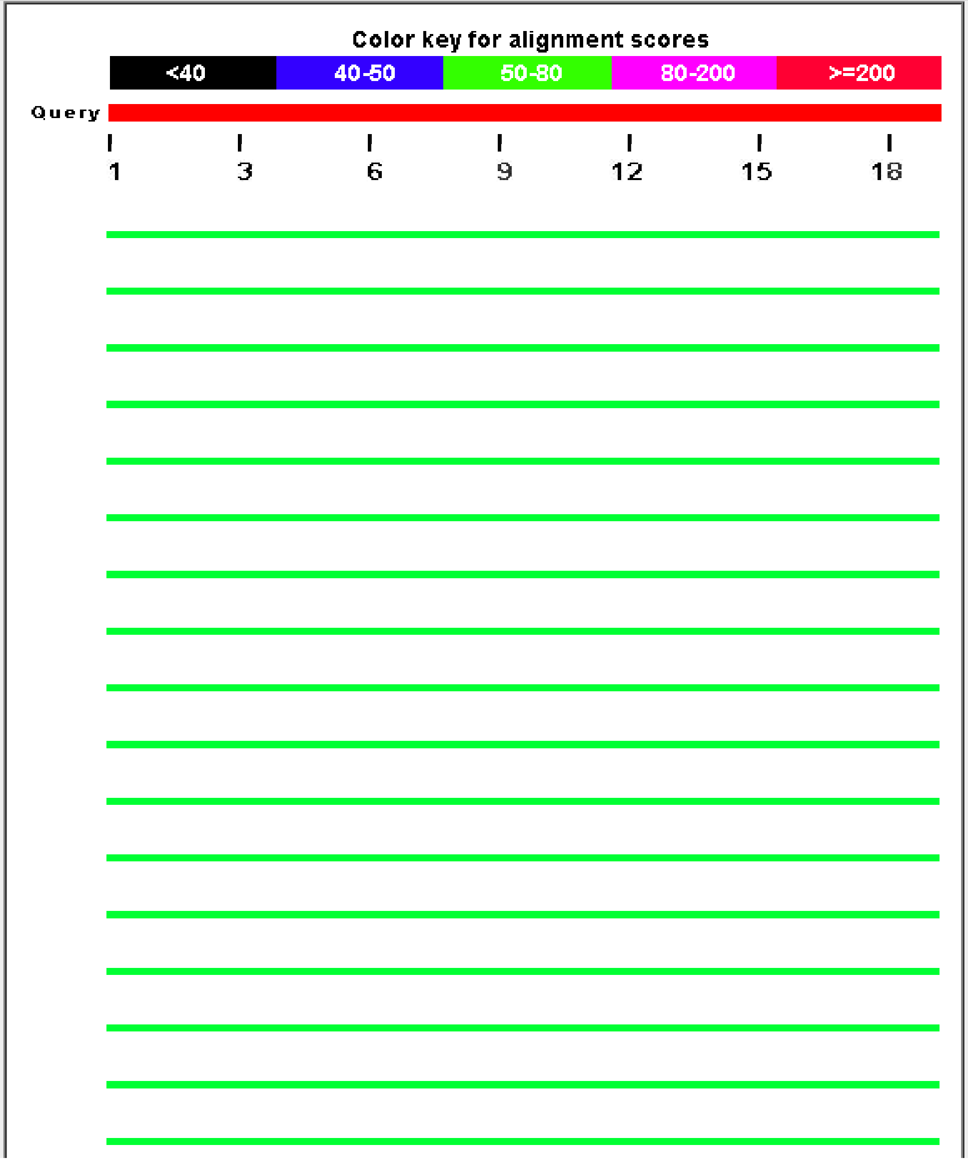
Graphic Summary

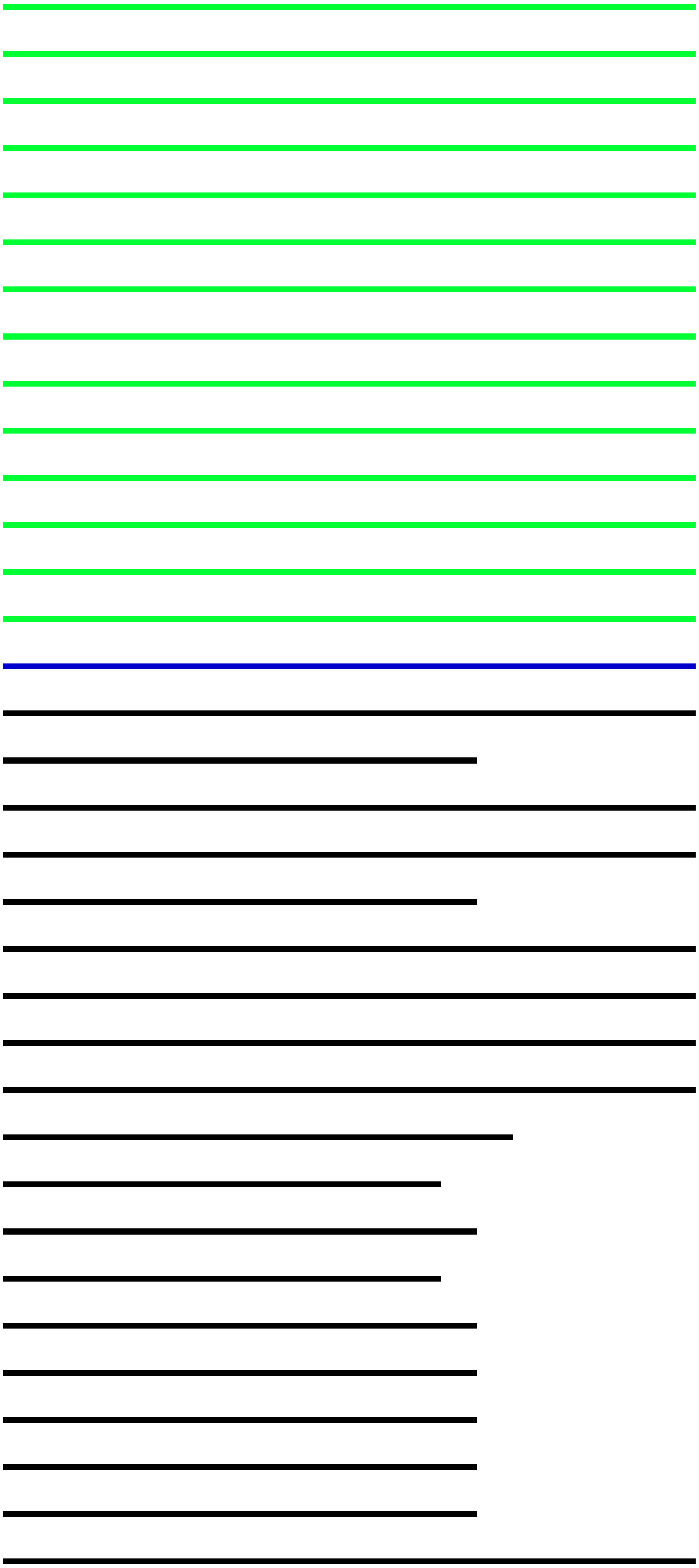
Show Conserved Domains

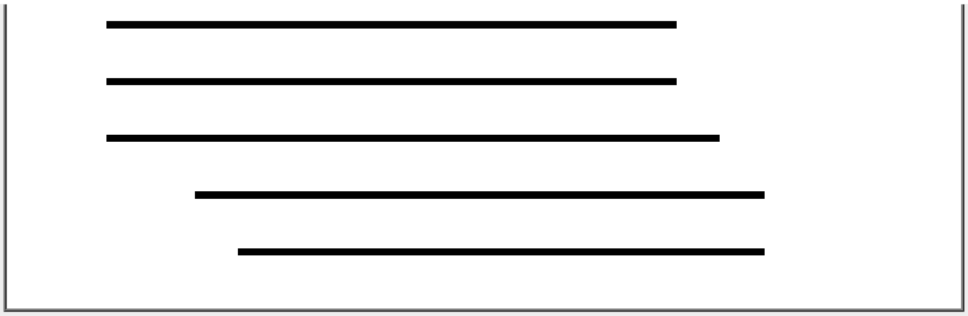
No putative conserved domains have been detected

Distribution of 103 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Unknown (protein for IMAGE:3354070) [Homo sapiens]	61.3	61.3	100%	2e-09	95%	AAH07614.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	61.3	61.3	100%	2e-09	95%	XP_008975042.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	61.3	61.3	100%	2e-09	95%	XP_005249075.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pongo ab	61.3	61.3	100%	2e-09	95%	XP_009239742.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	61.3	61.3	100%	2e-09	95%	CAC87068.1
☐	phospholipase D [Homo sapiens]	61.3	61.3	100%	2e-09	95%	AAA36445.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	61.3	61.3	100%	2e-09	95%	XP_003823243.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Homo sapien	61.3	61.3	100%	2e-09	95%	NP_001494.2
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Homo sapie	61.3	61.3	100%	2e-09	95%	AAG16627.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pan trogl	61.3	61.3	100%	2e-09	95%	XP_518268.4
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	61.3	61.3	100%	2e-09	95%	XP_008975041.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_c [Hom	61.3	61.3	100%	2e-09	95%	EAW55450.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Nomascu	61.3	61.3	100%	2e-09	95%	XP_003263611.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 2	59.2	59.2	100%	1e-08	89%	XP_004043389.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 1	59.2	59.2	100%	1e-08	89%	XP_004043388.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	56.6	56.6	100%	9e-08	84%	XP_009202774.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	56.6	56.6	100%	9e-08	84%	XP_009202773.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	56.6	56.6	100%	9e-08	84%	XP_007971742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	56.6	56.6	100%	9e-08	84%	XP_007971741.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	56.6	56.6	100%	9e-08	84%	XP_007971740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	56.6	56.6	100%	9e-08	84%	XP_007971746.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	56.6	56.6	100%	9e-08	84%	XP_003897171.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	56.6	56.6	100%	9e-08	84%	XP_009202772.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	53.7	100%	9e-07	79%	XP_005553977.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-like [Maca	53.7	53.7	100%	9e-07	79%	XP_002803682.1
☐	phospholipase D [Homo sapiens]	53.7	53.7	100%	9e-07	79%	AAA36444.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	53.7	100%	9e-07	79%	XP_005553976.1
☐	hypothetical protein EGM_13271 [Macaca fascicularis]	53.7	53.7	100%	1e-06	79%	EHH52757.1
☐	hypothetical protein EGK_21153 [Macaca mulatta]	53.7	53.7	100%	1e-06	79%	EHH25414.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	53.7	100%	1e-06	79%	XP_005553975.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Rhinopith	50.3	50.3	100%	1e-05	74%	XP_010363586.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	40.5	40.5	100%	0.021	63%	XP_003788429.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Leptonyc	39.7	39.7	100%	0.039	68%	XP_006739372.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Odobenu	38.8	38.8	68%	0.072	85%	XP_004406584.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Saimiri b	38.8	38.8	100%	0.072	63%	XP_003927350.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Camelus	38.0	38.0	100%	0.13	58%	XP_010944080.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ceratothe	38.0	38.0	68%	0.13	85%	XP_004432133.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Galeopte	37.5	37.5	100%	0.18	63%	XP_008578807.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	36.7	36.7	100%	0.34	58%	XP_006182298.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	36.7	36.7	100%	0.34	58%	XP_010978426.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Vicugna	36.7	36.7	100%	0.34	58%	XP_006198740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Jaculus j	36.3	36.3	73%	0.46	71%	XP_004669997.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	35.8	35.8	63%	0.63	83%	XP_004761311.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Tarsius s	35.8	35.8	68%	0.63	77%	XP_008048656.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	35.8	35.8	63%	0.63	83%	XP_004761310.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Eptesicus	35.4	35.4	68%	0.86	77%	XP_008145534.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Felis catu	35.4	35.4	68%	0.86	77%	XP_003985826.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Panthera	35.4	35.4	68%	0.86	77%	XP_007074479.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	35.0	35.0	68%	1.2	77%	XP_010621250.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	35.0	35.0	68%	1.2	77%	XP_010621248.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Loxodont	35.0	35.0	100%	1.2	58%	XP_003416488.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Fukomys damarensis]	35.0	35.0	68%	1.2	77%	KFO33840.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Erinaceus	33.7	33.7	68%	2.9	79%	XP_007526005.1
☐	hypothetical protein STEHIDRAFT_159394 [Stereum hirsutum FP-91666 SS1	32.9	102	73%	5.4	63%	XP_007306926.1
☐	DGPF domain-containing protein [Amycolatopsis halophila]	32.5	32.5	68%	6.6	77%	WP_034267665.1
☐	transcriptional regulator [Weissella ceti]	32.5	32.5	63%	6.7	83%	WP_009765332.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	32.5	32.5	68%	7.4	69%	XP_004847666.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Heterocephalus glaber]	32.5	32.5	68%	7.4	69%	EHB09593.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	32.5	32.5	68%	7.4	69%	XP_004847665.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	32.5	32.5	68%	7.4	69%	XP_004847664.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	32.5	32.5	68%	7.4	69%	XP_004847663.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Heteroce	32.5	32.5	68%	7.4	69%	XP_004895023.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Physeter	32.5	32.5	68%	7.4	69%	XP_007116306.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	32.5	32.5	68%	7.4	69%	XP_007197201.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	32.5	32.5	68%	7.4	69%	XP_007197200.1
☐	DEAD/DEAH box helicase domain protein [Desulfotomaculum gibsoniae]	32.5	32.5	68%	7.5	85%	WP_006520515.1
☐	hypothetical protein [Nocardia araoensis]	32.0	32.0	52%	9.4	90%	WP_039804003.1
☐	hypothetical protein [Lactobacillus rossiae]	32.0	32.0	73%	9.7	71%	WP_017261062.1
☐	Bacterial type II secretion system protein F domain (flaJ-A, flaJ) [uncultured m	32.0	32.0	89%	9.8	48%	AIF05804.1
☐	Bacterial type II secretion system protein F domain (flaJ-A, flaJ) [uncultured m	32.0	32.0	89%	9.8	48%	AIE95188.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Pteropus alecto]	32.0	32.0	100%	10	58%	ELK05805.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	32.0	32.0	100%	10	58%	XP_006919597.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Condylur	32.0	32.0	84%	10	69%	XP_004693375.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Microtus	32.0	32.0	57%	10	82%	XP_005355039.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	31.6	31.6	57%	14	82%	XP_008260728.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	31.6	31.6	57%	14	82%	XP_008260723.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	31.6	31.6	68%	14	69%	XP_007454575.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	31.6	31.6	68%	14	69%	XP_007454574.1
☐	hypothetical protein [Brachyspira pilosicoli]	31.2	31.2	73%	17	69%	WP_013245184.1
☐	hypothetical protein PANDA_003876 [Ailuropoda melanoleuca]	31.2	31.2	68%	19	69%	EFB28343.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-like [Ailur	31.2	31.2	68%	19	69%	XP_002915859.1
☐	hypothetical protein [Janthinobacterium sp. HH01]	30.8	30.8	68%	24	69%	WP_008451733.1
☐	hypothetical protein [Hassallia byssoidea]	30.8	30.8	57%	25	91%	WP_039749624.1
☐	hypothetical protein [Streptococcus mitis]	30.8	30.8	94%	25	61%	WP_033682715.1
☐	hypothetical protein HMPREF8571_0577 [Streptococcus mitis ATCC 6249]	30.8	30.8	94%	25	61%	EFM31924.1
☐	hypothetical protein [Streptococcus mitis]	30.8	30.8	94%	25	61%	WP_000241006.1
☐	Bacterial type II secretion system protein F domain (flaJ-A, flaJ) [uncultured m	30.8	30.8	78%	25	52%	AIF01437.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_a [Mus	30.8	30.8	47%	26	89%	EDL32465.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	30.8	30.8	47%	26	89%	XP_006253988.1
☐	RecName: Full=Phosphatidylinositol-glycan-specific phospholipase D; Short=	30.8	30.8	47%	26	89%	O70362.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_c [Mus	30.8	30.8	47%	26	89%	EDL32467.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Orycterop	30.8	30.8	100%	26	58%	XP_007948002.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	30.8	30.8	47%	26	89%	XP_008769857.1
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Mus muscul	30.8	30.8	47%	26	89%	AAP93132.1
☐	glycosylphosphatidylinositol phospholipase D [Mus musculus]	30.8	30.8	47%	26	89%	AAL87452.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Mus muscul	30.8	30.8	47%	26	89%	NP_032182.2
☐	unnamed protein product [Mus musculus]	30.8	30.8	47%	26	89%	BAB23698.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Rattus norve	30.8	30.8	47%	26	89%	NP_001093982.1
☐	RecName: Full=Phosphatidylinositol-glycan-specific phospholipase D; Short=	30.8	30.8	47%	26	89%	Q8R2H5.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Mesocri	30.8	30.8	47%	26	89%	XP_005066341.1

⊟ Alignments

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Unknown (protein for IMAGE:3354070), partial [Homo sapiens]

Sequence ID: gb|AAH07614.1| **Length:** 575 **Number of Matches:** 1

Range 1: 36 to 54 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1   KNDFHRDLTTSLTESVDRN  19
           KNDFHR+LTTSLTESVDRN
Sbjct  36  KNDFHRNLTTSLTESVDRN  54
```

Related Information

Gene - associated gene details

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Pan paniscus]

Sequence ID: ref|XP_008975042.1| **Length:** 677 **Number of Matches:** 1

Range 1: 138 to 156 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	18/19(95%)	19/19(100%)	0/19(0%)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

```
Query  1    KNDFHRDLTTSLTESVDRN  19
            KNDFHR+LTTSLTESVDRN
Sbjct  138  KNDFHRNLTTSLTESVDRN  156
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Homo sapiens]

Sequence ID: ref|XP_005249075.1| **Length:** 677 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 138 to 156 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KNDFHRDLTTSLTESVDRN  19
            KNDFHR+LTTSLTESVDRN
Sbjct  138  KNDFHRNLTTSLTESVDRN  156
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pongo abelii]

Sequence ID: ref|XP_009239742.1| **Length:** 754 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 235 to 253 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KNDFHRDLTTSLTESVDRN  19
            KNDFHR+LTTSLTESVDRN
Sbjct  235  KNDFHRNLTTSLTESVDRN  253
```

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glycosylphosphatidylinositol phospholipase D [Homo sapiens]

Sequence ID: emb|CAC87068.1| **Length:** 840 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 301 to 319 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KNDFHRDLTTSLTESVDRN  19
            KNDFHR+LTTSLTESVDRN
Sbjct  301  KNDFHRNLTTSLTESVDRN  319
```

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NCBI/ BLAST/ blastp suite/ **Formatting Results - B9EDC96A01R**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download

How to read this page Blast report description

GPLD1_KNDFHRNLTTSLTESVDRN_NonMod

RID B9EDC96A01R (Expires on 01-14 13:22 pm)

Query ID	lcl|383879	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	19		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

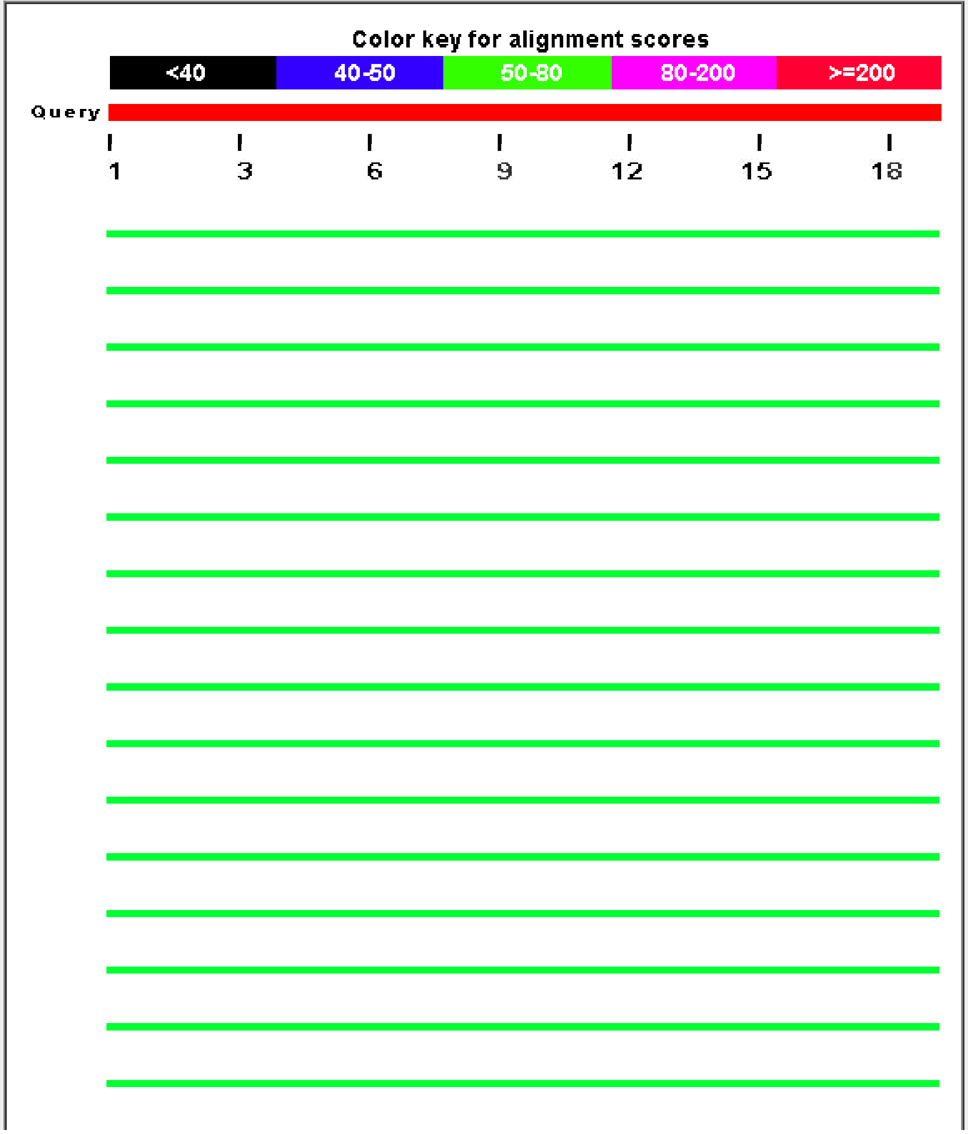
Graphic Summary

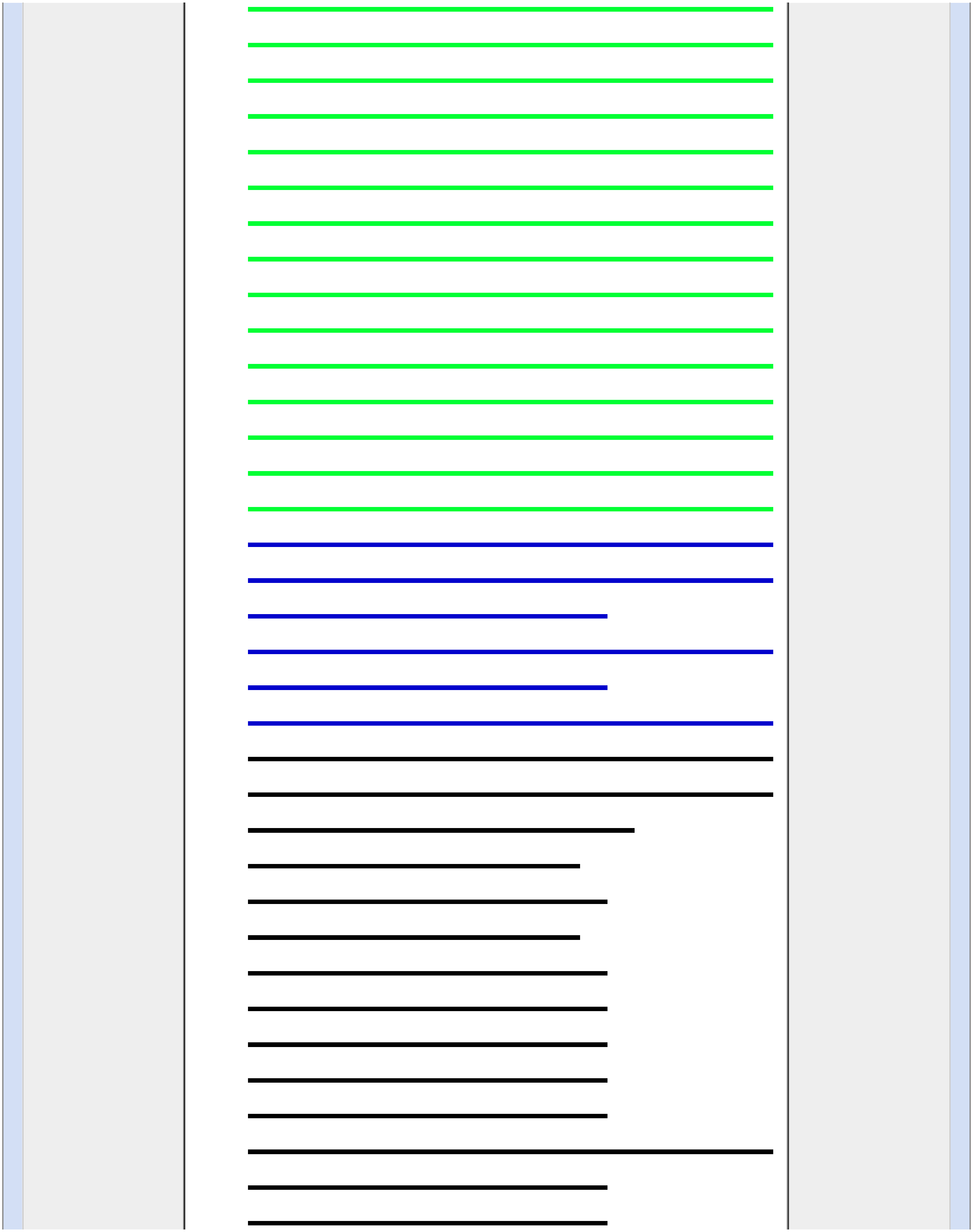
Show Conserved Domains

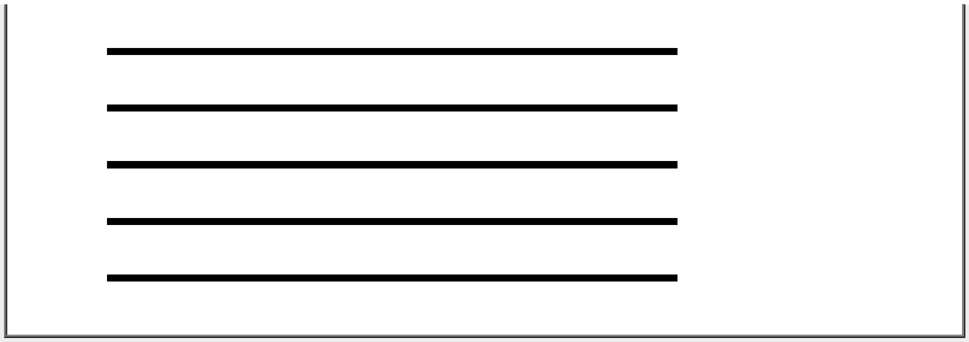
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Unknown (protein for IMAGE:3354070) [Homo sapiens]	63.8	63.8	100%	3e-10	100%	gi|14043248|AAH07614.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	63.8	63.8	100%	3e-10	100%	gi|675773160|XP_008975042.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	63.8	63.8	100%	3e-10	100%	gi|530381810|XP_005249075.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	63.8	63.8	100%	3e-10	100%	gi|686720936|XP_009239742.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	63.8	63.8	100%	3e-10	100%	gi|20269065|CAC87068.1
☐	phospholipase D [Homo sapiens]	63.8	63.8	100%	3e-10	100%	gi|388765|AAA36445.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	63.8	63.8	100%	3e-10	100%	gi|397505380|XP_003823243.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Ho	63.8	63.8	100%	3e-10	100%	gi|29171717|NP_001494.2
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Hc	63.8	63.8	100%	3e-10	100%	gi|14195001|AAG16627.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	63.8	63.8	100%	3e-10	100%	gi|410040317|XP_518268.4
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	63.8	63.8	100%	3e-10	100%	gi|675773152|XP_008975041.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CR,	63.8	63.8	100%	3e-10	100%	gi|119575854|EAW55450.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	63.8	63.8	100%	3e-10	100%	gi|332228866|XP_003263611.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	61.7	61.7	100%	2e-09	95%	gi|426351748|XP_004043389.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	61.7	61.7	100%	2e-09	95%	gi|426351746|XP_004043388.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	59.2	59.2	100%	1e-08	89%	gi|685535046|XP_009202774.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	59.2	59.2	100%	1e-08	89%	gi|685535044|XP_009202773.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	59.2	59.2	100%	1e-08	89%	gi|635096985|XP_007971742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	59.2	59.2	100%	1e-08	89%	gi|635096983|XP_007971741.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	59.2	59.2	100%	1e-08	89%	gi|635096981|XP_007971740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	59.2	59.2	100%	1e-08	89%	gi|635096993|XP_007971746.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	59.2	59.2	100%	1e-08	89%	gi|402865969|XP_003897171.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	59.2	59.2	100%	1e-08	89%	gi|685535041|XP_009202772.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	84%	gi|544429971|XP_005553977.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-	56.2	56.2	100%	1e-07	84%	gi|297290177|XP_002803682.1
☐	phospholipase D [Homo sapiens]	56.2	56.2	100%	1e-07	84%	gi|388763|AAA36444.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	84%	gi|544429969|XP_005553976.1
☐	hypothetical protein EGM_13271 [Macaca fascicularis]	56.2	56.2	100%	1e-07	84%	gi|355748274|EHH52757.1
☐							

	hypothetical protein EGK_21153 [Macaca mulatta]	56.2	56.2	100%	1e-07	84%	gi|355569342|EHH25414.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	56.2	100%	1e-07	84%	gi|544429967|XP_005553975.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	52.8	52.8	100%	2e-06	79%	gi|724798150|XP_010363586.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	43.1	43.1	100%	0.003	68%	gi|395830643|XP_003788429.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	42.2	42.2	100%	0.005	74%	gi|585175123|XP_006739372.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	41.4	41.4	68%	0.010	92%	gi|472374241|XP_004406584.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	41.4	41.4	100%	0.010	68%	gi|403270800|XP_003927350.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.5	40.5	68%	0.019	92%	gi|478515788|XP_004432133.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	40.1	40.1	100%	0.027	68%	gi|667294118|XP_008578807.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	39.2	39.2	100%	0.050	63%	gi|560912019|XP_006182298.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	39.2	39.2	100%	0.050	63%	gi|560952422|XP_006198740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	38.8	38.8	73%	0.068	79%	gi|507572817|XP_004669997.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	38.4	38.4	63%	0.093	92%	gi|511882880|XP_004761311.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	38.4	38.4	68%	0.093	85%	gi|640776034|XP_008048656.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	38.4	38.4	63%	0.093	92%	gi|511882878|XP_004761310.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	38.0	38.0	68%	0.13	85%	gi|641712629|XP_008145534.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	38.0	38.0	68%	0.13	85%	gi|410958439|XP_003985826.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	38.0	38.0	68%	0.13	85%	gi|591294474|XP_007074479.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.5	37.5	68%	0.17	85%	gi|731213592|XP_010621250.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.5	37.5	68%	0.17	85%	gi|731213588|XP_010621248.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	37.5	37.5	100%	0.17	63%	gi|344289516|XP_003416488.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Fukomys dar	37.5	37.5	68%	0.17	85%	gi|676279913|KFO33840.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	36.3	36.3	68%	0.44	86%	gi|617615072|XP_007526005.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.0	35.0	68%	1.1	77%	gi|512971062|XP_004847666.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Heterocepha	35.0	35.0	68%	1.1	77%	gi|351706674|EHB09593.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.0	35.0	68%	1.1	77%	gi|512971060|XP_004847665.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.0	35.0	68%	1.1	77%	gi|512971057|XP_004847664.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.0	35.0	68%	1.1	77%	gi|512971055|XP_004847663.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.0	35.0	68%	1.1	77%	gi|512880679|XP_004895023.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.0	35.0	68%	1.1	77%	gi|593754864|XP_007116306.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.0	35.0	68%	1.1	77%	gi|594700264|XP_007197201.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	35.0	35.0	68%	1.1	77%	gi|594700262|XP_007197200.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Pteropus ale	34.6	34.6	100%	1.5	63%	gi|431896393|ELK05805.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	34.6	34.6	100%	1.5	63%	gi|586529361|XP_006919597.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	34.6	34.6	84%	1.5	75%	gi|507979038|XP_004693375.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	34.6	34.6	57%	1.5	91%	gi|532023384|XP_005355039.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	34.1	34.1	57%	2.0	91%	gi|655839984|XP_008260728.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	34.1	34.1	57%	2.0	91%	gi|655839976|XP_008260723.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	34.1	34.1	68%	2.0	77%	gi|602684652|XP_007454575.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	34.1	34.1	68%	2.0	77%	gi|602684650|XP_007454574.1
☐	hypothetical protein PANDA_003876 [Ailuropoda melanoleuca]	33.7	33.7	68%	2.8	77%	gi|281352759|EFB28343.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-	33.7	33.7	68%	2.8	77%	gi|301760102|XP_002915859.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CR	33.3	33.3	47%	3.7	100%	gi|148700518|EDL32465.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	33.3	33.3	47%	3.8	100%	gi|564391385|XP_006253988.1
☐	RecName: Full=Phosphatidylinositol-glycan-specific phospholipase	33.3	33.3	47%	3.8	100%	gi|6225846|O70362.1

☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CR	33.3	33.3	47%	3.8	100%	gi|148700520|EDL32467.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	33.3	33.3	100%	3.8	63%	gi|634873155|XP_007948002.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	33.3	33.3	47%	3.8	100%	gi|672081759|XP_008769857.1
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Mu	33.3	33.3	47%	3.8	100%	gi|33088003|AAP93132.1
☐	glycosylphosphatidylinositol phospholipase D [Mus musculus]	33.3	33.3	47%	3.8	100%	gi|19547985|AAL87452.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Mu	33.3	33.3	47%	3.8	100%	gi|111378397|NP_032182.2
☐	unnamed protein product [Mus musculus]	33.3	33.3	47%	3.8	100%	gi|12836535|BAB23698.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Ra	33.3	33.3	47%	3.8	100%	gi|213688382|NP_001093982.1
☐	RecName: Full=Phosphatidylinositol-glycan-specific phospholipase	33.3	33.3	47%	3.8	100%	gi|81871416|Q8R2H5.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	33.3	33.3	47%	3.8	100%	gi|524924187|XP_005066341.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.9	32.9	68%	5.1	77%	gi|545837650|XP_001925944.5
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.5	32.5	68%	7.0	85%	gi|664709546|XP_008511735.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.5	32.5	100%	7.0	63%	gi|545554532|XP_005640137.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.5	32.5	68%	7.0	85%	gi|664709544|XP_008511734.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.5	32.5	100%	7.0	63%	gi|74003954|XP_535902.2
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	32.5	32.5	84%	7.0	69%	gi|488541031|XP_004462113.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.5	32.5	68%	7.0	85%	gi|149732005|XP_001497586.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.5	32.5	100%	7.0	63%	gi|545554529|XP_005640136.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.5	32.5	68%	7.0	85%	gi|664709542|XP_008511732.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.5	32.5	68%	7.0	85%	gi|664709540|XP_008511731.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	32.5	32.5	68%	7.0	85%	gi|664709538|XP_008511730.1
☐	ATP-dependent helicase [Haloterrigena thermotolerans]	32.5	32.5	89%	7.0	65%	gi|493699931|WP_006649723.1
☐	helicase [Natrinema pellirubrum]	32.5	32.5	89%	7.0	65%	gi|493181691|WP_006179974.1
☐	Signal transduction histidine kinase [Magnetospirillum magneticum]	32.0	32.0	68%	9.5	77%	gi|499703955|WP_011384689.1
☐	Signal transduction histidine kinase [Magnetospirillum sp. SO-1]	31.6	31.6	68%	13	77%	gi|495889881|WP_008614460.1
☐	malate dehydrogenase [candidate division WWE1 bacterium JGI O	30.8	30.8	47%	24	100%	gi|661254578|WP_029950068.1
☐	MULTISPECIES: malate dehydrogenase [unclassified candidate di	30.8	30.8	47%	24	100%	gi|635657985|WP_024304809.1

Alignments

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Unknown (protein for IMAGE:3354070), partial [Homo sapiens]

Sequence ID: gi|14043248|gb|AAH07614.1| **Length:** 575 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 36 to 54 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	3e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KNDFHRNLTTSLTESVDRN  19
            KNDFHRNLTTSLTESVDRN
Sbjct  36   KNDFHRNLTTSLTESVDRN  54
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Pan paniscus]

Sequence ID: gi|675773160|ref|XP_008975042.1| **Length:** 677 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 138 to 156 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	3e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KNDFHRNLTTSLTESVDRN  19
```

```
               KNDFHRNLTTSLTESVDRN
Sbjct  138  KNDFHRNLTTSLTESVDRN  156
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Homo sapiens]

Sequence ID: gi|530381810|ref|XP_005249075.1| **Length:** 677 **Number of Matches:** 1

Range 1: 138 to 156 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	3e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KNDFHRNLTTSLTESVDRN  19
            KNDFHRNLTTSLTESVDRN
Sbjct  138  KNDFHRNLTTSLTESVDRN  156
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pongo abelii]

Sequence ID: gi|686720936|ref|XP_009239742.1| **Length:** 754 **Number of Matches:** 1

Range 1: 235 to 253 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	3e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KNDFHRNLTTSLTESVDRN  19
            KNDFHRNLTTSLTESVDRN
Sbjct  235  KNDFHRNLTTSLTESVDRN  253
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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glycosylphosphatidylinositol phospholipase D [Homo sapiens]

Sequence ID: gi|20269065|emb|CAC87068.1| **Length:** 840 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 301 to 319 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	3e-10	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KNDFHRNLTTSLTESVDRN  19
            KNDFHRNLTTSLTESVDRN
Sbjct  301  KNDFHRNLTTSLTESVDRN  319
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

BLAST ®

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVE65GHE01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

GPLD1_RGEEDFSWFGYSLHGVTVDDRT_Mod

RID BVE65GHE01R (Expires on 01-21 09:09 am)

Query ID lcl|290501
Description None
Molecule type amino acid
Query Length 22

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

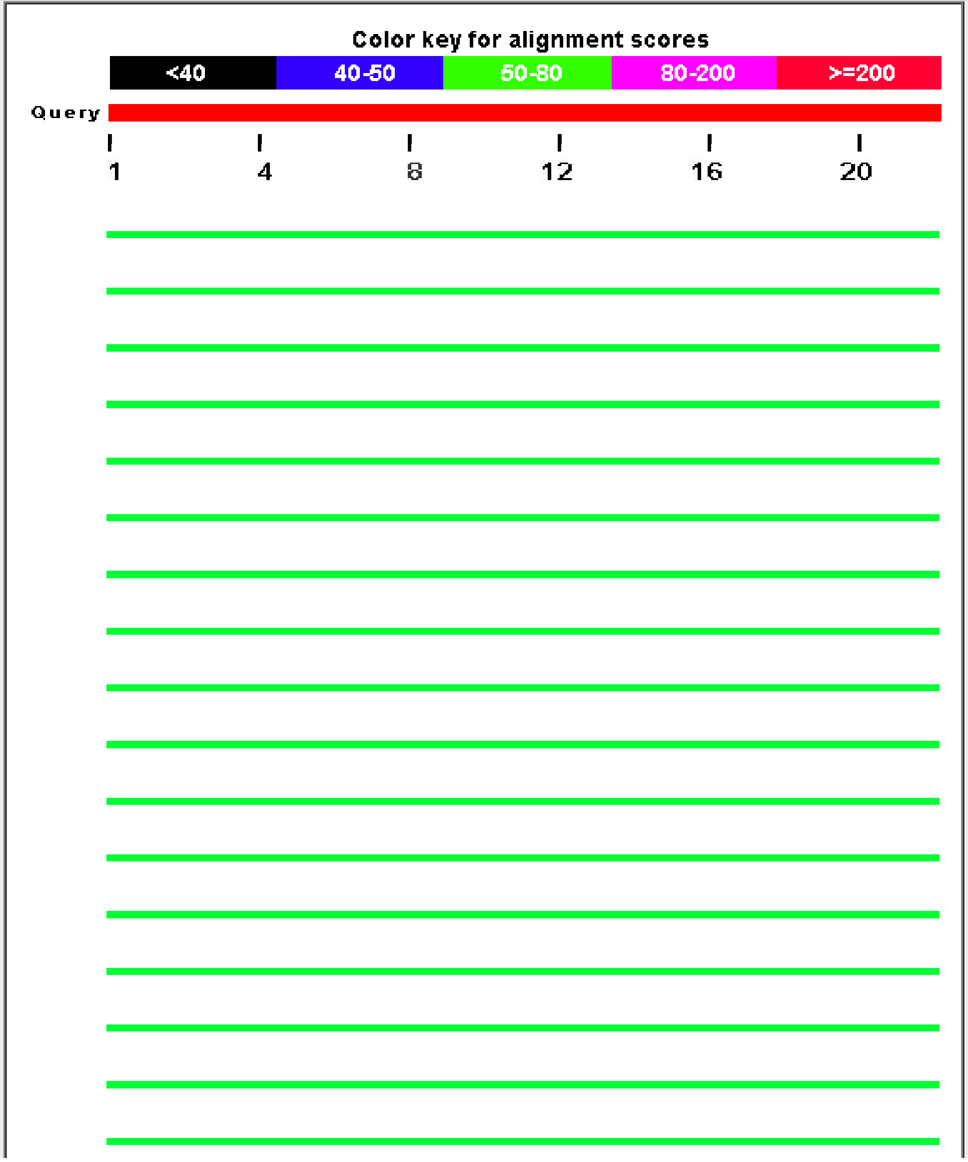
Graphic Summary

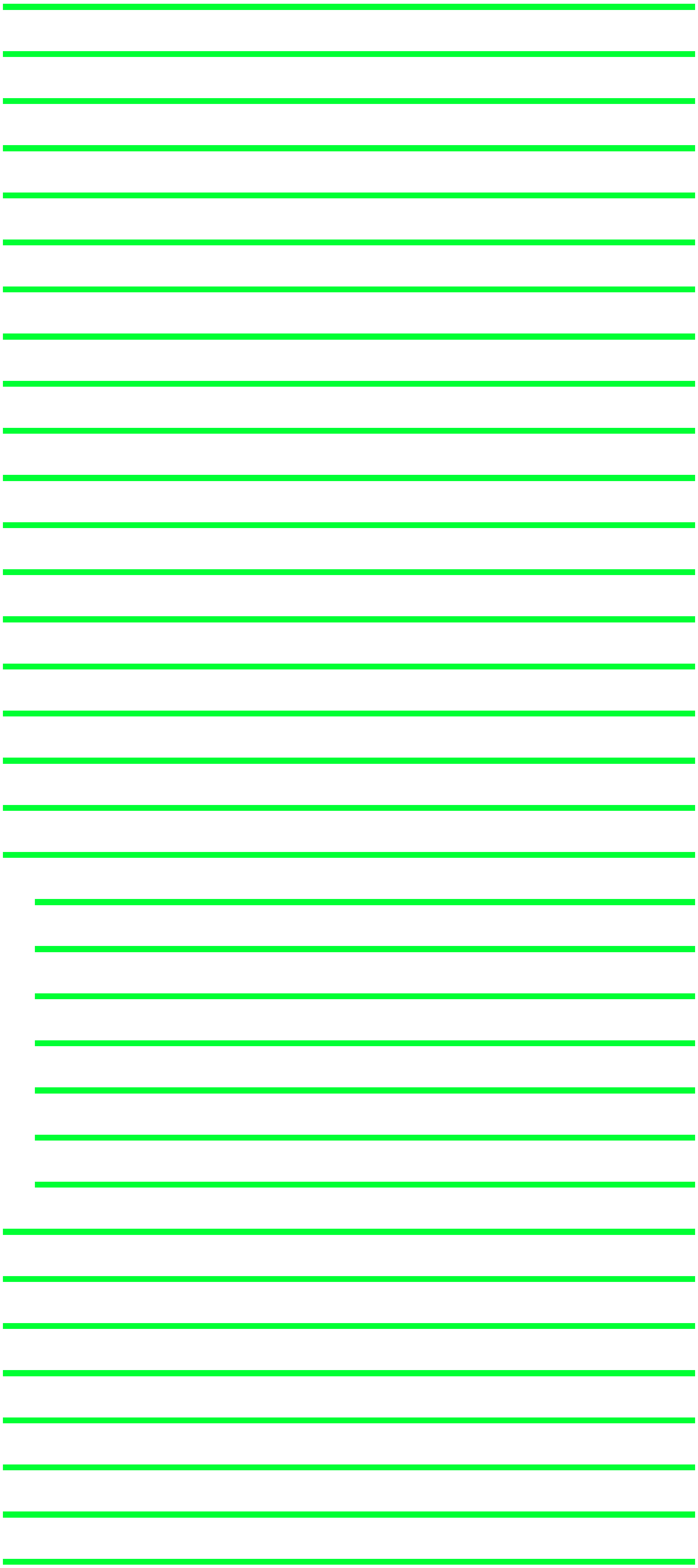
Show Conserved Domains

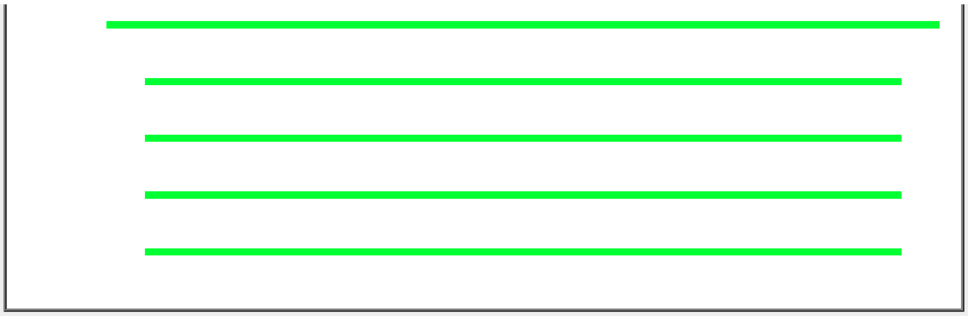
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	73.2	73.2	100%	3e-13	95%	CAC14844.1
☐	Unknown (protein for IMAGE:3354070) [Homo sapiens]	73.2	73.2	100%	3e-13	95%	AAH07614.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	73.2	73.2	100%	3e-13	95%	XP_008975042.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	73.2	73.2	100%	3e-13	95%	XP_005249075.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pongo ab	73.2	73.2	100%	3e-13	95%	XP_009239742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 2	73.2	73.2	100%	3e-13	95%	XP_004043389.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 1	73.2	73.2	100%	3e-13	95%	XP_004043388.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	73.2	73.2	100%	3e-13	95%	CAC87068.1
☐	phospholipase D [Homo sapiens]	73.2	73.2	100%	3e-13	95%	AAA36445.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	73.2	73.2	100%	3e-13	95%	XP_003823243.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Homo sapien	73.2	73.2	100%	3e-13	95%	NP_001494.2
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Homo sapier	73.2	73.2	100%	3e-13	95%	AAG16627.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Rhinopith	73.2	73.2	100%	3e-13	95%	XP_010363586.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pan trogl	73.2	73.2	100%	3e-13	95%	XP_518268.4
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	73.2	73.2	100%	3e-13	95%	XP_008975041.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_c [Hom	73.2	73.2	100%	3e-13	95%	EAW55450.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Nomascu	73.2	73.2	100%	3e-13	95%	XP_003263611.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	70.6	70.6	100%	2e-12	91%	XP_009202774.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	70.6	70.6	100%	2e-12	91%	XP_005553977.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	70.6	70.6	100%	2e-12	91%	XP_009202773.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	70.6	70.6	100%	2e-12	91%	XP_007971742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-like [Maca	70.6	70.6	100%	2e-12	91%	XP_002803682.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	70.6	70.6	100%	2e-12	91%	XP_007971741.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	70.6	70.6	100%	2e-12	91%	XP_007971740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	70.6	70.6	100%	2e-12	91%	XP_007971746.1
☐	phospholipase D [Homo sapiens]	70.6	70.6	100%	2e-12	91%	AAA36444.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	70.6	70.6	100%	2e-12	91%	XP_005553976.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	70.6	70.6	100%	2e-12	91%	XP_003897171.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	70.6	70.6	100%	2e-12	91%	XP_009202772.1

☐	hypothetical protein EGM_13271 [Macaca fascicularis]	70.6	70.6	100%	2e-12	91%	EHH52757.1
☐	hypothetical protein EGK_21153 [Macaca mulatta]	70.6	70.6	100%	2e-12	91%	EHH25414.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	70.6	70.6	100%	2e-12	91%	XP_005553975.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Tarsius s	68.1	68.1	100%	2e-11	86%	XP_008048656.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	66.0	66.0	100%	1e-10	86%	XP_010621250.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	66.0	66.0	100%	1e-10	86%	XP_010621248.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Fukomys damarensis]	66.0	66.0	100%	1e-10	86%	KFO33840.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	64.3	64.3	95%	4e-10	90%	XP_007627730.1
☐	phosphatidylinositol-glycan-specific phospholipase D-like protein [Cricetulus g	64.3	64.3	95%	4e-10	90%	ERE77282.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Cricetulus griseus]	64.3	64.3	95%	4e-10	90%	EGV94314.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Peromys	64.3	64.3	95%	4e-10	90%	XP_006977193.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Microtus	64.3	64.3	95%	4e-10	90%	XP_005355039.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	64.3	64.3	95%	4e-10	90%	XP_003502241.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Mesocric	64.3	64.3	95%	4e-10	90%	XP_005066341.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Panthera	63.8	63.8	100%	5e-10	86%	XP_007074479.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	63.4	63.4	100%	7e-10	82%	XP_004847666.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Heterocephalus glaber]	63.4	63.4	100%	7e-10	82%	EHB09593.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	63.4	63.4	100%	7e-10	82%	XP_004847665.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	63.4	63.4	100%	7e-10	82%	XP_004847664.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	63.4	63.4	100%	7e-10	82%	XP_004847663.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Heteroce	63.4	63.4	100%	7e-10	82%	XP_004895023.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Chinchill	63.4	63.4	100%	7e-10	82%	XP_005403486.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Condylur	62.6	62.6	100%	1e-09	82%	XP_004693375.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_a [Mus	62.1	62.1	90%	2e-09	90%	EDL32465.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	62.1	62.1	90%	2e-09	90%	XP_006253988.1
☐	RecName: Full=Phosphatidylinositol-glycan-specific phospholipase D; Short=	62.1	62.1	90%	2e-09	90%	O70362.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_c [Mus	62.1	62.1	90%	2e-09	90%	EDL32467.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Saimiri b	62.1	62.1	100%	2e-09	82%	XP_003927350.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Erinaceu	62.1	62.1	95%	2e-09	86%	XP_007526005.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	62.1	62.1	90%	2e-09	90%	XP_008769857.1
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Mus muscul	62.1	62.1	90%	2e-09	90%	AAP93132.1
☐	glycosylphosphatidylinositol phospholipase D [Mus musculus]	62.1	62.1	90%	2e-09	90%	AAL87452.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Mus muscul	62.1	62.1	90%	2e-09	90%	NP_032182.2
☐	unnamed protein product [Mus musculus]	62.1	62.1	90%	2e-09	90%	BAB23698.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Rattus norve	62.1	62.1	90%	2e-09	90%	NP_001093982.1
☐	RecName: Full=Phosphatidylinositol-glycan-specific phospholipase D; Short=	62.1	62.1	90%	2e-09	90%	Q8R2H5.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Callithrix	62.1	62.1	100%	2e-09	82%	XP_002746229.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Chrysoch	61.7	61.7	100%	3e-09	77%	XP_006878008.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Octodon	60.9	60.9	100%	5e-09	77%	XP_004640232.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Nannosp	60.9	60.9	90%	5e-09	85%	XP_008845321.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	60.0	60.0	100%	1e-08	82%	XP_005640137.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoformX1	60.0	60.0	100%	1e-08	82%	XP_535902.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	60.0	60.0	100%	1e-08	77%	XP_007454575.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	60.0	60.0	100%	1e-08	77%	XP_007454574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Physeter	60.0	60.0	100%	1e-08	77%	XP_007116306.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pantholo	60.0	60.0	100%	1e-08	77%	XP_005973908.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Capra hir	60.0	60.0	100%	1e-08	77%	XP_005696842.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ochotona	60.0	60.0	100%	1e-08	77%	XP_004593176.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ovis aries	60.0	60.0	100%	1e-08	77%	XP_004019154.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Vicugna p	60.0	60.0	100%	1e-08	77%	XP_006198740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	60.0	60.0	100%	1e-08	82%	XP_005640136.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	60.0	60.0	100%	1e-08	77%	XP_003788429.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Galeopte	59.6	59.6	95%	1e-08	76%	XP_008578807.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	59.2	59.2	100%	2e-08	77%	XP_006051268.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Trichechu	59.2	59.2	100%	2e-08	77%	XP_004384046.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	59.2	59.2	100%	2e-08	77%	XP_006051267.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	59.2	59.2	100%	2e-08	77%	XP_006051266.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	59.2	59.2	100%	2e-08	77%	XP_006051265.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	59.2	59.2	100%	2e-08	77%	XP_006051264.1
☐	hypothetical protein CB1_000595062 [Camelus ferus]	57.9	57.9	100%	5e-08	73%	EPY83136.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	57.9	57.9	100%	5e-08	73%	XP_006182298.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Camelus	57.9	57.9	100%	5e-08	73%	XP_010944080.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Loxodont	57.9	57.9	100%	5e-08	73%	XP_003416488.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	57.9	57.9	100%	5e-08	73%	XP_010978426.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Orcinus o	57.5	57.5	100%	7e-08	73%	XP_004273574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Tursiops	57.5	57.5	100%	7e-08	73%	XP_004313968.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	56.6	56.6	100%	1e-07	73%	XP_007197201.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	56.6	56.6	100%	1e-07	73%	XP_007197200.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Pteropus alecto]	55.8	55.8	100%	3e-07	73%	ELK05805.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	55.8	55.8	95%	3e-07	76%	XP_005903212.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Bos mutus]	55.8	55.8	95%	3e-07	76%	ELR50996.1

Alignments

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glycosylphosphatidylinositol phospholipase D [Homo sapiens]

Sequence ID: emb|CAC14844.1| **Length:** 457 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 189 to 210 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.2 bits(165)	3e-13	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1    RGEEDFSWFGYSLHGVTVDDRT  22
            RGEEDFSWFGYSLHGVTVD+RT
Sbjct  189  RGEEDFSWFGYSLHGVTVDNRT  210
```

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Unknown (protein for IMAGE:3354070), partial [Homo sapiens]

Sequence ID: gb|AAH07614.1| **Length:** 575 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 307 to 328 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.2 bits(165)	3e-13	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1    RGEEDFSWFGYSLHGVTVDDRT  22
            RGEEDFSWFGYSLHGVTVD+RT
Sbjct  307  RGEEDFSWFGYSLHGVTVDNRT  328
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Pan paniscus]

Sequence ID: ref|XP_008975042.1| **Length:** 677 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 409 to 430 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.2 bits(165)	3e-13	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1    RGEEDFSWFGYSLHGVTVDDRT  22
            RGEEDFSWFGYSLHGVTVD+RT
Sbjct  409  RGEEDFSWFGYSLHGVTVDNRT  430
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Homo sapiens]

Sequence ID: ref|XP_005249075.1| **Length:** 677 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 409 to 430 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.2 bits(165)	3e-13	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1    RGEEDFSWFGYSLHGVTVDDRT  22
            RGEEDFSWFGYSLHGVTVD+RT
Sbjct  409  RGEEDFSWFGYSLHGVTVDNRT  430
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pongo abelii]

Sequence ID: ref|XP_009239742.1| **Length:** 754 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 506 to 527 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
73.2 bits(165)	3e-13	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1    RGEEDFSWFGYSLHGVTVDDRT  22
            RGEEDFSWFGYSLHGVTVD+RT
Sbjct  506  RGEEDFSWFGYSLHGVTVDNRT  527
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - B9EHPJXX01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download

How to read this page   Blast report description

GPLD1_RGEEDFSWFGYSLHGVTVDNRT_NonMod

RID	B9EHPJXX01R (Expires on 01-14 13:24 pm)
Query ID	lcl|329909
Description	None
Molecule type	amino acid
Query Length	22
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

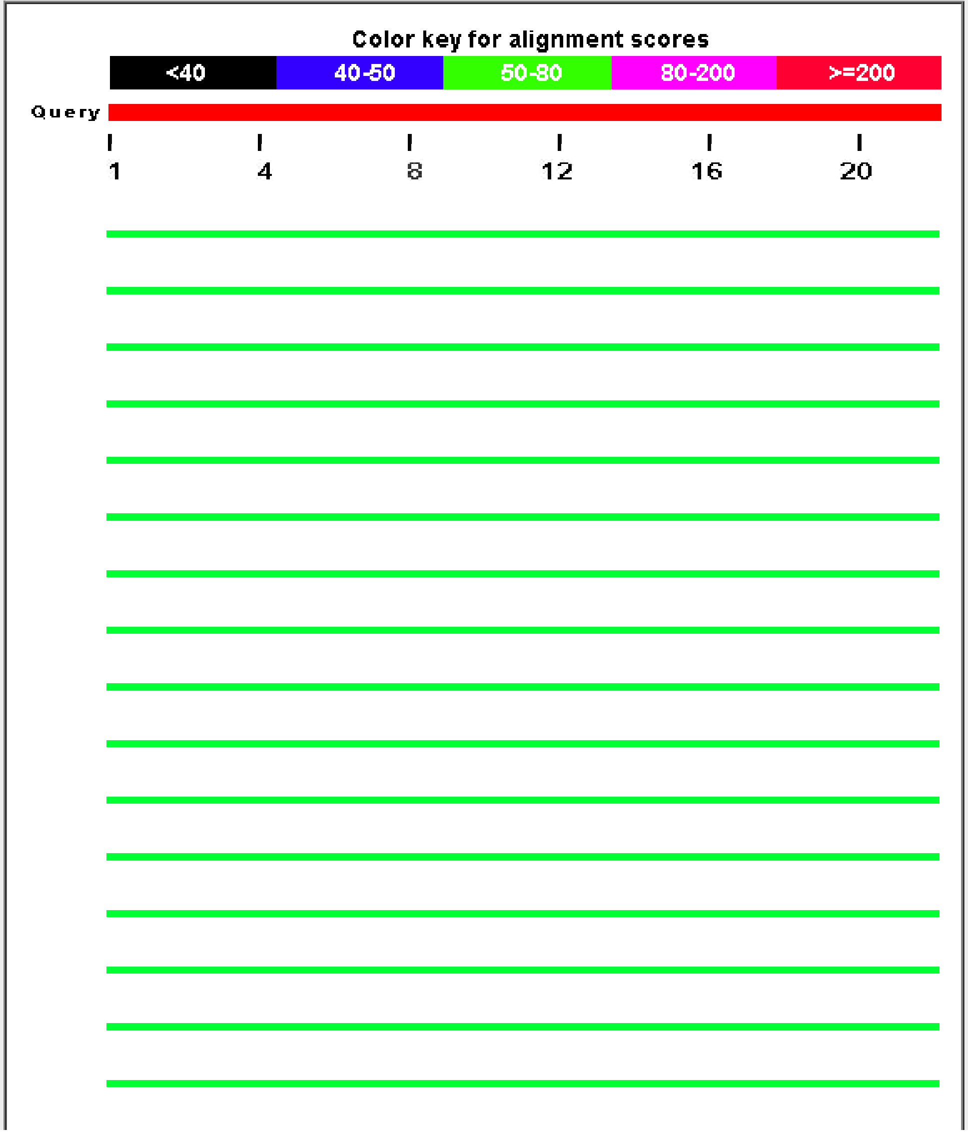
Graphic Summary

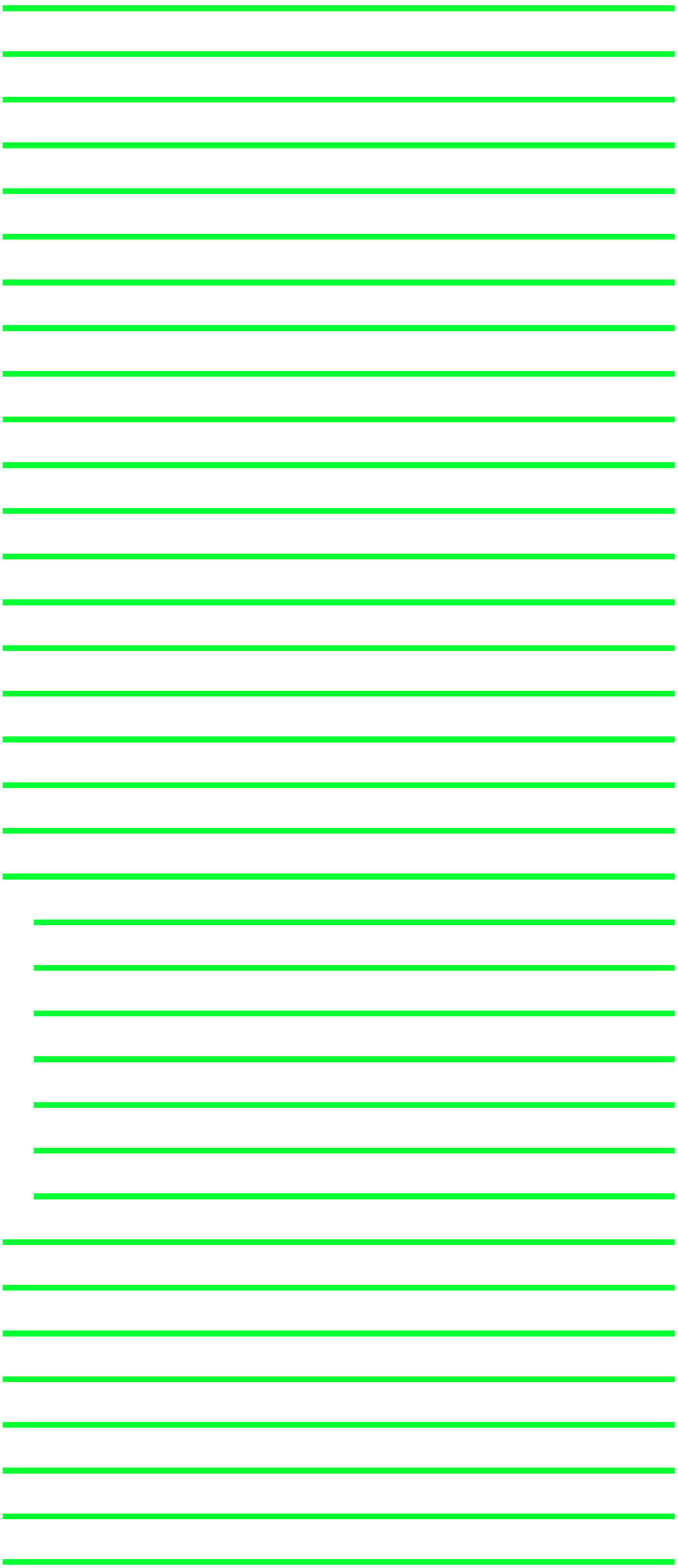
Show Conserved Domains

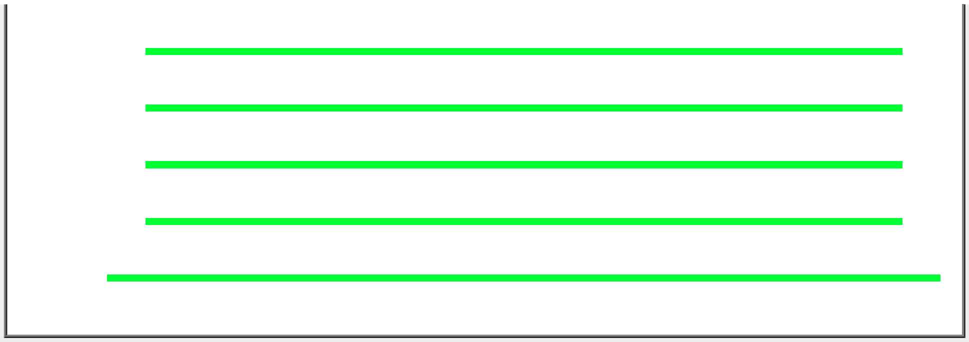
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	75.7	75.7	100%	4e-14	100%	gi|11122875|CAC14844.1
☐	Unknown (protein for IMAGE:3354070) [Homo sapiens]	75.7	75.7	100%	4e-14	100%	gi|14043248|AAH07614.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	75.7	75.7	100%	4e-14	100%	gi|675773160|XP_008975042.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	75.7	75.7	100%	4e-14	100%	gi|530381810|XP_005249075.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	75.7	75.7	100%	4e-14	100%	gi|686720936|XP_009239742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	75.7	75.7	100%	4e-14	100%	gi|426351748|XP_004043389.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	75.7	75.7	100%	4e-14	100%	gi|426351746|XP_004043388.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	75.7	75.7	100%	4e-14	100%	gi|20269065|CAC87068.1
☐	phospholipase D [Homo sapiens]	75.7	75.7	100%	4e-14	100%	gi|388765|AAA36445.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	75.7	75.7	100%	4e-14	100%	gi|397505380|XP_003823243.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Ho	75.7	75.7	100%	4e-14	100%	gi|29171717|NP_001494.2
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Hc	75.7	75.7	100%	4e-14	100%	gi|14195001|AAG16627.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	75.7	75.7	100%	4e-14	100%	gi|724798150|XP_010363586.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	75.7	75.7	100%	4e-14	100%	gi|410040317|XP_518268.4
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	75.7	75.7	100%	4e-14	100%	gi|675773152|XP_008975041.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CR	75.7	75.7	100%	4e-14	100%	gi|119575854|EAW55450.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	75.7	75.7	100%	4e-14	100%	gi|332228866|XP_003263611.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	73.2	73.2	100%	3e-13	95%	gi|685535046|XP_009202774.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	73.2	73.2	100%	3e-13	95%	gi|544429971|XP_005553977.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	73.2	73.2	100%	3e-13	95%	gi|685535044|XP_009202773.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	73.2	73.2	100%	3e-13	95%	gi|635096985|XP_007971742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	73.2	73.2	100%	3e-13	95%	gi|297290177|XP_002803682.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	73.2	73.2	100%	3e-13	95%	gi|635096983|XP_007971741.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	73.2	73.2	100%	3e-13	95%	gi|635096981|XP_007971740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	73.2	73.2	100%	3e-13	95%	gi|635096993|XP_007971746.1
☐	phospholipase D [Homo sapiens]	73.2	73.2	100%	3e-13	95%	gi|388763|AAA36444.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	73.2	73.2	100%	3e-13	95%	gi|544429969|XP_005553976.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	73.2	73.2	100%	3e-13	95%	gi|402865969|XP_003897171.1
☐							

	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	73.2	73.2	100%	3e-13	95%	gi|685535041|XP_009202772.1
☐	hypothetical protein EGM_13271 [Macaca fascicularis]	73.2	73.2	100%	3e-13	95%	gi|355748274|EHH52757.1
☐	hypothetical protein EGK_21153 [Macaca mulatta]	73.2	73.2	100%	3e-13	95%	gi|355569342|EHH25414.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	73.2	73.2	100%	3e-13	95%	gi|544429967|XP_005553975.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	70.6	70.6	100%	2e-12	91%	gi|640776034|XP_008048656.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	68.5	68.5	100%	1e-11	91%	gi|731213592|XP_010621250.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	68.5	68.5	100%	1e-11	91%	gi|731213588|XP_010621248.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Fukomys dar	68.5	68.5	100%	1e-11	91%	gi|676279913|KFO33840.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	66.8	66.8	95%	5e-11	95%	gi|625272320|XP_007627730.1
☐	phosphatidylinositol-glycan-specific phospholipase D-like protein [C	66.8	66.8	95%	5e-11	95%	gi|537192249|ERE77282.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Cricetulus gri	66.8	66.8	95%	5e-11	95%	gi|344238211|EGV94314.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	66.8	66.8	95%	5e-11	95%	gi|589928750|XP_006977193.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	66.8	66.8	95%	5e-11	95%	gi|532023384|XP_005355039.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	66.8	66.8	95%	5e-11	95%	gi|354480090|XP_003502241.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	66.8	66.8	95%	5e-11	95%	gi|524924187|XP_005066341.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	66.0	66.0	100%	9e-11	86%	gi|512971062|XP_004847666.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Heterocepha	66.0	66.0	100%	9e-11	86%	gi|351706674|EHB09593.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	66.0	66.0	100%	9e-11	86%	gi|512971060|XP_004847665.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	66.0	66.0	100%	9e-11	86%	gi|512971057|XP_004847664.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	66.0	66.0	100%	9e-11	86%	gi|512971055|XP_004847663.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	66.0	66.0	100%	9e-11	86%	gi|512880679|XP_004895023.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	66.0	66.0	100%	9e-11	86%	gi|533180623|XP_005403486.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	65.1	65.1	100%	2e-10	86%	gi|507979038|XP_004693375.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CR	64.7	64.7	90%	2e-10	95%	gi|148700518|EDL32465.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	64.7	64.7	90%	2e-10	95%	gi|564391385|XP_006253988.1
☐	RecName: Full=Phosphatidylinositol-glycan-specific phospholipase	64.7	64.7	90%	2e-10	95%	gi|6225846|O70362.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CR	64.7	64.7	90%	2e-10	95%	gi|148700520|EDL32467.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	64.7	64.7	100%	2e-10	86%	gi|403270800|XP_003927350.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	64.7	64.7	95%	2e-10	90%	gi|617615072|XP_007526005.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	64.7	64.7	90%	2e-10	95%	gi|672081759|XP_008769857.1
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Mu	64.7	64.7	90%	2e-10	95%	gi|33088003|AAP93132.1
☐	glycosylphosphatidylinositol phospholipase D [Mus musculus]	64.7	64.7	90%	2e-10	95%	gi|19547985|AAL87452.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Mu	64.7	64.7	90%	2e-10	95%	gi|111378397|NP_032182.2
☐	unnamed protein product [Mus musculus]	64.7	64.7	90%	2e-10	95%	gi|12836535|BAB23698.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Rat	64.7	64.7	90%	2e-10	95%	gi|213688382|NP_001093982.1
☐	RecName: Full=Phosphatidylinositol-glycan-specific phospholipase	64.7	64.7	90%	2e-10	95%	gi|81871416|Q8R2H5.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	64.7	64.7	100%	2e-10	86%	gi|675650934|XP_002746229.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	64.3	64.3	100%	3e-10	82%	gi|586495128|XP_006878008.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	63.4	63.4	100%	7e-10	82%	gi|507684247|XP_004640232.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	63.4	63.4	90%	7e-10	90%	gi|674075950|XP_008845321.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	62.6	62.6	100%	1e-09	86%	gi|545554532|XP_005640137.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	62.6	62.6	100%	1e-09	86%	gi|74003954|XP_535902.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	62.6	62.6	100%	1e-09	82%	gi|602684652|XP_007454575.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	62.6	62.6	100%	1e-09	82%	gi|602684650|XP_007454574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	62.6	62.6	100%	1e-09	82%	gi|593754864|XP_007116306.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	62.6	62.6	100%	1e-09	82%	gi|556757122|XP_005973908.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	62.6	62.6	100%	1e-09	82%	gi|548518368|XP_005696842.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	62.6	62.6	100%	1e-09	82%	gi|504166674|XP_004593176.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	62.6	62.6	100%	1e-09	82%	gi|426250866|XP_004019154.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	62.6	62.6	100%	1e-09	82%	gi|560952422|XP_006198740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	62.6	62.6	100%	1e-09	86%	gi|545554529|XP_005640136.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	62.6	62.6	100%	1e-09	82%	gi|395830643|XP_003788429.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	62.1	62.1	95%	2e-09	81%	gi|667294118|XP_008578807.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	61.7	61.7	100%	2e-09	82%	gi|594053987|XP_006051268.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	61.7	61.7	100%	2e-09	82%	gi|594053985|XP_006051267.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	61.7	61.7	100%	2e-09	82%	gi|594053983|XP_006051266.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	61.7	61.7	100%	2e-09	82%	gi|594053981|XP_006051265.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	61.7	61.7	100%	2e-09	82%	gi|594053979|XP_006051264.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	61.3	61.3	100%	3e-09	82%	gi|591294474|XP_007074479.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	60.9	60.9	100%	5e-09	77%	gi|471403600|XP_004384046.1
☐	hypothetical protein CB1_000595062 [Camelus ferus]	60.4	60.4	100%	7e-09	77%	gi|528763477|EPY83136.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	60.4	60.4	100%	7e-09	77%	gi|560912019|XP_006182298.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	60.4	60.4	100%	7e-09	77%	gi|344289516|XP_003416488.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	60.0	60.0	100%	9e-09	77%	gi|466027702|XP_004273574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	60.0	60.0	100%	9e-09	77%	gi|470605744|XP_004313968.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	59.2	59.2	100%	2e-08	77%	gi|594700264|XP_007197201.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	59.2	59.2	100%	2e-08	77%	gi|594700262|XP_007197200.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Pteropus ale	58.3	58.3	100%	3e-08	77%	gi|431896393|ELK05805.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	58.3	58.3	95%	3e-08	81%	gi|555982613|XP_005903212.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Bos mutus]	58.3	58.3	95%	3e-08	81%	gi|440899735|ELR50996.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Bos	58.3	58.3	95%	3e-08	81%	gi|27807363|NP_777241.1
☐	TPA: phosphatidylinositol-glycan-specific phospholipase D [Bos tau	58.3	58.3	95%	3e-08	81%	gi|296474001|DAA16116.1

⊟ Alignments

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glycosylphosphatidylinositol phospholipase D [Homo sapiens]

Sequence ID: gi|11122875|emb|CAC14844.1| **Length:** 457 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 189 to 210 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.7 bits(171)	4e-14	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1    RGEEDFSWFGYSLHGVTVDNRT  22
            RGEEDFSWFGYSLHGVTVDNRT
Sbjct  189  RGEEDFSWFGYSLHGVTVDNRT  210
```

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Unknown (protein for IMAGE:3354070), partial [Homo sapiens]

Sequence ID: gi|14043248|gb|AAH07614.1| **Length:** 575 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 307 to 328 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.7 bits(171)	4e-14	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1    RGEEDFSWFGYSLHGVTVDNRT  22
```

```
               RGEEDFSWFGYSLHGVTVDNRT
Sbjct  307  RGEEDFSWFGYSLHGVTVDNRT  328
```

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Pan paniscus]

Sequence ID: gi|675773160|ref|XP_008975042.1| **Length:** 677 **Number of Matches:** 1

Range 1: 409 to 430 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.7 bits(171)	4e-14	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1    RGEEDFSWFGYSLHGVTVDNRT  22
            RGEEDFSWFGYSLHGVTVDNRT
Sbjct  409  RGEEDFSWFGYSLHGVTVDNRT  430
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Homo sapiens]

Sequence ID: gi|530381810|ref|XP_005249075.1| **Length:** 677 **Number of Matches:** 1

Range 1: 409 to 430 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.7 bits(171)	4e-14	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1    RGEEDFSWFGYSLHGVTVDNRT  22
            RGEEDFSWFGYSLHGVTVDNRT
Sbjct  409  RGEEDFSWFGYSLHGVTVDNRT  430
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pongo abelii]

Sequence ID: gi|686720936|ref|XP_009239742.1| **Length:** 754 **Number of Matches:** 1

Range 1: 506 to 527 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.7 bits(171)	4e-14	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1    RGEEDFSWFGYSLHGVTVDNRT  22
            RGEEDFSWFGYSLHGVTVDNRT
Sbjct  506  RGEEDFSWFGYSLHGVTVDNRT  527
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVE75ZC201R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download   How to read this page   Blast report description

GPLD1_RTLLLVGSPTWKDASRL_Mod

RID BVE75ZC201R (Expires on 01-21 09:09 am)

Query ID lcl|52946
Description None
Molecule type amino acid
Query Length 17

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

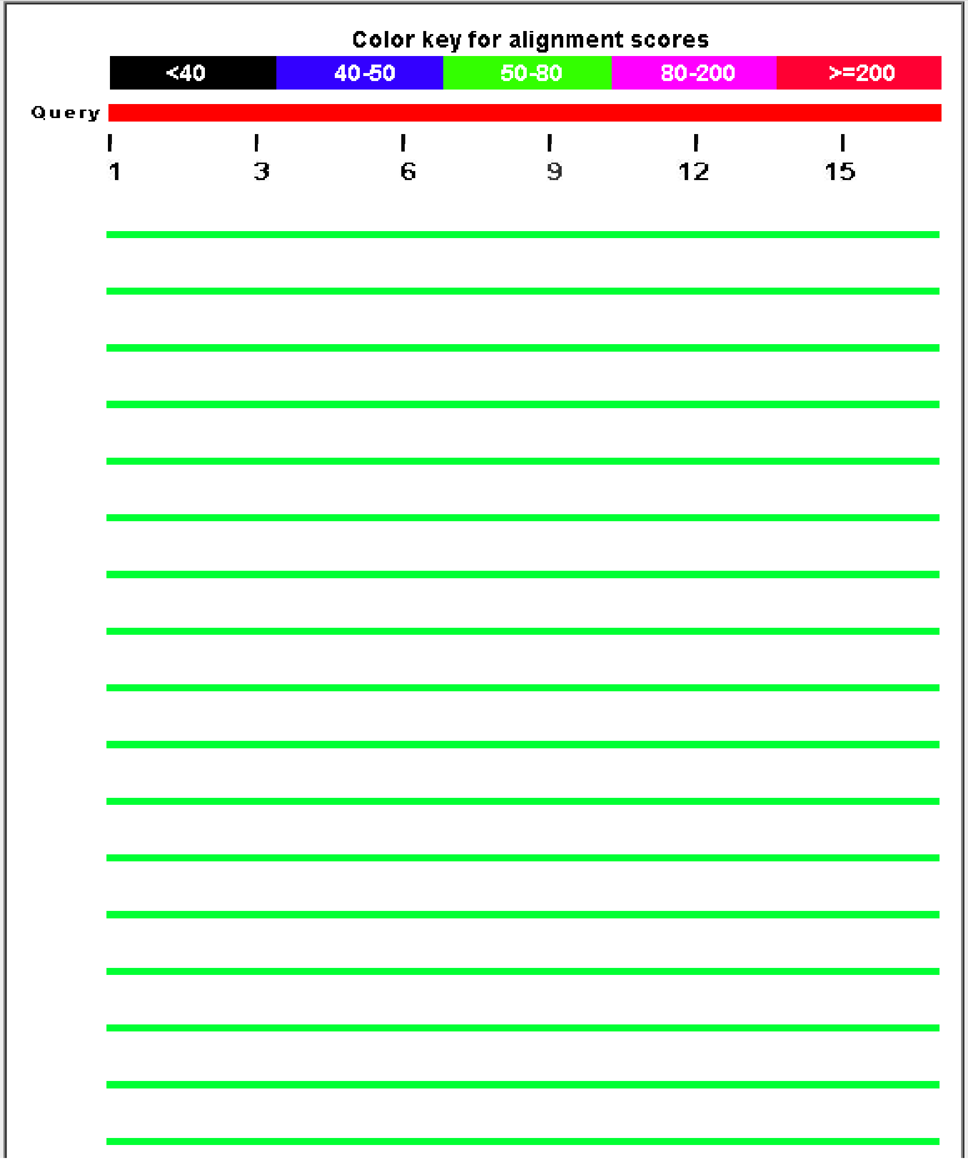
Graphic Summary

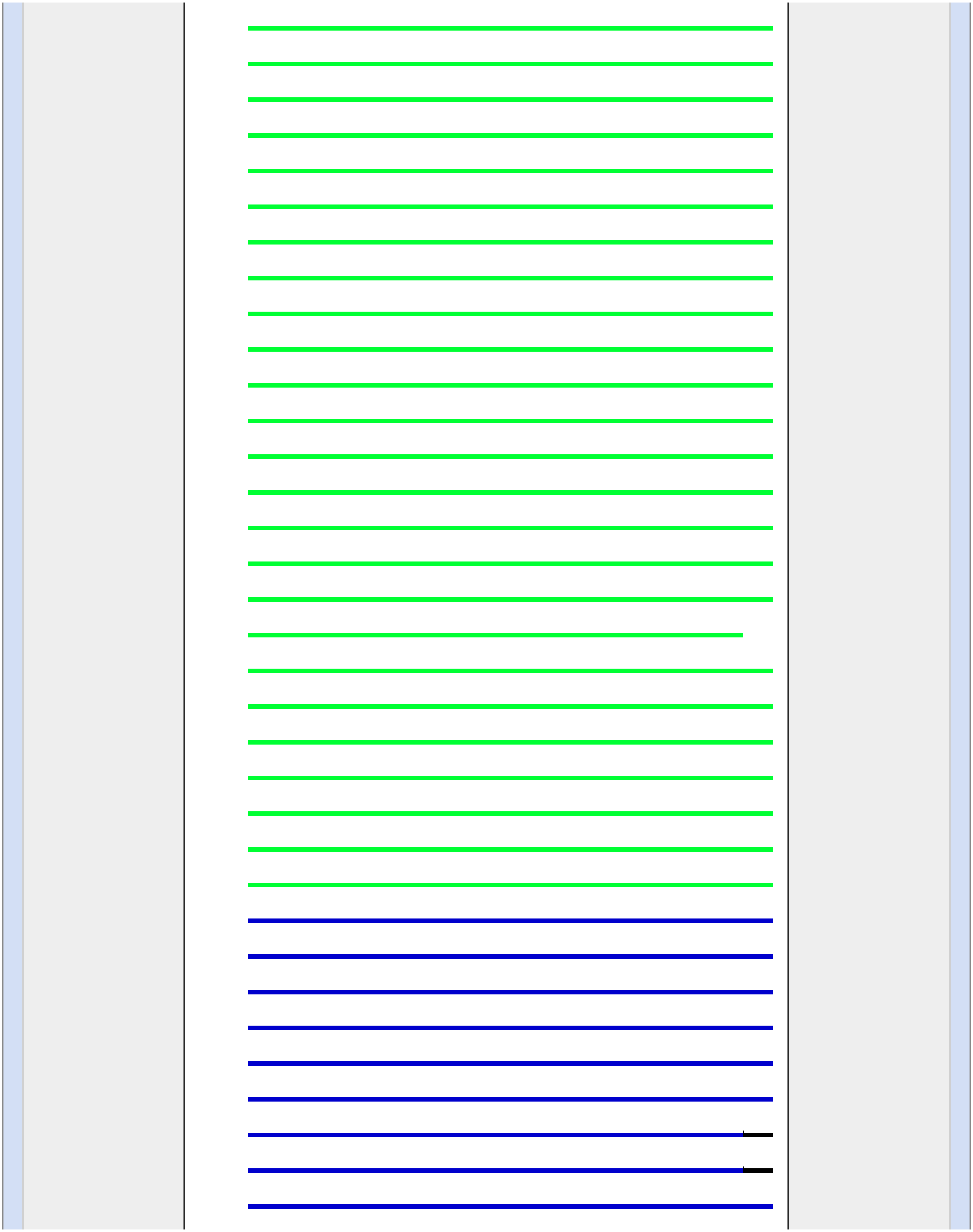
Show Conserved Domains

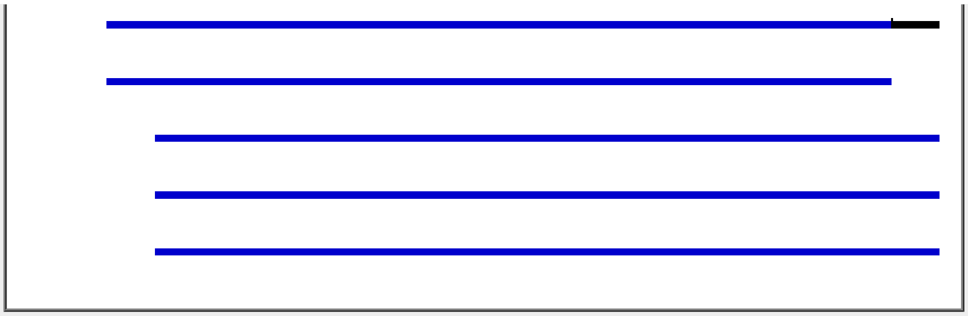
No putative conserved domains have been detected

Distribution of 198 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊖ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	53.7	76.8	100%	7e-07	94%	CAC14844.1
☐	Unknown (protein for IMAGE:3354070) [Homo sapiens]	53.7	76.8	100%	7e-07	94%	AAH07614.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	78.5	100%	7e-07	94%	XP_009202774.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	76.8	100%	7e-07	94%	XP_008975042.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	78.5	100%	7e-07	94%	XP_005553977.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	76.8	100%	7e-07	94%	XP_005249075.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	78.5	100%	7e-07	94%	XP_009202773.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	78.5	100%	7e-07	94%	XP_007971742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D-like [Maca	53.7	78.5	100%	7e-07	94%	XP_002803682.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pongo ab	53.7	75.9	100%	7e-07	94%	XP_009239742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	78.5	100%	7e-07	94%	XP_007971741.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	78.5	100%	7e-07	94%	XP_007971740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	78.5	100%	7e-07	94%	XP_007971746.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Tarsius s	53.7	76.4	100%	7e-07	94%	XP_008048656.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 2	53.7	78.1	100%	7e-07	94%	XP_004043389.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform 1	53.7	76.8	100%	7e-07	94%	XP_004043388.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	53.7	76.8	100%	7e-07	94%	CAC87068.1
☐	phospholipase D [Homo sapiens]	53.7	76.8	100%	7e-07	94%	AAA36445.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	76.8	100%	7e-07	94%	XP_003823243.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Homo sapien	53.7	76.8	100%	7e-07	94%	NP_001494.2
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Homo sapie	53.7	76.8	100%	7e-07	94%	AAG16627.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Rhinopith	53.7	78.5	100%	7e-07	94%	XP_010363586.1
☐	phospholipase D [Homo sapiens]	53.7	78.5	100%	7e-07	94%	AAA36444.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	78.5	100%	7e-07	94%	XP_005553976.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	78.5	100%	7e-07	94%	XP_003897171.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Pan trogl	53.7	75.5	100%	7e-07	94%	XP_518268.4
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	78.5	100%	7e-07	94%	XP_009202772.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	76.8	100%	7e-07	94%	XP_008975041.1
☐	hypothetical protein EGM_13271 [Macaca fascicularis]	53.7	78.5	100%	7e-07	94%	EHH52757.1

☐	hypothetical protein EGK_21153 [Macaca mulatta]	53.7	78.5	100%	7e-07	94%	EHH25414.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CRA_c [Hom	53.7	76.8	100%	7e-07	94%	EAW55450.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Nomascu	53.7	76.4	100%	7e-07	94%	XP_003263611.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	53.7	78.5	100%	7e-07	94%	XP_005553975.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Mesocric	53.7	76.4	100%	7e-07	94%	XP_005066341.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Octodon	50.7	71.7	94%	7e-06	94%	XP_004640232.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Saimiri b	50.7	73.4	100%	7e-06	88%	XP_003927350.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Callithrix	50.7	73.4	100%	7e-06	88%	XP_002746229.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	50.3	50.3	100%	1e-05	88%	XP_007627730.1
☐	phosphatidylinositol-glycan-specific phospholipase D-like protein [Cricetulus g	50.3	50.3	100%	1e-05	88%	ERE77282.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Cricetulus griseus]	50.3	50.3	100%	1e-05	88%	EGV94314.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Microtus	50.3	73.0	100%	1e-05	88%	XP_005355039.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	50.3	50.3	100%	1e-05	88%	XP_003502241.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Condylur	49.0	71.3	100%	3e-05	88%	XP_004693375.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Trichechu	49.0	70.8	100%	3e-05	88%	XP_004384046.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Erinaceu	49.0	74.2	100%	3e-05	88%	XP_007526005.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	49.0	92.7	100%	3e-05	88%	XP_007487938.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	49.0	92.7	100%	3e-05	88%	XP_001375600.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	49.0	92.7	100%	3e-05	88%	XP_007487937.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	47.7	70.4	100%	7e-05	88%	XP_008260728.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	47.7	70.4	100%	7e-05	88%	XP_008260723.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ictidomys	47.3	70.4	100%	1e-04	82%	XP_005337080.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Peromys	47.3	72.1	100%	1e-04	88%	XP_006977193.1
☐	hypothetical protein CB1_000595062 [Camelus ferus]	46.9	69.1	94%	1e-04	88%	EPY83136.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	46.9	70.8	94%	1e-04	88%	XP_010621250.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	46.9	70.8	94%	1e-04	88%	XP_010621248.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Fukomys damarensis]	46.9	70.8	94%	1e-04	88%	KFO33840.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	46.4	67.4	100%	2e-04	82%	XP_005640137.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoformX1	46.4	67.4	100%	2e-04	82%	XP_535902.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	46.4	67.4	100%	2e-04	82%	XP_005640136.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Pteropus alecto]	46.0	46.0	100%	3e-04	82%	ELK05805.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Chrysoch	46.0	67.9	100%	3e-04	82%	XP_006878008.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Orycterop	46.0	67.9	100%	3e-04	82%	XP_007948002.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	46.0	67.0	100%	3e-04	82%	XP_006919597.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	45.6	68.7	100%	4e-04	88%	XP_008511735.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	45.6	67.4	100%	4e-04	88%	XP_004614021.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	45.6	68.7	100%	4e-04	88%	XP_008511734.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Ceratothe	45.6	68.3	100%	4e-04	88%	XP_004432133.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Equus ca	45.6	68.7	100%	4e-04	88%	XP_001497586.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	45.6	68.7	100%	4e-04	88%	XP_008511732.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	45.6	68.7	100%	4e-04	88%	XP_008511731.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Sus scrof	45.6	70.4	100%	4e-04	88%	XP_001925944.5
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	45.6	68.7	100%	4e-04	88%	XP_008511730.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	45.2	67.4	100%	5e-04	82%	XP_006182298.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Camelus	45.2	67.4	100%	5e-04	82%	XP_010944080.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	45.2	66.2	100%	5e-04	82%	XP_007454575.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	45.2	66.2	100%	5e-04	82%	XP_007454574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Physeter	45.2	67.4	100%	5e-04	82%	XP_007116306.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	45.2	67.4	100%	5e-04	82%	XP_010978426.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Vicugna	45.2	67.4	100%	5e-04	82%	XP_006198740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	45.2	67.4	100%	5e-04	82%	XP_007197201.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	45.2	67.4	100%	5e-04	82%	XP_007197200.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	44.3	67.0	94%	0.001	88%	XP_004847666.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Heterocephalus glaber]	44.3	67.0	94%	0.001	88%	EHB09593.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	44.3	67.0	94%	0.001	88%	XP_004847665.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	44.3	67.0	94%	0.001	88%	XP_004847664.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	44.3	67.0	94%	0.001	88%	XP_004847663.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Heteroce	44.3	67.0	94%	0.001	88%	XP_004895023.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Panthera	43.9	64.9	100%	0.001	76%	XP_007074479.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Sarcophil	43.9	68.7	100%	0.001	87%	XP_003760182.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Elephant	43.5	64.5	82%	0.002	93%	XP_006888712.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glycan-specific	43.1	65.3	88%	0.003	87%	XP_005903212.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Bos mutus]	43.1	65.3	88%	0.003	87%	ELR50996.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	43.1	65.3	88%	0.003	87%	XP_010841812.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Bos taurus]	43.1	65.3	88%	0.003	87%	NP_777241.1
☐	TPA: phosphatidylinositol-glycan-specific phospholipase D [Bos taurus]	43.1	65.3	88%	0.003	87%	DAA16116.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D [Loxodont	43.1	64.9	88%	0.003	87%	XP_003416488.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	43.1	65.3	88%	0.003	87%	XP_010841810.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	43.1	65.3	88%	0.003	87%	XP_005223795.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	43.1	65.3	88%	0.003	87%	XP_005223794.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X	43.1	65.3	88%	0.003	87%	XP_010816770.1

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GPLD1_RTLLLVGSPTWKNASRL_NonMod

RID B9E8UW2A01R (Expires on 01-14 13:20 pm)

Query ID	lcl|254936	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	17		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

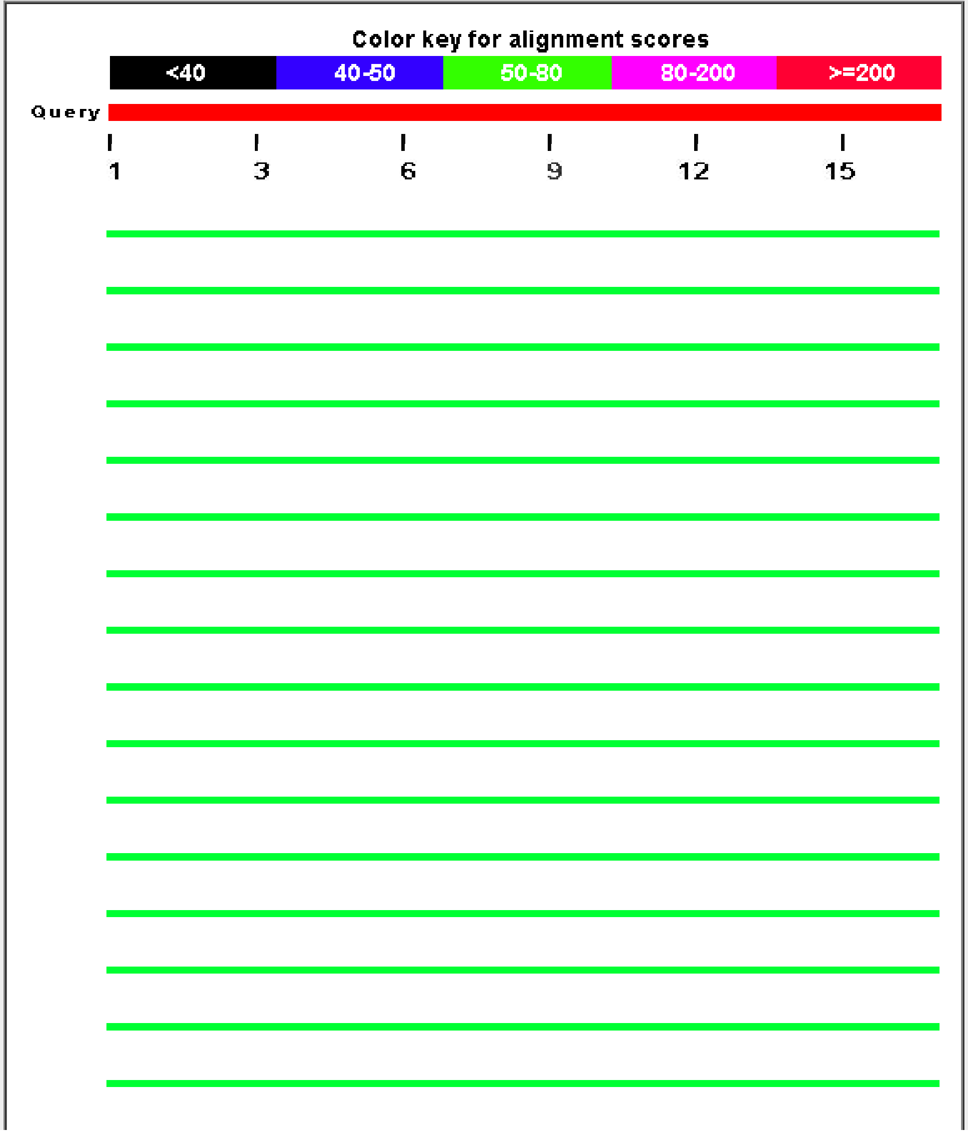
⊟ Graphic Summary

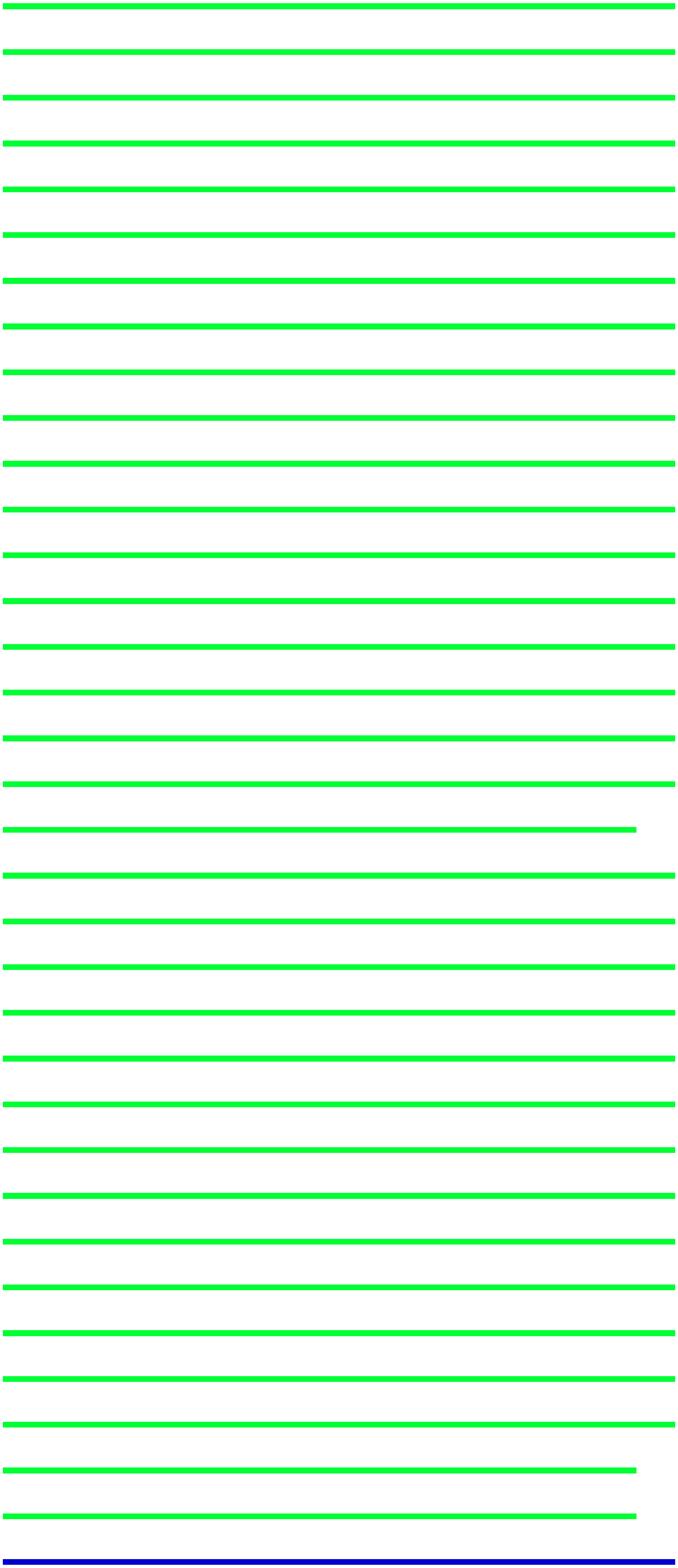
⊟ Show Conserved Domains

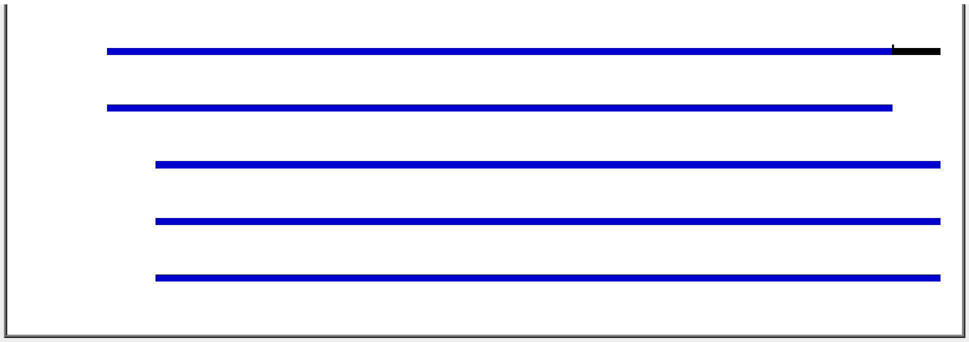
No putative conserved domains have been detected

Distribution of 197 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	56.2	78.1	100%	9e-08	100%	gi|11122875|CAC14844.1
☐	Unknown (protein for IMAGE:3354070) [Homo sapiens]	56.2	78.1	100%	9e-08	100%	gi|14043248|AAH07614.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.5	100%	9e-08	100%	gi|685535046|XP_009202774.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.1	100%	9e-08	100%	gi|675773160|XP_008975042.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.5	100%	9e-08	100%	gi|544429971|XP_005553977.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.1	100%	9e-08	100%	gi|530381810|XP_005249075.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.5	100%	9e-08	100%	gi|685535044|XP_009202773.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.5	100%	9e-08	100%	gi|635096985|XP_007971742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.5	100%	9e-08	100%	gi|297290177|XP_002803682.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.1	100%	9e-08	100%	gi|686720936|XP_009239742.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.5	100%	1e-07	100%	gi|635096983|XP_007971741.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.5	100%	1e-07	100%	gi|635096981|XP_007971740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.5	100%	1e-07	100%	gi|635096993|XP_007971746.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.1	100%	1e-07	100%	gi|640776034|XP_008048656.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.1	100%	1e-07	100%	gi|426351748|XP_004043389.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.1	100%	1e-07	100%	gi|426351746|XP_004043388.1
☐	glycosylphosphatidylinositol phospholipase D [Homo sapiens]	56.2	78.1	100%	1e-07	100%	gi|20269065|CAC87068.1
☐	phospholipase D [Homo sapiens]	56.2	78.1	100%	1e-07	100%	gi|388765|AAA36445.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.1	100%	1e-07	100%	gi|397505380|XP_003823243.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Ho	56.2	78.1	100%	1e-07	100%	gi|29171717|NP_001494.2
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [H	56.2	78.1	100%	1e-07	100%	gi|14195001|AAG16627.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.5	100%	1e-07	100%	gi|724798150|XP_010363586.1
☐	phospholipase D [Homo sapiens]	56.2	78.5	100%	1e-07	100%	gi|388763|AAA36444.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.5	100%	1e-07	100%	gi|544429969|XP_005553976.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.5	100%	1e-07	100%	gi|402865969|XP_003897171.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.1	100%	1e-07	100%	gi|410040317|XP_518268.4
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.5	100%	1e-07	100%	gi|685535041|XP_009202772.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.1	100%	1e-07	100%	gi|675773152|XP_008975041.1
☐							

	hypothetical protein EGM_13271 [Macaca fascicularis]	56.2	78.5	100%	1e-07	100%	gi|355748274|EHH52757.1
☐	hypothetical protein EGK_21153 [Macaca mulatta]	56.2	78.5	100%	1e-07	100%	gi|355569342|EHH25414.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CR	56.2	78.1	100%	1e-07	100%	gi|119575854|EAW55450.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.1	100%	1e-07	100%	gi|332228866|XP_003263611.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.5	100%	1e-07	100%	gi|544429967|XP_005553975.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	56.2	78.1	100%	1e-07	100%	gi|524924187|XP_005066341.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	53.2	74.2	94%	1e-06	100%	gi|507684247|XP_004640232.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	53.2	75.1	100%	1e-06	94%	gi|403270800|XP_003927350.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	53.2	75.1	100%	1e-06	94%	gi|675650934|XP_002746229.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	52.8	52.8	100%	1e-06	94%	gi|625272320|XP_007627730.1
☐	phosphatidylinositol-glycan-specific phospholipase D-like protein [C	52.8	52.8	100%	1e-06	94%	gi|537192249|ERE77282.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Cricetulus gri	52.8	52.8	100%	1e-06	94%	gi|344238211|EGV94314.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	52.8	74.7	100%	1e-06	94%	gi|532023384|XP_005355039.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	52.8	52.8	100%	1e-06	94%	gi|354480090|XP_003502241.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.5	73.0	100%	4e-06	94%	gi|507979038|XP_004693375.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.5	73.4	100%	4e-06	94%	gi|471403600|XP_004384046.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.5	74.2	100%	4e-06	94%	gi|617615072|XP_007526005.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.5	93.5	100%	4e-06	94%	gi|612008081|XP_007487938.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.5	93.5	100%	4e-06	94%	gi|612008079|XP_001375600.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	51.5	93.5	100%	4e-06	94%	gi|612008077|XP_007487937.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	50.3	72.1	94%	1e-05	94%	gi|655839984|XP_008260728.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	50.3	72.1	94%	1e-05	94%	gi|655839976|XP_008260723.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	49.8	72.1	100%	1e-05	88%	gi|532102948|XP_005337080.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	49.8	72.1	100%	1e-05	94%	gi|589928750|XP_006977193.1
☐	hypothetical protein CB1_000595062 [Camelus ferus]	49.4	71.7	94%	2e-05	94%	gi|528763477|EPY83136.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	49.4	71.3	94%	2e-05	94%	gi|731213592|XP_010621250.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	49.4	71.3	94%	2e-05	94%	gi|731213588|XP_010621248.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Fukomys dar	49.4	71.3	94%	2e-05	94%	gi|676279913|KFO33840.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	49.0	70.0	100%	3e-05	88%	gi|545554532|XP_005640137.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	49.0	70.0	100%	3e-05	88%	gi|74003954|XP_535902.2
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	49.0	70.0	100%	3e-05	88%	gi|545554529|XP_005640136.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Pteropus ale	48.6	48.6	100%	4e-05	88%	gi|431896393|ELK05805.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.6	69.6	100%	4e-05	88%	gi|586495128|XP_006878008.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.6	69.6	100%	4e-05	88%	gi|634873155|XP_007948002.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.6	69.6	100%	4e-05	88%	gi|586529361|XP_006919597.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.1	70.4	100%	5e-05	94%	gi|664709546|XP_008511735.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	48.1	69.6	100%	5e-05	94%	gi|505841011|XP_004614021.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.1	70.4	100%	5e-05	94%	gi|664709544|XP_008511734.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.1	70.4	100%	5e-05	94%	gi|478515788|XP_004432133.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.1	70.4	100%	5e-05	94%	gi|149732005|XP_001497586.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.1	70.4	100%	5e-05	94%	gi|664709542|XP_008511732.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.1	70.4	100%	5e-05	94%	gi|664709540|XP_008511731.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.1	70.4	100%	5e-05	94%	gi|545837650|XP_001925944.5
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	48.1	70.4	100%	5e-05	94%	gi|664709538|XP_008511730.1
☐	PREDICTED: LOW QUALITY PROTEIN: phosphatidylinositol-glyca	47.7	70.0	100%	7e-05	88%	gi|560912019|XP_006182298.1

☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	47.7	68.7	100%	7e-05	88%	gi|602684652|XP_007454575.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	47.7	68.7	100%	7e-05	88%	gi|602684650|XP_007454574.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	47.7	70.0	100%	7e-05	88%	gi|593754864|XP_007116306.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	47.7	70.0	100%	7e-05	88%	gi|560952422|XP_006198740.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	47.7	70.0	100%	7e-05	88%	gi|594700264|XP_007197201.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	47.7	70.0	100%	7e-05	88%	gi|594700262|XP_007197200.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	46.4	67.4	100%	2e-04	82%	gi|591294474|XP_007074479.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	46.4	68.7	100%	2e-04	93%	gi|395511886|XP_003760182.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	67.4	94%	3e-04	88%	gi|512971062|XP_004847666.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Heterocepha	45.6	67.4	94%	3e-04	88%	gi|351706674|EHB09593.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	67.4	94%	3e-04	88%	gi|512971060|XP_004847665.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	67.4	94%	3e-04	88%	gi|512971057|XP_004847664.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	67.4	94%	3e-04	88%	gi|512971055|XP_004847663.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	67.4	94%	3e-04	88%	gi|512880679|XP_004895023.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.6	67.4	88%	3e-04	93%	gi|344289516|XP_003416488.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CR	45.2	67.0	100%	5e-04	76%	gi|148700518|EDL32465.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.2	67.4	100%	5e-04	82%	gi|641712629|XP_008145534.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.2	67.0	94%	5e-04	88%	gi|514459231|XP_005003342.1
☐	RecName: Full=Phosphatidylinositol-glycan-specific phospholipase	45.2	67.0	100%	5e-04	76%	gi|6225846|O70362.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.2	67.0	94%	5e-04	88%	gi|348566244|XP_003468912.1
☐	glycosylphosphatidylinositol specific phospholipase D1, isoform CR	45.2	67.0	100%	5e-04	76%	gi|148700520|EDL32467.1
☐	PREDICTED: phosphatidylinositol-glycan-specific phospholipase D	45.2	67.0	100%	5e-04	75%	gi|667294118|XP_008578807.1
☐	glycosylphosphatidylinositol-specific phospholipase D precursor [Mu	45.2	67.0	100%	5e-04	76%	gi|33088003|AAP93132.1
☐	glycosylphosphatidylinositol phospholipase D [Mus musculus]	45.2	67.0	100%	5e-04	76%	gi|19547985|AAL87452.1
☐	phosphatidylinositol-glycan-specific phospholipase D precursor [Mu	45.2	67.0	100%	5e-04	76%	gi|111378397|NP_032182.2
☐	unnamed protein product [Mus musculus]	45.2	67.0	100%	5e-04	76%	gi|12836535|BAB23698.1
☐	Phosphatidylinositol-glycan-specific phospholipase D [Myotis brand	44.8	44.8	100%	7e-04	75%	gi|521024043|EPQ05831.1

⊟ Alignments

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glycosylphosphatidylinositol phospholipase D [Homo sapiens]

Sequence ID: gi|11122875|emb|CAC14844.1| **Length:** 457 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 209 to 225 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
56.2 bits(125)	9e-08	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RTLLLVGSPTWKNASRL  17
            RTLLLVGSPTWKNASRL
Sbjct  209  RTLLLVGSPTWKNASRL  225
```

Range 2: 278 to 289 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
21.8 bits(44)	20913	8/12(67%)	8/12(66%)	3/12(25%)

```
Query  2    TL---LLVGSPT  10
            TL   LLVG PT
Sbjct  278  TLKQVLLVGAPT  289
```

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Unknown (protein for IMAGE:3354070), partial [Homo sapiens]

Sequence ID: gi|14043248|gb|AAH07614.1| **Length:** 575 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 327 to 343 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
56.2 bits(125)	9e-08	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RTLLLVGSPTWKNASRL  17
            RTLLLVGSPTWKNASRL
Sbjct  327  RTLLLVGSPTWKNASRL  343
```

Range 2: 396 to 407 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
21.8 bits(44)	20945	8/12(67%)	8/12(66%)	3/12(25%)

```
Query  2    TL---LLVGSPT  10
            TL   LLVG PT
Sbjct  396  TLKQVLLVGAPT  407
```

Download GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X4 [Papio anubis]

Sequence ID: gi|685535046|ref|XP_009202774.1| **Length:** 677 **Number of Matches:** 2

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 429 to 445 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
56.2 bits(125)	9e-08	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RTLLLVGSPTWKNASRL  17
            RTLLLVGSPTWKNASRL
Sbjct  429  RTLLLVGSPTWKNASRL  445
```

Range 2: 498 to 516 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
22.3 bits(45)	14709	9/19(47%)	11/19(57%)	3/19(15%)

```
Query  2    TL---LLVGSPTWKNASRL  17
            TL   LLVG PT  + S +
Sbjct  498  TLTQVLLVGAPTRDDVSKM  516
```

Download GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Pan paniscus]

Sequence ID: gi|675773160|ref|XP_008975042.1| **Length:** 677 **Number of Matches:** 2

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 429 to 445 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
56.2 bits(125)	9e-08	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RTLLLVGSPTWKNASRL  17
            RTLLLVGSPTWKNASRL
Sbjct  429  RTLLLVGSPTWKNASRL  445
```

Range 2: 498 to 509 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
21.8 bits(44)	20964	8/12(67%)	8/12(66%)	3/12(25%)

```
Query  2    TL---LLVGSPT  10
            TL   LLVG PT
Sbjct  498  TLTQVLLVGAPT  509
```

Download GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

PREDICTED: phosphatidylinositol-glycan-specific phospholipase D isoform X3 [Macaca fascicularis]

Sequence ID: gi|544429971|ref|XP_005553977.1| **Length:** 677 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 429 to 445 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
56.2 bits(125)	9e-08	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RTLLLVGSPTWKNASRL  17
            RTLLLVGSPTWKNASRL
Sbjct  429  RTLLLVGSPTWKNASRL  445
```

Range 2: 498 to 516 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
22.3 bits(45)	14709	9/19(47%)	11/19(57%)	3/19(15%)

```
Query  2    TL---LLVGSPTWKNASRL  17
```

```
            TL   LLVG PT  + S +
Sbjct  498  TLTQVLLVGAPTRDDVSKM  516
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVE7ZF1W01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

GPR116_KANEQVVQSLDQTYKM_Mod

RID BVE7ZF1W01R (Expires on 01-21 09:10 am)

Query ID lcl|63041
Description None
Molecule type amino acid
Query Length 16

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

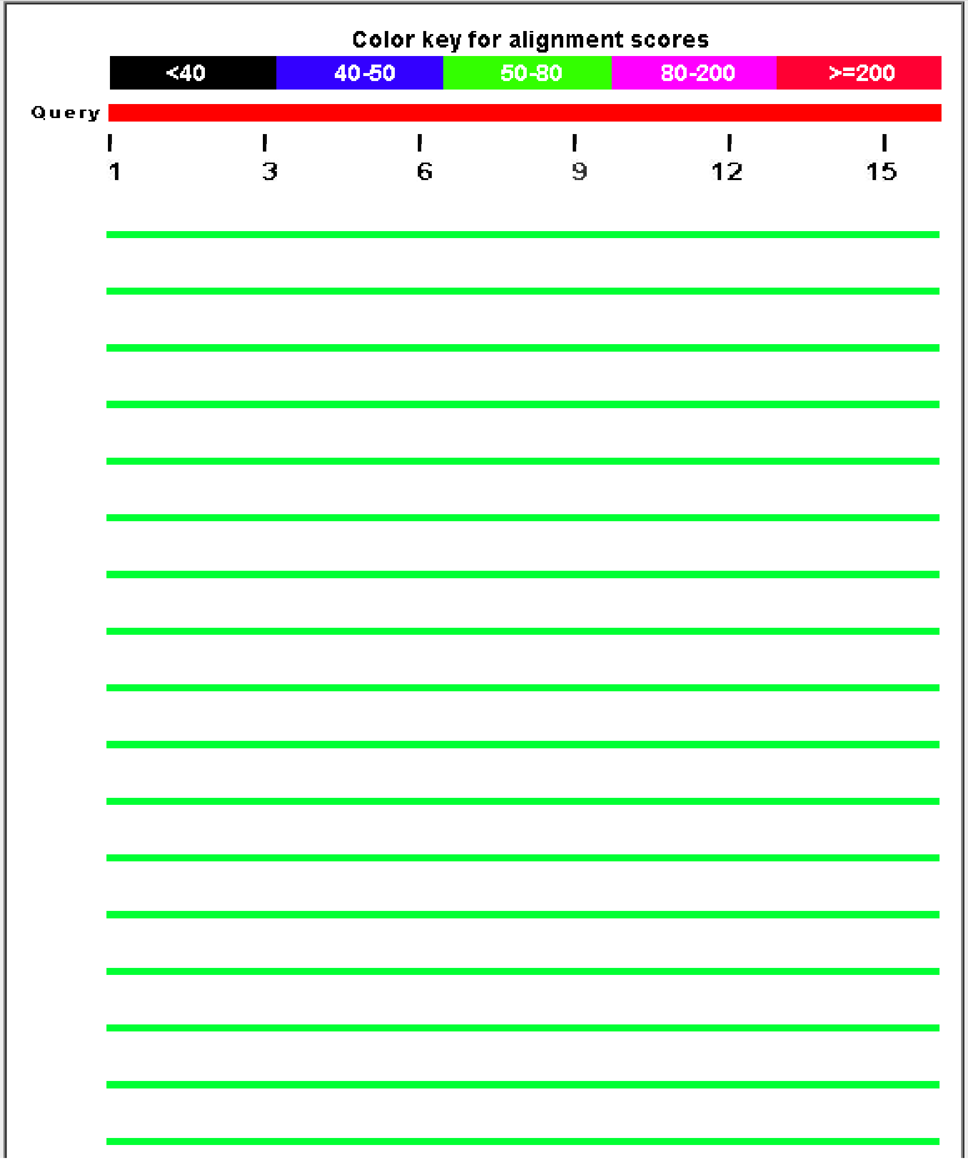
Graphic Summary

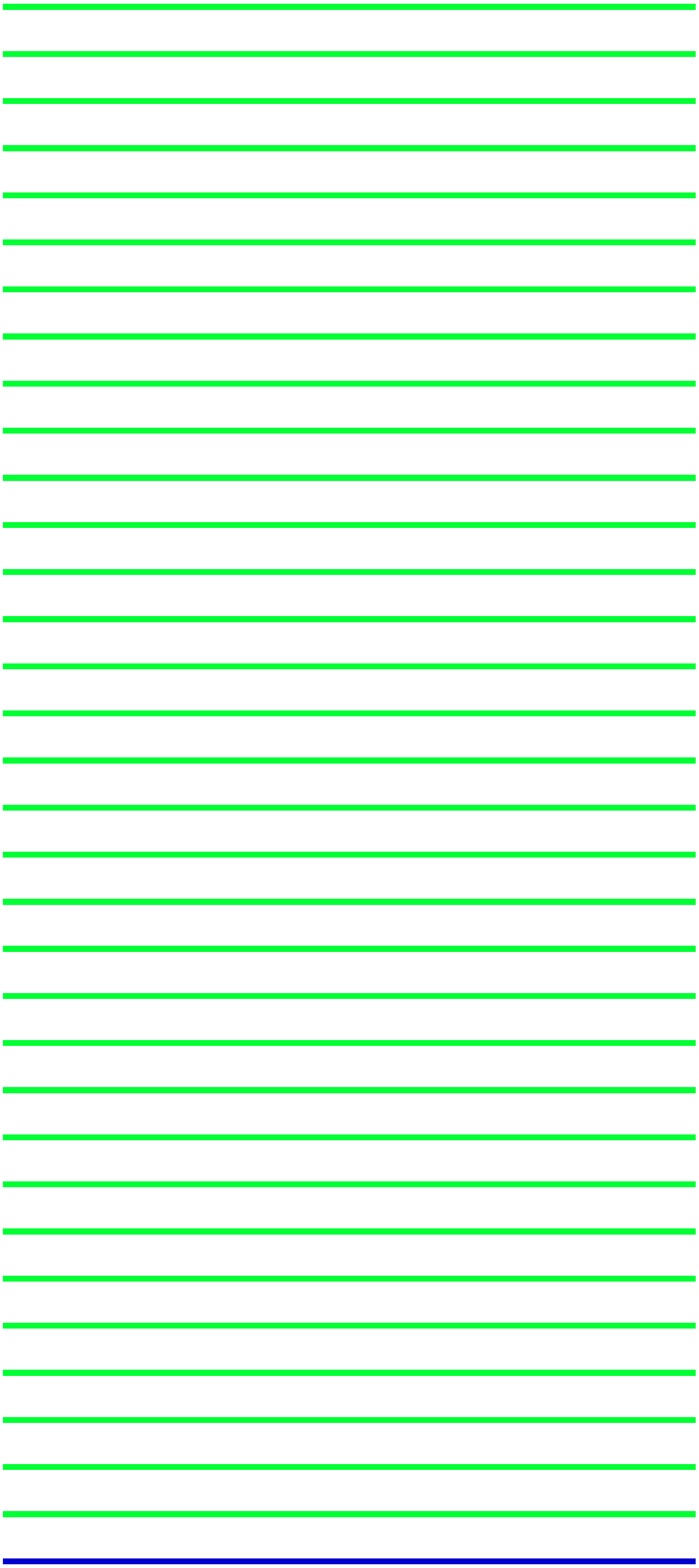
Show Conserved Domains

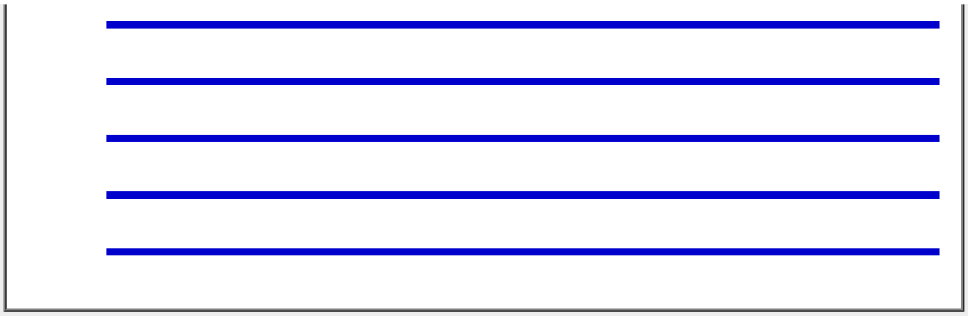
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	hypothetical protein [Homo sapiens]	52.8	52.8	100%	1e-06	94%	CAB43394.1
☐	hypothetical protein [synthetic construct]	52.8	52.8	100%	1e-06	94%	CAL38391.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Pongo ab	52.8	52.8	100%	1e-06	94%	XP_009240213.1
☐	G-protein coupled receptor GPR116 [Homo sapiens]	52.8	52.8	100%	1e-06	94%	AAN46672.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X5 [Papio anu	52.8	52.8	100%	1e-06	94%	XP_009203591.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4 [Papio anu	52.8	52.8	100%	1e-06	94%	XP_009203590.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X5 [Pan troglc	52.8	52.8	100%	1e-06	94%	XP_009449688.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4 [Pan panis	52.8	52.8	100%	1e-06	94%	XP_008956931.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2 [Rhinopith	52.8	52.8	100%	1e-06	94%	XP_010354809.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4 [Macaca fa	52.8	52.8	100%	1e-06	94%	XP_005552855.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Papio anu	52.8	52.8	100%	1e-06	94%	XP_003897745.1
☐	hypothetical protein EGM_13658 [Macaca fascicularis]	52.8	52.8	100%	1e-06	94%	EHH53094.1
☐	hypothetical protein EGK_14976 [Macaca mulatta]	52.8	52.8	100%	1e-06	94%	EHH18396.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 1 [Gorilla goril	52.8	52.8	100%	1e-06	94%	XP_004044192.1
☐	G protein-coupled receptor 116 [Homo sapiens]	52.8	52.8	100%	1e-06	94%	AAH66121.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Pan panis	52.8	52.8	100%	1e-06	94%	XP_003833242.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4 [Pan troglc	52.8	52.8	100%	1e-06	94%	XP_001140861.2
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 1 [Nomascus	52.8	52.8	100%	1e-06	94%	XP_003254249.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2 [Pongo ab	52.8	52.8	100%	1e-06	94%	XP_002817007.1
☐	unnamed protein product [Homo sapiens]	52.8	52.8	100%	1e-06	94%	BAF82192.1
☐	G protein-coupled receptor 116, isoform CRA_a [Homo sapiens]	52.8	52.8	100%	1e-06	94%	EAX04307.1
☐	G protein coupled receptor 116 [Homo sapiens]	52.8	52.8	100%	1e-06	94%	AAS21061.1
☐	probable G-protein coupled receptor 116 precursor [Homo sapiens]	52.8	52.8	100%	1e-06	94%	NP_001091988.1
☐	G protein-coupled receptor 116, isoform CRA_b [Homo sapiens]	52.8	52.8	100%	1e-06	94%	EAX04309.1
☐	KIAA0758 protein [Homo sapiens]	52.8	52.8	100%	1e-06	94%	BAA34478.2
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2 [Papio anu	52.8	52.8	100%	1e-06	94%	XP_009203589.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Macaca fa	52.8	52.8	100%	1e-06	94%	XP_005552854.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Pan troglc	52.8	52.8	100%	1e-06	94%	XP_009449687.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4 [Homo sap	52.8	52.8	100%	1e-06	94%	XP_005248952.1

☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2 [Pan troglo	52.8	52.8	100%	1e-06	94%	XP_009449686.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2 [Pan panis	52.8	52.8	100%	1e-06	94%	XP_008956930.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Homo sap	52.8	52.8	100%	1e-06	94%	XP_005248951.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Rhinopith	52.8	52.8	100%	1e-06	94%	XP_010354807.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Papio anu	52.8	52.8	100%	1e-06	94%	XP_009203587.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Macaca fa	52.8	52.8	100%	1e-06	94%	XP_005552852.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Pan troglo	52.8	52.8	100%	1e-06	94%	XP_009449683.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Pongo ab	52.8	52.8	100%	1e-06	94%	XP_009240212.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Pan panis	52.8	52.8	100%	1e-06	94%	XP_008956928.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Homo sap	52.8	52.8	100%	1e-06	94%	XP_005248949.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Macaca mulatta]	52.8	52.8	100%	1e-06	94%	XP_001103527.2
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 6 [Dasypus no	50.7	50.7	100%	6e-06	88%	XP_004452861.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 5 [Dasypus no	50.7	50.7	100%	7e-06	88%	XP_004452860.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Orycteropus afer afer	50.7	50.7	100%	7e-06	88%	XP_007934357.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 4 [Dasypus no	50.7	50.7	100%	7e-06	88%	XP_004452859.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Trichechus manatus l	50.7	50.7	100%	7e-06	88%	XP_004379588.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 3 [Dasypus no	50.7	50.7	100%	7e-06	88%	XP_004452858.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 1 [Dasypus no	50.7	50.7	100%	7e-06	88%	XP_004452856.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Chloroceb	50.3	50.3	100%	9e-06	88%	XP_007970519.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2 [Chloroceb	50.3	50.3	100%	9e-06	88%	XP_007970518.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Chloroceb	50.3	50.3	100%	9e-06	88%	XP_007970516.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Echinops telfairi]	49.4	49.4	100%	2e-05	88%	XP_004710942.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Otolemur garnettii]	49.4	49.4	100%	2e-05	88%	XP_003789395.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Ictidomys tridecemlin	48.1	48.1	100%	5e-05	81%	XP_005318657.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Tarsius syrichta]	48.1	48.1	100%	5e-05	81%	XP_008056651.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Sorex araneus]	48.1	48.1	100%	5e-05	81%	XP_004605897.1
☐	probable G-protein coupled receptor 116 precursor [Rattus norvegicus]	48.1	48.1	100%	5e-05	81%	NP_620810.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X5 [Rattus no	48.1	48.1	100%	5e-05	81%	XP_008765057.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4 [Rattus no	48.1	48.1	100%	5e-05	81%	XP_006244656.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Rattus no	48.1	48.1	100%	5e-05	81%	XP_008765056.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2 [Rattus no	48.1	48.1	100%	5e-05	81%	XP_008765054.1
☐	hypothetical protein PANDA_007624 [Ailuropoda melanoleuca]	46.9	46.9	100%	1e-04	81%	EFB13334.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Tupaia chinensis]	46.9	46.9	100%	1e-04	81%	XP_006149150.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Ursus ma	46.9	46.9	100%	1e-04	81%	XP_008690048.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Leptonychotes wedde	46.9	46.9	100%	1e-04	81%	XP_006727631.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X7 [Mustela p	46.9	46.9	100%	1e-04	81%	XP_004739803.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Odobenus rosmarus	46.9	46.9	100%	1e-04	81%	XP_004408503.1
☐	PREDICTED: probable G-protein coupled receptor 116-like [Ailuropoda melan	46.9	46.9	100%	1e-04	81%	XP_002919049.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Oryctolag	46.9	46.9	100%	1e-04	81%	XP_008261239.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X6 [Mustela p	46.9	46.9	100%	1e-04	81%	XP_004739802.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2 [Ursus ma	46.9	46.9	100%	1e-04	81%	XP_008690046.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2 [Oryctolag	46.9	46.9	100%	1e-04	81%	XP_008261237.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Ursus ma	46.9	46.9	100%	1e-04	81%	XP_008690044.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Oryctolag	46.9	46.9	100%	1e-04	81%	XP_008261235.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X5 [Mustela p	46.9	46.9	100%	1e-04	81%	XP_004739801.1

☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Mustela p	46.9	46.9	100%	1e-04	81%	XP_004739799.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Mustela p	46.9	46.9	100%	1e-04	81%	XP_004739797.1
☐	putative G-protein coupled receptor 116 [Tupaia chinensis]	46.9	46.9	100%	1e-04	81%	ELW65642.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 2 [Ceratotheri	46.4	46.4	100%	2e-04	81%	XP_004424105.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Ochotona princeps]	46.4	46.4	100%	2e-04	81%	XP_004590480.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X5 [Equus cal	46.4	46.4	100%	2e-04	81%	XP_005604037.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 1 [Ceratotheri	46.4	46.4	100%	2e-04	81%	XP_004424104.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoformX1 [Equus cab	46.4	46.4	100%	2e-04	81%	XP_001498309.2
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4 [Equus cal	46.4	46.4	100%	2e-04	81%	XP_005604036.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X6 [Equus prz	46.4	46.4	100%	2e-04	81%	XP_008540805.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2 [Equus cal	46.4	46.4	100%	2e-04	81%	XP_005604034.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X5 [Equus prz	46.4	46.4	100%	2e-04	81%	XP_008540804.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4 [Equus prz	46.4	46.4	100%	2e-04	81%	XP_008540803.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Equus prz	46.4	46.4	100%	2e-04	81%	XP_008540802.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2 [Equus prz	46.4	46.4	100%	2e-04	81%	XP_008540801.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Equus prz	46.4	46.4	100%	2e-04	81%	XP_008540800.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Physeter catodon]	46.0	46.0	100%	2e-04	81%	XP_007120943.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Lipotes vexillifer]	46.0	46.0	100%	2e-04	81%	XP_007451968.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Loxodonta africana]	46.0	46.0	100%	2e-04	88%	XP_010587260.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4 [Callithrix j	45.6	45.6	100%	3e-04	81%	XP_008992789.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2 [Saimiri bo	45.6	45.6	100%	3e-04	81%	XP_003923134.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Callithrix j	45.6	45.6	100%	3e-04	81%	XP_008992788.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2 [Callithrix j	45.6	45.6	100%	3e-04	81%	XP_008992787.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Callithrix j	45.6	45.6	100%	3e-04	81%	XP_008992785.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1 [Saimiri bo	45.6	45.6	100%	3e-04	81%	XP_010332277.1
☐	probable G-protein coupled receptor 116 precursor [Mus musculus]	45.2	45.2	100%	5e-04	75%	NP_001074647.1

⊟ Alignments

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hypothetical protein [Homo sapiens]

Sequence ID: emb|CAB43394.1| **Length:** 618 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 246 to 261 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.8 bits(117)	1e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    KANEQVVQSLDQTYKM  16
            KANEQVVQSL+QTYKM
Sbjct  246  KANEQVVQSLNQTYKM  261
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

hypothetical protein [synthetic construct]

Sequence ID: emb|CAL38391.1| **Length:** 1204 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 246 to 261 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.8 bits(117)	1e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    KANEQVVQSLDQTYKM  16
            KANEQVVQSL+QTYKM
Sbjct  246  KANEQVVQSLNQTYKM  261
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Pongo abelii]

Sequence ID: ref|XP_009240213.1| **Length:** 1289 **Number of Matches:** 1

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

Range 1: 246 to 261 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.8 bits(117)	1e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    KANEQVVQSLDQTYKM  16
            KANEQVVQSL+QTYKM
Sbjct  246  KANEQVVQSLNQTYKM  261
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

G-protein coupled receptor GPR116 [Homo sapiens]

Sequence ID: gb|AAN46672.1| **Length:** 1300 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 246 to 261 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.8 bits(117)	1e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    KANEQVVQSLDQTYKM  16
            KANEQVVQSL+QTYKM
Sbjct  246  KANEQVVQSLNQTYKM  261
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: probable G-protein coupled receptor 116 isoform X5 [Papio anubis]

Sequence ID: ref|XP_009203591.1| **Length:** 1338 **Number of Matches:** 1

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

Range 1: 198 to 213 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.8 bits(117)	1e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    KANEQVVQSLDQTYKM  16
            KANEQVVQSL+QTYKM
Sbjct  198  KANEQVVQSLNQTYKM  213
```

BLAST® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ **Formatting Results - B9FDBUXS01R**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download

You Tube How to read this page   Blast report description

GPR116_KANEQVVQSLNQTYKM_NonMod

RID B9FDBUXS01R (Expires on 01-14 13:39 pm)

Query ID	lcl|257423	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ ▷Citation
Query Length	16		

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

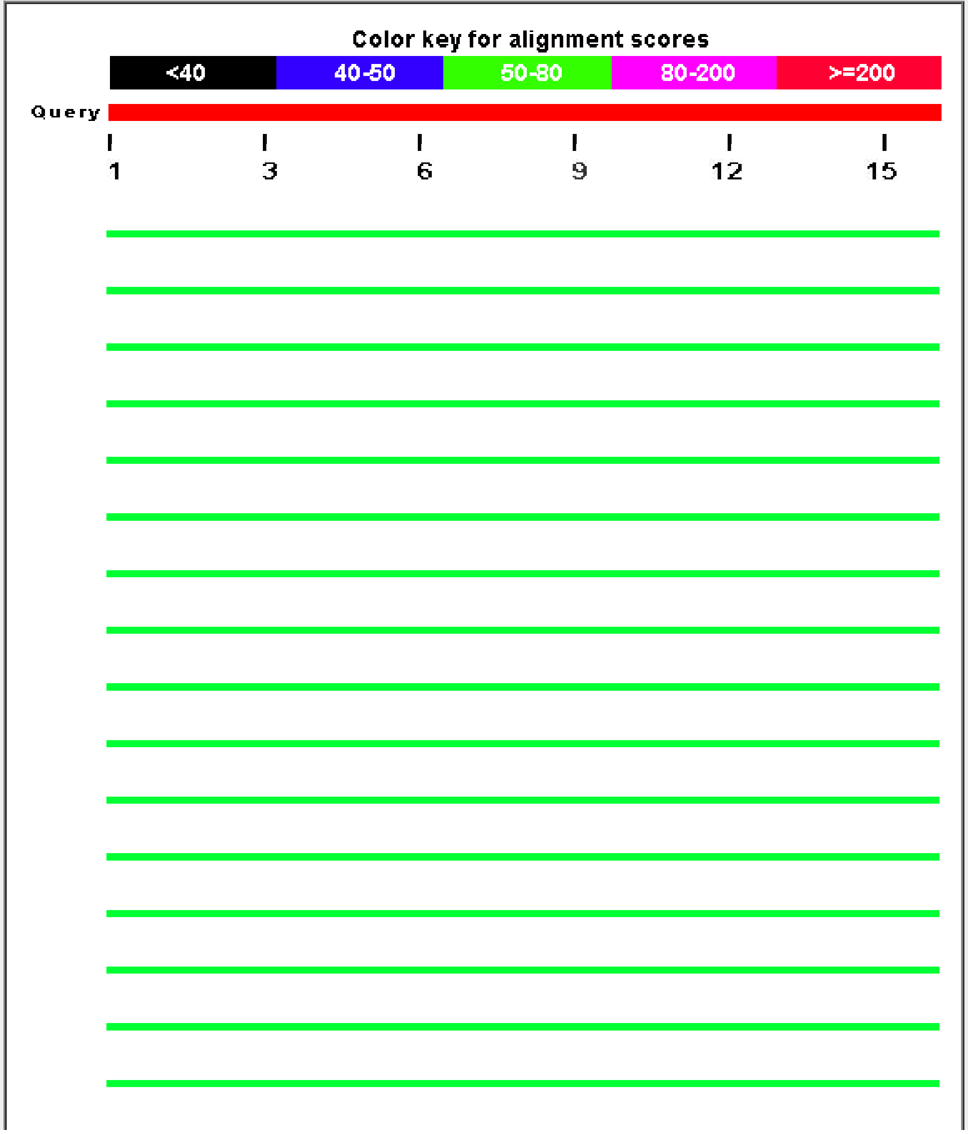
⊟ Graphic Summary

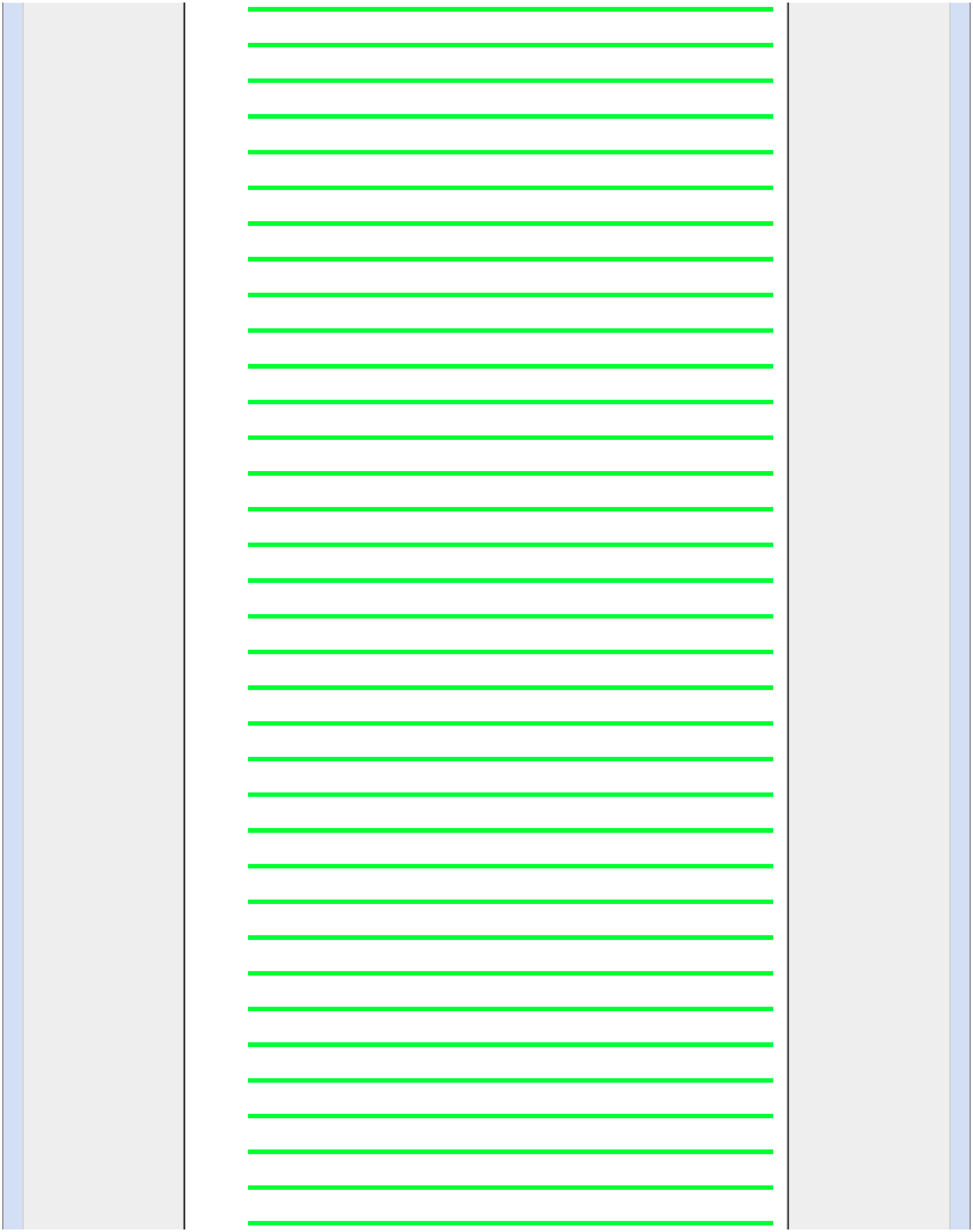
⊟ Show Conserved Domains

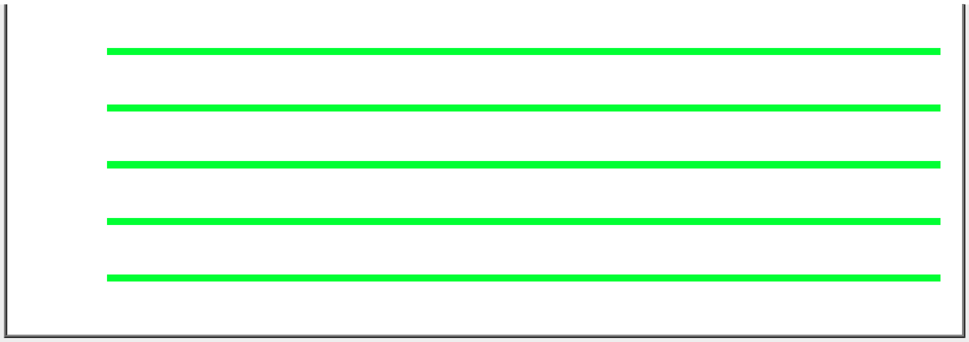
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	hypothetical protein [Homo sapiens]	55.4	55.4	100%	2e-07	100%	gi|4886491|CAB43394.1
☐	hypothetical protein [synthetic construct]	55.4	55.4	100%	2e-07	100%	gi|117645848|CAL38391.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3	55.4	55.4	100%	2e-07	100%	gi|686722337|XP_009240213.1
☐	G-protein coupled receptor GPR116 [Homo sapiens]	55.4	55.4	100%	2e-07	100%	gi|24286029|AAN46672.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X5	55.4	55.4	100%	2e-07	100%	gi|685537071|XP_009203591.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4	55.4	55.4	100%	2e-07	100%	gi|685537069|XP_009203590.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X5	55.4	55.4	100%	2e-07	100%	gi|694916767|XP_009449688.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4	55.4	55.4	100%	2e-07	100%	gi|675802057|XP_008956931.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2	55.4	55.4	100%	2e-07	100%	gi|724961251|XP_010354809.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4	55.4	55.4	100%	2e-07	100%	gi|544427534|XP_005552855.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3	55.4	55.4	100%	2e-07	100%	gi|402867181|XP_003897745.1
☐	hypothetical protein EGM_13658 [Macaca fascicularis]	55.4	55.4	100%	2e-07	100%	gi|355748611|EHH53094.1
☐	hypothetical protein EGK_14976 [Macaca mulatta]	55.4	55.4	100%	2e-07	100%	gi|355561764|EHH18396.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 1 [C	55.4	55.4	100%	2e-07	100%	gi|426353420|XP_004044192.1
☐	G protein-coupled receptor 116 [Homo sapiens]	55.4	55.4	100%	2e-07	100%	gi|42490767|AAH66121.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3	55.4	55.4	100%	2e-07	100%	gi|397526671|XP_003833242.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4	55.4	55.4	100%	2e-07	100%	gi|332824352|XP_001140861.2
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 1 [N	55.4	55.4	100%	2e-07	100%	gi|332210305|XP_003254249.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2	55.4	55.4	100%	2e-07	100%	gi|297678285|XP_002817007.1
☐	unnamed protein product [Homo sapiens]	55.4	55.4	100%	2e-07	100%	gi|158260029|BAF82192.1
☐	G protein-coupled receptor 116, isoform CRA_a [Homo sapiens]	55.4	55.4	100%	2e-07	100%	gi|119624712|EAX04307.1
☐	G protein coupled receptor 116 [Homo sapiens]	55.4	55.4	100%	2e-07	100%	gi|42566596|AAS21061.1
☐	probable G-protein coupled receptor 116 precursor [Homo sapiens]	55.4	55.4	100%	2e-07	100%	gi|148719671|NP_001091988.1
☐	G protein-coupled receptor 116, isoform CRA_b [Homo sapiens]	55.4	55.4	100%	2e-07	100%	gi|119624714|EAX04309.1
☐	KIAA0758 protein [Homo sapiens]	55.4	55.4	100%	2e-07	100%	gi|71891679|BAA34478.2
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2	55.4	55.4	100%	2e-07	100%	gi|685537065|XP_009203589.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3	55.4	55.4	100%	2e-07	100%	gi|544427532|XP_005552854.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3	55.4	55.4	100%	2e-07	100%	gi|694916763|XP_009449687.1
☐							

	PREDICTED: probable G-protein coupled receptor 116 isoform X4	55.4	55.4	100%	2e-07	100%	gi|530381555|XP_005248952.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2	55.4	55.4	100%	2e-07	100%	gi|694916761|XP_009449686.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2	55.4	55.4	100%	2e-07	100%	gi|675802053|XP_008956930.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3	55.4	55.4	100%	2e-07	100%	gi|530381553|XP_005248951.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1	55.4	55.4	100%	2e-07	100%	gi|724961247|XP_010354807.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1	55.4	55.4	100%	2e-07	100%	gi|685537061|XP_009203587.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1	55.4	55.4	100%	2e-07	100%	gi|544427528|XP_005552852.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1	55.4	55.4	100%	2e-07	100%	gi|694916757|XP_009449683.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1	55.4	55.4	100%	2e-07	100%	gi|686722333|XP_009240212.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1	55.4	55.4	100%	2e-07	100%	gi|675802049|XP_008956928.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1	55.4	55.4	100%	2e-07	100%	gi|530381549|XP_005248949.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Macaca mu	55.4	55.4	100%	2e-07	100%	gi|297290986|XP_001103527.2
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 6 [D	53.2	53.2	100%	8e-07	94%	gi|488521900|XP_004452861.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 5 [D	53.2	53.2	100%	9e-07	94%	gi|488521898|XP_004452860.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Orycteropu	53.2	53.2	100%	9e-07	94%	gi|634835124|XP_007934357.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 4 [D	53.2	53.2	100%	9e-07	94%	gi|488521896|XP_004452859.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Trichechus	53.2	53.2	100%	9e-07	94%	gi|471389220|XP_004379588.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 3 [D	53.2	53.2	100%	9e-07	94%	gi|488521894|XP_004452858.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 1 [D	53.2	53.2	100%	9e-07	94%	gi|488521890|XP_004452856.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3	52.8	52.8	100%	1e-06	94%	gi|635094630|XP_007970519.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2	52.8	52.8	100%	1e-06	94%	gi|635094628|XP_007970518.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1	52.8	52.8	100%	1e-06	94%	gi|635094624|XP_007970516.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Echinops te	52.0	52.0	100%	2e-06	94%	gi|507682428|XP_004710942.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Otolemur g	52.0	52.0	100%	2e-06	94%	gi|395832700|XP_003789395.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Ictidomys t	50.7	50.7	100%	6e-06	88%	gi|532065597|XP_005318657.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Tarsius syr	50.7	50.7	100%	6e-06	88%	gi|640800780|XP_008056651.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Sorex aran	50.7	50.7	100%	6e-06	88%	gi|505791455|XP_004605897.1
☐	probable G-protein coupled receptor 116 precursor [Rattus norvegic	50.7	50.7	100%	6e-06	88%	gi|20806161|NP_620810.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X5	50.7	50.7	100%	6e-06	88%	gi|672064229|XP_008765057.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4	50.7	50.7	100%	6e-06	88%	gi|564367517|XP_006244656.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3	50.7	50.7	100%	6e-06	88%	gi|672064226|XP_008765056.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2	50.7	50.7	100%	6e-06	88%	gi|672064222|XP_008765054.1
☐	hypothetical protein PANDA_007624 [Ailuropoda melanoleuca]	49.4	49.4	100%	2e-05	88%	gi|281337750|EFB13334.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Tupaia chir	49.4	49.4	100%	2e-05	88%	gi|562840007|XP_006149150.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3	49.4	49.4	100%	2e-05	88%	gi|670998310|XP_008690048.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Leptonycho	49.4	49.4	100%	2e-05	88%	gi|585150307|XP_006727631.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X7	49.4	49.4	100%	2e-05	88%	gi|511830214|XP_004739803.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Odobenus	49.4	49.4	100%	2e-05	88%	gi|472378162|XP_004408503.1
☐	PREDICTED: probable G-protein coupled receptor 116-like [Ailurop	49.4	49.4	100%	2e-05	88%	gi|301767272|XP_002919049.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3	49.4	49.4	100%	2e-05	88%	gi|655841660|XP_008261239.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X6	49.4	49.4	100%	2e-05	88%	gi|511830212|XP_004739802.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2	49.4	49.4	100%	2e-05	88%	gi|670998308|XP_008690046.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2	49.4	49.4	100%	2e-05	88%	gi|655841657|XP_008261237.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1	49.4	49.4	100%	2e-05	88%	gi|670998304|XP_008690044.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1	49.4	49.4	100%	2e-05	88%	gi|655841651|XP_008261235.1

☐	PREDICTED: probable G-protein coupled receptor 116 isoform X5	49.4	49.4	100%	2e-05	88%	gi|511830210|XP_004739801.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3	49.4	49.4	100%	2e-05	88%	gi|511830206|XP_004739799.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1	49.4	49.4	100%	2e-05	88%	gi|511830202|XP_004739797.1
☐	putative G-protein coupled receptor 116 [Tupaia chinensis]	49.4	49.4	100%	2e-05	88%	gi|444725062|ELW65642.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 2 [C	49.0	49.0	100%	2e-05	88%	gi|478499560|XP_004424105.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Ochotona p	49.0	49.0	100%	2e-05	88%	gi|504157919|XP_004590480.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X5	49.0	49.0	100%	2e-05	88%	gi|545198452|XP_005604037.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform 1 [C	49.0	49.0	100%	2e-05	88%	gi|478499558|XP_004424104.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoformX1 [	49.0	49.0	100%	2e-05	88%	gi|194223572|XP_001498309.2
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4	49.0	49.0	100%	2e-05	88%	gi|545198450|XP_005604036.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X6	49.0	49.0	100%	2e-05	88%	gi|664766618|XP_008540805.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2	49.0	49.0	100%	2e-05	88%	gi|545198446|XP_005604034.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X5	49.0	49.0	100%	2e-05	88%	gi|664766616|XP_008540804.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4	49.0	49.0	100%	2e-05	88%	gi|664766614|XP_008540803.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3	49.0	49.0	100%	2e-05	88%	gi|664766612|XP_008540802.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2	49.0	49.0	100%	2e-05	88%	gi|664766610|XP_008540801.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1	49.0	49.0	100%	2e-05	88%	gi|664766608|XP_008540800.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Physeter ca	48.6	48.6	100%	3e-05	88%	gi|593764740|XP_007120943.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Lipotes vex	48.6	48.6	100%	3e-05	88%	gi|602733162|XP_007451968.1
☐	PREDICTED: probable G-protein coupled receptor 116 [Loxodonta	48.6	48.6	100%	3e-05	94%	gi|731454283|XP_010587260.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X4	48.1	48.1	100%	4e-05	88%	gi|675652897|XP_008992789.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2	48.1	48.1	100%	4e-05	88%	gi|403261451|XP_003923134.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X3	48.1	48.1	100%	4e-05	88%	gi|675652895|XP_008992788.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X2	48.1	48.1	100%	4e-05	88%	gi|675652893|XP_008992787.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1	48.1	48.1	100%	4e-05	88%	gi|675652889|XP_008992785.1
☐	PREDICTED: probable G-protein coupled receptor 116 isoform X1	48.1	48.1	100%	4e-05	88%	gi|725556657|XP_010332277.1
☐	probable G-protein coupled receptor 116 precursor [Mus musculus]	47.7	47.7	100%	6e-05	81%	gi|124487171|NP_001074647.1

⊟ Alignments

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hypothetical protein [Homo sapiens]

Sequence ID: gi|4886491|emb|CAB43394.1| **Length:** 618 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 246 to 261 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.4 bits(123)	2e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    KANEQVVQSLNQTYKM  16
            KANEQVVQSLNQTYKM
Sbjct  246  KANEQVVQSLNQTYKM  261
```

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hypothetical protein [synthetic construct]

Sequence ID: gi|117645848|emb|CAL38391.1| **Length:** 1204 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 246 to 261 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.4 bits(123)	2e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    KANEQVVQSLNQTYKM  16
```

```
                KANEQVVQSLNQTYKM
Sbjct  246   KANEQVVQSLNQTYKM  261
```

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PREDICTED: probable G-protein coupled receptor 116 isoform X3 [Pongo abelii]

Sequence ID: gi|686722337|ref|XP_009240213.1| **Length:** 1289 **Number of Matches:** 1

Range 1: 246 to 261 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.4 bits(123)	2e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1     KANEQVVQSLNQTYKM  16
             KANEQVVQSLNQTYKM
Sbjct  246   KANEQVVQSLNQTYKM  261
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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G-protein coupled receptor GPR116 [Homo sapiens]

Sequence ID: gi|24286029|gb|AAN46672.1| **Length:** 1300 **Number of Matches:** 1

Range 1: 246 to 261 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.4 bits(123)	2e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1     KANEQVVQSLNQTYKM  16
             KANEQVVQSLNQTYKM
Sbjct  246   KANEQVVQSLNQTYKM  261
```

Related Information

Gene - associated gene details

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PREDICTED: probable G-protein coupled receptor 116 isoform X5 [Papio anubis]

Sequence ID: gi|685537071|ref|XP_009203591.1| **Length:** 1338 **Number of Matches:** 1

Range 1: 198 to 213 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.4 bits(123)	2e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1     KANEQVVQSLNQTYKM  16
             KANEQVVQSLNQTYKM
Sbjct  198   KANEQVVQSLNQTYKM  213
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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NCBI/ BLAST/ blastp suite/ Formatting Results - BE8AVDBH014

Your search parameters were adjusted to search for a short input sequence.

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THBS1_KVVNSTTGPGEHLRN_NonMod

RID	BE8AVDBH014 (Expires on 01-16 09:09 am)		
Query ID	lcl|15533	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	15		
		Program	BLASTP 2.2.30+ Citation

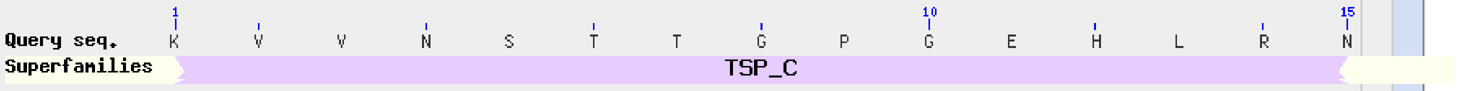
Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

New DELTA-BLAST a more sensitive protein-protein search Go

Graphic Summary

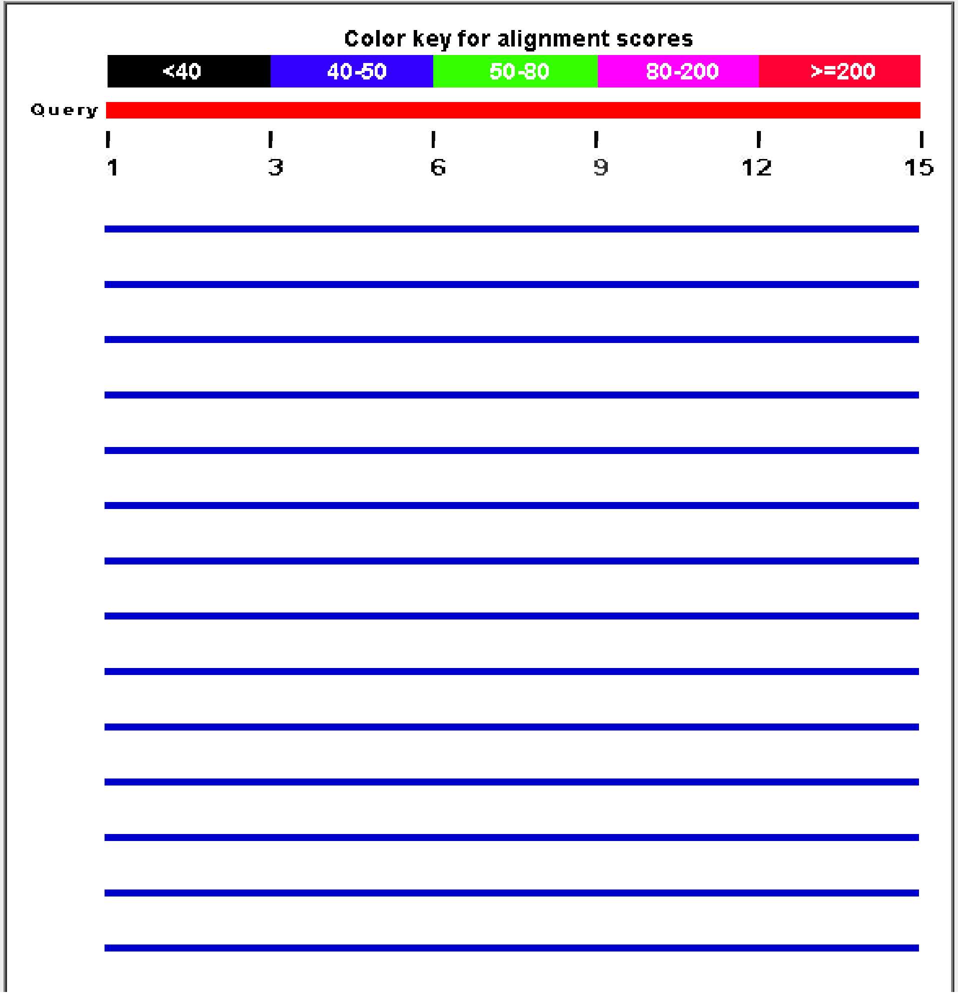
Show Conserved Domains

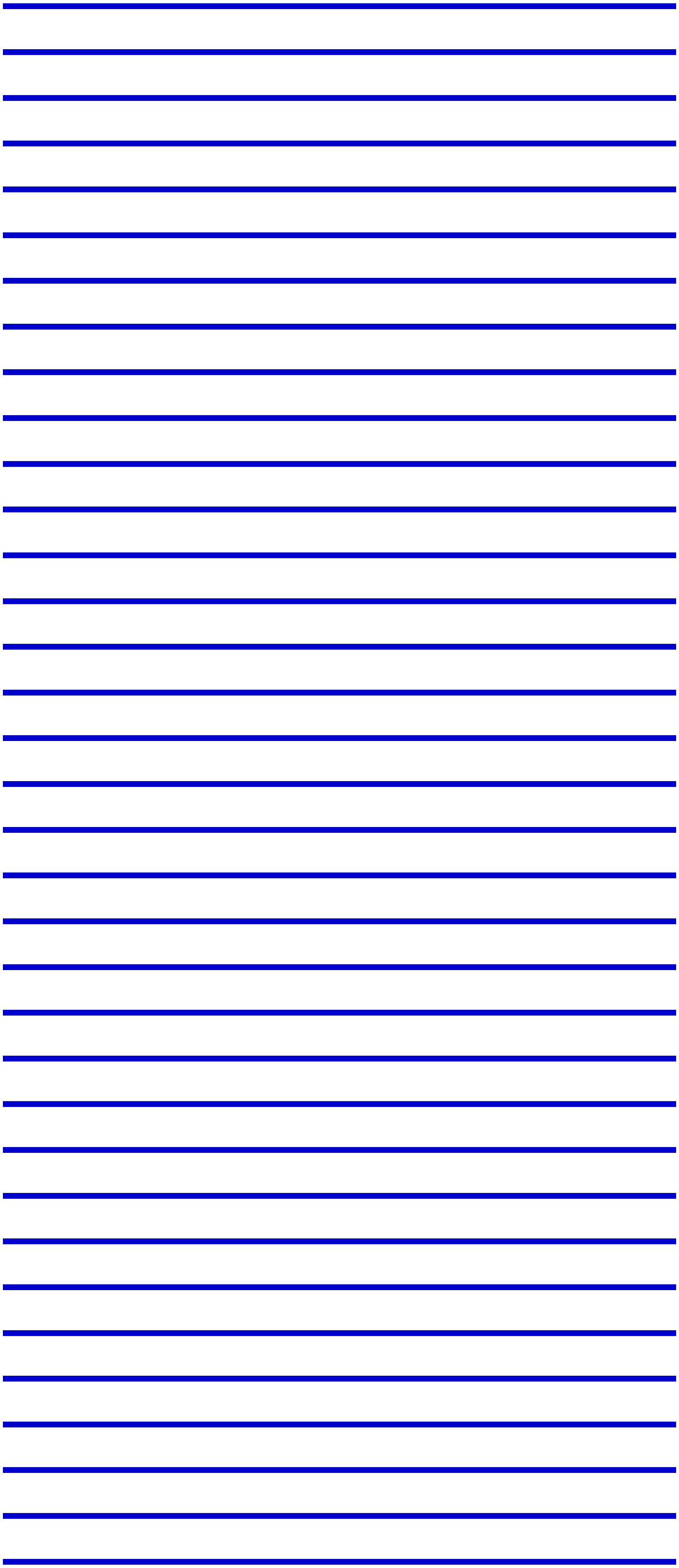
Putative conserved domains have been detected, click on the image below for detailed results.

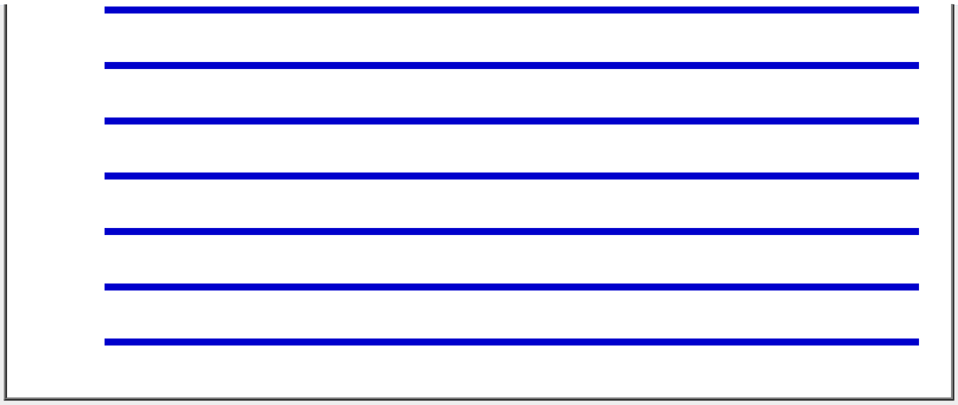


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	thrombospondin [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|339669|AAB59366.1
☐	Thrombospondin-1 [Calypte anna]	49.4	49.4	100%	1e-05	100%	gi|676764737|KFO95071.1
☐	PREDICTED: thrombospondin-1-like [Taeniopygia guttata]	49.4	49.4	100%	1e-05	100%	gi|449511879|XP_002188235.2
☐	unnamed protein product [Mus musculus]	49.4	49.4	100%	1e-05	100%	gi|74218775|BAE37804.1
☐	unnamed protein product [Mus musculus]	49.4	49.4	100%	1e-05	100%	gi|74224666|BAE37878.1
☐	unnamed protein product [Oncorhynchus mykiss]	49.4	49.4	100%	1e-05	100%	gi|641983478|CDQ99562.1
☐	unnamed protein product [Oncorhynchus mykiss]	49.4	49.4	100%	1e-05	100%	gi|642012171|CDQ96481.1
☐	thrombospondin [Bos taurus]	49.4	49.4	100%	1e-05	100%	gi|860883|CAA60950.1
☐	Thrombospondin-1 [Cricetulus griseus]	49.4	49.4	100%	1e-05	100%	gi|344248202|EGW04306.1
☐	PREDICTED: thrombospondin-1-like [Danio rerio]	49.4	49.4	100%	2e-05	100%	gi|528505376|XP_002667003.3
☐	PREDICTED: thrombospondin-1-like [Xiphophorus maculatus]	49.4	49.4	100%	2e-05	100%	gi|551507462|XP_005805261.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Latimeria chalumnae]	49.4	49.4	100%	2e-05	100%	gi|556952909|XP_005988415.1
☐	PREDICTED: thrombospondin-1-like [Poecilia reticulata]	49.4	49.4	100%	2e-05	100%	gi|658912204|XP_008396149.1
☐	PREDICTED: thrombospondin-1 [Ornithorhynchus anatinus]	49.4	49.4	100%	2e-05	100%	gi|620951278|XP_007664158.1
☐	thrombospondin 1, isoform CRA_a [Mus musculus]	49.4	49.4	100%	2e-05	100%	gi|148695954|EDL27901.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Eptesicus fuscus]	49.4	49.4	100%	2e-05	100%	gi|641704796|XP_008141208.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Orycteropus afer afer]	49.4	49.4	100%	2e-05	100%	gi|634847136|XP_007938654.1
☐	unnamed protein product [Homo sapiens]	49.4	49.4	100%	2e-05	100%	gi|194388250|BAG65509.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Leptonychotes wedde	49.4	49.4	100%	2e-05	100%	gi|585180878|XP_006742087.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Pantholops hodgsonii]	49.4	49.4	100%	2e-05	100%	gi|556766553|XP_005978527.1
☐	PREDICTED: thrombospondin-1 isoform 2 [Ovis aries]	49.4	49.4	100%	2e-05	100%	gi|426232960|XP_004010485.1
☐	PREDICTED: thrombospondin-1 [Macaca mulatta]	49.4	49.4	100%	2e-05	100%	gi|297296130|XP_001093770.2
☐	PREDICTED: thrombospondin-1-like [Alligator mississippiensis]	49.4	49.4	100%	2e-05	100%	gi|564252372|XP_006265214.1
☐	Thrombospondin-1 [Corvus brachyrhynchos]	49.4	49.4	100%	2e-05	100%	gi|676421514|KFO63667.1
☐	Thrombospondin-1 [Buceros rhinoceros silvestris]	49.4	49.4	100%	2e-05	100%	gi|676717688|KFO88878.1
☐	Thrombospondin-1 [Calypte anna]	49.4	49.4	100%	2e-05	100%	gi|676766381|KFO96190.1
☐	Thrombospondin-1 [Nestor notabilis]	49.4	49.4	100%	2e-05	100%	gi|677450281|KFQ42080.1
☐	Thrombospondin-1 [Apaloderma vittatum]	49.4	49.4	100%	2e-05	100%	gi|677298994|KFP81422.1

☐	Thrombospondin-1 [Charadrius vociferus]	49.4	49.4	100%	2e-05	100%	gi|697454601|KGL92027.1
☐	Thrombospondin-1 [Manacus vitellinus]	49.4	49.4	100%	2e-05	100%	gi|679183398|KFW75047.1
☐	Thrombospondin-1 [Fulmarus glacialis]	49.4	49.4	100%	2e-05	100%	gi|678980495|KFV92396.1
☐	Thrombospondin-1 [Acanthisitta chloris]	49.4	49.4	100%	2e-05	100%	gi|677304493|KFP86921.1
☐	Thrombospondin-1 [Podiceps cristatus]	49.4	49.4	100%	2e-05	100%	gi|683474149|KFZ68358.1
☐	Thrombospondin-1 [Phalacrocorax carbo]	49.4	49.4	100%	2e-05	100%	gi|679241896|KFW95848.1
☐	Thrombospondin-1 [Pygoscelis adeliae]	49.4	49.4	100%	2e-05	100%	gi|679135448|KFW65009.1
☐	Thrombospondin-1 [Eurypyga helias]	49.4	49.4	100%	2e-05	100%	gi|679001503|KFW04094.1
☐	Thrombospondin-1 [Struthio camelus australis]	49.4	49.4	100%	2e-05	100%	gi|678211234|KFV78213.1
☐	Thrombospondin-1 [Gavia stellata]	49.4	49.4	100%	2e-05	100%	gi|678187521|KFV55243.1
☐	Thrombospondin-1 [Tyto alba]	49.4	49.4	100%	2e-05	100%	gi|678174761|KFV42717.1
☐	Thrombospondin-1 [Tauraco erythrolophus]	49.4	49.4	100%	2e-05	100%	gi|678130136|KFU99322.1
☐	Thrombospondin-1 [Pterocles gutturalis]	49.4	49.4	100%	2e-05	100%	gi|678127604|KFU96792.1
☐	Thrombospondin-1 [Chaetura pelagica]	49.4	49.4	100%	2e-05	100%	gi|678107932|KFU85223.1
☐	Thrombospondin-1 [Nipponia nippon]	49.4	49.4	100%	2e-05	100%	gi|677546093|KFR07154.1
☐	Thrombospondin-1 [Opisthocomus hoazin]	49.4	49.4	100%	2e-05	100%	gi|677545920|KFR07008.1
☐	Thrombospondin-1 [Pelecanus crispus]	49.4	49.4	100%	2e-05	100%	gi|677471751|KFQ61165.1
☐	Thrombospondin-1 [Merops nubicus]	49.4	49.4	100%	2e-05	100%	gi|677408397|KFQ17938.1
☐	Thrombospondin-1 [Leptosomus discolor]	49.4	49.4	100%	2e-05	100%	gi|677395134|KFQ12753.1
☐	Thrombospondin-1 [Haliaeetus albicilla]	49.4	49.4	100%	2e-05	100%	gi|677384050|KFQ05795.1
☐	Thrombospondin-1 [Cariama cristata]	49.4	49.4	100%	2e-05	100%	gi|677248464|KFP58732.1
☐	Thrombospondin-1 [Cathartes aura]	49.4	49.4	100%	2e-05	100%	gi|677245954|KFP57718.1
☐	Thrombospondin-1 [Colius striatus]	49.4	49.4	100%	2e-05	100%	gi|677085189|KFP29490.1
☐	Thrombospondin-1 [Egretta garzetta]	49.4	49.4	100%	2e-05	100%	gi|676816388|KFP12089.1
☐	Thrombospondin-1 [Balearica pavonina gibbericeps]	49.4	49.4	100%	2e-05	100%	gi|676248881|KFO12753.1
☐	Thrombospondin-1 [Tinamus guttatus]	49.4	49.4	100%	2e-05	100%	gi|697424097|KGL85097.1
☐	Thrombospondin-1 [Bos mutus]	49.4	49.4	100%	2e-05	100%	gi|440911658|ELR61299.1
☐	thrombospondin 1, isoform CRA_b [Mus musculus]	49.4	49.4	100%	2e-05	100%	gi|148695955|EDL27902.1
☐	Thrombospondin-1 [Macaca fascicularis]	49.4	49.4	100%	2e-05	100%	gi|355777934|EHH62970.1
☐	thrombospondin-1a precursor [Oreochromis niloticus]	49.4	49.4	100%	2e-05	100%	gi|525344264|NP_001266664.1
☐	PREDICTED: thrombospondin-1-like [Takifugu rubripes]	49.4	49.4	100%	2e-05	100%	gi|410916673|XP_003971811.1
☐	PREDICTED: thrombospondin-1 [Gorilla gorilla gorilla]	49.4	49.4	100%	2e-05	100%	gi|426378604|XP_004056005.1
☐	PREDICTED: thrombospondin-1 isoform 1 [Ovis aries]	49.4	49.4	100%	2e-05	100%	gi|426232958|XP_004010484.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Mus musculus]	49.4	49.4	100%	2e-05	100%	gi|568916267|XP_006499215.1
☐	RecName: Full=Thrombospondin-1; Flags: Precursor [Mus musculu	49.4	49.4	100%	2e-05	100%	gi|549134|P35441.1
☐	precursor polypeptide (AA -31 to 1139) [Homo sapiens]	49.4	49.4	100%	2e-05	100%	gi|37465|CAA32889.1
☐	thrombospondin-1 precursor [Bos taurus]	49.4	49.4	100%	2e-05	100%	gi|41386685|NP_776621.1
☐	PREDICTED: thrombospondin-1 [Felis catus]	49.4	49.4	100%	2e-05	100%	gi|410961529|XP_003987333.1
☐	PREDICTED: thrombospondin-1 [Saimiri boliviensis boliviensis]	49.4	49.4	100%	2e-05	100%	gi|403289260|XP_003935780.1
☐	PREDICTED: thrombospondin-1 [Papio anubis]	49.4	49.4	100%	2e-05	100%	gi|402873929|XP_003900802.1
☐	PREDICTED: thrombospondin-1 [Pan paniscus]	49.4	49.4	100%	2e-05	100%	gi|397512548|XP_003826603.1
☐	PREDICTED: thrombospondin-1 [Otolemur garnettii]	49.4	49.4	100%	2e-05	100%	gi|395837664|XP_003791750.1
☐	PREDICTED: thrombospondin-1 [Canis lupus familiaris]	49.4	49.4	100%	2e-05	100%	gi|345794639|XP_544610.3
☐	PREDICTED: thrombospondin-1 [Pan troglodytes]	49.4	49.4	100%	2e-05	100%	gi|332843483|XP_510294.3
☐	PREDICTED: thrombospondin-1 isoform 1 [Nomascus leucogenys]	49.4	49.4	100%	2e-05	100%	gi|332235127|XP_003266759.1
☐	PREDICTED: thrombospondin-1-like [Ailuropoda melanoleuca]	49.4	49.4	100%	2e-05	100%	gi|301754930|XP_002913278.1

☐	PREDICTED: thrombospondin-1 [Pongo abelii]	49.4	49.4	100%	2e-05	100%	gi|297696281|XP_002825327.1
☐	TPA: thrombospondin 1 precursor [Bos taurus]	49.4	49.4	100%	2e-05	100%	gi|296483305|DAA25420.1
☐	thrombospondin-1 precursor [synthetic construct]	49.4	49.4	100%	2e-05	100%	gi|168278042|BAG10999.1
☐	unnamed protein product [Homo sapiens]	49.4	49.4	100%	2e-05	100%	gi|158256710|BAF84328.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Danio rerio]	49.4	49.4	100%	2e-05	100%	gi|292624775|XP_690395.4
☐	PREDICTED: thrombospondin-1 [Equus caballus]	49.4	49.4	100%	2e-05	100%	gi|149692076|XP_001503649.1
☐	thrombospondin-1 precursor [Homo sapiens]	49.4	49.4	100%	2e-05	100%	gi|40317626|NP_003237.2
☐	thrombospondin-1 precursor [Rattus norvegicus]	49.4	49.4	100%	2e-05	100%	gi|61556835|NP_001013080.1
☐	unnamed protein product [Tetraodon nigroviridis]	49.4	49.4	100%	2e-05	100%	gi|47230253|CAG10667.1
☐	Thrombospondin 1 [Mus musculus]	49.4	49.4	100%	2e-05	100%	gi|27502731|AAH42422.1
☐	PREDICTED: thrombospondin-1-like [Takifugu rubripes]	49.4	49.4	100%	2e-05	100%	gi|410898329|XP_003962650.1
☐	thrombospondin-1b precursor [Oreochromis niloticus]	49.4	49.4	100%	2e-05	100%	gi|525344287|NP_001266666.1
☐	PREDICTED: thrombospondin-1 [Monodelphis domestica]	49.4	49.4	100%	2e-05	100%	gi|126278346|XP_001380945.1
☐	thrombospondin-1 precursor [Gallus gallus]	49.4	49.4	100%	2e-05	100%	gi|313661364|NP_001186382.1
☐	thrombospondin-1 [Ambystoma mexicanum]	49.4	49.4	100%	2e-05	100%	gi|323301354|ADX36088.1
☐	PREDICTED: thrombospondin-1 [Meleagris gallopavo]	49.4	49.4	100%	2e-05	100%	gi|733889736|XP_010709922.1
☐	Thrombospondin-1 [Tupaia chinensis]	49.4	49.4	100%	2e-05	100%	gi|444706864|ELW48182.1
☐	thrombospondin-1a precursor [Oryzias latipes]	49.4	49.4	100%	2e-05	100%	gi|253314439|NP_001156590.1
☐	unnamed protein product [Tetraodon nigroviridis]	49.4	49.4	100%	2e-05	100%	gi|47224540|CAG03524.1
☐	Thrombospondin-1 [Pteropus alecto]	49.4	49.4	100%	2e-05	100%	gi|431896138|ELK05556.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Cavia	49.4	49.4	100%	2e-05	100%	gi|348579399|XP_003475467.1
☐	thrombospondin-1b precursor [Oryzias latipes]	49.4	49.4	100%	2e-05	100%	gi|253314468|NP_001156600.1
☐	thrombospondin 1 precursor variant [Homo sapiens]	49.4	49.4	100%	2e-05	100%	gi|62089410|BAD93149.1
☐	Thrombospondin-1 [Macaca mulatta]	49.4	49.4	100%	2e-05	100%	gi|355692594|EHH27197.1
☐	PREDICTED: thrombospondin-1 [Sarcophilus harrisii]	49.4	49.4	100%	2e-05	100%	gi|395503381|XP_003756045.1
☐	Thrombospondin-1 [Heterocephalus glaber]	49.4	49.4	100%	2e-05	100%	gi|351707373|EHB10292.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

thrombospondin, partial [Homo sapiens]

Sequence ID: gi|339669|gb|AAB59366.1| **Length:** 143 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 37 to 51 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1   KVVNSTTGPGEHLRN  15
           KVVNSTTGPGEHLRN
Sbjct  37  KVVNSTTGPGEHLRN  51
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Thrombospondin-1, partial [Calypte anna]

Sequence ID: gi|676764737|gb|KFO95071.1| **Length:** 172 **Number of Matches:** 1

Related Information

Range 1: 66 to 80 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1   KVVNSTTGPGEHLRN  15
           KVVNSTTGPGEHLRN
Sbjct  66  KVVNSTTGPGEHLRN  80
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: thrombospondin-1-like, partial [Taeniopygia guttata]

Sequence ID: gi|449511879|ref|XP_002188235.2| **Length:** 245 **Number of Matches:** 1

Range 1: 141 to 155 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KVVNSTTGPGEHLRN  15
            KVVNSTTGPGEHLRN
Sbjct  141  KVVNSTTGPGEHLRN  155
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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unnamed protein product [Mus musculus]

Sequence ID: gi|74218775|dbj|BAE37804.1| **Length:** 259 **Number of Matches:** 1

Range 1: 153 to 167 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KVVNSTTGPGEHLRN  15
            KVVNSTTGPGEHLRN
Sbjct  153  KVVNSTTGPGEHLRN  167
```

Related Information

Gene - associated gene details

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unnamed protein product [Mus musculus]

Sequence ID: gi|74224666|dbj|BAE37878.1| **Length:** 262 **Number of Matches:** 1

Range 1: 156 to 170 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KVVNSTTGPGEHLRN  15
            KVVNSTTGPGEHLRN
Sbjct  156  KVVNSTTGPGEHLRN  170
```

Related Information

Gene - associated gene details

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BVE9KCHS01R**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

HEG1_KSHAASDAPEDLTLLAETADARG_Mod

RID BVE9KCHS01R (Expires on 01-21 09:10 am)

Query ID lcl|83063
Description None
Molecule type amino acid
Query Length 23

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

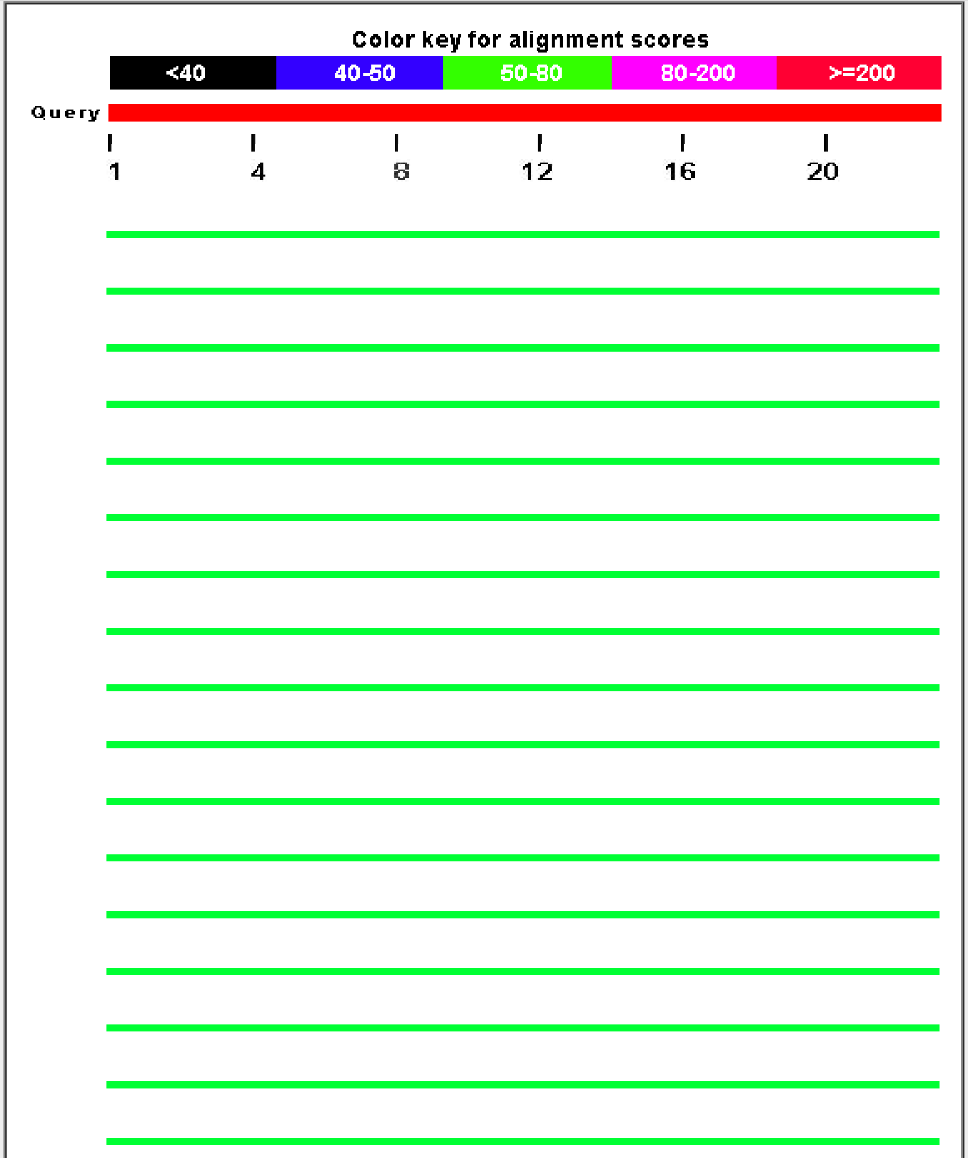
Graphic Summary

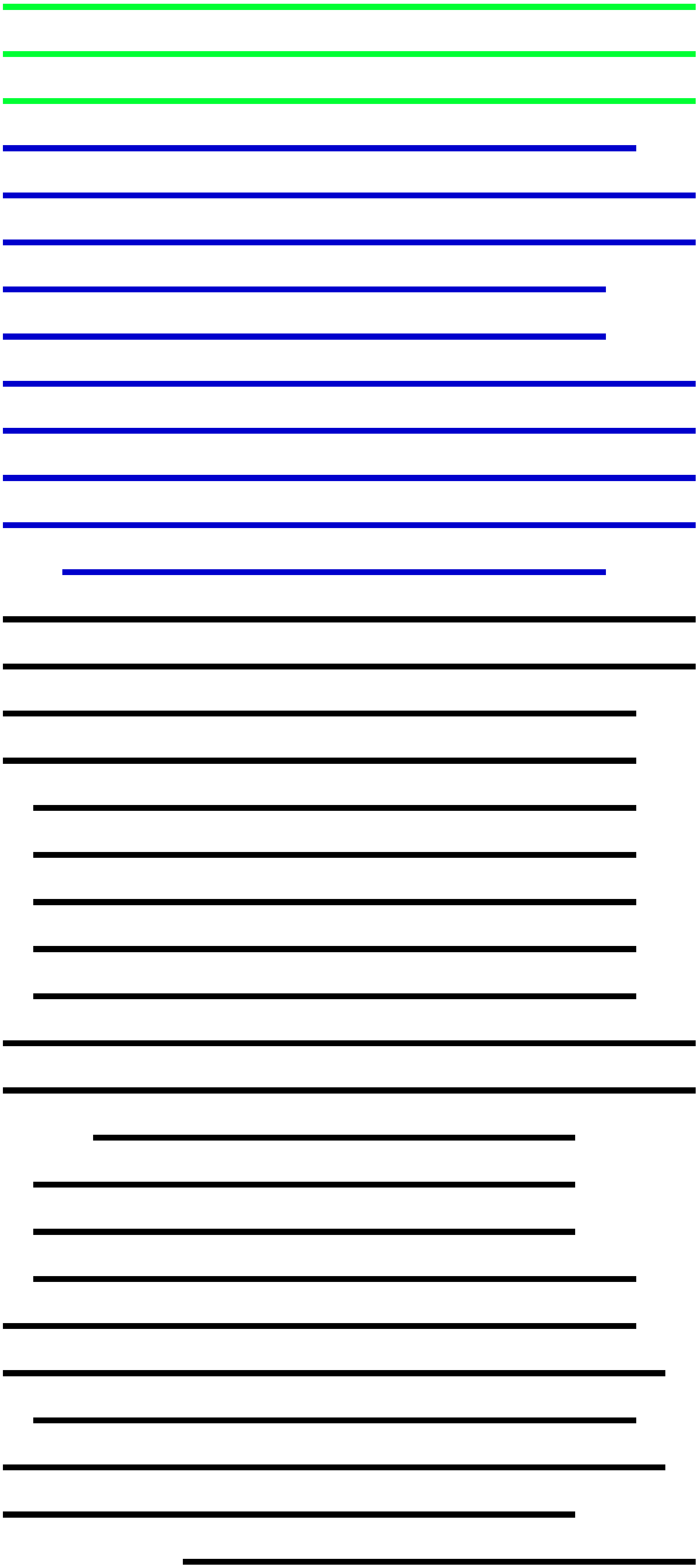
Show Conserved Domains

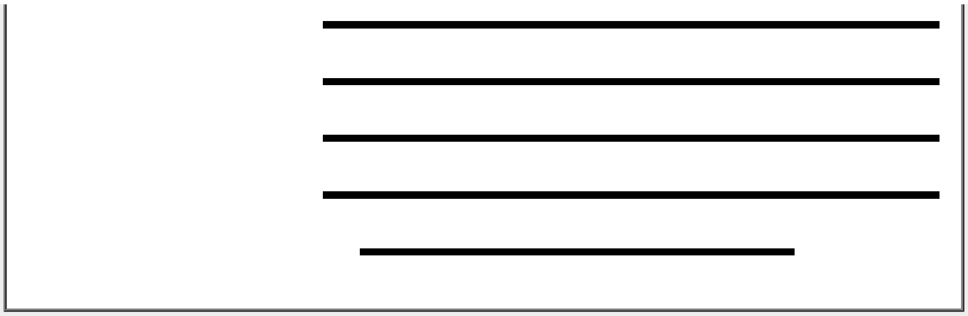
No putative conserved domains have been detected

Distribution of 104 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: protein HEG homolog 1 [Nomascus	68.9	68.9	100%	1e-11	96%	XP_003275622.1
☐	KIAA1237 protein [Homo sapiens]	68.9	68.9	100%	1e-11	96%	BAA86551.2
☐	PREDICTED: protein HEG homolog 1 [Pan paniscus]	68.9	68.9	100%	1e-11	96%	XP_008948773.1
☐	protein HEG homolog 1 precursor [Homo sapiens]	68.9	68.9	100%	1e-11	96%	NP_065784.1
☐	PREDICTED: protein HEG homolog 1 isoform X2 [Pan troglodytes]	68.9	68.9	100%	1e-11	96%	XP_516708.4
☐	PREDICTED: protein HEG homolog 1 [Gorilla gorilla gorilla]	68.9	68.9	100%	1e-11	96%	XP_004036264.1
☐	PREDICTED: protein HEG homolog 1 isoform X1 [Homo sapiens]	68.9	68.9	100%	1e-11	96%	XP_005247723.1
☐	HEG homolog 1 [synthetic construct]	68.9	68.9	100%	1e-11	96%	BAG10442.1
☐	PREDICTED: protein HEG homolog 1 isoform X1 [Pan troglodytes]	68.9	68.9	100%	1e-11	96%	XP_009444603.1
☐	PREDICTED: protein HEG homolog 1 isoform X1 [Rhinopithecus roxellana]	63.8	63.8	100%	6e-10	91%	XP_010353116.1
☐	PREDICTED: protein HEG homolog 1 isoform X5 [Chlorocebus sabaeus]	61.3	61.3	100%	4e-09	87%	XP_007983733.1
☐	PREDICTED: protein HEG homolog 1 isoform X1 [Chlorocebus sabaeus]	61.3	61.3	100%	4e-09	87%	XP_007983729.1
☐	PREDICTED: protein HEG homolog 1 isoform X7 [Chlorocebus sabaeus]	61.3	61.3	100%	4e-09	87%	XP_007983735.1
☐	PREDICTED: protein HEG homolog 1 [Papio anubis]	61.3	61.3	100%	4e-09	87%	XP_009198408.1
☐	PREDICTED: protein HEG homolog 1-like [Saimiri boliviensis boliviensis]	59.2	59.2	100%	2e-08	87%	XP_010350754.1
☐	PREDICTED: protein HEG homolog 1 isoform X3 [Callithrix jacchus]	58.7	58.7	100%	3e-08	83%	XP_008980554.1
☐	PREDICTED: protein HEG homolog 1 isoform X2 [Callithrix jacchus]	58.7	117	100%	3e-08	83%	XP_008980553.1
☐	PREDICTED: protein HEG homolog 1 isoform X1 [Callithrix jacchus]	58.7	117	100%	3e-08	83%	XP_008980552.1
☐	PREDICTED: protein HEG homolog 1 [Macaca fascicularis]	55.4	55.4	100%	4e-07	83%	XP_005547989.1
☐	PREDICTED: protein HEG homolog 1-like [Macaca mulatta]	55.4	55.4	100%	4e-07	83%	XP_002802724.1
☐	PREDICTED: protein HEG homolog 1 [Tarsius syrichta]	45.6	45.6	91%	6e-04	76%	XP_008071068.1
☐	PREDICTED: protein HEG homolog 1 [Canis lupus familiaris]	43.5	43.5	100%	0.003	65%	XP_005639641.1
☐	PREDICTED: protein HEG homolog 1 isoform X1 [Mustela putorius furo]	43.5	43.5	100%	0.003	65%	XP_004745464.1
☐	PREDICTED: protein HEG homolog 1 [Loxodonta africana]	42.6	42.6	86%	0.006	70%	XP_010591299.1
☐	PREDICTED: protein HEG homolog 1 [Trichechus manatus latirostris]	42.2	42.2	86%	0.008	70%	XP_004373773.1
☐	PREDICTED: protein HEG homolog 1 [Capra hircus]	40.9	40.9	100%	0.020	65%	XP_005675295.1
☐	PREDICTED: LOW QUALITY PROTEIN: protein HEG homolog 1 [Ovis aries]	40.9	40.9	100%	0.020	65%	XP_004003855.1
☐	PREDICTED: protein HEG homolog 1 [Pantholops hodgsonii]	40.9	40.9	100%	0.020	65%	XP_005982396.1
☐	PREDICTED: protein HEG homolog 1 [Bubalus bubalis]	40.9	40.9	100%	0.020	65%	XP_006078628.1

☐	PREDICTED: protein HEG homolog 1 [Galeopterus variegatus]	40.1	40.1	78%	0.037	72%	XP_008575868.1
☐	PREDICTED: protein HEG homolog 1 [Vicugna pacos]	39.7	39.7	100%	0.050	65%	XP_006201131.1
☐	PREDICTED: protein HEG homolog 1 [Camelus ferus]	39.7	39.7	100%	0.050	65%	XP_006195026.1
☐	PREDICTED: protein HEG homolog 1 [Chrysochloris asiatica]	39.2	39.2	91%	0.068	73%	XP_006869492.1
☐	PREDICTED: protein HEG homolog 1 [Oryctolagus cuniculus]	39.2	39.2	91%	0.068	73%	XP_008264981.1
☐	PREDICTED: protein HEG homolog 1 [Myotis davidii]	39.2	39.2	86%	0.068	70%	XP_006775087.1
☐	PREDICTED: protein HEG homolog 1 [Myotis lucifugus]	38.8	38.8	86%	0.092	70%	XP_006092920.1
☐	PREDICTED: protein HEG homolog 1 [Heterocephalus glaber]	38.0	38.0	86%	0.17	65%	XP_004878675.1
☐	PREDICTED: protein HEG homolog 1 [Heterocephalus glaber]	38.0	38.0	86%	0.17	65%	XP_004835845.1
☐	HEG-like protein 1 [Heterocephalus glaber]	38.0	38.0	86%	0.17	65%	EHA99185.1
☐	PREDICTED: protein HEG homolog 1 [Felis catus]	38.0	38.0	100%	0.17	61%	XP_006936214.1
☐	PREDICTED: protein HEG homolog 1 [Panthera tigris altaica]	38.0	38.0	100%	0.17	61%	XP_007098431.1
☐	PREDICTED: protein HEG homolog 1 [Otolemur garnettii]	37.5	37.5	69%	0.23	75%	XP_003795152.1
☐	PREDICTED: protein HEG homolog 1 [Fukomys damarensis]	37.1	37.1	78%	0.32	67%	XP_010616571.1
☐	Integrin beta-5 [Fukomys damarensis]	37.1	57.3	78%	0.32	67%	KFO38306.1
☐	PREDICTED: protein HEG homolog 1 [Cavia porcellus]	36.7	36.7	86%	0.43	65%	XP_003464197.2
☐	PREDICTED: protein HEG homolog 1 [Ceratotherium simum simum]	36.3	36.3	91%	0.59	67%	XP_004424850.1
☐	hypothetical protein PANDA_004926 [Ailuropoda melanoleuca]	36.3	36.3	95%	0.59	59%	EFB14274.1
☐	PREDICTED: protein HEG homolog 1 [Eptesicus fuscus]	36.3	36.3	86%	0.59	70%	XP_008153759.1
☐	PREDICTED: protein HEG homolog 1-like [Ailuropoda melanoleuca]	36.3	36.3	95%	0.59	59%	XP_002916796.1
☐	PREDICTED: protein HEG homolog 1 [Balaenoptera acutorostrata scammoni	36.3	36.3	82%	0.59	68%	XP_007182838.1
☐	Protein HEG-like protein 1 [Bos mutus]	35.8	35.8	73%	0.80	71%	ELR45395.1
☐	TPA: neurogenic locus notch homolog protein 2-like [Bos taurus]	35.8	35.8	73%	0.80	71%	DAA33474.1
☐	PREDICTED: protein HEG homolog 1 [Bos mutus]	35.8	35.8	73%	0.80	71%	XP_005910670.1
☐	PREDICTED: protein HEG homolog 1 [Bison bison bison]	35.8	35.8	73%	0.80	71%	XP_010832714.1
☐	PREDICTED: protein HEG homolog 1 [Bos taurus]	35.8	35.8	73%	0.80	71%	XP_005196144.1
☐	fumarate hydratase [Propionibacteriaceae bacterium P6A17]	34.6	34.6	52%	2.0	92%	WP_028705241.1
☐	PREDICTED: protein HEG homolog 1 [Octodon degus]	34.6	34.6	60%	2.0	71%	XP_004642279.1
☐	hypothetical protein THAOC_18311 [Thalassiosira oceanica]	34.1	34.1	73%	2.6	71%	EJK61241.1
☐	hypothetical protein COCSUDRAFT_42503 [Coccomyxa subellipsoidea C-16	33.7	33.7	82%	3.7	60%	XP_005646654.1
☐	siroheme synthase [Citromicrobium bathyomarinum]	33.3	33.3	73%	5.0	64%	WP_010238762.1
☐	beta-ketoacyl synthase [Saccharomonospora xinjiangensis]	33.3	33.3	73%	5.1	72%	WP_006236443.1
☐	aminopeptidase N [Pluralibacter gergoviae]	33.3	33.3	56%	5.2	67%	AIR02013.1
☐	PREDICTED: aminopeptidase N-like [Ceratitis capitata]	33.3	33.3	56%	5.2	67%	XP_004528055.1
☐	Protein HEG like protein 1 [Myotis brandtii]	33.3	33.3	86%	5.2	65%	EPQ11995.1
☐	PREDICTED: protein HEG homolog 1 [Myotis brandtii]	33.3	33.3	86%	5.2	65%	XP_005873280.1
☐	probable PHO8-repressible alkaline phosphatase vacuolar [Claviceps purpure	33.3	33.3	69%	5.2	76%	CCE27560.1
☐	polyketide synthase family protein [Saccharomonospora xinjiangensis]	33.3	33.3	73%	5.3	72%	WP_006236454.1
☐	2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase [Mycobacteri	32.9	32.9	82%	7.0	68%	WP_005147008.1
☐	glycosyltransferase [Rothia mucilaginosa]	32.9	32.9	65%	7.0	74%	WP_005506238.1
☐	transcriptional regulator [Streptomyces cellulosae]	32.9	32.9	65%	7.1	65%	WP_030669364.1
☐	PREDICTED: protein HEG homolog 1 [Pteropus alecto]	32.9	32.9	91%	7.2	62%	XP_006905661.1
☐	Protein HEG like protein 1 [Pteropus alecto]	32.9	32.9	91%	7.2	62%	ELK18108.1
☐	phage gp6-like head-tail connector protein [Caulobacter vibrioides]	32.5	32.5	73%	8.8	63%	WP_024265851.1
☐	hypothetical protein [Caulobacter segnis]	32.5	32.5	73%	8.8	63%	WP_013078162.1

☐	hypothetical protein PPTG_19648 [Phytophthora parasitica INRA-310]	32.5	32.5	86%	9.6	50%	XP_008916451.1
☐	lysine decarboxylase [Agrobacterium tumefaciens]	32.5	32.5	56%	9.6	73%	WP_035241982.1
☐	hypothetical protein Agau_C101591 [Agrobacterium tumefaciens F2]	32.5	32.5	56%	9.6	73%	EGP58724.1
☐	lysine decarboxylase [Rhizobium sp. PDO1-076]	32.5	32.5	60%	9.7	76%	WP_007607716.1
☐	histidine kinase [Hyphomonas jannaschiana]	32.5	32.5	60%	9.8	75%	WP_035581823.1
☐	histidine kinase [Hyphomonas adhaerens]	32.5	32.5	60%	9.8	75%	WP_035571639.1
☐	histidine kinase [Hyphomonas sp. CY54-11-8]	32.5	32.5	60%	9.8	75%	WP_034767069.1
☐	sensor histidine kinase [Hyphomonas jannaschiana VP2]	32.5	32.5	60%	9.8	75%	KCZ88660.1
☐	histidine kinase [Hyphomonas sp. CY54-11-8]	32.5	32.5	60%	9.8	75%	KCZ47047.1
☐	sensor histidine kinase [Hyphomonas adhaerens MHS-3]	32.5	32.5	60%	9.8	75%	KCZ84965.1
☐	chemotaxis protein histidine kinase-like protein [Microcoleus sp. PCC 7113]	32.5	32.5	65%	9.9	76%	WP_015182642.1
☐	PREDICTED: protein HEG homolog 1 [Nannospalax galili]	32.5	32.5	86%	9.9	60%	XP_008841199.1
☐	PREDICTED: protein HEG homolog 1 [Erinaceus europaeus]	32.5	32.5	91%	10.0	57%	XP_007536091.1
☐	PREDICTED: protein HEG homolog 1 [Rattus norvegicus]	32.5	32.5	73%	10.0	59%	XP_006221221.1
☐	DNA-binding protein [Isosphaera pallida]	32.0	32.0	56%	13	77%	WP_013565862.1
☐	hypothetical protein [Nocardiopsis chromatogenes]	32.0	32.0	52%	13	92%	WP_017626765.1
☐	hypothetical protein [Leifsonia aquatica]	32.0	32.0	56%	13	85%	WP_025157970.1
☐	hypothetical protein [Streptomyces xanthophaeus]	32.0	32.0	56%	13	85%	WP_031151916.1
☐	hypothetical protein [Streptomyces xanthophaeus]	32.0	32.0	56%	13	85%	WP_031138202.1
☐	hypothetical protein [Pseudomonas nitroreducens]	32.0	53.4	60%	13	82%	WP_017518469.1
☐	beta-glucosidase [Deinococcus misasensis]	32.0	32.0	91%	14	57%	WP_034342803.1
☐	hypothetical protein [Paracoccus pantotrophus]	32.0	32.0	69%	14	65%	WP_028710187.1
☐	unnamed protein product [Blastocystis hominis]	32.0	32.0	47%	14	91%	CBK25175.2
☐	thiamine pyrophosphate domain-containing TPP-binding protein [Natrialba cha	32.0	32.0	73%	14	71%	WP_006169172.1
☐	fumarate hydratase [Mobiluncus curtisii]	32.0	32.0	52%	14	83%	WP_004010370.1
☐	fumarate hydratase [Mobiluncus curtisii]	32.0	32.0	52%	14	83%	WP_004009960.1

Alignments

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PREDICTED: LOW QUALITY PROTEIN: protein HEG homolog 1 [Nomascus leucogenys]

Sequence ID: ref|XP_003275622.1| **Length:** 1211 **Number of Matches:** 1

Range 1: 150 to 172 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(155)	1e-11	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    KSHAASDAPEDLTLLAETADARG  23
            KSHAASDAPE+LTLLAETADARG
Sbjct  150  KSHAASDAPENLTLLAETADARG  172
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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KIAA1237 protein [Homo sapiens]

Sequence ID: dbj|BAA86551.2| **Length:** 1268 **Number of Matches:** 1

Range 1: 36 to 58 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(155)	1e-11	22/23(96%)	23/23(100%)	0/23(0%)

Related Information

Gene - associated gene details

```
Query  1   KSHAASDAPEDLTLLAETADARG  23
           KSHAASDAPE+LTLLAETADARG
Sbjct  36  KSHAASDAPENLTLLAETADARG  58
```

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PREDICTED: protein HEG homolog 1 [Pan paniscus]

Sequence ID: ref|XP_008948773.1| **Length:** 1349 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 7 to 29 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(155)	1e-11	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1   KSHAASDAPEDLTLLAETADARG  23
           KSHAASDAPE+LTLLAETADARG
Sbjct  7   KSHAASDAPENLTLLAETADARG  29
```

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protein HEG homolog 1 precursor [Homo sapiens]

Sequence ID: ref|NP_065784.1| **Length:** 1381 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 149 to 171 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(155)	1e-11	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    KSHAASDAPEDLTLLAETADARG  23
            KSHAASDAPE+LTLLAETADARG
Sbjct  149  KSHAASDAPENLTLLAETADARG  171
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: protein HEG homolog 1 isoform X2 [Pan troglodytes]

Sequence ID: ref|XP_516708.4| **Length:** 1391 **Number of Matches:** 1

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Range 1: 149 to 171 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(155)	1e-11	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    KSHAASDAPEDLTLLAETADARG  23
            KSHAASDAPE+LTLLAETADARG
Sbjct  149  KSHAASDAPENLTLLAETADARG  171
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download

How to read this page   Blast report description

HEG1_KSHAASDAPENLTLLAETADARG_NonMod

RID B9FJDRCG01R (Expires on 01-14 13:42 pm)

Query ID lcl|226166
Description None
Molecule type amino acid
Query Length 23

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

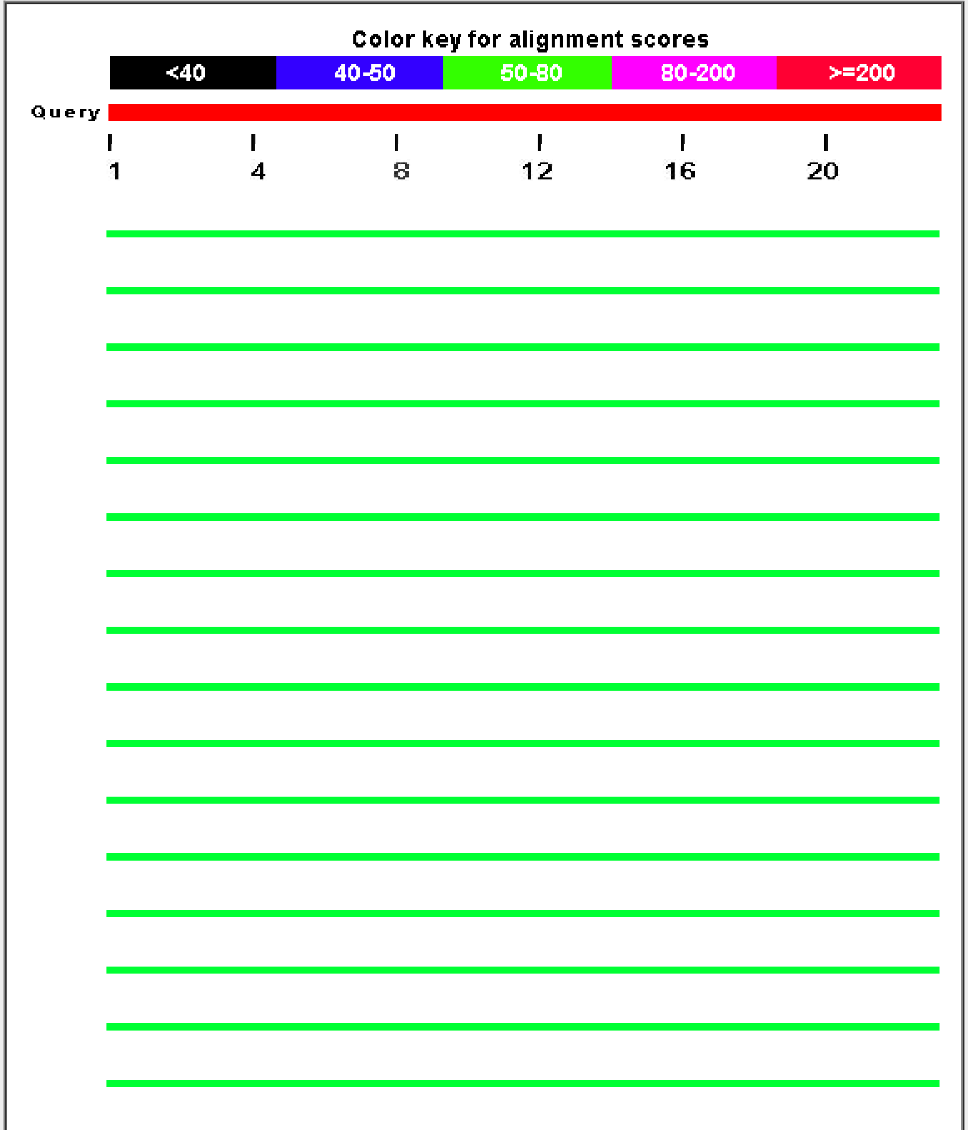
Graphic Summary

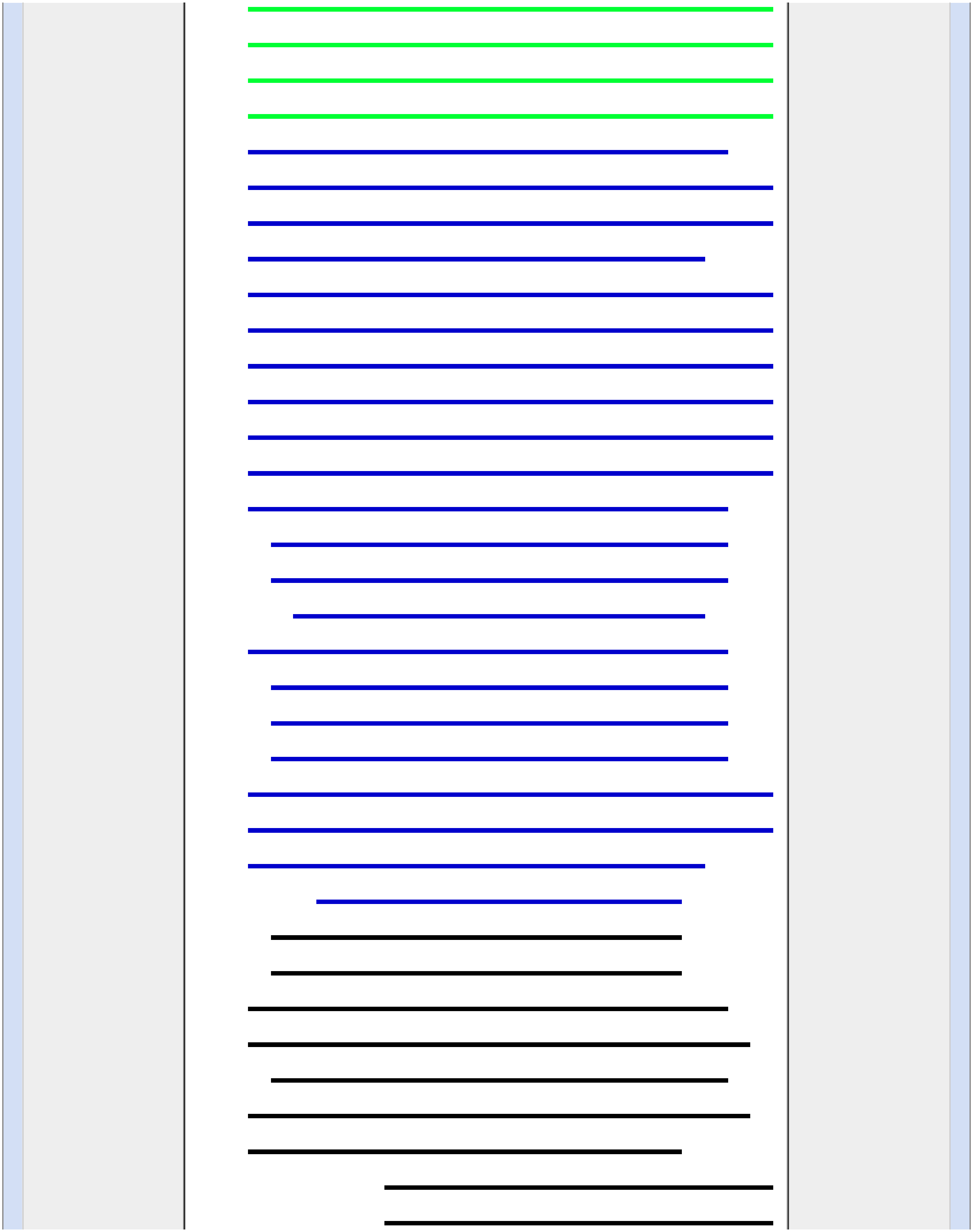
Show Conserved Domains

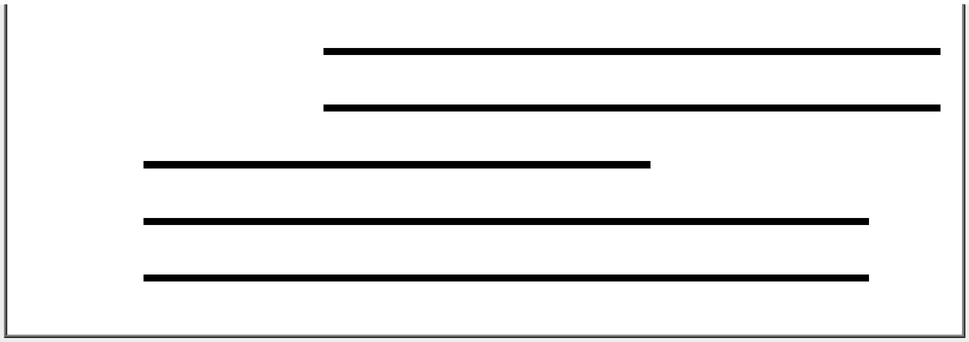
No putative conserved domains have been detected

Distribution of 102 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: protein HEG homolog 1 [N	71.5	71.5	100%	1e-12	100%	gi|332252962|XP_003275622.1
☐	KIAA1237 protein [Homo sapiens]	71.5	71.5	100%	1e-12	100%	gi|34327974|BAA86551.2
☐	PREDICTED: protein HEG homolog 1 [Pan paniscus]	71.5	71.5	100%	1e-12	100%	gi|675781584|XP_008948773.1
☐	protein HEG homolog 1 precursor [Homo sapiens]	71.5	71.5	100%	1e-12	100%	gi|153792110|NP_065784.1
☐	PREDICTED: protein HEG homolog 1 isoform X2 [Pan troglodytes]	71.5	71.5	100%	1e-12	100%	gi|410037372|XP_516708.4
☐	PREDICTED: protein HEG homolog 1 [Gorilla gorilla gorilla]	71.5	71.5	100%	1e-12	100%	gi|426341907|XP_004036264.1
☐	PREDICTED: protein HEG homolog 1 isoform X1 [Homo sapiens]	71.5	71.5	100%	1e-12	100%	gi|530375053|XP_005247723.1
☐	HEG homolog 1 [synthetic construct]	71.5	71.5	100%	1e-12	100%	gi|168273206|BAG10442.1
☐	PREDICTED: protein HEG homolog 1 isoform X1 [Pan troglodytes]	71.5	71.5	100%	1e-12	100%	gi|694903827|XP_009444603.1
☐	PREDICTED: protein HEG homolog 1 isoform X1 [Rhinopithecus ro	66.4	66.4	100%	8e-11	96%	gi|724956033|XP_010353116.1
☐	PREDICTED: protein HEG homolog 1 isoform X5 [Chlorocebus sab	63.8	63.8	100%	6e-10	91%	gi|635121296|XP_007983733.1
☐	PREDICTED: protein HEG homolog 1 isoform X1 [Chlorocebus sab	63.8	63.8	100%	6e-10	91%	gi|635121288|XP_007983729.1
☐	PREDICTED: protein HEG homolog 1 isoform X7 [Chlorocebus sab	63.8	63.8	100%	6e-10	91%	gi|635121300|XP_007983735.1
☐	PREDICTED: protein HEG homolog 1 [Papio anubis]	63.8	63.8	100%	6e-10	91%	gi|685523313|XP_009198408.1
☐	PREDICTED: protein HEG homolog 1 isoform X3 [Callithrix jacchus	61.3	61.3	100%	4e-09	87%	gi|675731167|XP_008980554.1
☐	PREDICTED: protein HEG homolog 1 isoform X2 [Callithrix jacchus	61.3	122	100%	4e-09	87%	gi|675731165|XP_008980553.1
☐	PREDICTED: protein HEG homolog 1 isoform X1 [Callithrix jacchus	61.3	122	100%	4e-09	87%	gi|675731163|XP_008980552.1
☐	PREDICTED: protein HEG homolog 1-like [Saimiri boliviensis bolivi	60.9	60.9	100%	4e-09	87%	gi|725601602|XP_010350754.1
☐	PREDICTED: protein HEG homolog 1 [Macaca fascicularis]	57.9	57.9	100%	6e-08	87%	gi|544416142|XP_005547989.1
☐	PREDICTED: protein HEG homolog 1-like [Macaca mulatta]	57.9	57.9	100%	6e-08	87%	gi|297285172|XP_002802724.1
☐	PREDICTED: protein HEG homolog 1 [Tarsius syrichta]	48.1	48.1	91%	9e-05	81%	gi|640830988|XP_008071068.1
☐	PREDICTED: protein HEG homolog 1 [Canis lupus familiaris]	46.0	46.0	100%	4e-04	70%	gi|545553118|XP_005639641.1
☐	PREDICTED: protein HEG homolog 1 isoform X1 [Mustela putorius	46.0	46.0	100%	4e-04	70%	gi|511841975|XP_004745464.1
☐	PREDICTED: protein HEG homolog 1 [Trichechus manatus latirost	44.8	44.8	86%	0.001	75%	gi|471366480|XP_004373773.1
☐	PREDICTED: protein HEG homolog 1 [Capra hircus]	43.5	43.5	100%	0.003	70%	gi|548450985|XP_005675295.1
☐	PREDICTED: LOW QUALITY PROTEIN: protein HEG homolog 1 [C	43.5	43.5	100%	0.003	70%	gi|426219281|XP_004003855.1
☐	PREDICTED: protein HEG homolog 1 [Pantholops hodgsonii]	43.5	43.5	100%	0.003	70%	gi|556774526|XP_005982396.1
☐	PREDICTED: protein HEG homolog 1 [Bubalus bubalis]	43.5	43.5	100%	0.003	70%	gi|594111623|XP_006078628.1
☐							

	PREDICTED: protein HEG homolog 1 [Vicugna pacos]	42.2	42.2	100%	0.007	70%	gi|560957313|XP_006201131.1
☐	PREDICTED: protein HEG homolog 1 [Camelus ferus]	42.2	42.2	100%	0.007	70%	gi|560938470|XP_006195026.1
☐	PREDICTED: protein HEG homolog 1 [Chrysochloris asiatica]	41.8	41.8	91%	0.010	77%	gi|586477913|XP_006869492.1
☐	PREDICTED: protein HEG homolog 1 [Myotis davidii]	41.8	41.8	86%	0.010	75%	gi|584061295|XP_006775087.1
☐	PREDICTED: protein HEG homolog 1 [Myotis lucifugus]	41.4	41.4	86%	0.014	75%	gi|558143649|XP_006092920.1
☐	PREDICTED: protein HEG homolog 1 [Galeopterus variegatus]	41.4	41.4	78%	0.014	72%	gi|667285651|XP_008575868.1
☐	PREDICTED: protein HEG homolog 1 [Oryctolagus cuniculus]	40.9	40.9	91%	0.019	73%	gi|655854339|XP_008264981.1
☐	PREDICTED: protein HEG homolog 1 [Heterocephalus glaber]	40.5	40.5	86%	0.025	70%	gi|512817826|XP_004878675.1
☐	PREDICTED: protein HEG homolog 1 [Heterocephalus glaber]	40.5	40.5	86%	0.025	70%	gi|512946721|XP_004835845.1
☐	HEG-like protein 1 [Heterocephalus glaber]	40.5	40.5	86%	0.025	70%	gi|351696267|EHA99185.1
☐	PREDICTED: protein HEG homolog 1 [Felis catus]	40.5	40.5	100%	0.025	65%	gi|586999546|XP_006936214.1
☐	PREDICTED: protein HEG homolog 1 [Panthera tigris altaica]	40.5	40.5	100%	0.025	65%	gi|591346369|XP_007098431.1
☐	PREDICTED: protein HEG homolog 1 [Loxodonta africana]	40.1	40.1	86%	0.035	65%	gi|731491397|XP_010591299.1
☐	PREDICTED: protein HEG homolog 1 [Otolemur garnettii]	40.1	40.1	69%	0.035	81%	gi|395844827|XP_003795152.1
☐	PREDICTED: protein HEG homolog 1 [Fukomys damarensis]	39.7	39.7	78%	0.047	72%	gi|731191401|XP_010616571.1
☐	Integrin beta-5 [Fukomys damarensis]	39.7	39.7	78%	0.048	72%	gi|676287424|KFO38306.1
☐	PREDICTED: protein HEG homolog 1 [Ceratotherium simum simun	38.8	38.8	91%	0.087	71%	gi|478501073|XP_004424850.1
☐	hypothetical protein PANDA_004926 [Ailuropoda melanoleuca]	38.8	38.8	95%	0.087	64%	gi|281338690|EFB14274.1
☐	PREDICTED: protein HEG homolog 1 [Eptesicus fuscus]	38.8	38.8	86%	0.087	75%	gi|641727343|XP_008153759.1
☐	PREDICTED: protein HEG homolog 1-like [Ailuropoda melanoleuca	38.8	38.8	95%	0.087	64%	gi|301762794|XP_002916796.1
☐	PREDICTED: protein HEG homolog 1 [Balaenoptera acutorostrata	38.8	38.8	82%	0.087	74%	gi|594669717|XP_007182838.1
☐	Protein HEG-like protein 1 [Bos mutus]	38.4	38.4	73%	0.12	76%	gi|440892002|ELR45395.1
☐	PREDICTED: protein HEG homolog 1 isoform X2 [Bos taurus]	38.4	38.4	73%	0.12	76%	gi|194664090|XP_589074.4
☐	PREDICTED: protein HEG homolog 1 [Bos mutus]	38.4	38.4	73%	0.12	76%	gi|555997906|XP_005910670.1
☐	PREDICTED: protein HEG homolog 1 isoform X1 [Bos taurus]	38.4	38.4	73%	0.12	76%	gi|528899646|XP_005196144.1
☐	PREDICTED: protein HEG homolog 1 [Octodon degus]	37.1	37.1	60%	0.30	79%	gi|507692540|XP_004642279.1
☐	Protein HEG like protein 1 [Myotis brandtii]	35.8	35.8	86%	0.75	70%	gi|521030208|EPQ11995.1
☐	PREDICTED: protein HEG homolog 1 [Myotis brandtii]	35.8	35.8	86%	0.75	70%	gi|554557733|XP_005873280.1
☐	PREDICTED: protein HEG homolog 1 [Pteropus alecto]	35.4	35.4	91%	1.0	67%	gi|586541026|XP_006905661.1
☐	Protein HEG like protein 1 [Pteropus alecto]	35.4	35.4	91%	1.0	67%	gi|431919751|ELK18108.1
☐	PREDICTED: protein HEG homolog 1 [Erinaceus europaeus]	35.0	35.0	91%	1.4	62%	gi|617657334|XP_007536091.1
☐	PREDICTED: protein HEG homolog 1 [Rattus norvegicus]	35.0	35.0	73%	1.4	65%	gi|564314514|XP_006221221.1
☐	hypothetical protein [Pseudomonas nitroreducens]	34.6	34.6	47%	1.9	91%	gi|516087889|WP_017518469.1
☐	PREDICTED: protein HEG homolog 1 [Condylura cristata]	34.6	34.6	91%	1.9	57%	gi|507928473|XP_004675488.1
☐	PREDICTED: protein HEG homolog 1 [Ictidomys tridecemlineatus]	34.6	34.6	86%	1.9	70%	gi|532108416|XP_005338931.1
☐	fumarate hydratase [Propionibacteriaceae bacterium P6A17]	34.1	34.1	52%	2.6	92%	gi|655296257|WP_028705241.1
☐	PREDICTED: protein HEG homolog 1 [Cavia porcellus]	34.1	34.1	86%	2.6	60%	gi|514450244|XP_003464197.2
☐	PREDICTED: protein HEG homolog 1-like [Lipotes vexillifer]	33.7	33.7	82%	3.6	68%	gi|602724388|XP_007447667.1
☐	PREDICTED: protein HEG homolog 1 [Tupaia chinensis]	33.7	33.7	91%	3.6	62%	gi|562851896|XP_006154654.1
☐	PREDICTED: protein HEG homolog 1-like [Physeter catodon]	33.7	33.7	82%	3.6	68%	gi|593768203|XP_007122570.1
☐	ATP-binding protein [Streptomyces lividans]	33.3	33.3	86%	4.9	55%	gi|490072157|WP_003974332.1
☐	ATP/GTP binding protein [Streptomyces lividans TK24]	33.3	33.3	86%	4.9	55%	gi|672370134|AIJ14016.1
☐	putative ATP/GTP binding protein [Streptomyces lividans]	33.3	33.3	86%	4.9	55%	gi|511096551|WP_016327021.1
☐	PREDICTED: protein HEG homolog 1 [Nannospalax galili]	33.3	33.3	86%	4.9	60%	gi|674068341|XP_008841199.1
☐	PREDICTED: LOW QUALITY PROTEIN: protein HEG homolog 1 [	32.9	32.9	91%	6.8	57%	gi|545865686|XP_005670209.1

☐	putative lypase [Nocardia cyriacigeorgica]	32.5	32.5	86%	8.9	67%	gi|504119683|WP_014353669.1
☐	transcriptional regulator [Streptomyces bicolor]	32.0	32.0	60%	12	71%	gi|671496762|WP_031485889.1
☐	DNA recombination protein RecO [Arthrobacter sp. H20]	32.0	32.0	86%	13	52%	gi|651491855|WP_026552230.1
☐	hypothetical protein SMCB_0775 [Comamonadaceae bacterium B1	32.0	32.0	78%	13	64%	gi|635597847|BAO83003.1
☐	rRNA methylase [Bifidobacterium callitrichos DSM 23973]	32.0	32.0	65%	13	75%	gi|672955716|KFI51333.1
☐	tetratricopeptide domain protein [Burkholderiales bacterium GJ-E10	32.0	32.0	65%	13	73%	gi|723004031|BAP89185.1
☐	unnamed protein product [Blastocystis hominis]	32.0	32.0	47%	13	91%	gi|300123904|CBK25175.2
☐	unnamed protein product [Blastocystis hominis]	32.0	32.0	47%	13	91%	gi|300123935|CBK25206.2
☐	alpha-amylase [Variovorax sp. CF313]	32.0	32.0	95%	13	52%	gi|495108088|WP_007832910.1
☐	conserved hypothetical protein [Leishmania braziliensis MHOM/BR/	32.0	32.0	52%	13	92%	gi|154341182|XP_001566544.1
☐	hypothetical protein THAOC_18311 [Thalassiosira oceanica]	31.6	31.6	73%	17	65%	gi|397611241|EJK61241.1
☐	transcriptional regulator [Streptomyces cellulosae]	31.6	31.6	65%	18	60%	gi|664132708|WP_030669364.1
☐	phosphoribosylaminoimidazolecarboxamide formyltransferase [Bifid	31.6	31.6	78%	18	68%	gi|705400339|WP_033496408.1
☐	fumarate hydratase [Mobiluncus curtisii]	31.6	31.6	52%	18	83%	gi|490109655|WP_004010370.1
☐	fumarate hydratase [Mobiluncus curtisii]	31.6	31.6	52%	18	83%	gi|490109230|WP_004009960.1
☐	fumarate hydratase [Arsenicicoccus bolidensis]	31.6	31.6	52%	18	83%	gi|656265923|WP_029211857.1
☐	GH17958 [Drosophila grimshawi]	31.6	31.6	82%	18	70%	gi|195060409|XP_001995800.1
☐	probable PHO8-repressible alkaline phosphatase vacuolar [Clavicep	31.6	31.6	69%	18	76%	gi|399171823|CCE27560.1
☐	PREDICTED: LOW QUALITY PROTEIN: laminin subunit gamma-1-	31.6	31.6	65%	18	73%	gi|584028919|XP_006808984.1
☐	PREDICTED: protein HEG homolog 1 [Chinchilla lanigera]	31.6	31.6	91%	18	57%	gi|533144146|XP_005386602.1
☐	PREDICTED: laminin subunit gamma-1-like isoform X2 [Oreochron	31.6	31.6	65%	18	73%	gi|542257771|XP_005464262.1
☐	PREDICTED: laminin subunit gamma-1-like [Pundamilia nyererei]	31.6	31.6	65%	18	73%	gi|548523070|XP_005751418.1
☐	PREDICTED: laminin subunit gamma-1-like [Haplochromis burtoni]	31.6	31.6	65%	18	73%	gi|554871791|XP_005945845.1
☐	PREDICTED: laminin subunit gamma-1-like isoform X2 [Maylandia	31.6	31.6	65%	18	73%	gi|499045975|XP_004573568.1
☐	PREDICTED: laminin subunit gamma-1-like isoform X1 [Oreochron	31.6	31.6	65%	18	73%	gi|348543037|XP_003458990.1
☐	PREDICTED: laminin subunit gamma-1-like isoform X1 [Maylandia	31.6	31.6	65%	18	73%	gi|499045973|XP_004573567.1
☐	PREDICTED: uncharacterized protein LOC103455671 [Malus dome	31.2	31.2	69%	24	75%	gi|657948135|XP_008393478.1

⊟ Alignments

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PREDICTED: LOW QUALITY PROTEIN: protein HEG homolog 1 [Nomascus leucogenys]

Sequence ID: gi|332252962|ref|XP_003275622.1| **Length:** 1211 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 150 to 172 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
71.5 bits(161)	1e-12	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    KSHAASDAPENLTLLAETADARG  23
            KSHAASDAPENLTLLAETADARG
Sbjct  150  KSHAASDAPENLTLLAETADARG  172
```

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KIAA1237 protein [Homo sapiens]

Sequence ID: gi|34327974|dbj|BAA86551.2| **Length:** 1268 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 36 to 58 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
71.5 bits(161)	1e-12	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1   KSHAASDAPENLTLLAETADARG  23
```

```
                KSHAASDAPENLTLLAETADARG
Sbjct  36   KSHAASDAPENLTLLAETADARG  58
```

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PREDICTED: protein HEG homolog 1 [Pan paniscus]

Sequence ID: gi|675781584|ref|XP_008948773.1| **Length:** 1349 **Number of Matches:** 1

Range 1: 7 to 29 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
71.5 bits(161)	1e-12	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    KSHAASDAPENLTLLAETADARG  23
            KSHAASDAPENLTLLAETADARG
Sbjct  7    KSHAASDAPENLTLLAETADARG  29
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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protein HEG homolog 1 precursor [Homo sapiens]

Sequence ID: gi|153792110|ref|NP_065784.1| **Length:** 1381 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 149 to 171 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
71.5 bits(161)	1e-12	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    KSHAASDAPENLTLLAETADARG  23
            KSHAASDAPENLTLLAETADARG
Sbjct  149  KSHAASDAPENLTLLAETADARG  171
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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PREDICTED: protein HEG homolog 1 isoform X2 [Pan troglodytes]

Sequence ID: gi|410037372|ref|XP_516708.4| **Length:** 1391 **Number of Matches:** 1

Range 1: 149 to 171 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
71.5 bits(161)	1e-12	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    KSHAASDAPENLTLLAETADARG  23
            KSHAASDAPENLTLLAETADARG
Sbjct  149  KSHAASDAPENLTLLAETADARG  171
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVGGW1N701R

Your search parameters were adjusted to search for a short input sequence.

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HGFAC_RDSVSVVLGQHFFDRT_Mod

RID BVGGW1N701R (Expires on 01-21 09:49 am)

Query ID	lcl|239321	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ ▷ Citation
Query Length	16		

Other reports: ▷ Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

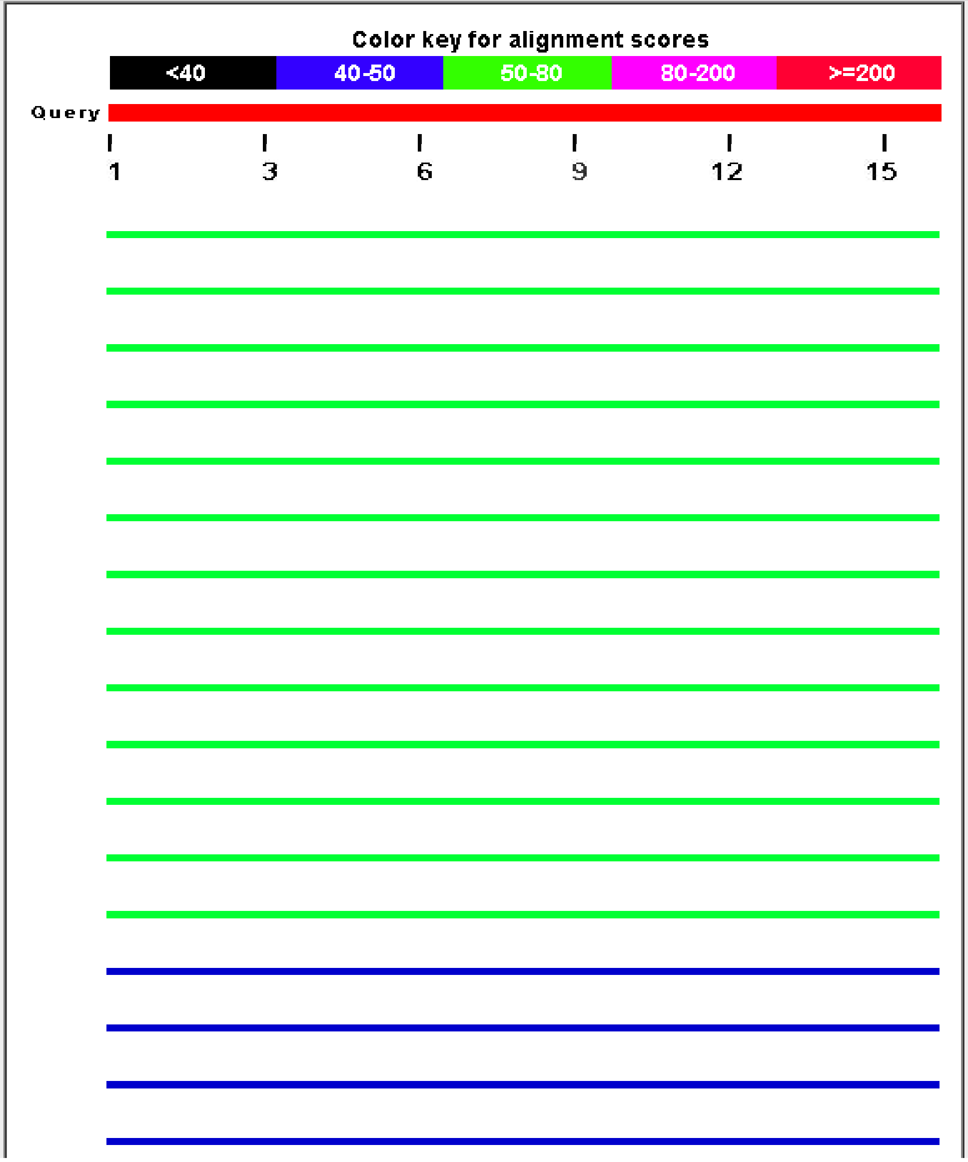
Graphic Summary

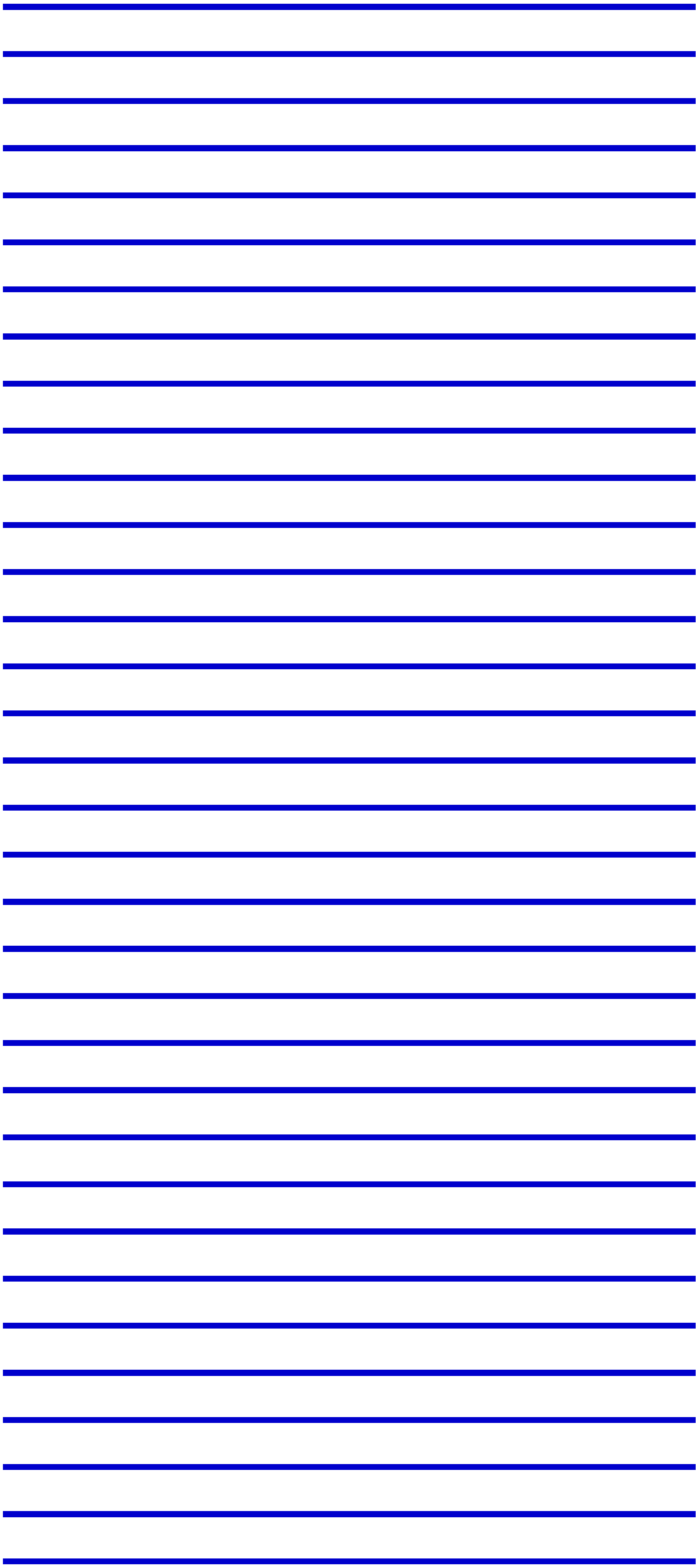
Show Conserved Domains

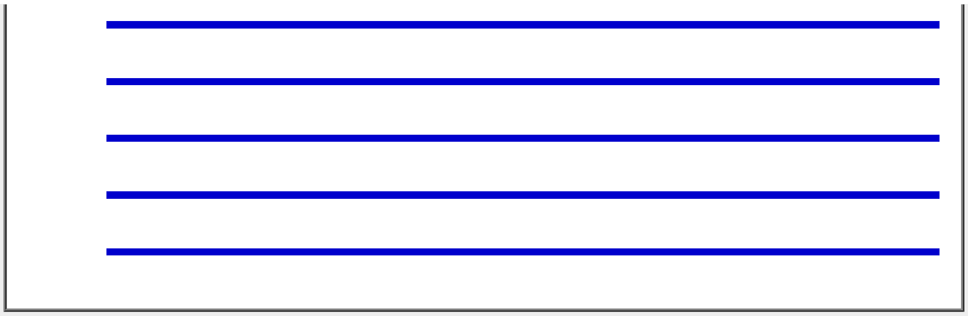
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Short Form Hgfa With Inhibitory Fab75 [Homo sapiens]	51.5	51.5	100%	3e-06	94%	2R0L_A
☐	Chain A, Crystal Structure Of Hgfa In Complex With The Allosteric Non-Inhibit	51.5	51.5	100%	3e-06	94%	2WUB_A
☐	Chain A, Protease Domain Of Hgfa With No Inhibitor [Homo sapiens]	51.5	51.5	100%	3e-06	94%	1YBW_A
☐	PREDICTED: hepatocyte growth factor activator isoform X3 [Callithrix jacchus	51.5	51.5	100%	3e-06	94%	XP_008991932.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Callithrix jacchus	51.5	51.5	100%	3e-06	94%	XP_008991931.1
☐	PREDICTED: hepatocyte growth factor activator [Ceratotherium simum simum	51.5	51.5	100%	3e-06	94%	XP_004432296.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Callithrix jacchus	51.5	51.5	100%	3e-06	94%	XP_002746077.1
☐	HGF activator, preproprotein [Homo sapiens]	51.5	51.5	100%	3e-06	94%	AAI12193.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor activator [	51.5	51.5	100%	3e-06	94%	XP_004038404.1
☐	hepatocyte growth factor activator isoform 2 preproprotein [Homo sapiens]	51.5	51.5	100%	3e-06	94%	NP_001519.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Pan paniscus]	51.5	51.5	100%	3e-06	94%	XP_003804416.1
☐	PREDICTED: hepatocyte growth factor activator [Pan troglodytes]	51.5	51.5	100%	3e-06	94%	XP_001174601.2
☐	hepatocyte growth factor activator isoform 1 preproprotein [Homo sapiens]	51.5	51.5	100%	3e-06	94%	NP_001284368.1
☐	PREDICTED: hepatocyte growth factor activator [Sorex araneus]	49.4	49.4	100%	2e-05	88%	XP_004617524.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor activator [	49.4	49.4	100%	2e-05	88%	XP_006919081.1
☐	PREDICTED: hepatocyte growth factor activator-like [Equus przewalskii]	49.0	49.0	100%	2e-05	88%	XP_008509987.1
☐	PREDICTED: hepatocyte growth factor activator [Dasypus novemcinctus]	49.0	49.0	100%	2e-05	88%	XP_004481097.1
☐	PREDICTED: hepatocyte growth factor activator [Ovis aries]	49.0	49.0	100%	2e-05	88%	XP_004010188.1
☐	PREDICTED: hepatocyte growth factor activator [Tarsius syrichta]	49.0	49.0	100%	2e-05	88%	XP_008046016.1
☐	PREDICTED: hepatocyte growth factor activator [Capra hircus]	49.0	49.0	100%	2e-05	88%	XP_005682051.1
☐	TPA: HGF activator preproprotein-like [Bos taurus]	49.0	49.0	100%	2e-05	88%	DAA28460.1
☐	PREDICTED: hepatocyte growth factor activator [Physeter catodon]	49.0	49.0	100%	2e-05	88%	XP_007109331.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Balaenoptera ac	49.0	49.0	100%	2e-05	88%	XP_007172367.1
☐	Hepatocyte growth factor activator [Macaca fascicularis]	49.0	49.0	100%	2e-05	88%	EHH49413.1
☐	PREDICTED: hepatocyte growth factor activator-like [Macaca mulatta]	49.0	49.0	100%	2e-05	88%	XP_001114822.2
☐	PREDICTED: hepatocyte growth factor activator isoform X3 [Heterocephalus	49.0	49.0	100%	2e-05	88%	XP_004847421.1
☐	PREDICTED: hepatocyte growth factor activator-like isoform X2 [Sus scrofa]	49.0	49.0	100%	2e-05	88%	XP_005666566.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Macaca fascicula	49.0	49.0	100%	2e-05	88%	XP_005554416.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor activator [	49.0	49.0	100%	2e-05	88%	XP_005609072.1

☐	PREDICTED: hepatocyte growth factor activator [Rhinopithecus roxellana]	49.0	49.0	100%	2e-05	88%	XP_010382705.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Macaca fascicula	49.0	49.0	100%	2e-05	88%	XP_005554415.1
☐	PREDICTED: hepatocyte growth factor activator [Chlorocebus sabaeus]	49.0	49.0	100%	2e-05	88%	XP_008016229.1
☐	hepatocyte growth factor activator preproprotein [Bos taurus]	49.0	49.0	100%	2e-05	88%	NP_001193958.1
☐	PREDICTED: hepatocyte growth factor activator [Mesocricetus auratus]	49.0	49.0	100%	2e-05	88%	XP_005068916.1
☐	Hepatocyte growth factor activator [Bos mutus]	49.0	49.0	100%	2e-05	88%	ELR57284.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Galeopterus vari	49.0	49.0	100%	2e-05	88%	XP_008566189.1
☐	PREDICTED: hepatocyte growth factor activator-like isoform X1 [Sus scrofa]	49.0	49.0	100%	2e-05	88%	XP_003482383.1
☐	PREDICTED: hepatocyte growth factor activator [Lipotes vexillifer]	49.0	49.0	100%	2e-05	88%	XP_007456919.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Balaenoptera ac	49.0	49.0	100%	2e-05	88%	XP_007172366.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Heterocephalus	49.0	49.0	100%	2e-05	88%	XP_004847420.1
☐	PREDICTED: hepatocyte growth factor activator [Nannospalax galili]	49.0	49.0	100%	2e-05	88%	XP_008840096.1
☐	PREDICTED: hepatocyte growth factor activator [Ictidomys tridecemlineatus]	49.0	49.0	100%	2e-05	88%	XP_005319055.1
☐	PREDICTED: hepatocyte growth factor activator [Nomascus leucogenys]	49.0	49.0	100%	2e-05	88%	XP_003279052.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Galeopterus vari	49.0	49.0	100%	2e-05	88%	XP_008566259.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor activator [	49.0	49.0	100%	2e-05	88%	XP_009238032.1
☐	PREDICTED: hepatocyte growth factor activator [Tursiops truncatus]	49.0	49.0	100%	2e-05	88%	XP_004311082.1
☐	PREDICTED: hepatocyte growth factor activator [Orcinus orca]	49.0	49.0	100%	2e-05	88%	XP_004265212.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Heterocephalus	49.0	49.0	100%	2e-05	88%	XP_004847419.1
☐	PREDICTED: hepatocyte growth factor activator [Bison bison bison]	49.0	49.0	100%	2e-05	88%	XP_010846427.1
☐	PREDICTED: hepatocyte growth factor activator [Bos mutus]	49.0	49.0	100%	2e-05	88%	XP_005894504.1
☐	PREDICTED: hepatocyte growth factor activator [Bubalus bubalis]	49.0	49.0	100%	2e-05	88%	XP_006074671.1
☐	PREDICTED: hepatocyte growth factor activator [Pantholops hodgsonii]	49.0	49.0	100%	2e-05	88%	XP_005984423.1
☐	PREDICTED: hepatocyte growth factor activator [Papio anubis]	49.0	49.0	100%	2e-05	88%	XP_009209400.1
☐	Hepatocyte growth factor activator [Macaca mulatta]	49.0	49.0	100%	2e-05	88%	EHH14171.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Rattus norvegicu	46.9	46.9	100%	1e-04	81%	XP_008768574.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Mus musculus]	46.9	46.9	100%	1e-04	81%	XP_006504095.1
☐	PREDICTED: hepatocyte growth factor activator [Cavia porcellus]	46.9	46.9	100%	1e-04	88%	XP_003461921.2
☐	PREDICTED: hepatocyte growth factor activator [Peromyscus maniculatus ba	46.9	46.9	100%	1e-04	81%	XP_006985637.1
☐	PREDICTED: hepatocyte growth factor activator [Cricetulus griseus]	46.9	46.9	100%	1e-04	81%	XP_007624029.1
☐	PREDICTED: hepatocyte growth factor activator [Cricetulus griseus]	46.9	46.9	100%	1e-04	81%	XP_003496650.1
☐	hepatocyte growth factor activator precursor [Rattus norvegicus]	46.9	46.9	100%	1e-04	81%	NP_445772.1
☐	hepatocyte growth factor activator HGFA [Mus musculus]	46.9	46.9	100%	1e-04	81%	AAF34712.1
☐	unnamed protein product [Mus musculus]	46.9	46.9	100%	1e-04	81%	BAE41500.1
☐	hepatocyte growth factor activator preproprotein [Mus musculus]	46.9	46.9	100%	1e-04	81%	NP_062320.2
☐	Hepatocyte growth factor activator [Mus musculus]	46.9	46.9	100%	1e-04	81%	AAH19376.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Mus musculus]	46.9	46.9	100%	1e-04	81%	XP_006504094.1
☐	hepatocyte growth factor activator [Cricetulus griseus]	46.9	46.9	100%	1e-04	81%	ERE89786.1
☐	Hepatocyte growth factor activator [Cricetulus griseus]	46.9	46.9	100%	1e-04	81%	EGV91591.1
☐	PREDICTED: hepatocyte growth factor activator [Fukomys damarensis]	46.9	46.9	100%	1e-04	88%	XP_010640070.1
☐	Hepatocyte growth factor activator [Fukomys damarensis]	46.9	46.9	100%	1e-04	88%	KFO25725.1
☐	PREDICTED: hepatocyte growth factor activator [Jaculus jaculus]	46.4	46.4	100%	2e-04	88%	XP_004656058.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor activator [	45.2	45.2	100%	5e-04	81%	XP_010995899.1
☐	PREDICTED: hepatocyte growth factor activator [Vicugna pacos]	45.2	45.2	100%	5e-04	81%	XP_006213089.1
☐	PREDICTED: hepatocyte growth factor activator [Camelus bactrianus]	45.2	45.2	100%	5e-04	81%	XP_010957586.1

☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor activator [(	45.2	45.2	100%	5e-04	81%	XP_006181198.1
☐	PREDICTED: hepatocyte growth factor activator [Erinaceus europaeus]	45.2	45.2	100%	5e-04	81%	XP_007536851.1
☐	PREDICTED: hepatocyte growth factor activator [Microtus ochrogaster]	44.3	44.3	100%	9e-04	75%	XP_005365974.1
☐	Hepatocyte growth factor activator [Myotis davidii]	42.6	42.6	87%	0.003	86%	ELK32958.1
☐	PREDICTED: hepatocyte growth factor activator [Myotis davidii]	42.6	42.6	87%	0.003	86%	XP_006760204.1
☐	PREDICTED: hepatocyte growth factor activator [Eptesicus fuscus]	42.6	42.6	87%	0.003	86%	XP_008149119.1
☐	PREDICTED: hepatocyte growth factor activator [Echinops telfairi]	42.6	42.6	87%	0.003	86%	XP_004715151.1
☐	PREDICTED: hepatocyte growth factor activator [Elephantulus edwardii]	42.6	42.6	87%	0.003	86%	XP_006893724.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Chinchilla lanige	42.2	42.2	100%	0.004	81%	XP_005408819.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Chinchilla lanige	42.2	42.2	100%	0.004	81%	XP_005408818.1
☐	PREDICTED: hepatocyte growth factor activator [Odobenus rosmarus diverge	41.4	41.4	100%	0.008	81%	XP_004396253.1
☐	PREDICTED: hepatocyte growth factor activator isoform X3 [Tupaia chinensis	40.5	40.5	100%	0.016	75%	XP_006153008.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Tupaia chinensis	40.5	40.5	100%	0.016	75%	XP_006153007.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Tupaia chinensis	40.5	40.5	100%	0.016	75%	XP_006153006.1
☐	PREDICTED: hepatocyte growth factor activator [Otolemur garnettii]	39.7	39.7	93%	0.028	80%	XP_003801207.1
☐	PREDICTED: hepatocyte growth factor activator [Myotis brandtii]	39.2	39.2	81%	0.041	85%	XP_005886528.1
☐	PREDICTED: hepatocyte growth factor activator [Chrysochloris asiatica]	39.2	39.2	81%	0.041	85%	XP_006875389.1
☐	PREDICTED: hepatocyte growth factor activator [Panthera tigris altaica]	38.8	38.8	100%	0.055	75%	XP_007089521.1
☐	PREDICTED: hepatocyte growth factor activator isoform X5 [Mustela putorius	38.8	38.8	100%	0.055	75%	XP_004772296.1
☐	PREDICTED: hepatocyte growth factor activator isoform X6 [Mustela putorius	38.8	38.8	100%	0.056	75%	XP_004801526.1
☐	PREDICTED: hepatocyte growth factor activator [Ursus maritimus]	38.8	38.8	100%	0.056	75%	XP_008704513.1
☐	PREDICTED: hepatocyte growth factor activator isoform X4 [Mustela putorius	38.8	38.8	100%	0.056	75%	XP_004772295.1
☐	PREDICTED: hepatocyte growth factor activator isoform X5 [Mustela putorius	38.8	38.8	100%	0.056	75%	XP_004801525.1
☐	PREDICTED: hepatocyte growth factor activator [Ochotona princeps]	38.8	38.8	93%	0.056	73%	XP_004579433.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor activator-lil	38.8	38.8	100%	0.056	75%	XP_002916611.1
☐	PREDICTED: hepatocyte growth factor activator isoform X3 [Mustela putorius	38.8	38.8	100%	0.056	75%	XP_004772294.1

⊟ Alignments

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Chain A, Short Form Hgfa With Inhibitory Fab75

Sequence ID: pdb|2R0L|A **Length:** 248 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 48 to 63 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	3e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1   RDSVSVVLGQHFFDRT  16
           RDSVSVVLGQHFF+RT
Sbjct  48  RDSVSVVLGQHFFNRT  63
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of Hgfa In Complex With The Allosteric Non-Inhibitory Antibody Fab40.Deltatrp

Sequence ID: pdb|2WUB|A **Length:** 257 **Number of Matches:** 1

▷ See 3 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins

Range 1: 48 to 63 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	3e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1   RDSVSVVLGQHFFDRT  16
           RDSVSVVLGQHFF+RT
Sbjct  48  RDSVSVVLGQHFFNRT  63
```

identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Protease Domain Of Hgfa With No Inhibitor

Sequence ID: pdb|1YBW|A **Length:** 283 **Number of Matches:** 1

See 3 more title(s)

Range 1: 83 to 98 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	3e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1   RDSVSVVLGQHFFDRT  16
           RDSVSVVLGQHFF+RT
Sbjct  83  RDSVSVVLGQHFFNRT  98
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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PREDICTED: hepatocyte growth factor activator isoform X3 [Callithrix jacchus]

Sequence ID: ref|XP_008991932.1| **Length:** 539 **Number of Matches:** 1

Range 1: 339 to 354 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	3e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RDSVSVVLGQHFFDRT  16
            RDSVSVVLGQHFF+RT
Sbjct  339  RDSVSVVLGQHFFNRT  354
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: hepatocyte growth factor activator isoform X2 [Callithrix jacchus]

Sequence ID: ref|XP_008991931.1| **Length:** 607 **Number of Matches:** 1

Range 1: 454 to 469 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	3e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RDSVSVVLGQHFFDRT  16
            RDSVSVVLGQHFF+RT
Sbjct  454  RDSVSVVLGQHFFNRT  469
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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NCBI/ BLAST/ blastp suite/ **Formatting Results - B9HE25MV01R**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | ▷Formatting options | ▷Download

How to read this page | Blast report description

HGFAC_RDSVSVVLGQHFFNRT_NonMod

RID B9HE25MV01R (Expires on 01-14 14:14 pm)

Query ID	lcl|124214	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	16	**Program**	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

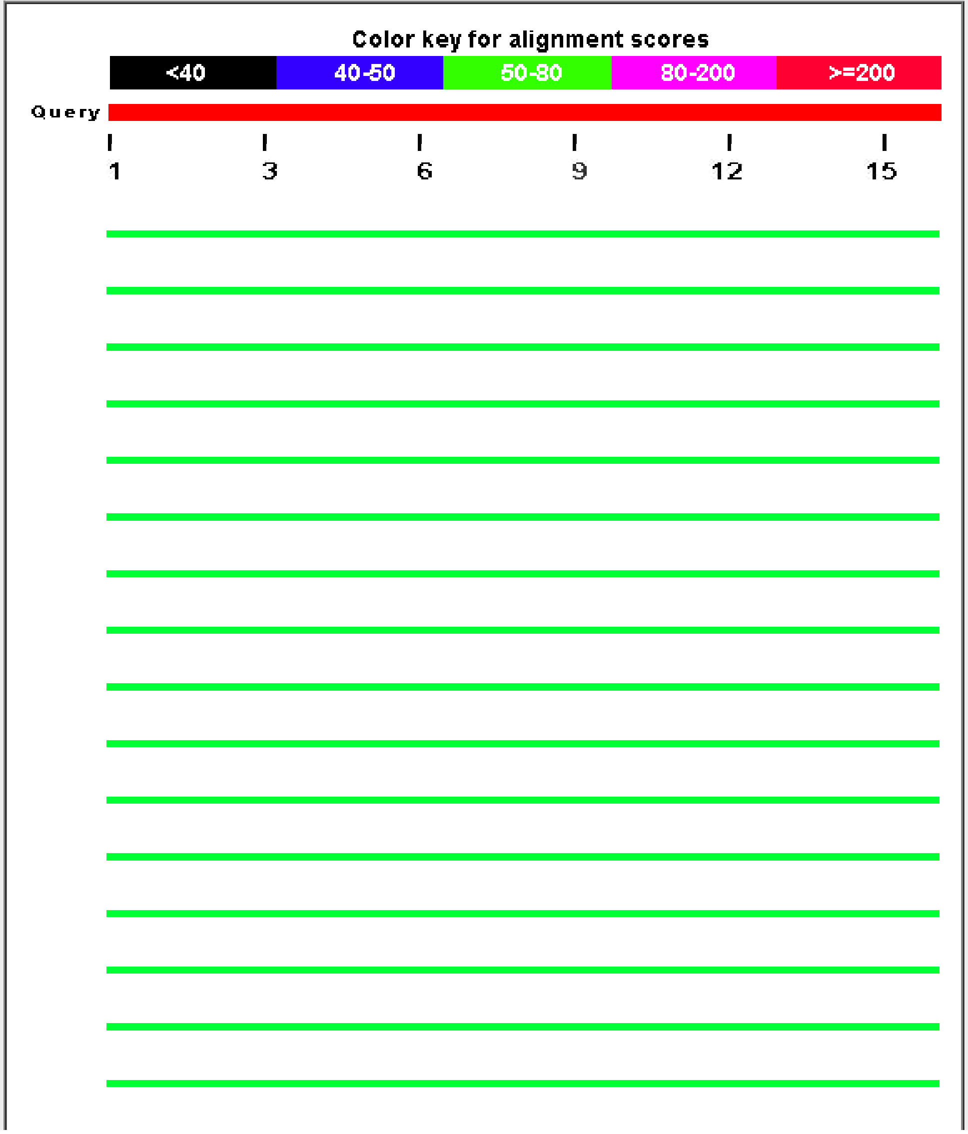
Graphic Summary

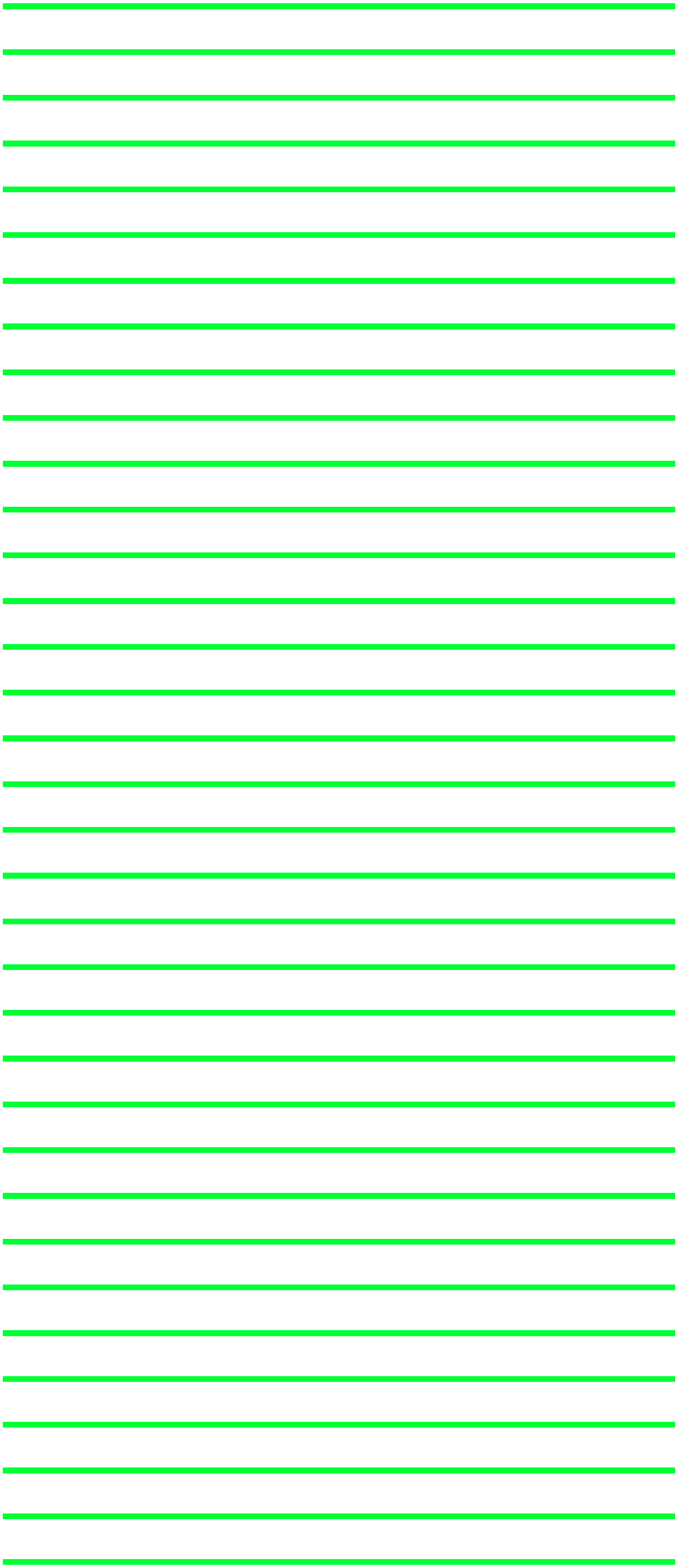
Show Conserved Domains

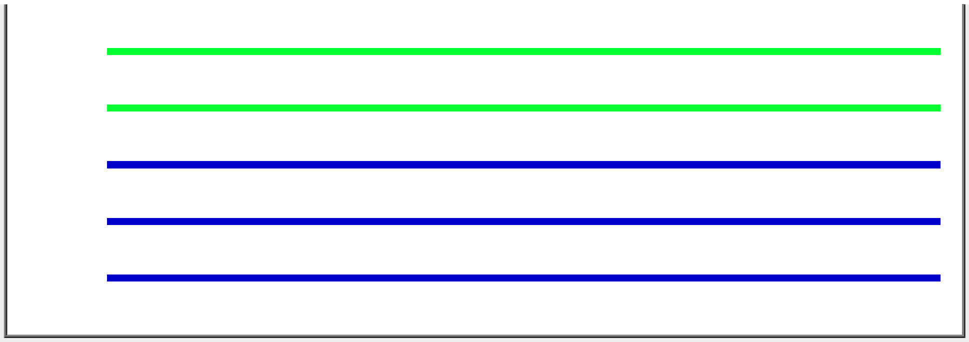
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Short Form Hgfa With Inhibitory Fab75 [Homo sapiens]	54.1	54.1	100%	4e-07	100%	gi|163931039|2R0L_A
☐	Chain A, Crystal Structure Of Hgfa In Complex With The Allosteric I	54.1	54.1	100%	4e-07	100%	gi|281306940|2WUB_A
☐	Chain A, Protease Domain Of Hgfa With No Inhibitor [Homo sapien	54.1	54.1	100%	4e-07	100%	gi|61680579|1YBW_A
☐	PREDICTED: hepatocyte growth factor activator isoform X3 [Callith	54.1	54.1	100%	4e-07	100%	gi|675650394|XP_008991932.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Callith	54.1	54.1	100%	4e-07	100%	gi|675650392|XP_008991931.1
☐	PREDICTED: hepatocyte growth factor activator [Ceratotherium sin	54.1	54.1	100%	4e-07	100%	gi|478516120|XP_004432296.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Callith	54.1	54.1	100%	4e-07	100%	gi|296196985|XP_002746077.1
☐	HGF activator, preproprotein [Homo sapiens]	54.1	54.1	100%	4e-07	100%	gi|85567253|AAI12193.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor a	54.1	54.1	100%	4e-07	100%	gi|426343647|XP_004038404.1
☐	hepatocyte growth factor activator isoform 2 preproprotein [Homo sa	54.1	54.1	100%	4e-07	100%	gi|4504383|NP_001519.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Pan pa	54.1	54.1	100%	4e-07	100%	gi|397465226|XP_003804416.1
☐	PREDICTED: hepatocyte growth factor activator [Pan troglodytes]	54.1	54.1	100%	4e-07	100%	gi|332818997|XP_001174601.2
☐	hepatocyte growth factor activator isoform 1 preproprotein [Homo sa	54.1	54.1	100%	4e-07	100%	gi|661903023|NP_001284368.1
☐	PREDICTED: hepatocyte growth factor activator [Sorex araneus]	52.0	52.0	100%	2e-06	94%	gi|505848131|XP_004617524.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor a	52.0	52.0	100%	2e-06	94%	gi|586528318|XP_006919081.1
☐	PREDICTED: hepatocyte growth factor activator-like [Equus przewa	51.5	51.5	100%	3e-06	94%	gi|664781339|XP_008509987.1
☐	PREDICTED: hepatocyte growth factor activator [Dasypus novemci	51.5	51.5	100%	3e-06	94%	gi|488591674|XP_004481097.1
☐	PREDICTED: hepatocyte growth factor activator [Ovis aries]	51.5	51.5	100%	3e-06	94%	gi|426232343|XP_004010188.1
☐	PREDICTED: hepatocyte growth factor activator [Tarsius syrichta]	51.5	51.5	100%	3e-06	94%	gi|640780818|XP_008046016.1
☐	PREDICTED: hepatocyte growth factor activator [Capra hircus]	51.5	51.5	100%	3e-06	94%	gi|548471340|XP_005682051.1
☐	TPA: HGF activator preproprotein-like [Bos taurus]	51.5	51.5	100%	3e-06	94%	gi|296486347|DAA28460.1
☐	PREDICTED: hepatocyte growth factor activator [Physeter catodon]	51.5	51.5	100%	3e-06	94%	gi|593726599|XP_007109331.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Balaer	51.5	51.5	100%	3e-06	94%	gi|594638131|XP_007172367.1
☐	Hepatocyte growth factor activator [Macaca fascicularis]	51.5	51.5	100%	3e-06	94%	gi|355744788|EHH49413.1
☐	PREDICTED: hepatocyte growth factor activator-like [Macaca mula	51.5	51.5	100%	3e-06	94%	gi|297281947|XP_001114822.2
☐	PREDICTED: hepatocyte growth factor activator isoform X3 [Heterc	51.5	51.5	100%	3e-06	94%	gi|512970560|XP_004847421.1
☐	PREDICTED: hepatocyte growth factor activator-like isoform X2 [Su	51.5	51.5	100%	3e-06	94%	gi|545843795|XP_005666566.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Macac	51.5	51.5	100%	3e-06	94%	gi|544431060|XP_005554416.1
☐							

	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor	51.5	51.5	100%	3e-06	94%	gi|545213511|XP_005609072.1
☐	PREDICTED: hepatocyte growth factor activator [Rhinopithecus rox	51.5	51.5	100%	3e-06	94%	gi|724928379|XP_010382705.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Macac	51.5	51.5	100%	3e-06	94%	gi|544431058|XP_005554415.1
☐	PREDICTED: hepatocyte growth factor activator [Chlorocebus saba	51.5	51.5	100%	3e-06	94%	gi|635138752|XP_008016229.1
☐	hepatocyte growth factor activator preproprotein [Bos taurus]	51.5	51.5	100%	3e-06	94%	gi|333360891|NP_001193958.1
☐	PREDICTED: hepatocyte growth factor activator [Mesocricetus aura	51.5	51.5	100%	3e-06	94%	gi|524929421|XP_005068916.1
☐	Hepatocyte growth factor activator [Bos mutus]	51.5	51.5	100%	3e-06	94%	gi|440907097|ELR57284.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Galeo	51.5	51.5	100%	3e-06	94%	gi|667239445|XP_008566189.1
☐	PREDICTED: hepatocyte growth factor activator-like isoform X1 [Su	51.5	51.5	100%	3e-06	94%	gi|350587301|XP_003482383.1
☐	PREDICTED: hepatocyte growth factor activator [Lipotes vexillifer]	51.5	51.5	100%	3e-06	94%	gi|602689402|XP_007456919.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Balae	51.5	51.5	100%	3e-06	94%	gi|594638129|XP_007172366.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Heter	51.5	51.5	100%	3e-06	94%	gi|512970558|XP_004847420.1
☐	PREDICTED: hepatocyte growth factor activator [Nannospalax galil	51.5	51.5	100%	3e-06	94%	gi|674066317|XP_008840096.1
☐	PREDICTED: hepatocyte growth factor activator [Ictidomys tridece	51.5	51.5	100%	3e-06	94%	gi|532066402|XP_005319055.1
☐	PREDICTED: hepatocyte growth factor activator [Nomascus leucog	51.5	51.5	100%	3e-06	94%	gi|332259962|XP_003279052.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Galeo	51.5	51.5	100%	3e-06	94%	gi|667239448|XP_008566259.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor	51.5	51.5	100%	3e-06	94%	gi|686715189|XP_009238032.1
☐	PREDICTED: hepatocyte growth factor activator [Tursiops truncatu	51.5	51.5	100%	3e-06	94%	gi|470596733|XP_004311082.1
☐	PREDICTED: hepatocyte growth factor activator [Orcinus orca]	51.5	51.5	100%	3e-06	94%	gi|465982188|XP_004265212.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Heter	51.5	51.5	100%	3e-06	94%	gi|512970556|XP_004847419.1
☐	PREDICTED: hepatocyte growth factor activator [Bos mutus]	51.5	51.5	100%	3e-06	94%	gi|555964887|XP_005894504.1
☐	PREDICTED: hepatocyte growth factor activator [Bubalus bubalis]	51.5	51.5	100%	3e-06	94%	gi|594103282|XP_006074671.1
☐	PREDICTED: hepatocyte growth factor activator [Pantholops hodgs	51.5	51.5	100%	3e-06	94%	gi|556778715|XP_005984423.1
☐	PREDICTED: hepatocyte growth factor activator [Papio anubis]	51.5	51.5	100%	3e-06	94%	gi|685511454|XP_009209400.1
☐	Hepatocyte growth factor activator [Macaca mulatta]	51.5	51.5	100%	3e-06	94%	gi|355557391|EHH14171.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Rattus	49.4	49.4	100%	2e-05	88%	gi|672076919|XP_008768574.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Mus m	49.4	49.4	100%	2e-05	88%	gi|568934380|XP_006504095.1
☐	PREDICTED: hepatocyte growth factor activator [Cavia porcellus]	49.4	49.4	100%	2e-05	94%	gi|514445291|XP_003461921.2
☐	PREDICTED: hepatocyte growth factor activator [Peromyscus mani	49.4	49.4	100%	2e-05	88%	gi|589945912|XP_006985637.1
☐	PREDICTED: hepatocyte growth factor activator [Cricetulus griseus	49.4	49.4	100%	2e-05	88%	gi|625265138|XP_007624029.1
☐	PREDICTED: hepatocyte growth factor activator [Cricetulus griseus	49.4	49.4	100%	2e-05	88%	gi|354468418|XP_003496650.1
☐	hepatocyte growth factor activator precursor [Rattus norvegicus]	49.4	49.4	100%	2e-05	88%	gi|61097947|NP_445772.1
☐	hepatocyte growth factor activator HGFA [Mus musculus]	49.4	49.4	100%	2e-05	88%	gi|6980072|AAF34712.1
☐	unnamed protein product [Mus musculus]	49.4	49.4	100%	2e-05	88%	gi|74199664|BAE41500.1
☐	hepatocyte growth factor activator preproprotein [Mus musculus]	49.4	49.4	100%	2e-05	88%	gi|188219651|NP_062320.2
☐	Hepatocyte growth factor activator [Mus musculus]	49.4	49.4	100%	2e-05	88%	gi|18044173|AAH19376.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Mus m	49.4	49.4	100%	2e-05	88%	gi|568934378|XP_006504094.1
☐	hepatocyte growth factor activator [Cricetulus griseus]	49.4	49.4	100%	2e-05	88%	gi|537259644|ERE89786.1
☐	Hepatocyte growth factor activator [Cricetulus griseus]	49.4	49.4	100%	2e-05	88%	gi|344235488|EGV91591.1
☐	PREDICTED: hepatocyte growth factor activator [Fukomys damare	49.4	49.4	100%	2e-05	94%	gi|731254756|XP_010640070.1
☐	Hepatocyte growth factor activator [Fukomys damarensis]	49.4	49.4	100%	2e-05	94%	gi|676270515|KFO25725.1
☐	PREDICTED: hepatocyte growth factor activator [Jaculus jaculus]	49.0	49.0	100%	2e-05	94%	gi|507544157|XP_004656058.1
☐	PREDICTED: hepatocyte growth factor activator [Vicugna pacos]	47.7	47.7	100%	6e-05	88%	gi|560981704|XP_006213089.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor	47.7	47.7	100%	6e-05	88%	gi|560909785|XP_006181198.1
☐	PREDICTED: hepatocyte growth factor activator [Erinaceus europa	47.7	47.7	100%	6e-05	88%	gi|617659508|XP_007536851.1

☐	PREDICTED: hepatocyte growth factor activator [Microtus ochrogas	46.9	46.9	100%	1e-04	81%	gi|532046356|XP_005365974.1
☐	Hepatocyte growth factor activator [Myotis davidii]	45.2	45.2	87%	4e-04	93%	gi|432107907|ELK32958.1
☐	PREDICTED: hepatocyte growth factor activator [Myotis davidii]	45.2	45.2	87%	4e-04	93%	gi|584080689|XP_006760204.1
☐	PREDICTED: hepatocyte growth factor activator [Eptesicus fuscus]	45.2	45.2	87%	4e-04	93%	gi|641719053|XP_008149119.1
☐	PREDICTED: hepatocyte growth factor activator [Echinops telfairi]	45.2	45.2	87%	4e-04	93%	gi|507700282|XP_004715151.1
☐	PREDICTED: hepatocyte growth factor activator [Elephantulus edw	45.2	45.2	87%	4e-04	93%	gi|585687633|XP_006893724.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Chincl	44.8	44.8	100%	6e-04	88%	gi|533191952|XP_005408819.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Chincl	44.8	44.8	100%	6e-04	88%	gi|533191950|XP_005408818.1
☐	PREDICTED: hepatocyte growth factor activator [Odobenus rosmar	43.9	43.9	100%	0.001	88%	gi|472353164|XP_004396253.1
☐	PREDICTED: hepatocyte growth factor activator isoform X3 [Tupaia	43.1	43.1	100%	0.002	81%	gi|562848375|XP_006153008.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Tupaia	43.1	43.1	100%	0.002	81%	gi|562848373|XP_006153007.1
☐	PREDICTED: hepatocyte growth factor activator isoform X1 [Tupaia	43.1	43.1	100%	0.002	81%	gi|562848371|XP_006153006.1
☐	PREDICTED: hepatocyte growth factor activator [Otolemur garnettii	42.2	42.2	93%	0.004	87%	gi|395857659|XP_003801207.1
☐	PREDICTED: hepatocyte growth factor activator [Myotis brandtii]	41.8	41.8	81%	0.006	92%	gi|554590398|XP_005886528.1
☐	PREDICTED: hepatocyte growth factor activator [Chrysochloris asia	41.8	41.8	81%	0.006	92%	gi|586489842|XP_006875389.1
☐	PREDICTED: hepatocyte growth factor activator [Panthera tigris alt	41.4	41.4	100%	0.008	81%	gi|591327132|XP_007089521.1
☐	PREDICTED: hepatocyte growth factor activator isoform X5 [Mustel	41.4	41.4	100%	0.008	81%	gi|511905650|XP_004772296.1
☐	PREDICTED: hepatocyte growth factor activator isoform X6 [Mustel	41.4	41.4	100%	0.008	81%	gi|511966828|XP_004801526.1
☐	PREDICTED: hepatocyte growth factor activator [Ursus maritimus]	41.4	41.4	100%	0.008	81%	gi|670981313|XP_008704513.1
☐	PREDICTED: hepatocyte growth factor activator isoform X4 [Mustel	41.4	41.4	100%	0.008	81%	gi|511905648|XP_004772295.1
☐	PREDICTED: hepatocyte growth factor activator isoform X5 [Mustel	41.4	41.4	100%	0.008	81%	gi|511966826|XP_004801525.1
☐	PREDICTED: hepatocyte growth factor activator [Ochotona princep	41.4	41.4	93%	0.008	80%	gi|504133750|XP_004579433.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor a	41.4	41.4	100%	0.008	81%	gi|301762376|XP_002916611.1
☐	PREDICTED: hepatocyte growth factor activator isoform X3 [Mustel	41.4	41.4	100%	0.008	81%	gi|511905646|XP_004772294.1
☐	hepatocyte growth factor activator precursor [Canis lupus familiaris]	41.4	41.4	100%	0.008	81%	gi|73532760|NP_001026985.1
☐	PREDICTED: hepatocyte growth factor activator [Felis catus]	41.4	41.4	100%	0.008	81%	gi|410958042|XP_003985632.1
☐	PREDICTED: hepatocyte growth factor activator isoform X2 [Mustel	41.4	41.4	100%	0.008	81%	gi|511905644|XP_004772293.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Short Form Hgfa With Inhibitory Fab75

Sequence ID: gi|163931039|pdb|2R0L|A **Length:** 248 **Number of Matches:** 1

Range 1: 48 to 63 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	4e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RDSVSVVLGQHFFNRT  16
            RDSVSVVLGQHFFNRT
Sbjct  48   RDSVSVVLGQHFFNRT  63
```

Related Information

Structure - 3D structure displays

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of Hgfa In Complex With The Allosteric Non-Inhibitory Antibody Fab40.Deltatrp

Sequence ID: gi|281306940|pdb|2WUB|A **Length:** 257 **Number of Matches:** 1

▸ See 3 more title(s)

Range 1: 48 to 63 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	4e-07	16/16(100%)	16/16(100%)	0/16(0%)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

```
Query  1   RDSVSVVLGQHFFNRT  16
           RDSVSVVLGQHFFNRT
Sbjct  48  RDSVSVVLGQHFFNRT  63
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Protease Domain Of Hgfa With No Inhibitor

Sequence ID: gi|61680579|pdb|1YBW|A **Length:** 283 **Number of Matches:** 1

See 3 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 83 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	4e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1   RDSVSVVLGQHFFNRT  16
           RDSVSVVLGQHFFNRT
Sbjct  83  RDSVSVVLGQHFFNRT  98
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: hepatocyte growth factor activator isoform X3 [Callithrix jacchus]

Sequence ID: gi|675650394|ref|XP_008991932.1| **Length:** 539 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 339 to 354 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	4e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RDSVSVVLGQHFFNRT  16
            RDSVSVVLGQHFFNRT
Sbjct  339  RDSVSVVLGQHFFNRT  354
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: hepatocyte growth factor activator isoform X2 [Callithrix jacchus]

Sequence ID: gi|675650392|ref|XP_008991931.1| **Length:** 607 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 454 to 469 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	4e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RDSVSVVLGQHFFNRT  16
            RDSVSVVLGQHFFNRT
Sbjct  454  RDSVSVVLGQHFFNRT  469
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVGSCDJR01R

Your search parameters were adjusted to search for a short input sequence.

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ICAM1_RADLTVVLLRG_Mod

RID BVGSCDJR01R (Expires on 01-21 09:53 am)

Query ID	lcl|334439	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	11	**Program**	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

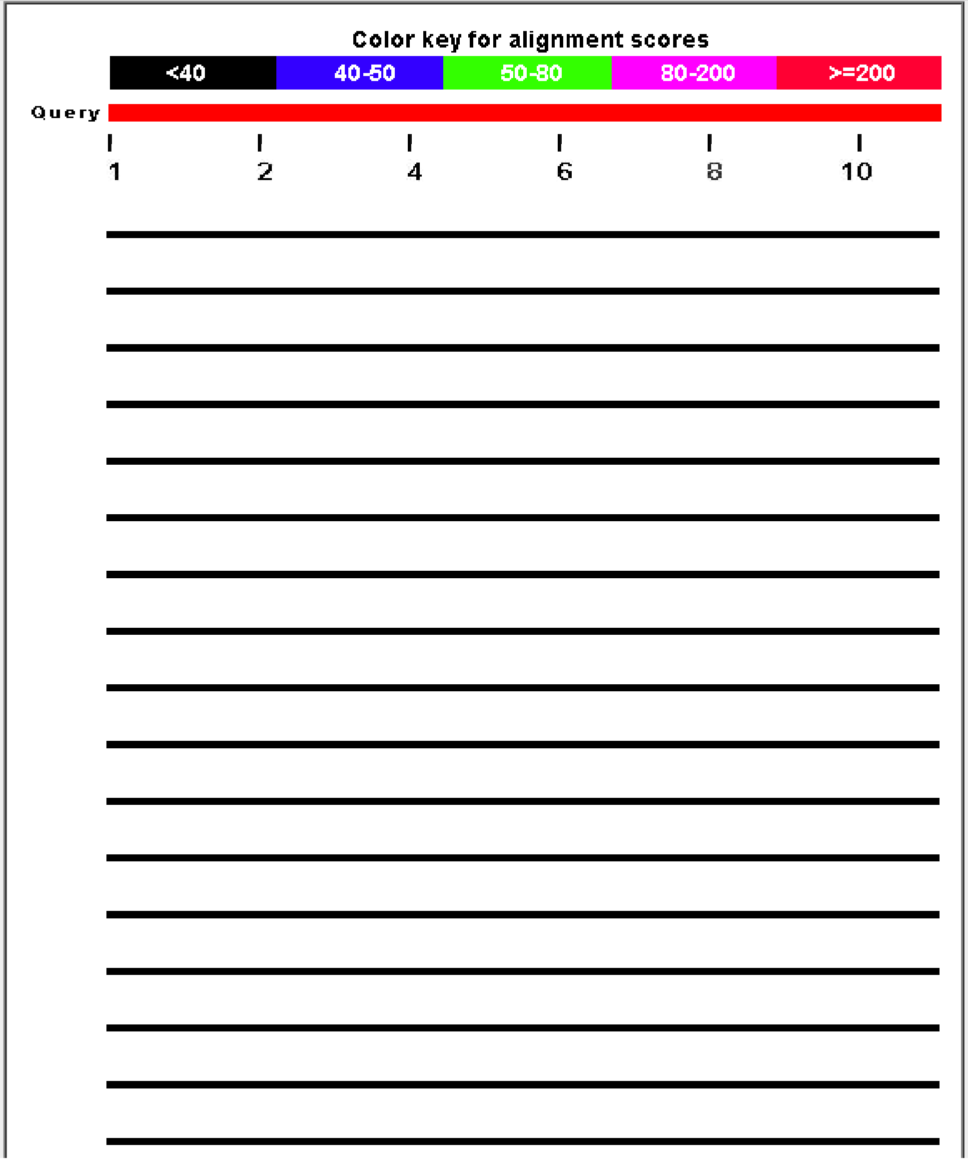
⊟ Graphic Summary

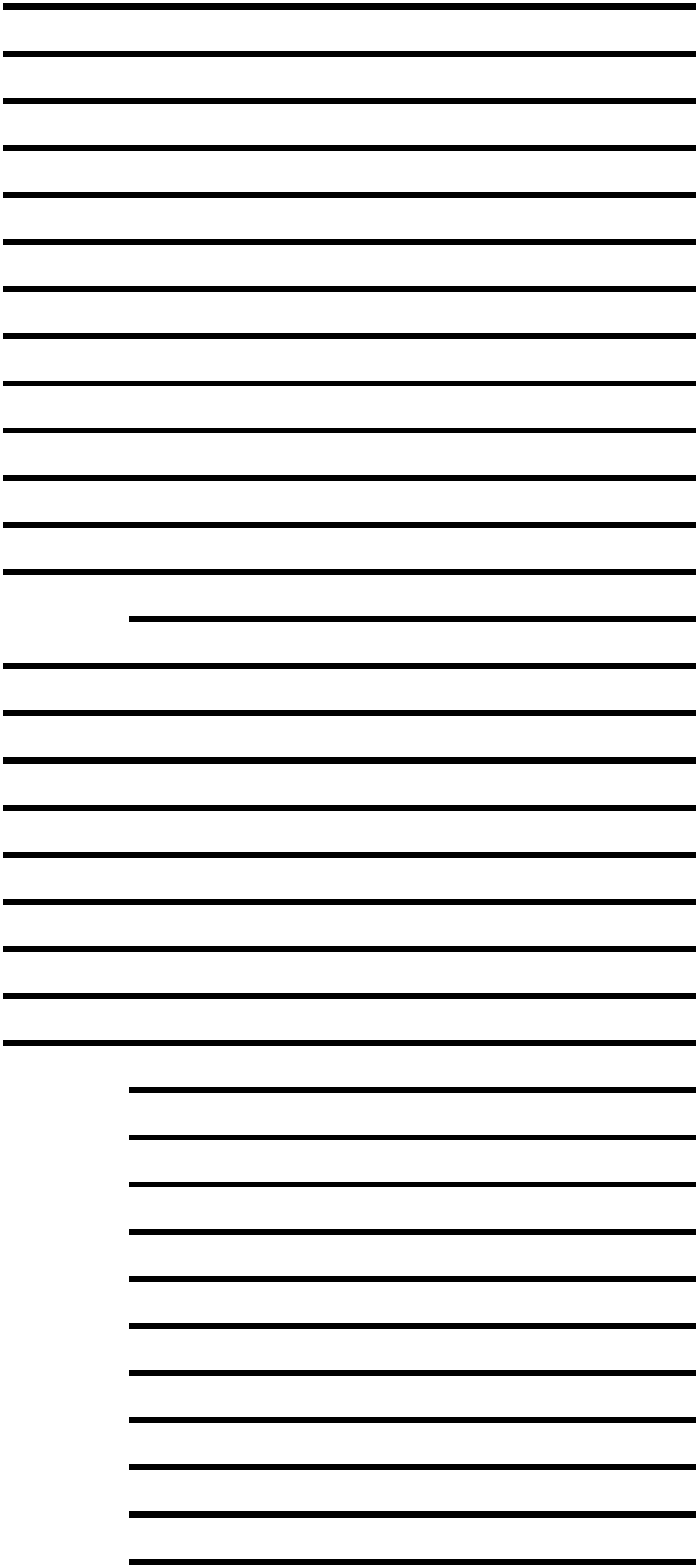
⊟ Show Conserved Domains

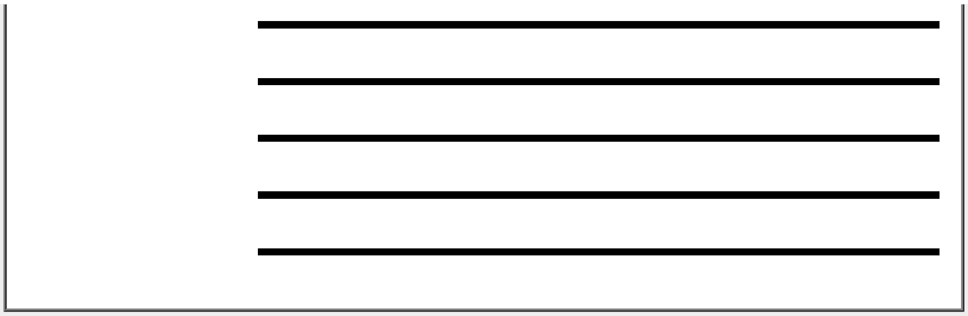
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	cell surface glycoprotein [Homo sapiens]	33.7	33.7	100%	1.3	91%	AAA60392.1
☐	Chain A, D1d2-Icam-1 Fully Glycosylated, Variation Of D1-D2 Interdomain An	33.7	33.7	100%	1.4	91%	1D3L_A
☐	Chain A, The Crystal Structure For The N-Terminal Two Domains Of Icam-1 [	33.7	33.7	100%	1.4	91%	1IC1_A
☐	Chain B, The Crystal Structure For The N-Terminal Two Domains Of Icam-1 [	33.7	33.7	100%	1.4	91%	1IC1_B
☐	Chain A, Crystal Structure Of Alphal I Domain In Complex With Icam-1 [Homo	33.7	33.7	100%	1.5	91%	1MQ8_A
☐	unnamed protein product [Homo sapiens]	33.7	33.7	100%	1.5	91%	BAG60348.1
☐	unnamed protein product [Homo sapiens]	33.7	33.7	100%	1.5	91%	BAG61077.1
☐	Chain I, Cryo-Em Structure Of Human Coxsackievirus A21 Complexed With F	33.7	33.7	100%	1.5	91%	1Z7Z_I
☐	PREDICTED: intercellular adhesion molecule 1 [Pongo abelii]	33.7	33.7	100%	1.5	91%	XP_002828698.2
☐	intercellular adhesion molecule 1 [Pan troglodytes]	33.7	33.7	100%	1.5	91%	AAA35415.1
☐	intercellular adhesion molecule 1 [Homo sapiens]	33.7	33.7	100%	1.5	91%	AAQ14902.1
☐	intercellular adhesion molecule 1 [Pongo pygmaeus]	33.7	33.7	100%	1.5	91%	AAQ14904.1
☐	PREDICTED: intercellular adhesion molecule 1 [Nomascus leucogenys]	33.7	33.7	100%	1.5	91%	XP_003275780.1
☐	PREDICTED: intercellular adhesion molecule 1 [Chlorocebus sabaeus]	33.7	33.7	100%	1.5	91%	XP_007993410.1
☐	intercellular adhesion molecule-1 precursor [Homo sapiens]	33.7	33.7	100%	1.5	91%	AAA52709.1
☐	PREDICTED: intercellular adhesion molecule 1 [Pan paniscus]	33.7	33.7	100%	1.5	91%	XP_003809639.1
☐	intercellular adhesion molecule 1 precursor [Pan troglodytes]	33.7	33.7	100%	1.5	91%	NP_001009946.1
☐	intercellular adhesion molecule 1 precursor [Homo sapiens]	33.7	33.7	100%	1.5	91%	NP_000192.2
☐	PREDICTED: intercellular adhesion molecule 1 [Papio anubis]	33.7	33.7	100%	1.5	91%	XP_009191725.1
☐	intercellular adhesion molecule 1 [Homo sapiens]	33.7	33.7	100%	1.5	91%	AAQ14901.1
☐	Homo sapiens intercellular adhesion molecule 1 (CD54), human rhinovirus re	33.7	33.7	100%	1.5	91%	AAP36234.1
☐	PREDICTED: intercellular adhesion molecule 1 [Saimiri boliviensis boliviensis	33.7	33.7	100%	1.5	91%	XP_003938996.1
☐	PREDICTED: intercellular adhesion molecule 1 [Elephantulus edwardii]	33.7	33.7	100%	1.5	91%	XP_006898825.1
☐	PREDICTED: intercellular adhesion molecule 3 [Trichechus manatus latirostri	33.7	33.7	100%	1.6	91%	XP_004378609.1
☐	PREDICTED: intercellular adhesion molecule 3 [Elephantulus edwardii]	33.7	33.7	100%	1.6	91%	XP_006898902.1
☐	Snap ICAM-1 fusion protein [synthetic construct]	33.7	33.7	100%	1.6	91%	AIZ77117.1
☐	Chain A, Structure Of The Two Amino-Terminal Domains Of Human Intercellu	32.0	32.0	100%	5.0	91%	1IAM_A
☐	PREDICTED: intercellular adhesion molecule 1 [Ceratotherium simum simum	31.2	31.2	100%	10	91%	XP_004442677.1
☐	PREDICTED: intercellular adhesion molecule 1 [Galeopterus variegatus]	31.2	31.2	100%	10	91%	XP_008576239.1

☐	PREDICTED: intercellular adhesion molecule 3 [Ceratotherium simum simum	31.2	31.2	100%	10	91%	XP_004442732.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	30.3	30.3	81%	13	100%	WP_031350797.1
☐	enoyl-CoA hydratase [Achromobacter xylosoxidans AXX-A]	30.8	30.8	100%	14	91%	EGP42811.1
☐	enoyl-CoA hydratase [Achromobacter insuavis]	30.8	30.8	100%	14	91%	WP_035360557.1
☐	PREDICTED: intercellular adhesion molecule 1 isoform X2 [Felis catus]	30.8	30.8	100%	14	82%	XP_006928451.1
☐	RecName: Full=Intercellular adhesion molecule 1; Short=ICAM-1; AltName: C	30.8	30.8	100%	14	82%	P33729.2
☐	intercellular adhesion molecule 1 precursor [Canis lupus familiaris]	30.8	30.8	100%	14	82%	NP_001003291.1
☐	PREDICTED: intercellular adhesion molecule 1 isoform X1 [Felis catus]	30.8	30.8	100%	14	82%	XP_003981899.1
☐	PREDICTED: intercellular adhesion molecule 3 isoform X1 [Felis catus]	30.8	30.8	100%	14	82%	XP_003981917.1
☐	PREDICTED: intercellular adhesion molecule 3 [Canis lupus familiaris]	30.8	30.8	100%	14	82%	XP_003432901.1
☐	PREDICTED: intercellular adhesion molecule 1 [Loxodonta africana]	30.8	30.8	100%	14	82%	XP_003413428.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	30.3	30.3	81%	19	100%	WP_031350798.1
☐	enoyl-CoA hydratase [Mycobacterium avium subsp. paratuberculosis 10-4404	30.3	30.3	81%	19	100%	ETB04169.1
☐	enoyl-CoA hydratase [Mycobacterium vulneris]	30.3	30.3	81%	19	100%	WP_036445570.1
☐	enoyl-CoA hydratase/isomerase family protein [Mycobacterium avium 2285 (F	30.3	30.3	81%	19	100%	EUA41425.1
☐	enoyl-CoA hydratase/isomerase family protein [Mycobacterium intracellulare	30.3	30.3	81%	19	100%	ETZ37455.1
☐	enoyl-CoA hydratase [Mycobacterium indicus pranii]	30.3	30.3	81%	19	100%	WP_014941527.1
☐	enoyl-CoA hydratase [Mycobacterium intracellulare]	30.3	30.3	81%	19	100%	WP_014384111.1
☐	enoyl-CoA hydratase [Mycobacterium intracellulare]	30.3	30.3	81%	19	100%	WP_014382115.1
☐	enoyl-CoA hydratase [Mycobacterium intracellulare]	30.3	30.3	81%	19	100%	WP_014379614.1
☐	enoyl-CoA hydratase/isomerase [Mycobacterium vulneris]	30.3	30.3	81%	19	100%	CDO27409.1
☐	enoyl-CoA hydratase [Mycobacterium smegmatis]	30.3	30.3	81%	19	100%	WP_003893595.1
☐	enoyl-CoA hydratase [Mycobacterium farcinogenes]	30.3	30.3	81%	19	100%	WP_036388478.1
☐	enoyl-CoA hydratase [Mycobacterium hassiacum]	30.3	30.3	81%	19	100%	WP_005626218.1
☐	enoyl-CoA hydratase [Mycobacterium fortuitum]	30.3	30.3	81%	19	100%	WP_003881307.1
☐	enoyl-CoA hydratase [Mycobacterium thermoresistibile]	30.3	30.3	81%	19	100%	WP_003927267.1
☐	enoyl-CoA hydratase [Mycobacterium triplex]	30.3	30.3	81%	19	100%	WP_036470614.1
☐	enoyl-CoA hydratase [Mycobacterium smegmatis]	30.3	30.3	81%	19	100%	WP_014877338.1
☐	enoyl-CoA hydratase [Mycobacterium rhodesiae]	30.3	30.3	81%	19	100%	WP_014214268.1
☐	enoyl-CoA hydratase [Mycobacterium sp. URHD0025]	30.3	30.3	81%	19	100%	WP_029111550.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	30.3	30.3	81%	19	100%	WP_003877383.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	30.3	30.3	81%	19	100%	WP_023897844.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	30.3	30.3	81%	19	100%	WP_023865499.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	30.3	30.3	81%	19	100%	WP_023868654.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	30.3	30.3	81%	19	100%	WP_003873168.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	30.3	30.3	81%	19	100%	WP_009975789.1
☐	MULTISPECIES: enoyl-CoA hydratase [Mycobacterium]	30.3	30.3	81%	19	100%	WP_011724238.1
☐	enoyl-CoA hydratase [Mycobacterium asiaticum]	30.3	30.3	81%	19	100%	WP_036358004.1
☐	enoyl-CoA hydratase [Mycobacterium intracellulare]	30.3	30.3	81%	19	100%	WP_036458505.1
☐	enoyl-CoA hydratase [Mycobacterium parascrofulaceum]	30.3	30.3	81%	19	100%	WP_007169328.1
☐	hypothetical protein [Mycobacterium yongonense]	30.3	30.3	81%	19	100%	WP_020822025.1
☐	enoyl-CoA hydratase [Mycobacterium intracellulare]	30.3	30.3	81%	19	100%	WP_020188779.1
☐	MULTISPECIES: enoyl-CoA hydratase/isomerase [Mycobacterium]	30.3	30.3	81%	19	100%	WP_008254944.1
☐	enoyl-CoA hydratase [Mycobacterium sp. MOTT36Y]	30.3	30.3	81%	19	100%	WP_014711113.1
☐	enoyl-CoA hydratase [Mycobacterium intracellulare]	30.3	30.3	81%	19	100%	WP_009957717.1

☐	enoyl-CoA hydratase [Mycobacterium setense]	30.3	30.3	81%	19	100%	WP_039318073.1
☐	enoyl-CoA hydratase [Mycobacterium setense]	30.3	30.3	81%	19	100%	WP_039378841.1
☐	hypothetical protein K875_04408 [Mycobacterium tuberculosis TKK-01-0051]	30.3	30.3	81%	19	100%	KBZ61452.1
☐	enoyl-CoA hydratase [Mycobacterium colombiense]	30.3	30.3	81%	19	100%	WP_007773968.1
☐	enoyl-CoA hydratase [Nocardia sp. 348MFTsu5.1]	30.3	30.3	81%	19	100%	WP_020106389.1
☐	enoyl-CoA hydratase [Mycobacterium sp. JLS]	30.3	30.3	81%	19	100%	WP_011855230.1
☐	MULTISPECIES: enoyl-CoA hydratase [Mycobacterium]	30.3	30.3	81%	19	100%	WP_011559168.1
☐	enoyl-CoA hydratase [Mycobacterium vaccae]	30.3	30.3	81%	19	100%	WP_003928815.1
☐	enoyl-CoA hydratase [Mycobacterium tusciae]	30.3	30.3	81%	19	100%	WP_006245820.1
☐	PREDICTED: intercellular adhesion molecule 1 [Macaca fascicularis]	30.3	30.3	100%	20	82%	XP_005587991.1
☐	intercellular adhesion molecule 1 precursor [Macaca mulatta]	30.3	30.3	100%	20	82%	NP_001040600.1
☐	Intercellular adhesion molecule 1 [Macaca mulatta]	30.3	30.3	100%	20	82%	EHH29617.1
☐	PREDICTED: intercellular adhesion molecule 1 [Callithrix jacchus]	30.3	30.3	100%	20	82%	XP_008985482.1
☐	AraC family transcriptional regulator [Frankia sp. EuI1c]	29.9	29.9	100%	25	91%	WP_013425582.1
☐	PREDICTED: LOW QUALITY PROTEIN: intercellular adhesion molecule 1 [E	29.9	29.9	100%	27	82%	XP_005612007.1
☐	intercellular adhesion molecule 1 precursor [Gorilla gorilla]	29.9	29.9	100%	27	82%	NP_001266532.1
☐	PREDICTED: intercellular adhesion molecule 3 [Equus przewalskii]	29.9	29.9	100%	27	82%	XP_008508983.1
☐	PREDICTED: LOW QUALITY PROTEIN: intercellular adhesion molecule 3 [E	29.9	29.9	100%	27	82%	XP_005612008.1
☐	PREDICTED: intercellular adhesion molecule 1 [Equus przewalskii]	29.9	29.9	100%	27	82%	XP_008529085.1
☐	PREDICTED: intercellular adhesion molecule 3 [Erinaceus europaeus]	29.5	29.5	100%	37	82%	XP_007526090.1
☐	hypothetical protein IV02_14020 [Pseudomonas syringae]	29.1	29.1	90%	46	83%	KFE51120.1
☐	hypothetical protein [Bradyrhizobium diazoefficiens]	28.6	28.6	90%	58	80%	WP_011090401.1
☐	pentapeptide repeat-containing protein [Paracoccus denitrificans]	28.6	28.6	100%	65	82%	WP_011750157.1
☐	hydrolase [Nocardia araoensis]	28.6	28.6	90%	66	90%	WP_039800000.1
☐	hydrolase [Nocardia araoensis]	28.6	28.6	90%	66	90%	WP_039798989.1
☐	hypothetical protein [Sphingomonas sp. PAMC 26621]	28.2	28.2	100%	83	83%	WP_026046693.1

⊟ Alignments

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cell surface glycoprotein, partial [Homo sapiens]

Sequence ID: gb|AAA60392.1| **Length:** 151 **Number of Matches:** 1

Related Information

Range 1: 58 to 68 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
33.7 bits(72)	1.3	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1   RADLTVVLLRG  11
           RA+LTVVLLRG
Sbjct  58  RANLTVVLLRG  68
```

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Chain A, D1d2-Icam-1 Fully Glycosylated, Variation Of D1-D2 Interdomain Angle In Different Crystal Structures.

Sequence ID: pdb|1D3L|A **Length:** 185 **Number of Matches:** 1

▸ See 2 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins

Range 1: 116 to 126 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
33.7 bits(72)	1.4	10/11(91%)	11/11(100%)	0/11(0%)

identical to the subject

```
Query  1    RADLTVVLLRG  11
            RA+LTVVLLRG
Sbjct  116  RANLTVVLLRG  126
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, The Crystal Structure For The N-Terminal Two Domains Of Icam-1

Sequence ID: pdb|1IC1|A **Length:** 190 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 116 to 126 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
33.7 bits(72)	1.4	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    RADLTVVLLRG  11
            RA+LTVVLLRG
Sbjct  116  RANLTVVLLRG  126
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain B, The Crystal Structure For The N-Terminal Two Domains Of Icam-1

Sequence ID: pdb|1IC1|B **Length:** 190 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 116 to 126 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
33.7 bits(72)	1.4	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    RADLTVVLLRG  11
            RA+LTVVLLRG
Sbjct  116  RANLTVVLLRG  126
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of Alphal I Domain In Complex With Icam-1

Sequence ID: pdb|1MQ8|A **Length:** 291 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 116 to 126 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
33.7 bits(72)	1.5	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    RADLTVVLLRG  11
            RA+LTVVLLRG
Sbjct  116  RANLTVVLLRG  126
```

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How to read this page Blast report description

ICAM1_RANLTVVLLRG_NonMod

RID B9FFCEMB01R (Expires on 01-14 13:40 pm)

Query ID lcl|203444
Description None
Molecule type amino acid
Query Length 11

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

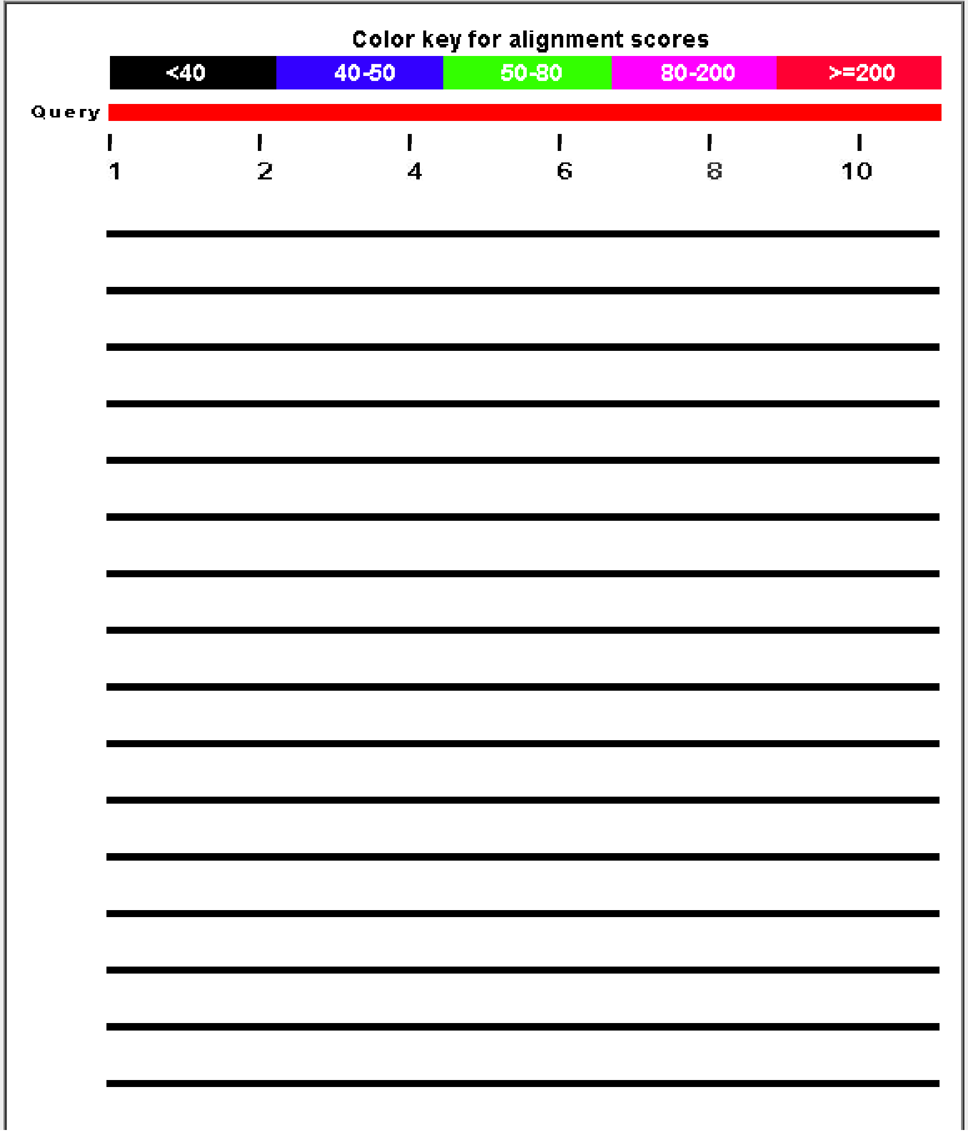
Graphic Summary

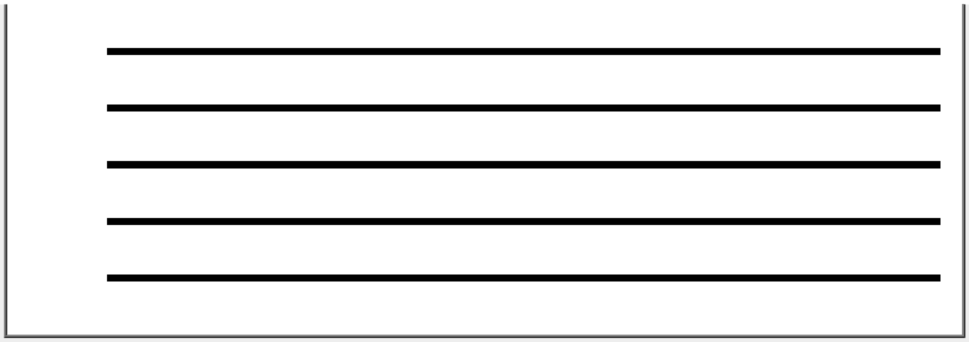
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	cell surface glycoprotein [Homo sapiens]	36.3	36.3	100%	0.18	100%	gi|338068|AAA60392.1
☐	Chain A, D1d2-Icam-1 Fully Glycosylated, Variation Of D1-D2 Inter	36.3	36.3	100%	0.19	100%	gi|6573330|1D3L_A
☐	Chain A, The Crystal Structure For The N-Terminal Two Domains C	36.3	36.3	100%	0.19	100%	gi|3318903|1IC1_A
☐	Chain B, The Crystal Structure For The N-Terminal Two Domains C	36.3	36.3	100%	0.19	100%	gi|3318904|1IC1_B
☐	Chain A, Crystal Structure Of Alphal I Domain In Complex With Icar	36.3	36.3	100%	0.20	100%	gi|28373771|1MQ8_A
☐	unnamed protein product [Homo sapiens]	36.3	36.3	100%	0.21	100%	gi|194388760|BAG60348.1
☐	unnamed protein product [Homo sapiens]	36.3	36.3	100%	0.21	100%	gi|194386534|BAG61077.1
☐	Chain I, Cryo-Em Structure Of Human Coxsackievirus A21 Complex	36.3	36.3	100%	0.21	100%	gi|73535843|1Z7Z_I
☐	PREDICTED: intercellular adhesion molecule 1 [Pongo abelii]	36.3	36.3	100%	0.21	100%	gi|395750443|XP_002828698.2
☐	intercellular adhesion molecule 1 [Pan troglodytes]	36.3	36.3	100%	0.21	100%	gi|176796|AAA35415.1
☐	intercellular adhesion molecule 1 [Homo sapiens]	36.3	36.3	100%	0.21	100%	gi|33340675|AAQ14902.1
☐	intercellular adhesion molecule 1 [Pongo pygmaeus]	36.3	36.3	100%	0.21	100%	gi|33340679|AAQ14904.1
☐	PREDICTED: intercellular adhesion molecule 1 [Nomascus leucoge	36.3	36.3	100%	0.21	100%	gi|332253293|XP_003275780.1
☐	PREDICTED: intercellular adhesion molecule 1 [Chlorocebus sabae	36.3	36.3	100%	0.21	100%	gi|635036004|XP_007993410.1
☐	intercellular adhesion molecule-1 precursor [Homo sapiens]	36.3	36.3	100%	0.21	100%	gi|306896|AAA52709.1
☐	PREDICTED: intercellular adhesion molecule 1 [Pan paniscus]	36.3	36.3	100%	0.21	100%	gi|397476504|XP_003809639.1
☐	intercellular adhesion molecule 1 precursor [Pan troglodytes]	36.3	36.3	100%	0.21	100%	gi|57977287|NP_001009946.1
☐	intercellular adhesion molecule 1 precursor [Homo sapiens]	36.3	36.3	100%	0.21	100%	gi|167466198|NP_000192.2
☐	PREDICTED: intercellular adhesion molecule 1 [Papio anubis]	36.3	36.3	100%	0.21	100%	gi|685605924|XP_009191725.1
☐	intercellular adhesion molecule 1 [Homo sapiens]	36.3	36.3	100%	0.21	100%	gi|33340673|AAQ14901.1
☐	Homo sapiens intercellular adhesion molecule 1 (CD54), human rhi	36.3	36.3	100%	0.21	100%	gi|30583971|AAP36234.1
☐	PREDICTED: intercellular adhesion molecule 1 [Saimiri boliviensis	36.3	36.3	100%	0.21	100%	gi|403296180|XP_003938996.1
☐	PREDICTED: intercellular adhesion molecule 1 [Elephantulus edwa	36.3	36.3	100%	0.21	100%	gi|585706580|XP_006898825.1
☐	PREDICTED: intercellular adhesion molecule 3 [Trichechus manatu	36.3	36.3	100%	0.21	100%	gi|471381636|XP_004378609.1
☐	PREDICTED: intercellular adhesion molecule 3 [Elephantulus edwa	36.3	36.3	100%	0.21	100%	gi|585706861|XP_006898902.1
☐	PREDICTED: intercellular adhesion molecule 1 isoform X2 [Felis ca	33.3	33.3	100%	2.0	91%	gi|586976762|XP_006928451.1
☐	RecName: Full=Intercellular adhesion molecule 1; Short=ICAM-1; A	33.3	33.3	100%	2.0	91%	gi|2506778|P33729.2
☐	intercellular adhesion molecule 1 precursor [Canis lupus familiaris]	33.3	33.3	100%	2.0	91%	gi|308081738|NP_001003291.1
☐							

	PREDICTED: intercellular adhesion molecule 1 isoform X1 [Felis ca	33.3	33.3	100%	2.0	91%	gi|410950410|XP_003981899.1
☐	PREDICTED: intercellular adhesion molecule 3 isoform X1 [Felis ca	33.3	33.3	100%	2.0	91%	gi|410950448|XP_003981917.1
☐	PREDICTED: intercellular adhesion molecule 3 [Canis lupus familia	33.3	33.3	100%	2.0	91%	gi|345787203|XP_003432901.1
☐	PREDICTED: intercellular adhesion molecule 1 [Loxodonta africana	33.3	33.3	100%	2.0	91%	gi|344283337|XP_003413428.1
☐	PREDICTED: intercellular adhesion molecule 1 [Ceratotherium simu	32.9	32.9	100%	2.8	91%	gi|478537121|XP_004442677.1
☐	PREDICTED: intercellular adhesion molecule 1 [Galeopterus varieg	32.9	32.9	100%	2.8	91%	gi|667286704|XP_008576239.1
☐	PREDICTED: intercellular adhesion molecule 1 [Macaca fascicularis	32.9	32.9	100%	2.8	91%	gi|544508624|XP_005587991.1
☐	intercellular adhesion molecule 1 precursor [Macaca mulatta]	32.9	32.9	100%	2.8	91%	gi|114051944|NP_001040600.1
☐	Intercellular adhesion molecule 1 [Macaca mulatta]	32.9	32.9	100%	2.8	91%	gi|355703126|EHH29617.1
☐	PREDICTED: intercellular adhesion molecule 1 [Callithrix jacchus]	32.9	32.9	100%	2.8	91%	gi|675757750|XP_008985482.1
☐	PREDICTED: intercellular adhesion molecule 3 [Ceratotherium simu	32.9	51.8	100%	2.8	91%	gi|478537234|XP_004442732.1
☐	PREDICTED: LOW QUALITY PROTEIN: intercellular adhesion mol	32.5	32.5	100%	3.8	91%	gi|545222252|XP_005612007.1
☐	intercellular adhesion molecule 1 precursor [Gorilla gorilla]	32.5	32.5	100%	3.8	91%	gi|525342618|NP_001266532.1
☐	PREDICTED: intercellular adhesion molecule 3 [Equus przewalskii]	32.5	32.5	100%	3.8	91%	gi|664779359|XP_008508983.1
☐	PREDICTED: LOW QUALITY PROTEIN: intercellular adhesion mol	32.5	32.5	100%	3.8	91%	gi|545222257|XP_005612008.1
☐	PREDICTED: intercellular adhesion molecule 1 [Equus przewalskii]	32.5	32.5	100%	3.8	91%	gi|664743540|XP_008529085.1
☐	PREDICTED: intercellular adhesion molecule 3 [Erinaceus europae	32.0	32.0	100%	5.2	91%	gi|617615325|XP_007526090.1
☐	Chain A, Structure Of The Two Amino-Terminal Domains Of Humar	31.6	31.6	100%	6.5	91%	gi|157831419|1IAM_A
☐	PREDICTED: intercellular adhesion molecule 3 isoform X2 [Mustela	30.8	30.8	100%	13	91%	gi|511848267|XP_004748507.1
☐	PREDICTED: intercellular adhesion molecule 3 isoform X1 [Mustela	30.8	30.8	100%	13	91%	gi|511848265|XP_004748506.1
☐	PREDICTED: intercellular adhesion molecule 1 [Mustela putorius fu	30.8	30.8	100%	13	91%	gi|512013981|XP_004824339.1
☐	PREDICTED: intercellular adhesion molecule 1 [Mustela putorius fu	30.8	30.8	100%	13	91%	gi|511848273|XP_004748510.1
☐	PREDICTED: intercellular adhesion molecule 1 [Trichechus manatu	30.3	30.3	81%	18	100%	gi|471381640|XP_004378611.1
☐	Intercellular adhesion molecule 1 [Bos mutus]	29.9	29.9	100%	25	82%	gi|440899924|ELR51165.1
☐	hypothetical protein PANDA_010324 [Ailuropoda melanoleuca]	29.9	29.9	100%	25	82%	gi|281337407|EFB12991.1
☐	hypothetical protein PANDA_010318 [Ailuropoda melanoleuca]	29.9	29.9	100%	25	82%	gi|281337401|EFB12985.1
☐	PREDICTED: intercellular adhesion molecule 3-like [Ailuropoda me	29.9	29.9	100%	25	82%	gi|301772028|XP_002921447.1
☐	intercellular adhesion molecule 1 precursor [Bos taurus]	29.9	29.9	100%	25	82%	gi|27805931|NP_776773.1
☐	TPA: intercellular adhesion molecule 1 precursor [Bos taurus]	29.9	29.9	100%	25	82%	gi|296485887|DAA28002.1
☐	intercellular adhesion molecule 1 [Bos taurus]	29.9	29.9	100%	25	82%	gi|161701470|ABX75547.1
☐	intercellular adhesion molecule 3 precursor [Bos taurus]	29.9	29.9	100%	25	82%	gi|41386693|NP_776774.1
☐	TPA: intercellular adhesion molecule 3 precursor [Bos taurus]	29.9	29.9	100%	25	82%	gi|296485888|DAA28003.1
☐	PREDICTED: intercellular adhesion molecule 3 [Ursus maritimus]	29.9	29.9	100%	25	82%	gi|671031024|XP_008706311.1
☐	PREDICTED: intercellular adhesion molecule 1-like [Ailuropoda me	29.9	29.9	100%	25	82%	gi|301772040|XP_002921450.1
☐	PREDICTED: intercellular adhesion molecule 1 [Ursus maritimus]	29.9	29.9	100%	25	82%	gi|671031105|XP_008706351.1
☐	PREDICTED: intercellular adhesion molecule 3 [Galeopterus varieg	29.1	29.1	100%	46	82%	gi|667286729|XP_008576247.1
☐	PREDICTED: intercellular adhesion molecule 3 [Orcinus orca]	29.1	29.1	100%	47	82%	gi|466047921|XP_004277724.1
☐	PREDICTED: intercellular adhesion molecule 3 [Chrysochloris asiat	28.6	28.6	100%	64	82%	gi|586489511|XP_006875225.1
☐	enoyl-CoA hydratase [Achromobacter insuavis]	28.2	28.2	100%	84	82%	gi|493440403|WP_006395856.1
☐	FTR1 family iron permease [Pseudomonas sp. TKP]	28.2	28.2	90%	85	90%	gi|568200678|WP_024075042.1
☐	PREDICTED: LOW QUALITY PROTEIN: intercellular adhesion mol	28.2	28.2	100%	88	82%	gi|505846701|XP_004616823.1
☐	PREDICTED: intercellular adhesion molecule 1 [Rhinopithecus roxe	28.2	28.2	100%	88	82%	gi|724876734|XP_010372081.1
☐	PREDICTED: pentatricopeptide repeat-containing protein At5g1501	28.2	28.2	90%	88	80%	gi|502107026|XP_004493133.1
☐	PREDICTED: ribonucleoprotein PTB-binding 1 [Sorex araneus]	28.2	28.2	100%	89	82%	gi|505846707|XP_004616826.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	27.8	27.8	81%	90	89%	gi|665984837|WP_031350797.1

☐	enoyl-CoA hydratase [Mycobacterium avium]	27.8	27.8	81%	116	89%	gi|665984838|WP_031350798.1
☐	enoyl-CoA hydratase [Mycobacterium avium subsp. paratuberculos	27.8	27.8	81%	116	89%	gi|564160320|ETB04169.1
☐	enoyl-CoA hydratase/isomerase family protein [Mycobacterium aviu	27.8	27.8	81%	116	89%	gi|576447784|EUA41425.1
☐	enoyl-CoA hydratase/isomerase family protein [Mycobacterium intra	27.8	27.8	81%	116	89%	gi|576342910|ETZ37455.1
☐	enoyl-CoA hydratase [Mycobacterium indicus pranii]	27.8	27.8	81%	116	89%	gi|504754425|WP_014941527.1
☐	enoyl-CoA hydratase [Mycobacterium intracellulare]	27.8	27.8	81%	116	89%	gi|504197009|WP_014384111.1
☐	enoyl-CoA hydratase [Mycobacterium intracellulare]	27.8	27.8	81%	116	89%	gi|504195013|WP_014382115.1
☐	enoyl-CoA hydratase [Mycobacterium intracellulare]	27.8	27.8	81%	116	89%	gi|504192512|WP_014379614.1
☐	enoyl-CoA hydratase/isomerase [Mycobacterium vulneris]	27.8	27.8	81%	116	89%	gi|602522334|CDO27409.1
☐	enoyl-CoA hydratase [Mycobacterium smegmatis]	27.8	27.8	81%	116	89%	gi|489990538|WP_003893595.1
☐	enoyl-CoA hydratase/isomerase [Mycobacterium farcinogenes]	27.8	27.8	81%	116	89%	gi|633838277|CDP84038.1
☐	enoyl-CoA hydratase [Mycobacterium hassiacum]	27.8	27.8	81%	116	89%	gi|491838896|WP_005626218.1
☐	enoyl-CoA hydratase [Mycobacterium fortuitum]	27.8	27.8	81%	116	89%	gi|489978170|WP_003881307.1
☐	enoyl-CoA hydratase [Mycobacterium thermoresistibile]	27.8	27.8	81%	116	89%	gi|490024790|WP_003927267.1
☐	enoyl-CoA hydratase/carnithine racemase [Mycobacterium triplex]	27.8	27.8	81%	116	89%	gi|620041031|CDO89870.1
☐	enoyl-CoA hydratase [Mycobacterium smegmatis]	27.8	27.8	81%	116	89%	gi|504690236|WP_014877338.1
☐	enoyl-CoA hydratase [Mycobacterium rhodesiae]	27.8	27.8	81%	116	89%	gi|503980274|WP_014214268.1
☐	enoyl-CoA hydratase [Mycobacterium sp. URHD0025]	27.8	27.8	81%	116	89%	gi|656080510|WP_029111550.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	27.8	27.8	81%	116	89%	gi|489974194|WP_003877383.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	27.8	27.8	81%	116	89%	gi|565650440|WP_023897844.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	27.8	27.8	81%	116	89%	gi|564856878|WP_023865499.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	27.8	27.8	81%	116	89%	gi|564861315|WP_023868654.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	27.8	27.8	81%	116	89%	gi|489969930|WP_003873168.1
☐	enoyl-CoA hydratase [Mycobacterium avium]	27.8	27.8	81%	116	89%	gi|497661605|WP_009975789.1
☐	MULTISPECIES: enoyl-CoA hydratase [Mycobacterium]	27.8	27.8	81%	116	89%	gi|500043520|WP_011724238.1
☐	hypothetical protein [Mycobacterium yongonense]	27.8	27.8	81%	116	89%	gi|523909424|WP_020822025.1
☐	enoyl-CoA hydratase [Mycobacterium intracellulare]	27.8	27.8	81%	116	89%	gi|519032904|WP_020188779.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

cell surface glycoprotein, partial [Homo sapiens]

Sequence ID: gi|338068|gb|AAA60392.1| **Length:** 151 **Number of Matches:** 1

Related Information

Range 1: 58 to 68 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
36.3 bits(78)	0.18	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RANLTVVLLRG  11
            RANLTVVLLRG
Sbjct  58   RANLTVVLLRG  68
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, D1d2-Icam-1 Fully Glycosylated, Variation Of D1-D2 Interdomain Angle In Different Crystal Structures.

Sequence ID: gi|6573330|pdb|1D3L|A **Length:** 185 **Number of Matches:** 1

▷ See 2 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 116 to 126 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
36.3 bits(78)	0.19	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RANLTVVLLRG  11
            RANLTVVLLRG
Sbjct  116  RANLTVVLLRG  126
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, The Crystal Structure For The N-Terminal Two Domains Of Icam-1

Sequence ID: gi|3318903|pdb|1IC1|A **Length:** 190 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 116 to 126 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
36.3 bits(78)	0.19	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RANLTVVLLRG  11
            RANLTVVLLRG
Sbjct  116  RANLTVVLLRG  126
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain B, The Crystal Structure For The N-Terminal Two Domains Of Icam-1

Sequence ID: gi|3318904|pdb|1IC1|B **Length:** 190 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 116 to 126 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
36.3 bits(78)	0.19	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RANLTVVLLRG  11
            RANLTVVLLRG
Sbjct  116  RANLTVVLLRG  126
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of Alphal I Domain In Complex With Icam-1

Sequence ID: gi|28373771|pdb|1MQ8|A **Length:** 291 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 116 to 126 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
36.3 bits(78)	0.20	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RANLTVVLLRG  11
            RANLTVVLLRG
Sbjct  116  RANLTVVLLRG  126
```

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVGXJJG701R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   Formatting options   Download   How to read this page   Blast report description

ICAM1_RLNPTVTYGDDSFSAKA_Mod

RID BVGXJJG701R (Expires on 01-21 09:55 am)

Query ID	lcl|386285	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	17	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

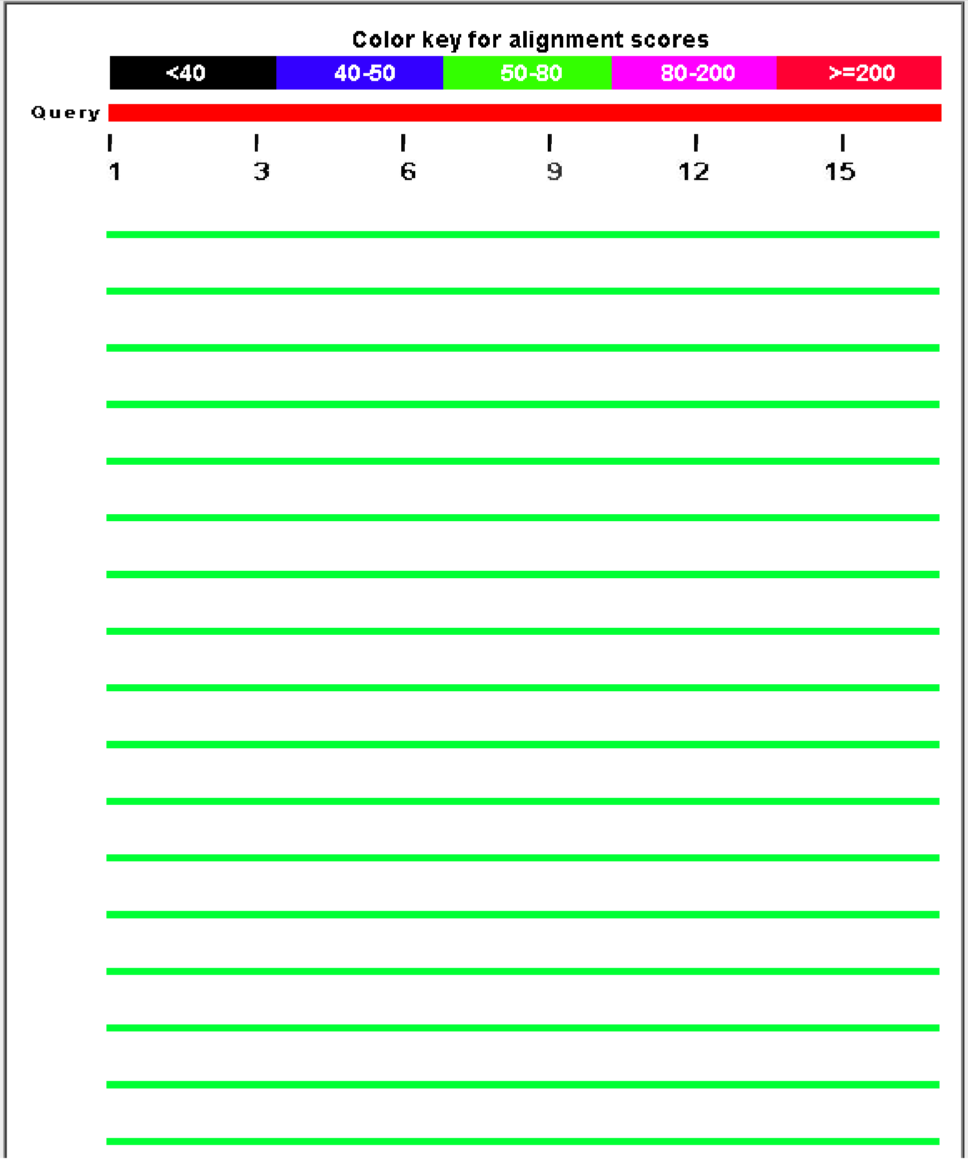
Graphic Summary

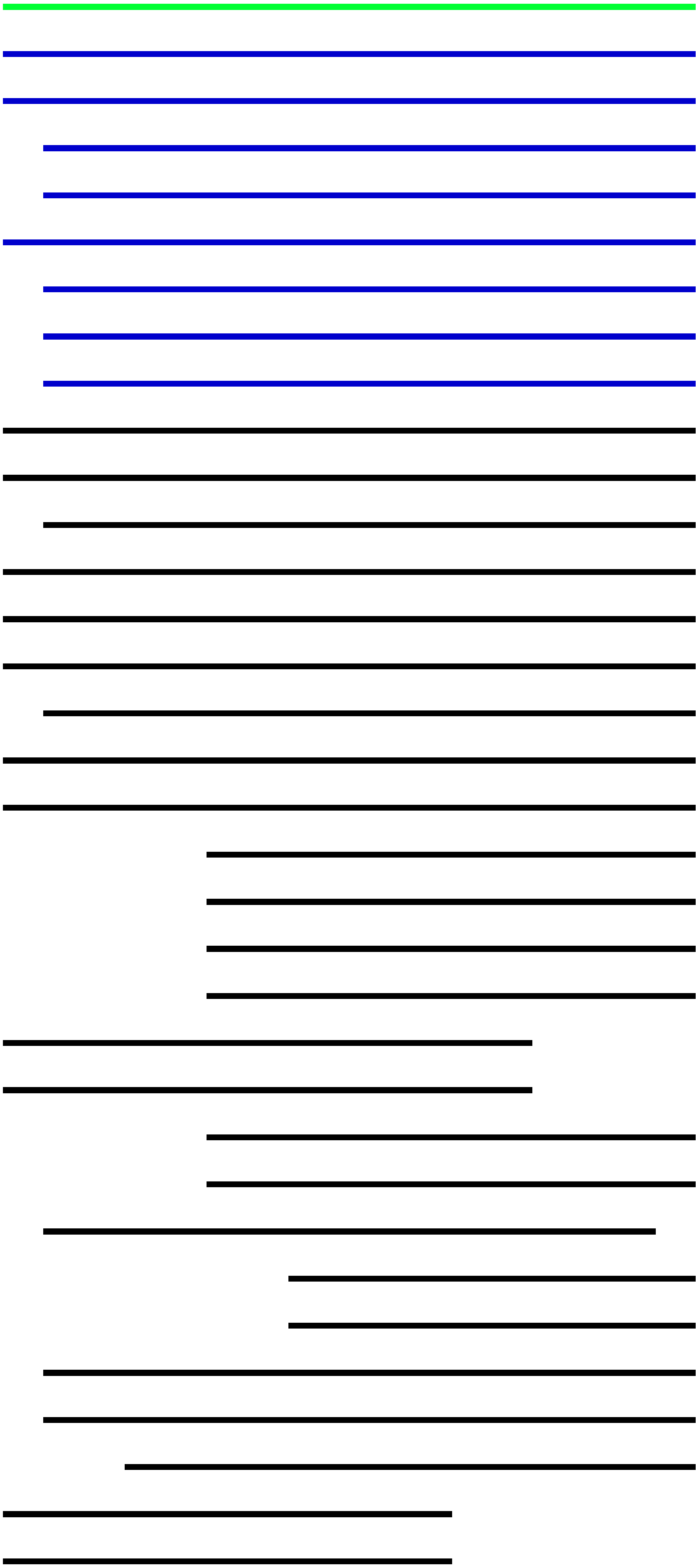
Show Conserved Domains

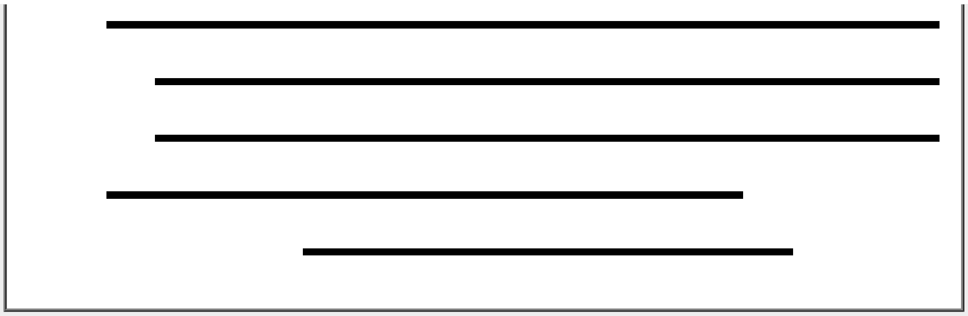
No putative conserved domains have been detected

Distribution of 107 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Structural Plasticity In Igsf Domain 4 Of Icam-1 Mediates Cell Surfac	53.2	53.2	100%	9e-07	94%	2OZ4_A
☐	Chain A, The Crystal Structure Of Icam-1 D3-D5 Fragment [Homo sapiens]	53.2	53.2	100%	9e-07	94%	1P53_A
☐	cell surface glycoprotein [Homo sapiens]	53.2	53.2	100%	9e-07	94%	AAA60393.1
☐	Chain A, Crystal Structure Of Alphal I Domain In Complex With Icam-1 [Homo	53.2	53.2	100%	9e-07	94%	1MQ8_A
☐	unnamed protein product [Homo sapiens]	53.2	53.2	100%	9e-07	94%	BAG62944.1
☐	unnamed protein product [Homo sapiens]	53.2	53.2	100%	1e-06	94%	BAG60348.1
☐	unnamed protein product [Homo sapiens]	53.2	53.2	100%	1e-06	94%	BAG61077.1
☐	Chain I, Cryo-Em Structure Of Human Coxsackievirus A21 Complexed With F	53.2	53.2	100%	1e-06	94%	1Z7Z_I
☐	intercellular adhesion molecule 1 [Pan troglodytes]	53.2	53.2	100%	1e-06	94%	AAA35415.1
☐	intercellular adhesion molecule 1 [Homo sapiens]	53.2	53.2	100%	1e-06	94%	AAQ14902.1
☐	intercellular adhesion molecule-1 precursor [Homo sapiens]	53.2	53.2	100%	1e-06	94%	AAA52709.1
☐	PREDICTED: intercellular adhesion molecule 1 [Pan paniscus]	53.2	53.2	100%	1e-06	94%	XP_003809639.1
☐	intercellular adhesion molecule 1 precursor [Gorilla gorilla]	53.2	53.2	100%	1e-06	94%	NP_001266532.1
☐	intercellular adhesion molecule 1 precursor [Pan troglodytes]	53.2	53.2	100%	1e-06	94%	NP_001009946.1
☐	intercellular adhesion molecule 1 precursor [Homo sapiens]	53.2	53.2	100%	1e-06	94%	NP_000192.2
☐	intercellular adhesion molecule 1 [Homo sapiens]	53.2	53.2	100%	1e-06	94%	AAQ14901.1
☐	Homo sapiens intercellular adhesion molecule 1 (CD54), human rhinovirus rec	53.2	53.2	100%	1e-06	94%	AAP36234.1
☐	Snap ICAM-1 fusion protein [synthetic construct]	53.2	53.2	100%	1e-06	94%	AIZ77117.1
☐	PREDICTED: intercellular adhesion molecule 1 [Pongo abelii]	43.9	43.9	100%	0.001	88%	XP_002828698.2
☐	intercellular adhesion molecule 1 [Pongo pygmaeus]	43.9	43.9	100%	0.001	88%	AAQ14904.1
☐	PREDICTED: intercellular adhesion molecule 1 [Papio anubis]	42.6	42.6	94%	0.003	81%	XP_009191725.1
☐	PREDICTED: intercellular adhesion molecule 1 [Rhinopithecus roxellana]	42.2	42.2	94%	0.005	81%	XP_010372081.1
☐	PREDICTED: intercellular adhesion molecule 1 [Nomascus leucogenys]	41.4	41.4	100%	0.009	82%	XP_003275780.1
☐	PREDICTED: intercellular adhesion molecule 1 [Chlorocebus sabaeus]	40.1	40.1	94%	0.023	75%	XP_007993410.1
☐	intercellular adhesion molecule 1 precursor [Macaca mulatta]	40.1	40.1	94%	0.023	75%	NP_001040600.1
☐	Intercellular adhesion molecule 1 [Macaca mulatta]	40.1	40.1	94%	0.023	75%	EHH29617.1
☐	PREDICTED: intercellular adhesion molecule 1 [Tarsius syrichta]	39.7	39.7	100%	0.031	71%	XP_008058814.1
☐	PREDICTED: intercellular adhesion molecule 1 [Ceratotherium simum simum]	36.7	36.7	100%	0.29	76%	XP_004442677.1
☐	PREDICTED: intercellular adhesion molecule 1 [Macaca fascicularis]	35.0	35.0	94%	1.0	69%	XP_005587991.1

☐	PREDICTED: intercellular adhesion molecule 1 [Ictidomys tridecemlineatus]	35.0	35.0	100%	1.0	71%	XP_005336176.1
☐	PREDICTED: intercellular adhesion molecule 1 [Balaenoptera acutorostrata s	34.1	34.1	100%	1.9	71%	XP_007169059.1
☐	Intercellular adhesion molecule 1 [Heterocephalus glaber]	33.7	33.7	100%	2.6	71%	EHB03343.1
☐	PREDICTED: intercellular adhesion molecule 1 [Saimiri boliviensis boliviensis	33.7	33.7	94%	2.6	75%	XP_003938996.1
☐	PREDICTED: intercellular adhesion molecule 1 [Heterocephalus glaber]	33.7	33.7	100%	2.6	71%	XP_004865541.1
☐	PREDICTED: LOW QUALITY PROTEIN: intercellular adhesion molecule 1 [H	33.7	33.7	100%	2.6	71%	XP_004885318.1
☐	hypothetical protein [Bartonella queenslandensis]	32.0	32.0	70%	7.9	83%	WP_039760587.1
☐	hypothetical protein [Bartonella rattimassiliensis]	32.0	32.0	70%	7.9	83%	WP_007347503.1
☐	hypothetical protein [Bartonella elizabethae]	32.0	32.0	70%	7.9	83%	WP_005774841.1
☐	hypothetical protein [Bartonella tribocorum]	32.0	32.0	70%	7.9	83%	WP_012232107.1
☐	TonB-dependent heme/hemoglobin receptor family protein [Bartonella schoen	32.0	32.0	76%	8.9	67%	CBI81923.1
☐	outer membrane hemin receptor [Bartonella schoenbuchensis]	32.0	32.0	76%	8.9	67%	CDP79874.1
☐	hypothetical protein [Bartonella taylorii]	31.6	31.6	70%	11	75%	WP_004861272.1
☐	hypothetical protein [Bartonella sp. DB5-6]	31.6	31.6	70%	11	75%	WP_007553558.1
☐	hypothetical protein NDAI_0A00940 [Naumovozyma dairenensis CBS 421]	31.6	31.6	88%	12	61%	XP_003667495.1
☐	hypothetical protein [Bartonella sp. R4(2010)]	31.2	31.2	58%	15	90%	WP_019220110.1
☐	hypothetical protein [Bartonella birtlesii]	31.2	31.2	58%	15	90%	WP_006590415.1
☐	PREDICTED: intercellular adhesion molecule 1 [Callithrix jacchus]	31.2	31.2	94%	16	69%	XP_008985482.1
☐	PREDICTED: intercellular adhesion molecule 1 [Octodon degus]	31.2	31.2	94%	16	75%	XP_004633061.1
☐	hypothetical protein [Streptomyces sp. NRRL F-525]	31.2	31.2	82%	17	57%	WP_033281104.1
☐	nucleotide pyrophosphatase [Bifidobacterium saguini]	30.8	30.8	64%	22	82%	WP_033890129.1
☐	ATP-dependent DNA helicase RecQ [Cytophaga fermentans DSM 9555]	30.8	30.8	64%	23	83%	GAF04645.1
☐	PREDICTED: intercellular adhesion molecule 1 [Myotis lucifugus]	30.3	30.3	100%	30	59%	XP_006104121.1
☐	PREDICTED: intercellular adhesion molecule 1 isoform X2 [Chinchilla lanigera	30.3	30.3	94%	30	69%	XP_005405644.1
☐	PREDICTED: intercellular adhesion molecule 1 isoform X1 [Chinchilla lanigera	30.3	30.3	94%	30	69%	XP_005405643.1
☐	beta-galactosidase [Streptomyces violaceusniger]	30.3	30.3	76%	31	77%	WP_014056372.1
☐	hypothetical protein [Actinobacillus capsulatus]	29.9	29.9	58%	40	83%	WP_018651119.1
☐	hypothetical protein [Bacteroides finegoldii]	29.9	29.9	58%	41	80%	WP_007756738.1
☐	putative tetratricopeptide repeat-containing domain protein [Bacteroides fineg	29.9	29.9	58%	41	80%	WP_022275680.1
☐	hypothetical protein [Bacteroides finegoldii]	29.9	29.9	58%	41	80%	WP_007767617.1
☐	endoglucanase [Streptomyces sp. NRRL F-525]	29.9	29.9	76%	41	77%	WP_033281181.1
☐	hypothetical protein [Rhizobiales bacterium YIM 77505]	29.9	29.9	58%	42	71%	WP_037015194.1
☐	excinuclease ABC subunit A [Corynebacterium massiliense]	29.9	29.9	88%	42	57%	WP_022863416.1
☐	adhesion exoprotein [Pediococcus pentosaceus]	29.9	197	76%	42	58%	WP_011672852.1
☐	hypothetical protein [Bartonella grahamii]	29.5	29.5	70%	52	75%	WP_015856692.1
☐	hypothetical protein [Bartonella koehlerae]	29.5	29.5	70%	53	75%	WP_034460029.1
☐	hypothetical protein [Bartonella henselae]	29.5	29.5	70%	53	75%	WP_038525266.1
☐	hypothetical protein [Bartonella henselae]	29.5	29.5	70%	53	75%	WP_034454929.1
☐	hypothetical protein [Bartonella senegalensis]	29.5	29.5	70%	53	75%	WP_019222025.1
☐	hypothetical protein [Bartonella henselae]	29.5	29.5	70%	53	75%	WP_011181121.1
☐	hypothetical protein [Bartonella alsatica]	29.5	29.5	70%	53	75%	WP_005864603.1
☐	hypothetical protein [Inquilinus limosus]	29.5	29.5	47%	55	100%	WP_034830816.1
☐	PREDICTED: LOW QUALITY PROTEIN: intercellular adhesion molecule 1 [C	29.5	29.5	94%	56	69%	XP_003460914.2
☐	MULTISPECIES: type VI secretion protein VgrG [Enterobacter]	29.5	29.5	70%	56	79%	WP_032648936.1
☐	hypothetical protein CHLNCDRAFT_58365 [Chlorella variabilis]	29.5	29.5	58%	57	80%	XP_005846113.1

☐	Tubulin alpha-2/alpha-4 chain [Cerapachys biroi]	29.1	29.1	64%	68	82%	EZA57249.1
☐	hypothetical protein [Bacteroides fragilis]	29.1	29.1	64%	74	82%	WP_005811591.1
☐	hypothetical protein [Bacteroides fragilis]	29.1	29.1	64%	74	82%	WP_032535354.1
☐	polysaccharide deacetylase-like protein [Cytophaga hutchinsonii]	29.1	29.1	52%	76	89%	WP_011584100.1
☐	Eukaryotic aspartyl protease family protein, putative [Theobroma cacao]	29.1	29.1	52%	77	89%	XP_007029843.1
☐	tRNA adenylyltransferase [Frankia sp. QA3]	29.1	29.1	47%	77	100%	WP_009741483.1
☐	polynucleotide adenylyltransferase/metal dependent phosphohydrolase [Fran	29.1	29.1	47%	77	100%	WP_006543050.1
☐	poly(A) polymerase [Frankia sp. BMG5.12]	29.1	29.1	47%	77	100%	WP_018636676.1
☐	PREDICTED: intercellular adhesion molecule 1 [Lipotes vexillifer]	29.1	29.1	100%	77	65%	XP_007460718.1
☐	hypothetical protein [Bacteroides sp. UW]	29.1	29.1	64%	77	82%	WP_033572567.1
☐	hypothetical protein [Bacteroides fragilis]	29.1	29.1	64%	77	82%	WP_032543005.1
☐	hypothetical protein [Bacteroides fragilis]	29.1	29.1	64%	77	82%	WP_032543004.1
☐	hypothetical protein [Bacteroides fragilis]	29.1	29.1	64%	77	82%	WP_032530802.1
☐	hypothetical protein [Bacteroides fragilis]	29.1	29.1	64%	77	82%	WP_005811589.1
☐	vanomycin resistance protein VanB [Clostridiales bacterium 1_7_47FAA]	29.1	29.1	52%	77	89%	WP_008716619.1
☐	vanomycin resistance protein VanB [Clostridiales bacterium VE202-28]	29.1	29.1	52%	77	89%	WP_025487055.1
☐	Ig domain protein group 2 domain protein [Gemmatimonadetes bacterium KB	29.1	29.1	64%	77	82%	AHG89512.1
☐	hypothetical protein J421_2485 [Gemmatimonadetes bacterium KBS708]	29.1	29.1	64%	77	82%	AHG90022.1
☐	outer membrane hemin receptor [Bartonella bovis]	29.1	29.1	76%	77	60%	WP_010702223.1
☐	virulence protein E [Corynebacterium ulcerans]	29.1	29.1	52%	78	89%	WP_013911548.1
☐	Ig domain protein group 2 domain protein [Gemmatimonadetes bacterium KB	29.1	29.1	64%	78	82%	AHG90021.1
☐	thermostable neutral protease NprT precursor [Cytophaga fermentans DSM 9	29.1	29.1	52%	78	89%	GAF04339.1
☐	hypothetical protein [Micavibrio aeruginosavorus]	29.1	29.1	76%	78	69%	WP_015468607.1
☐	hypothetical protein [Bartonella washoensis]	28.6	28.6	58%	99	80%	WP_006924877.1
☐	hypothetical protein [Bartonella washoensis]	28.6	28.6	58%	99	80%	WP_006924204.1
☐	hypothetical protein SXBG_00145 [Synechococcus phage S-CAM1]	28.6	28.6	88%	103	43%	YP_007673059.1

Alignments

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Chain A, Structural Plasticity In Igsf Domain 4 Of Icam-1 Mediates Cell Surface Dimerization

Sequence ID: pdb|2OZ4|A **Length:** 265 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 46 to 62 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
53.2 bits(118)	9e-07	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   RLNPTVTYGDDSFSAKA  17
           RLNPTVTYG+DSFSAKA
Sbjct  46  RLNPTVTYGNDSFSAKA  62
```

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Chain A, The Crystal Structure Of Icam-1 D3-D5 Fragment

Sequence ID: pdb|1P53|A **Length:** 266 **Number of Matches:** 1

See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins

Range 1: 47 to 63 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
53.2 bits(118)	9e-07	16/17(94%)	17/17(100%)	0/17(0%)

identical to the subject

```
Query  1   RLNPTVTYGDDSFSAKA  17
           RLNPTVTYG+DSFSAKA
Sbjct  47  RLNPTVTYGNDSFSAKA  63
```

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cell surface glycoprotein, partial [Homo sapiens]

Sequence ID: gb|AAA60393.1| **Length:** 276 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 2 to 18 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
53.2 bits(118)	9e-07	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   RLNPTVTYGDDSFSAKA  17
           RLNPTVTYG+DSFSAKA
Sbjct  2   RLNPTVTYGNDSFSAKA  18
```

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Chain A, Crystal Structure Of Alphal I Domain In Complex With Icam-1

Sequence ID: pdb|1MQ8|A **Length:** 291 **Number of Matches:** 1

See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 231 to 247 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
53.2 bits(118)	9e-07	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1    RLNPTVTYGDDSFSAKA  17
            RLNPTVTYG+DSFSAKA
Sbjct  231  RLNPTVTYGNDSFSAKA  247
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG62944.1| **Length:** 310 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 36 to 52 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
53.2 bits(118)	9e-07	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   RLNPTVTYGDDSFSAKA  17
           RLNPTVTYG+DSFSAKA
Sbjct  36  RLNPTVTYGNDSFSAKA  52
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download

How to read this page Blast report description

ICAM1_RLNPTVTYGNDSFSAKA_NonMod

RID B9FFSHWS01R (Expires on 01-14 13:40 pm)

Query ID lcl|279146
Description None
Molecule type amino acid
Query Length 17

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

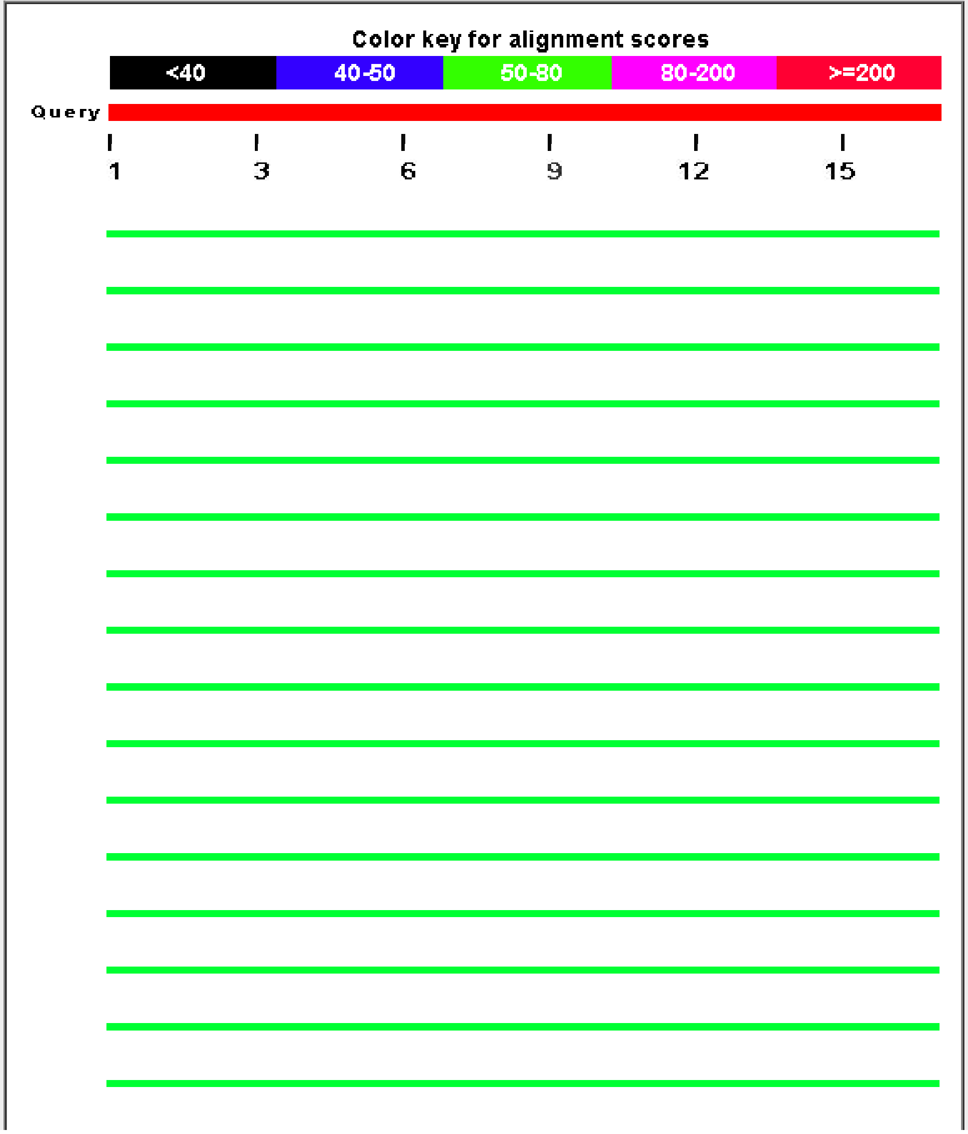
Graphic Summary

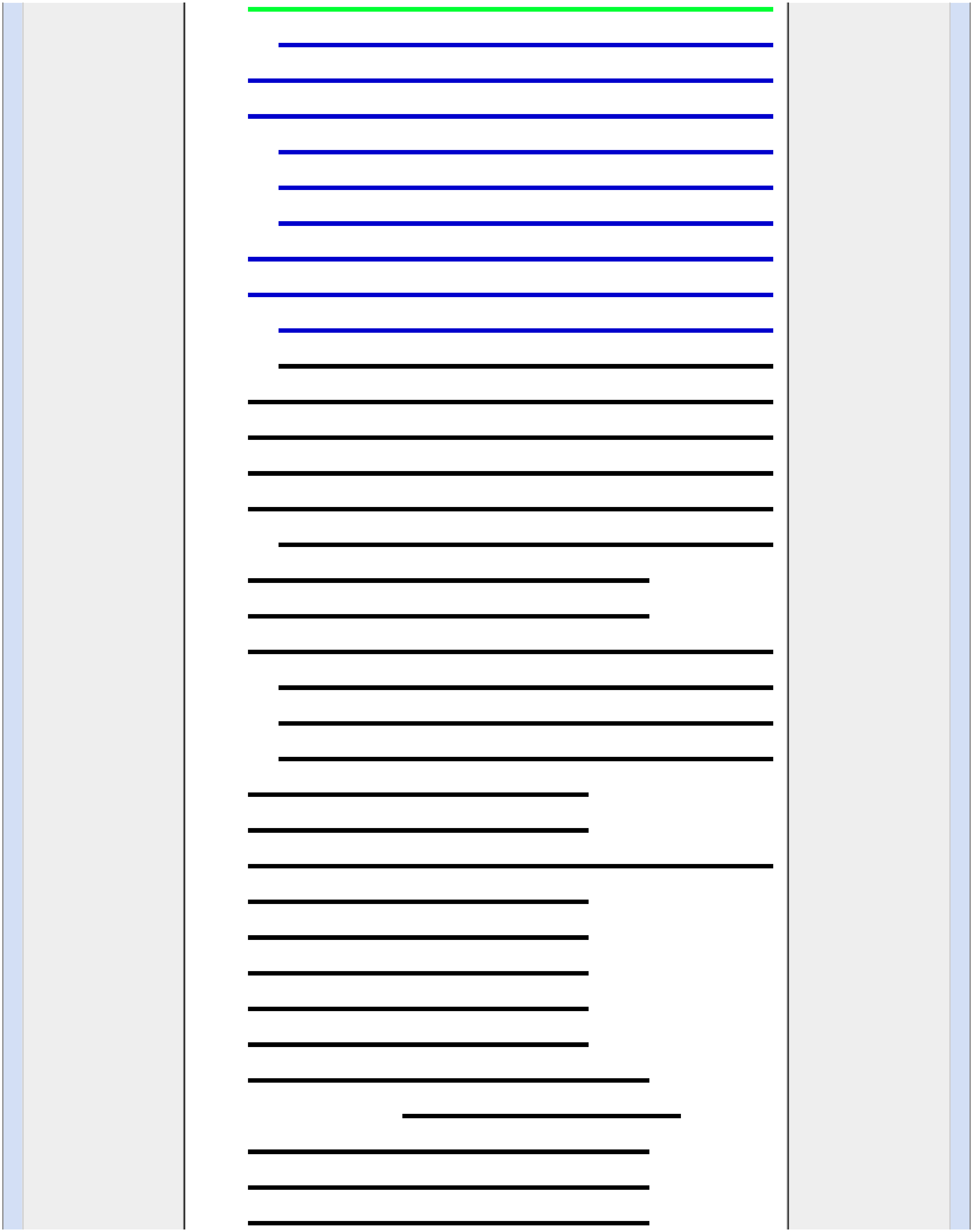
Show Conserved Domains

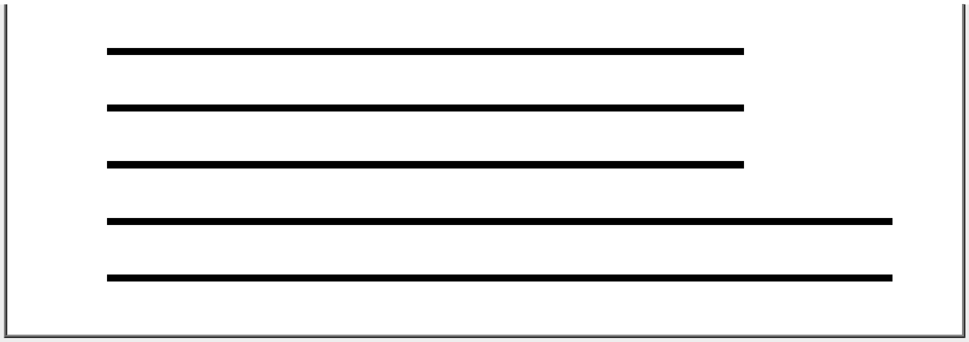
No putative conserved domains have been detected

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Structural Plasticity In Igsf Domain 4 Of Icam-1 Mediates (	55.8	55.8	100%	1e-07	100%	gi|158429270|2OZ4_A
☐	Chain A, The Crystal Structure Of Icam-1 D3-D5 Fragment [Homo s	55.8	55.8	100%	1e-07	100%	gi|48425199|1P53_A
☐	cell surface glycoprotein [Homo sapiens]	55.8	55.8	100%	1e-07	100%	gi|338069|AAA60393.1
☐	Chain A, Crystal Structure Of Alphal I Domain In Complex With Icar	55.8	55.8	100%	1e-07	100%	gi|28373771|1MQ8_A
☐	unnamed protein product [Homo sapiens]	55.8	55.8	100%	1e-07	100%	gi|194376370|BAG62944.1
☐	unnamed protein product [Homo sapiens]	55.8	55.8	100%	1e-07	100%	gi|194388760|BAG60348.1
☐	unnamed protein product [Homo sapiens]	55.8	55.8	100%	1e-07	100%	gi|194386534|BAG61077.1
☐	Chain I, Cryo-Em Structure Of Human Coxsackievirus A21 Complex	55.8	55.8	100%	1e-07	100%	gi|73535843|1Z7Z_I
☐	intercellular adhesion molecule 1 [Pan troglodytes]	55.8	55.8	100%	1e-07	100%	gi|176796|AAA35415.1
☐	intercellular adhesion molecule 1 [Homo sapiens]	55.8	55.8	100%	1e-07	100%	gi|33340675|AAQ14902.1
☐	intercellular adhesion molecule-1 precursor [Homo sapiens]	55.8	55.8	100%	1e-07	100%	gi|306896|AAA52709.1
☐	PREDICTED: intercellular adhesion molecule 1 [Pan paniscus]	55.8	55.8	100%	1e-07	100%	gi|397476504|XP_003809639.1
☐	intercellular adhesion molecule 1 precursor [Gorilla gorilla]	55.8	55.8	100%	1e-07	100%	gi|525342618|NP_001266532.1
☐	intercellular adhesion molecule 1 precursor [Pan troglodytes]	55.8	55.8	100%	1e-07	100%	gi|57977287|NP_001009946.1
☐	intercellular adhesion molecule 1 precursor [Homo sapiens]	55.8	55.8	100%	1e-07	100%	gi|167466198|NP_000192.2
☐	intercellular adhesion molecule 1 [Homo sapiens]	55.8	55.8	100%	1e-07	100%	gi|33340673|AAQ14901.1
☐	Homo sapiens intercellular adhesion molecule 1 (CD54), human rhi	55.8	55.8	100%	1e-07	100%	gi|30583971|AAP36234.1
☐	PREDICTED: intercellular adhesion molecule 1 [Rhinopithecus roxe	44.8	44.8	94%	6e-04	88%	gi|724876734|XP_010372081.1
☐	PREDICTED: intercellular adhesion molecule 1 [Pongo abelii]	43.9	43.9	100%	0.001	88%	gi|395750443|XP_002828698.2
☐	intercellular adhesion molecule 1 [Pongo pygmaeus]	43.9	43.9	100%	0.001	88%	gi|33340679|AAQ14904.1
☐	PREDICTED: intercellular adhesion molecule 1 [Chlorocebus sabae	42.6	42.6	94%	0.003	81%	gi|635036004|XP_007993410.1
☐	intercellular adhesion molecule 1 precursor [Macaca mulatta]	42.6	42.6	94%	0.003	81%	gi|114051944|NP_001040600.1
☐	Intercellular adhesion molecule 1 [Macaca mulatta]	42.6	42.6	94%	0.003	81%	gi|355703126|EHH29617.1
☐	PREDICTED: intercellular adhesion molecule 1 [Tarsius syrichta]	42.2	42.2	100%	0.004	76%	gi|640804811|XP_008058814.1
☐	PREDICTED: intercellular adhesion molecule 1 [Nomascus leucoge	41.4	41.4	100%	0.008	82%	gi|332253293|XP_003275780.1
☐	PREDICTED: intercellular adhesion molecule 1 [Papio anubis]	40.1	40.1	94%	0.022	75%	gi|685605924|XP_009191725.1
☐	PREDICTED: intercellular adhesion molecule 1 [Macaca fascicularis	37.5	37.5	94%	0.15	75%	gi|544508624|XP_005587991.1
☐	PREDICTED: intercellular adhesion molecule 1 [Ceratotherium simu	36.7	36.7	100%	0.27	76%	gi|478537121|XP_004442677.1
☐							

	Intercellular adhesion molecule 1 [Heterocephalus glaber]	35.0	35.0	100%	0.95	71%	gi|351700424|EHB03343.1
☐	PREDICTED: intercellular adhesion molecule 1 [Heterocephalus gla	35.0	35.0	100%	0.95	71%	gi|513008224|XP_004865541.1
☐	PREDICTED: LOW QUALITY PROTEIN: intercellular adhesion mol	35.0	35.0	100%	0.95	71%	gi|512843756|XP_004885318.1
☐	PREDICTED: intercellular adhesion molecule 1 [Saimiri boliviensis	34.6	34.6	94%	1.3	75%	gi|403296180|XP_003938996.1
☐	TonB-dependent heme/hemoglobin receptor family protein [Bartone	34.6	34.6	76%	1.3	73%	gi|319408270|CBI81923.1
☐	outer membrane hemin receptor [Bartonella schoenbuchensis]	34.6	34.6	76%	1.3	73%	gi|631776143|CDP79874.1
☐	PREDICTED: intercellular adhesion molecule 1 [Ictidomys tridecem	33.3	33.3	100%	3.3	71%	gi|532101112|XP_005336176.1
☐	PREDICTED: intercellular adhesion molecule 1 isoform X2 [Chinchi	32.9	32.9	94%	4.5	75%	gi|533185214|XP_005405644.1
☐	PREDICTED: intercellular adhesion molecule 1 isoform X1 [Chinchi	32.9	32.9	94%	4.5	75%	gi|533185212|XP_005405643.1
☐	PREDICTED: intercellular adhesion molecule 1 [Callithrix jacchus]	32.0	32.0	94%	8.3	69%	gi|675757750|XP_008985482.1
☐	hypothetical protein [Bacteroides fragilis]	31.6	31.6	64%	11	91%	gi|492329327|WP_005811591.1
☐	hypothetical protein [Bacteroides fragilis]	31.6	31.6	64%	11	91%	gi|695337898|WP_032535354.1
☐	PREDICTED: intercellular adhesion molecule 1 [Balaenoptera acutc	31.6	31.6	100%	11	65%	gi|594631039|XP_007169059.1
☐	hypothetical protein [Bacteroides sp. UW]	31.6	31.6	64%	11	91%	gi|723595040|WP_033572567.1
☐	hypothetical protein [Bacteroides fragilis]	31.6	31.6	64%	11	91%	gi|695346329|WP_032543005.1
☐	hypothetical protein [Bacteroides fragilis]	31.6	31.6	64%	11	91%	gi|695346328|WP_032543004.1
☐	hypothetical protein [Bacteroides fragilis]	31.6	31.6	64%	11	91%	gi|695332979|WP_032530802.1
☐	hypothetical protein [Bacteroides fragilis]	31.6	31.6	64%	11	91%	gi|492329325|WP_005811589.1
☐	outer membrane hemin receptor [Bartonella bovis]	31.6	31.6	76%	11	67%	gi|498388263|WP_010702223.1
☐	virulence protein E [Corynebacterium ulcerans]	31.6	31.6	52%	11	100%	gi|503677472|WP_013911548.1
☐	heme transporter CcmC [Bartonella quintana]	31.2	31.2	76%	16	67%	gi|504736811|WP_014923913.1
☐	TonB-dependent hemoglobin/transferrin/lactoferrin receptor family p	31.2	31.2	76%	16	67%	gi|654330448|KEC59997.1
☐	hypothetical protein Q651_01216 [Bartonella quintana BQ2-D70]	31.2	31.2	76%	16	67%	gi|572288853|ETS11689.1
☐	heme transporter CcmC [Bartonella quintana]	31.2	31.2	76%	16	67%	gi|499492564|WP_011179204.1
☐	heme transporter CcmC [Bartonella melophagi]	31.2	31.2	76%	16	67%	gi|494742022|WP_007477430.1
☐	outer membrane hemin receptor [Bartonella schoenbuchensis]	31.2	31.2	76%	16	67%	gi|498389607|WP_010703528.1
☐	cephalosporin-C deacetylase [Prevotella bryantii]	30.8	30.8	94%	21	38%	gi|493325652|WP_006282901.1
☐	acetyl xylan esterase [Prevotella bryantii]	30.8	30.8	94%	21	38%	gi|653247601|WP_027453062.1
☐	MULTISPECIES: type VI secretion protein VgrG [Enterobacter]	30.8	30.8	70%	21	79%	gi|695721986|WP_032648936.1
☐	hypothetical protein CD33_15155 [Lysinibacillus sinduriensis BLB-1	30.3	30.3	58%	27	91%	gi|704817868|KGR74435.1
☐	hypothetical protein [Ureibacillus thermosphaericus]	30.3	30.3	58%	27	91%	gi|648237934|WP_026019083.1
☐	endoglucanase [Streptomyces resistomycificus]	30.3	30.3	70%	28	83%	gi|662079400|WP_030042518.1
☐	PREDICTED: intercellular adhesion molecule 1 [Otolemur garnettii]	30.3	30.3	100%	29	65%	gi|395851075|XP_003798092.1
☐	n-acetylmuramoyl-L-alanine amidase [Eubacterium sp. CAG:38]	30.3	30.3	82%	29	73%	gi|548214048|WP_022433505.1
☐	hypothetical protein [Bacteroides finegoldii]	29.9	29.9	70%	38	75%	gi|495035370|WP_007760903.1
☐	beta-ketoacyl synthase [Niabella aurantiaca]	29.9	29.9	100%	39	71%	gi|517459815|WP_018630569.1
☐	hypothetical protein [Bartonella rattimassiliensis]	29.5	29.5	70%	49	75%	gi|494588908|WP_007347503.1
☐	hypothetical protein [Bartonella elizabethae]	29.5	29.5	70%	49	75%	gi|492193964|WP_005774841.1
☐	hypothetical protein [Bartonella tribocorum]	29.5	29.5	70%	49	75%	gi|501189089|WP_012232107.1
☐	fimbrial protein [Lysobacter defluvii]	29.5	29.5	70%	49	83%	gi|652750201|WP_027070646.1
☐	3-dehydroquinate dehydratase [Roseivivax sp. 22II-s10s]	29.5	29.5	82%	50	64%	gi|574574310|ETW11389.1
☐	hypothetical protein [Niabella aurantiaca]	29.5	29.5	76%	52	69%	gi|648618099|WP_026309850.1
☐	hypothetical protein P409_00850 [Inquilinus limosus MP06]	29.5	29.5	47%	52	100%	gi|699016581|KGM36053.1
☐	endoglucanase [Streptomyces sp. NRRL F-525]	29.5	29.5	76%	53	77%	gi|702842059|WP_033281181.1
☐	hypothetical protein [Bartonella taylorii]	29.1	29.1	70%	68	67%	gi|490999549|WP_004861272.1

☐	hypothetical protein [Bartonella sp. DB5-6]	29.1	29.1	70%	68	67%	gi|494818150|WP_007553558.1
☐	amino acid ABC transporter [Ketogulonicigenium vulgare]	29.1	29.1	58%	71	90%	gi|503148425|WP_013383086.1
☐	hypothetical protein NCAS_0A01150 [Naumovozyma castellii CBS	29.1	29.1	52%	71	89%	gi|366986599|XP_003673066.1
☐	multidrug ABC transporter ATP-binding protein [Chryseobacterium	29.1	29.1	88%	72	73%	gi|653130459|WP_027379845.1
☐	Intercellular adhesion molecule 1 [Myotis brandtii]	29.1	29.1	100%	72	59%	gi|521021531|EPQ03319.1
☐	PREDICTED: intercellular adhesion molecule 1 [Myotis brandtii]	29.1	29.1	100%	72	59%	gi|554528924|XP_005859267.1
☐	dNA gyrase B subunit protein [Firmicutes bacterium CAG:103]	29.1	29.1	64%	73	82%	gi|512388095|WP_016413966.1
☐	hypothetical protein NDAI_0A00940 [Naumovozyma dairenensis CE	29.1	29.1	88%	73	56%	gi|365981323|XP_003667495.1
☐	heme transporter CcmC [Bartonella rattaustraliani]	29.1	29.1	76%	73	67%	gi|648396501|WP_026088252.1
☐	heme transporter CcmC [Bartonella tamiae]	29.1	29.1	76%	73	60%	gi|495314328|WP_008039076.1
☐	virulence protein E [Corynebacterium ulcerans]	29.1	29.1	52%	73	89%	gi|504649320|WP_014836422.1
☐	hypothetical protein [Prevotella oralis]	29.1	29.1	76%	73	77%	gi|565957381|WP_023983492.1
☐	hypothetical protein [Prevotella oralis]	29.1	29.1	76%	73	77%	gi|514977012|WP_016665216.1
☐	peptidase M16 [Prevotella oralis]	29.1	29.1	76%	73	77%	gi|490503902|WP_004369982.1
☐	hypothetical protein [Sphaerochaeta pleomorpha]	29.1	50.5	82%	74	90%	gi|504035116|WP_014269110.1
☐	SprA protein [Flavobacterium soli]	29.1	29.1	82%	74	61%	gi|652112013|WP_026704586.1
☐	hypothetical protein [Bartonella birtlesii]	28.6	28.6	58%	93	80%	gi|493638664|WP_006590415.1
☐	hypothetical protein KAFR_0E03080 [Kazachstania africana CBS 2	28.6	28.6	47%	98	100%	gi|410080029|XP_003957595.1
☐	MULTISPECIES: branched-chain amino acid ABC transporter perm	28.6	28.6	52%	98	89%	gi|497479806|WP_009794004.1
☐	Similar to hypothetical protein [Botryotinia fuckeliana]; acc. no. CCD	28.6	28.6	94%	98	61%	gi|549054813|CCX06384.1
☐	branched-chain amino acid ABC transporter permease [Bacillus sp.	28.6	28.6	52%	98	89%	gi|560306555|WP_023615360.1
☐	branched-chain amino acid ABC transporter permease [Lysinibacilli	28.6	28.6	52%	98	89%	gi|640692002|WP_025116329.1
☐	branched-chain amino acid ABC transporter permease [Bacillus sp.	28.6	28.6	52%	98	89%	gi|495454026|WP_008178720.1
☐	2,3-butanediol dehydrogenase [Virgibacillus halodenitrificans]	28.6	28.6	70%	98	50%	gi|518206384|WP_019376592.1
☐	2,3-butanediol dehydrogenase [Salimicrobium sp. MJ3]	28.6	28.6	70%	98	50%	gi|495868148|WP_008592727.1
☐	hypothetical protein SEPMUDRAFT_146579 [Sphaerulina musiva S	28.6	28.6	70%	98	75%	gi|453089559|EMF17599.1
☐	peptidase S41 [Joostella marina]	28.6	28.6	52%	98	89%	gi|495887111|WP_008611690.1

Alignments

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Chain A, Structural Plasticity In Igsf Domain 4 Of Icam-1 Mediates Cell Surface Dimerization

Sequence ID: gi|158429270|pdb|2OZ4|A **Length:** 265 **Number of Matches:** 1

Range 1: 46 to 62 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.8 bits(124)	1e-07	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RLNPTVTYGNDSFSAKA  17
            RLNPTVTYGNDSFSAKA
Sbjct  46   RLNPTVTYGNDSFSAKA  62
```

Related Information

Structure - 3D structure displays

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, The Crystal Structure Of Icam-1 D3-D5 Fragment

Sequence ID: gi|48425199|pdb|1P53|A **Length:** 266 **Number of Matches:** 1

See 1 more title(s)

Range 1: 47 to 63 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.8 bits(124)	1e-07	17/17(100%)	17/17(100%)	0/17(0%)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

```
Query  1   RLNPTVTYGNDSFSAKA  17
           RLNPTVTYGNDSFSAKA
Sbjct  47  RLNPTVTYGNDSFSAKA  63
```

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cell surface glycoprotein, partial [Homo sapiens]

Sequence ID: gi|338069|gb|AAA60393.1| **Length:** 276 **Number of Matches:** 1

Range 1: 2 to 18 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.8 bits(124)	1e-07	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1   RLNPTVTYGNDSFSAKA  17
           RLNPTVTYGNDSFSAKA
Sbjct  2   RLNPTVTYGNDSFSAKA  18
```

Related Information

Gene - associated gene details

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Chain A, Crystal Structure Of Alphal I Domain In Complex With Icam-1

Sequence ID: gi|28373771|pdb|1MQ8|A **Length:** 291 **Number of Matches:** 1

▷ See 1 more title(s)

Range 1: 231 to 247 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.8 bits(124)	1e-07	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1     RLNPTVTYGNDSFSAKA  17
             RLNPTVTYGNDSFSAKA
Sbjct  231   RLNPTVTYGNDSFSAKA  247
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194376370|dbj|BAG62944.1| **Length:** 310 **Number of Matches:** 1

Range 1: 36 to 52 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.8 bits(124)	1e-07	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1   RLNPTVTYGNDSFSAKA  17
           RLNPTVTYGNDSFSAKA
Sbjct  36  RLNPTVTYGNDSFSAKA  52
```

Related Information

Gene - associated gene details

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

ICAM2_KAAPAPQEATATFDSTADRE_Mod

RID BVGYC30R01R (Expires on 01-21 09:56 am)

Query ID	lcl|4787	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	20		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

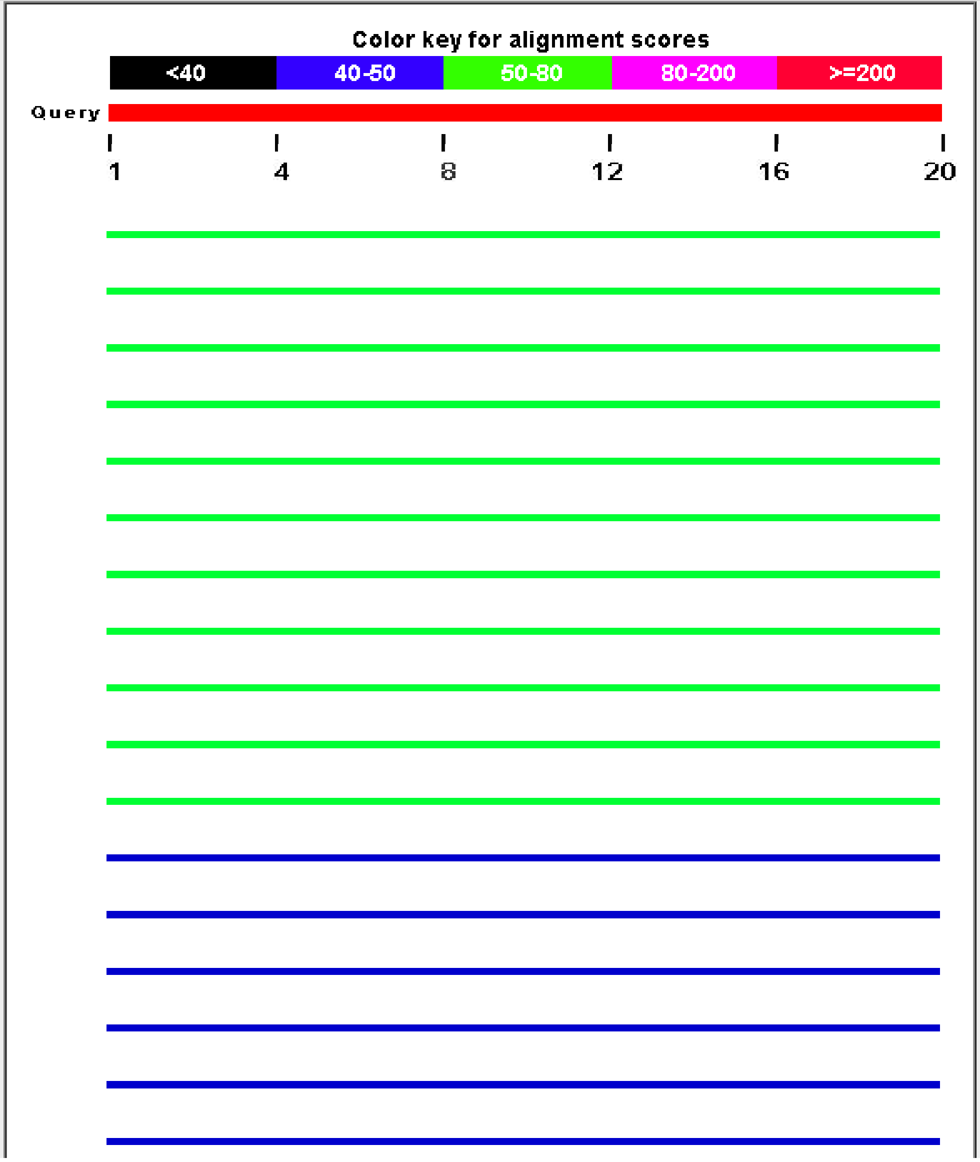
Graphic Summary

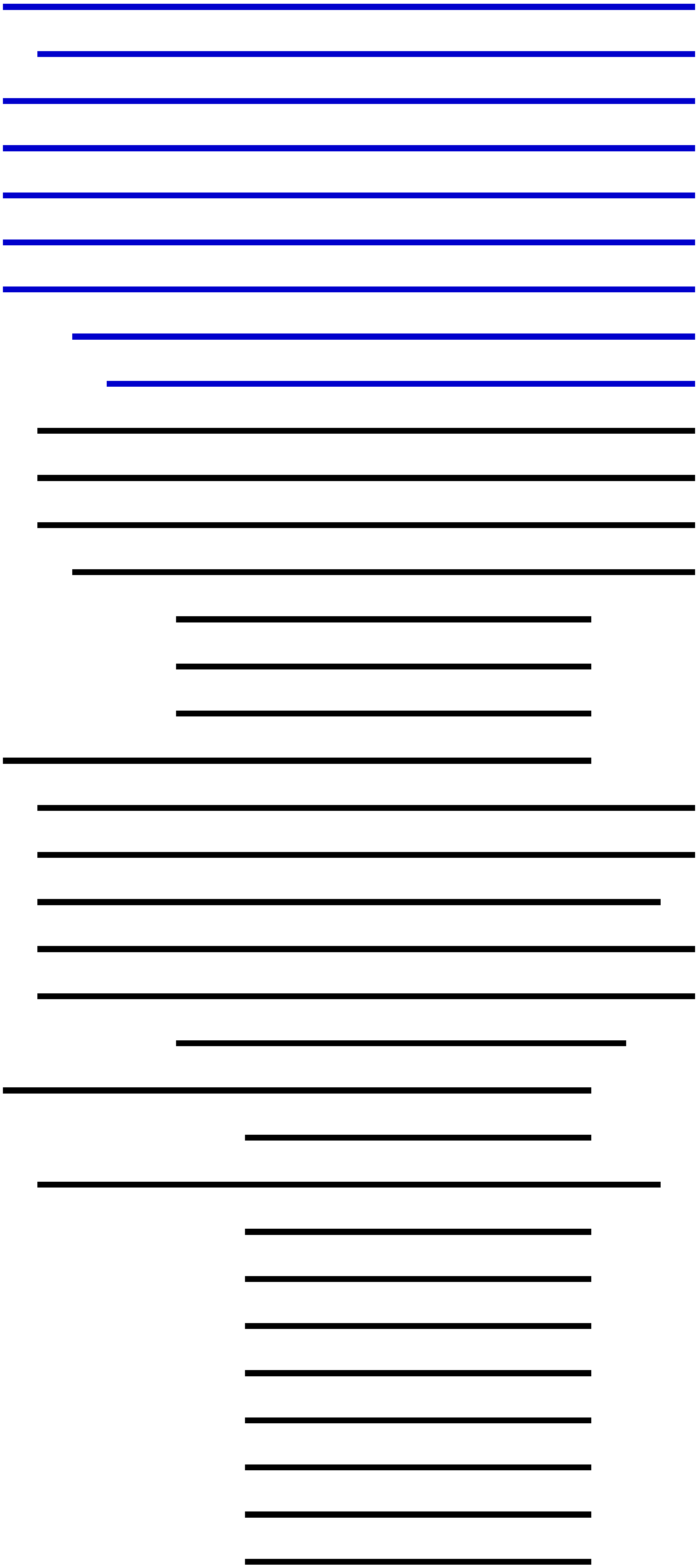
Show Conserved Domains

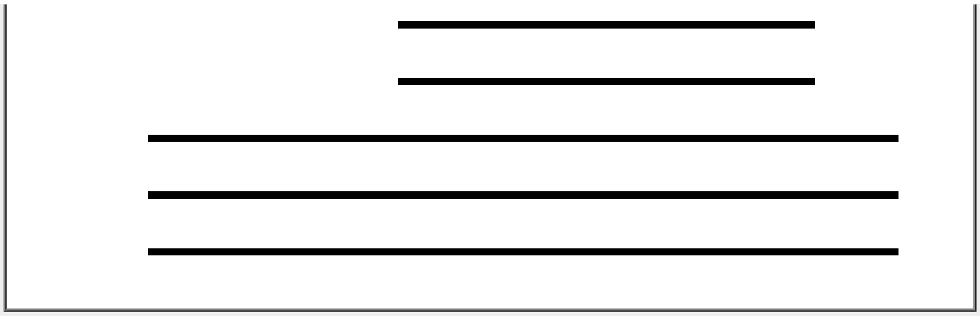
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊖ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, The Crystal Structure Of Icam-2 [Homo sapiens]	61.3	61.3	100%	2e-09	95%	1ZXQ_A
☐	intercellular adhesion molecule 2, isoform CRA_b [Homo sapiens]	61.3	61.3	100%	2e-09	95%	EAW94217.1
☐	intercellular adhesion molecule 2 precursor [Homo sapiens]	61.3	61.3	100%	2e-09	95%	NP_001093256.1
☐	ICAM-2 preprotein (AA -21 to 254) [Homo sapiens]	61.3	61.3	100%	2e-09	95%	CAA33630.1
☐	unnamed protein product [Homo sapiens]	61.3	61.3	100%	2e-09	95%	BAF85799.1
☐	intercellular adhesion molecule 2 [synthetic construct]	61.3	61.3	100%	2e-09	95%	AAX37087.1
☐	intercellular adhesion molecule 2, isoform CRA_c [Homo sapiens]	61.3	61.3	100%	2e-09	95%	EAW94218.1
☐	intercellular adhesion molecule 2, isoform CRA_d [Homo sapiens]	61.3	61.3	100%	3e-09	95%	EAW94220.1
☐	intercellular adhesion molecule 2 precursor variant [Homo sapiens]	61.3	61.3	100%	3e-09	95%	BAD93115.1
☐	intercellular adhesion molecule 2 precursor [Pan troglodytes]	55.4	55.4	100%	2e-07	85%	NP_001009166.1
☐	intercellular adhesion molecule 2 precursor [Gorilla gorilla]	54.9	54.9	100%	3e-07	90%	NP_001266588.1
☐	PREDICTED: intercellular adhesion molecule 2 [Pan paniscus]	49.0	49.0	100%	3e-05	80%	XP_003811403.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X2 [Rhinopithecus rox	47.3	47.3	100%	1e-04	85%	XP_010378323.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform 2 [Nomascus leucoge	47.3	47.3	100%	1e-04	85%	XP_003262689.1
☐	PREDICTED: intercellular adhesion molecule 2 [Pongo abelii]	47.3	47.3	100%	1e-04	85%	XP_002827759.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X1 [Rhinopithecus rox	47.3	47.3	100%	1e-04	85%	XP_010378321.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X2 [Saimiri boliviensis	46.0	46.0	100%	3e-04	80%	XP_010328611.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X1 [Saimiri boliviensis	46.0	46.0	100%	3e-04	80%	XP_003942508.1
☐	PREDICTED: intercellular adhesion molecule 2 [Dasypus novemcinctus]	46.0	46.0	95%	3e-04	79%	XP_004454118.1
☐	PREDICTED: intercellular adhesion molecule 2 [Callithrix jacchus]	43.9	43.9	100%	0.002	80%	XP_008995149.1
☐	intercellular adhesion molecule 2 [Macaca mulatta]	42.6	42.6	100%	0.004	80%	AAQ14911.1
☐	PREDICTED: intercellular adhesion molecule 2 [Papio anubis]	42.6	42.6	100%	0.004	80%	XP_003913334.2
☐	PREDICTED: intercellular adhesion molecule 2 [Chlorocebus sabaeus]	42.6	42.6	100%	0.004	80%	XP_008010305.1
☐	intercellular adhesion molecule 2 precursor [Macaca mulatta]	42.6	42.6	100%	0.004	80%	NP_001182318.1
☐	PREDICTED: intercellular adhesion molecule 2 [Tarsius syrichta]	41.4	41.4	90%	0.012	78%	XP_008058639.1
☐	PREDICTED: intercellular adhesion molecule 2 [Otolemur garnettii]	40.1	40.1	85%	0.028	71%	XP_003786673.1
☐	PREDICTED: intercellular adhesion molecule 2 [Heterocephalus glaber]	39.2	39.2	95%	0.052	74%	XP_004868694.1
☐	PREDICTED: intercellular adhesion molecule 2 [Heterocephalus glaber]	39.2	39.2	95%	0.052	74%	XP_004891551.1
☐	Intercellular adhesion molecule 2 [Heterocephalus glaber]	39.2	39.2	95%	0.053	74%	EHB07342.1

☐	PREDICTED: intercellular adhesion molecule 2 [Ochotona princeps]	38.8	38.8	90%	0.071	72%	XP_004597413.1
☐	unnamed protein product [Mus musculus]	37.1	37.1	60%	0.25	92%	BAB25266.1
☐	intercellular adhesion molecule 2 precursor [Mus musculus]	37.1	37.1	60%	0.25	92%	NP_034624.1
☐	intercellular adhesion molecule 2, isoform CRA_b [Mus musculus]	37.1	37.1	60%	0.25	92%	EDL34295.1
☐	hypothetical protein [Streptomyces alboviridis]	35.8	35.8	85%	0.55	76%	WP_032760839.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X2 [Fukomys damare	35.0	35.0	95%	1.2	68%	XP_010615058.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X1 [Fukomys damare	35.0	35.0	95%	1.2	68%	XP_010615056.1
☐	NRPS protein [Streptomyces glaucescens]	33.7	33.7	90%	3.2	50%	AIS02180.1
☐	PREDICTED: intercellular adhesion molecule 2 [Echinops telfairi]	33.3	33.3	95%	4.1	68%	XP_004707596.1
☐	PREDICTED: intercellular adhesion molecule 2 [Chrysochloris asiatica]	33.3	33.3	95%	4.1	63%	XP_006833790.1
☐	hypothetical protein [Sphingomonas sp. KC8]	32.9	32.9	65%	5.0	77%	WP_029624715.1
☐	hypothetical protein [Streptomyces sp. NRRL S-623]	32.9	32.9	85%	5.1	71%	WP_031124043.1
☐	unknown [Saccharomyces cerevisiae]	32.9	32.9	50%	5.4	100%	CAA90367.1
☐	PREDICTED: intercellular adhesion molecule 2 [Jaculus jaculus]	32.9	32.9	90%	5.6	62%	XP_004655694.1
☐	Mkc7p [Saccharomyces cerevisiae x Saccharomyces kudriavzevii VIN7]	32.9	32.9	50%	5.7	100%	EHN08122.1
☐	Mkc7p [Saccharomyces cerevisiae Lalvin QA23]	32.9	32.9	50%	5.7	100%	EGA83540.1
☐	Mkc7p [Saccharomyces cerevisiae EC1118]	32.9	32.9	50%	5.7	100%	CAY78649.1
☐	aspartyl protease [Saccharomyces cerevisiae RM11-1a]	32.9	32.9	50%	5.7	100%	EDV08165.1
☐	prepro-aspartyl protease [Saccharomyces cerevisiae]	32.9	32.9	50%	5.7	100%	AAC49112.1
☐	Mkc7p [Saccharomyces cerevisiae S288c]	32.9	32.9	50%	5.7	100%	NP_010428.3
☐	K7_Mkc7p [Saccharomyces cerevisiae Kyokai no. 7]	32.9	32.9	50%	5.7	100%	GAA22376.1
☐	Mkc7p [Saccharomyces cerevisiae Vin13]	32.9	32.9	50%	5.7	100%	EGA79523.1
☐	Mkc7p [Saccharomyces cerevisiae FostersB]	32.9	32.9	50%	5.7	100%	EGA59395.1
☐	aspartyl protease [Saccharomyces cerevisiae YJM789]	32.9	32.9	50%	5.7	100%	EDN60484.1
☐	choline transporter [Corynebacterium efficiens]	32.9	32.9	90%	5.7	72%	WP_035109369.1
☐	transporter, betaine/carnitine/choline family [Corynebacterium efficiens YS-31	32.9	32.9	90%	5.8	72%	EEW51311.1
☐	choline transporter [Corynebacterium efficiens]	32.9	32.9	90%	5.8	72%	WP_011076076.1
☐	PREDICTED: intercellular adhesion molecule 2 [Galeopterus variegatus]	32.5	32.5	85%	7.6	65%	XP_008577292.1
☐	PREDICTED: intercellular adhesion molecule 2 [Orycteropus afer afer]	32.0	32.0	100%	10	60%	XP_007957911.1
☐	PREDICTED: intercellular adhesion molecule 2 [Oryctolagus cuniculus]	32.0	32.0	85%	10	65%	XP_002719249.1
☐	hypothetical protein [Salinispora arenicola]	32.0	32.0	80%	11	69%	WP_032725575.1
☐	lipoprotein, putative [Pseudomonas pseudoalcaligenes]	31.6	31.6	70%	14	71%	WP_003451105.1
☐	hypothetical protein [Streptomyces sp. R1-NS-10]	31.6	31.6	90%	15	67%	WP_019073029.1
☐	hypothetical protein MCAG_05516 [Micromonospora sp. ATCC 39149]	31.2	31.2	95%	17	58%	EEP75189.1
☐	YraI [Streptomyces fulvissimus]	31.2	31.2	85%	18	71%	WP_015609311.1
☐	cytochrome C551 [Bacillus akibai]	31.2	31.2	90%	18	52%	WP_035660838.1
☐	hypothetical protein [Micromonospora sp. ATCC 39149]	31.2	31.2	95%	19	58%	WP_036375681.1
☐	hypothetical protein [Idiomarina sediminum]	31.2	31.2	85%	19	62%	WP_026861196.1
☐	hypothetical protein [Arthrobacter sp. Rue61a]	31.2	31.2	85%	19	60%	WP_011928020.1
☐	FliK family flagellar hook-length control protein [Lactobacillus casei]	31.2	31.2	65%	20	77%	WP_003566634.1
☐	para-aminobenzoate synthase component I [Halorubrum saccharovorum]	31.2	31.2	90%	20	61%	WP_004049467.1
☐	translation initiation factor IF-2 [Deinococcus sp. RL]	31.2	31.2	95%	20	63%	WP_034403226.1
☐	translation initiation factor IF-2 [Deinococcus murrayi]	31.2	31.2	95%	20	63%	WP_027460791.1
☐	alpha-1,2-mannosidase [Actinosynnema mirum]	31.2	31.2	90%	20	46%	WP_015800710.1
☐	NADH-quinone oxidoreductase [Streptomyces rimosus]	30.8	30.8	80%	27	67%	WP_030676242.1

☐	hypothetical protein [Streptomyces griseofuscus]	30.8	30.8	90%	27	36%	WP_037660275.1
☐	hypothetical protein [Bifidobacterium animalis]	30.8	30.8	45%	27	100%	WP_014710615.1
☐	hypothetical protein AH67_06940 [Bifidobacterium pseudolongum PV8-2]	30.8	30.8	45%	27	100%	AIZ16684.1
☐	PE-PGRS family protein [Bifidobacterium animalis]	30.8	30.8	45%	27	100%	WP_022542999.1
☐	hypothetical protein [Bifidobacterium animalis]	30.8	30.8	45%	27	100%	WP_004218191.1
☐	hypothetical protein [Bifidobacterium pseudolongum]	30.8	30.8	45%	27	100%	WP_034882776.1
☐	hypothetical protein [Bifidobacterium pseudolongum]	30.8	30.8	45%	27	100%	WP_033489377.1
☐	hypothetical protein [Bifidobacterium pseudolongum]	30.8	30.8	45%	27	100%	WP_033502396.1
☐	hypothetical protein [Bifidobacterium animalis]	30.8	30.8	45%	27	100%	WP_012619744.1
☐	ABC transporter substrate-binding protein [Agromyces italicus]	30.8	30.8	80%	27	63%	WP_022889834.1
☐	branched-chain alpha-keto acid dehydrogenase subunit E2 [Dyella ginsengisc	30.8	30.8	100%	27	65%	WP_017460578.1
☐	RNA polymerase subunit sigma-54 [Granulicella mallensis]	30.8	30.8	85%	27	55%	WP_014265120.1
☐	pyruvate dehydrogenase [Pontibacter actiniarum]	30.8	30.8	55%	28	91%	WP_025606427.1
☐	flagellar motor protein MotB [Flavobacterium sp. CF136]	30.8	30.8	50%	28	90%	WP_007807960.1
☐	hypothetical protein [Streptomyces sp. NRRL S-1868]	30.8	30.8	85%	28	56%	WP_030874634.1
☐	hypothetical protein [Streptomyces sp. NRRL F-5053]	30.8	30.8	85%	28	56%	WP_030888993.1
☐	hypothetical protein F775_12460 [Aegilops tauschii]	30.8	30.8	75%	28	63%	EMT01600.1
☐	hypothetical protein F775_00996 [Aegilops tauschii]	30.8	30.8	75%	28	63%	EMT03056.1
☐	Peptidoglycan-binding LysM [Xylanimonas cellulosilytica]	30.8	30.8	80%	28	69%	WP_012880165.1
☐	hemagluttinin repeat protein [Phascolarctobacterium succinatutens]	30.8	30.8	55%	28	82%	WP_021720813.1
☐	Cytochrome c-type biogenesis protein ccmE [Methylobacterium oryzae CBMB	30.3	30.3	80%	36	75%	AIQ93447.1
☐	CcmE/CycJ protein [Methylobacterium mesophilicum]	30.3	30.3	80%	36	75%	WP_010684570.1
☐	membrane protein [Streptomyces sp. NRRL S-1022]	30.3	30.3	75%	37	73%	WP_030346687.1
☐	integral membrane protein [Eggerthella sp. CAG:298]	30.3	30.3	70%	37	79%	WP_022363249.1
☐	hypothetical protein EAH_00035580 [Eimeria acervulina]	30.3	30.3	55%	37	91%	CDI78608.1
☐	hypothetical protein [Haloferax prahovense]	30.3	30.3	70%	37	71%	WP_008092832.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, The Crystal Structure Of Icam-2

Sequence ID: pdb|1ZXQ|A **Length:** 192 **Number of Matches:** 1

Range 1: 139 to 158 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KAAPAPQEATATFDSTADRE  20
            KAAPAPQEATATF+STADRE
Sbjct  139  KAAPAPQEATATFNSTADRE  158
```

Related Information

Structure - 3D structure displays

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intercellular adhesion molecule 2, isoform CRA_b [Homo sapiens]

Sequence ID: gb|EAW94217.1| **Length:** 255 **Number of Matches:** 1

▶ See 1 more title(s)

Range 1: 163 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	19/20(95%)	20/20(100%)	0/20(0%)

Related Information

Gene - associated gene details

Identical Proteins - Proteins

```
Query  1    KAAPAPQEATATFDSTADRE  20
            KAAPAPQEATATF+STADRE
Sbjct  163  KAAPAPQEATATFNSTADRE  182
```

identical to the subject

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intercellular adhesion molecule 2 precursor [Homo sapiens]

Sequence ID: ref|NP_001093256.1| **Length:** 275 **Number of Matches:** 1

See 18 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 163 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KAAPAPQEATATFDSTADRE  20
            KAAPAPQEATATF+STADRE
Sbjct  163  KAAPAPQEATATFNSTADRE  182
```

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ICAM-2 preprotein (AA -21 to 254) [Homo sapiens]

Sequence ID: emb|CAA33630.1| **Length:** 275 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 163 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KAAPAPQEATATFDSTADRE  20
            KAAPAPQEATATF+STADRE
Sbjct  163  KAAPAPQEATATFNSTADRE  182
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAF85799.1| **Length:** 275 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 163 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.3 bits(137)	2e-09	19/20(95%)	20/20(100%)	0/20(0%)

```
Query  1    KAAPAPQEATATFDSTADRE  20
            KAAPAPQEATATF+STADRE
Sbjct  163  KAAPAPQEATATFNSTADRE  182
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   Formatting options   Download

How to read this page   Blast report description

ICAM2_KAAPAPQEATATFNSTADRE_NonMod

RID B9HHC4ED01R (Expires on 01-14 14:15 pm)

Query ID	lcl|54764	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	20		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

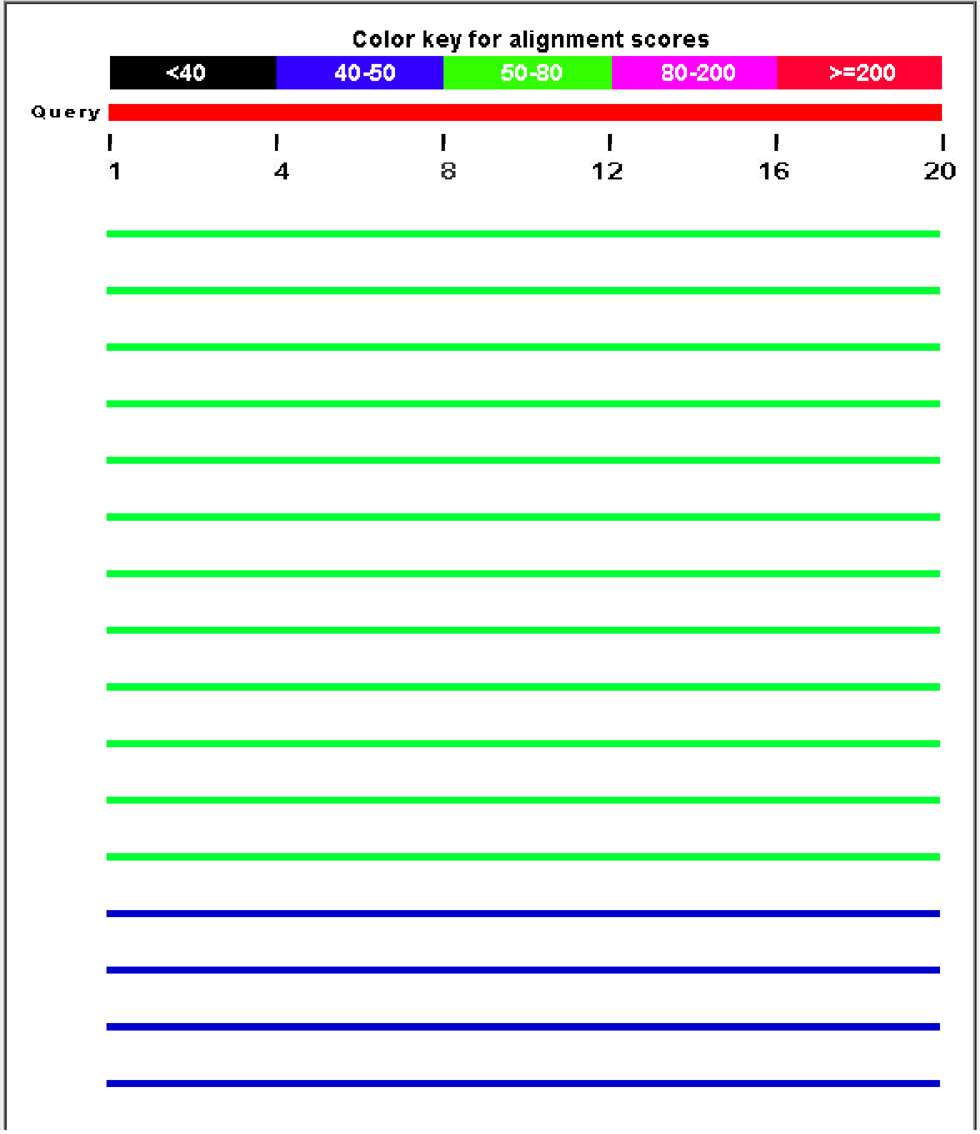
Graphic Summary

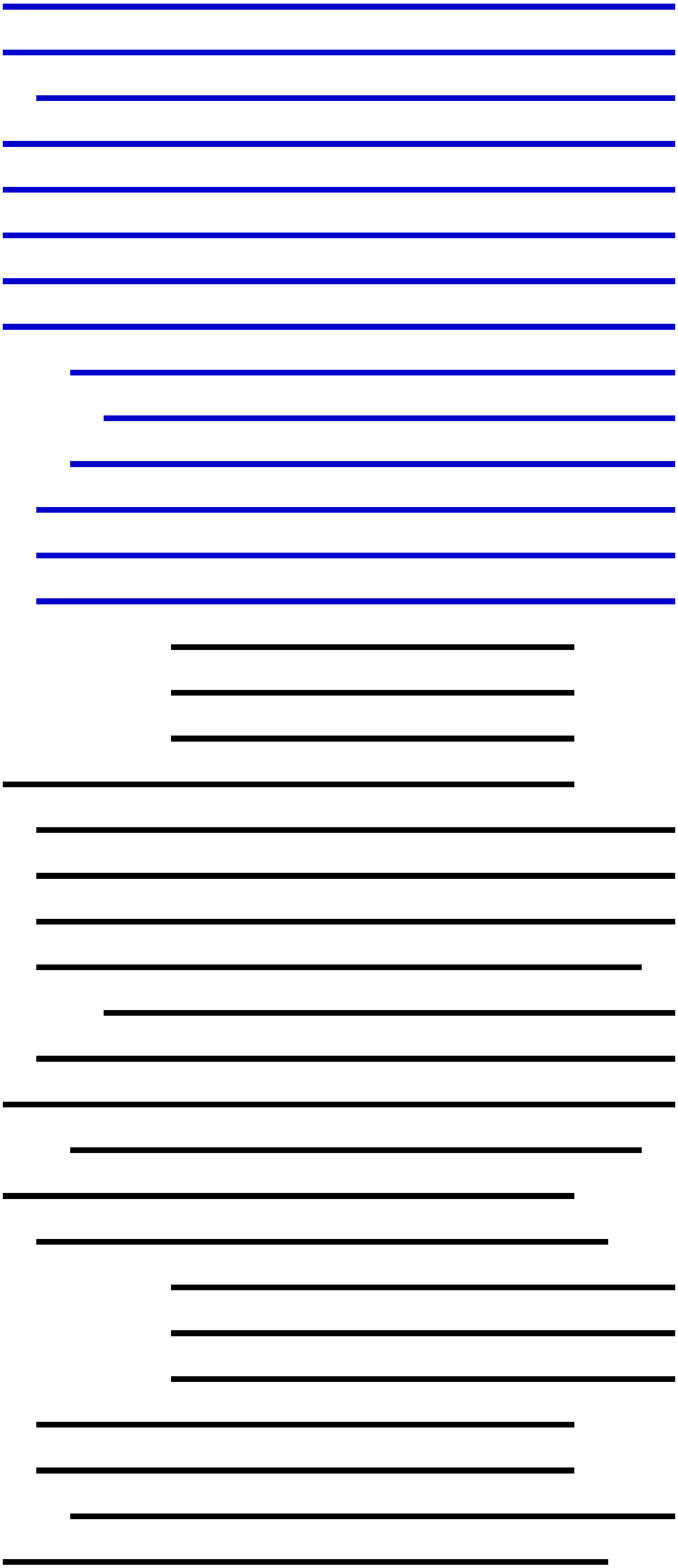
Show Conserved Domains

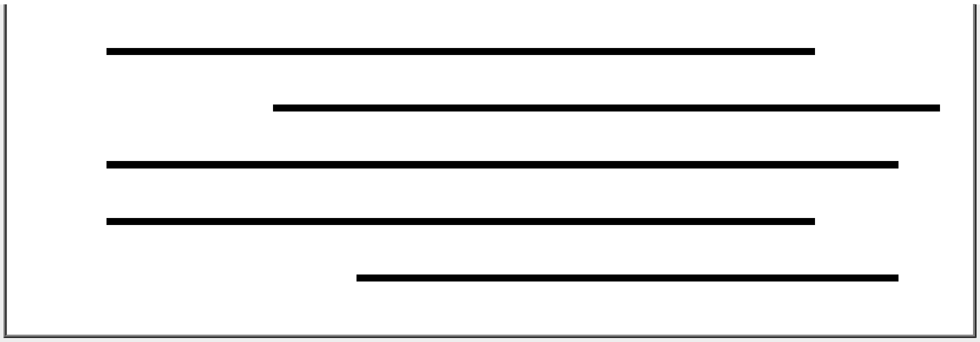
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊖ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, The Crystal Structure Of Icam-2 [Homo sapiens]	63.8	63.8	100%	3e-10	100%	gi|157834428|1ZXQ_A
☐	intercellular adhesion molecule 2, isoform CRA_b [Homo sapiens]	63.8	63.8	100%	3e-10	100%	gi|119614623|EAW94217.1
☐	intercellular adhesion molecule 2 precursor [Homo sapiens]	63.8	63.8	100%	3e-10	100%	gi|153082686|NP_001093256.1
☐	ICAM-2 preprotein (AA -21 to 254) [Homo sapiens]	63.8	63.8	100%	3e-10	100%	gi|32624|CAA33630.1
☐	unnamed protein product [Homo sapiens]	63.8	63.8	100%	3e-10	100%	gi|158259681|BAF85799.1
☐	intercellular adhesion molecule 2 [synthetic construct]	63.8	63.8	100%	3e-10	100%	gi|60834288|AAX37087.1
☐	intercellular adhesion molecule 2, isoform CRA_c [Homo sapiens]	63.8	63.8	100%	3e-10	100%	gi|119614624|EAW94218.1
☐	intercellular adhesion molecule 2, isoform CRA_d [Homo sapiens]	63.8	63.8	100%	3e-10	100%	gi|119614626|EAW94220.1
☐	intercellular adhesion molecule 2 precursor variant [Homo sapiens]	63.8	63.8	100%	3e-10	100%	gi|62089342|BAD93115.1
☐	intercellular adhesion molecule 2 precursor [Pan troglodytes]	57.9	57.9	100%	3e-08	90%	gi|57114204|NP_001009166.1
☐	intercellular adhesion molecule 2 precursor [Gorilla gorilla]	57.5	57.5	100%	4e-08	95%	gi|525343300|NP_001266588.1
☐	PREDICTED: intercellular adhesion molecule 2 [Pan paniscus]	51.5	51.5	100%	5e-06	85%	gi|397480257|XP_003811403.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X2 [Rhinopi	49.0	49.0	100%	3e-05	85%	gi|724907294|XP_010378323.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform 2 [Nomascu	49.0	49.0	100%	3e-05	85%	gi|332227028|XP_003262689.1
☐	PREDICTED: intercellular adhesion molecule 2 [Pongo abelii]	49.0	49.0	100%	3e-05	85%	gi|297701532|XP_002827759.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X1 [Rhinopi	49.0	49.0	100%	3e-05	85%	gi|724907287|XP_010378321.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X2 [Saimiri	48.6	48.6	100%	4e-05	85%	gi|725603673|XP_010328611.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X1 [Saimiri	48.6	48.6	100%	5e-05	85%	gi|403303795|XP_003942508.1
☐	PREDICTED: intercellular adhesion molecule 2 [Dasypus novemcin	48.6	48.6	95%	5e-05	84%	gi|488524498|XP_004454118.1
☐	PREDICTED: intercellular adhesion molecule 2 [Callithrix jacchus]	45.6	45.6	100%	4e-04	80%	gi|675659080|XP_008995149.1
☐	intercellular adhesion molecule 2 [Macaca mulatta]	44.3	44.3	100%	0.001	80%	gi|33340700|AAQ14911.1
☐	PREDICTED: intercellular adhesion molecule 2 [Papio anubis]	44.3	44.3	100%	0.001	80%	gi|685599161|XP_003913334.2
☐	PREDICTED: intercellular adhesion molecule 2 [Chlorocebus sabae	44.3	44.3	100%	0.001	80%	gi|635091279|XP_008010305.1
☐	intercellular adhesion molecule 2 precursor [Macaca mulatta]	44.3	44.3	100%	0.001	80%	gi|306035196|NP_001182318.1
☐	PREDICTED: intercellular adhesion molecule 2 [Tarsius syrichta]	43.9	43.9	90%	0.002	83%	gi|640804491|XP_008058639.1
☐	PREDICTED: intercellular adhesion molecule 2 [Otolemur garnettii]	42.6	42.6	85%	0.004	76%	gi|395826945|XP_003786673.1
☐	PREDICTED: intercellular adhesion molecule 2 [Ochotona princeps	41.4	41.4	90%	0.010	78%	gi|504175805|XP_004597413.1
☐	PREDICTED: intercellular adhesion molecule 2 [Heterocephalus gla	40.1	40.1	95%	0.026	74%	gi|513014697|XP_004868694.1
☐							

	PREDICTED: intercellular adhesion molecule 2 [Heterocephalus gla	40.1	40.1	95%	0.026	74%	gi|512867855|XP_004891551.1
☐	Intercellular adhesion molecule 2 [Heterocephalus glaber]	40.1	40.1	95%	0.027	74%	gi|351704423|EHB07342.1
☐	unnamed protein product [Mus musculus]	39.7	39.7	60%	0.036	100%	gi|12841581|BAB25266.1
☐	intercellular adhesion molecule 2 precursor [Mus musculus]	39.7	39.7	60%	0.036	100%	gi|6754274|NP_034624.1
☐	intercellular adhesion molecule 2, isoform CRA_b [Mus musculus]	39.7	39.7	60%	0.036	100%	gi|148702348|EDL34295.1
☐	hypothetical protein [Streptomyces alboviridis]	35.8	35.8	85%	0.52	76%	gi|695847583|WP_032760839.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X2 [Fukomy	35.8	35.8	95%	0.59	68%	gi|731294470|XP_010615058.1
☐	PREDICTED: intercellular adhesion molecule 2 [Chrysochloris asiat	35.8	35.8	95%	0.60	68%	gi|586449703|XP_006833790.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X1 [Fukomy	35.8	35.8	95%	0.60	68%	gi|731294465|XP_010615056.1
☐	PREDICTED: intercellular adhesion molecule 2 [Jaculus jaculus]	35.4	35.4	90%	0.81	67%	gi|507543407|XP_004655694.1
☐	PREDICTED: intercellular adhesion molecule 2 [Galeopterus varieg	35.0	35.0	85%	1.1	71%	gi|667289760|XP_008577292.1
☐	PREDICTED: intercellular adhesion molecule 2 [Echinops telfairi]	35.0	35.0	95%	1.1	68%	gi|507666534|XP_004707596.1
☐	PREDICTED: intercellular adhesion molecule 2 [Orycteropus afer af	34.6	34.6	100%	1.5	65%	gi|634829692|XP_007957911.1
☐	PREDICTED: intercellular adhesion molecule 2 [Oryctolagus cunicu	33.7	33.7	85%	2.8	65%	gi|291406375|XP_002719249.1
☐	hypothetical protein [Streptomyces sp. NRRL S-623]	32.9	32.9	85%	4.8	71%	gi|665521418|WP_031124043.1
☐	hypothetical protein [Arthrobacter sp. Rue61a]	32.9	32.9	85%	5.1	60%	gi|500342673|WP_011928020.1
☐	Intercellular adhesion molecule 2 [Pteropus alecto]	32.5	32.5	75%	7.1	73%	gi|431908872|ELK12464.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X2 [Pteropu	32.5	32.5	75%	7.2	73%	gi|586558152|XP_006912368.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X1 [Pteropu	32.5	32.5	75%	7.2	73%	gi|586558150|XP_006912367.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X2 [Chinchi	32.0	32.0	80%	9.8	69%	gi|533177935|XP_005402233.1
☐	PREDICTED: intercellular adhesion molecule 2 isoform X1 [Chinchi	32.0	32.0	80%	9.8	69%	gi|533177932|XP_005402232.1
☐	hypothetical protein PHYSODRAFT_484822 [Phytophthora sojae]	32.0	32.0	90%	10	57%	gi|695396271|XP_009521409.1
☐	dihydrolipoamide dehydrogenase [Thiothrix disciformis]	32.0	32.0	90%	10	68%	gi|648463207|WP_026154958.1
☐	hypothetical protein N784_07195 [Pontibacillus litoralis JSM 072002	31.6	31.6	85%	13	65%	gi|717929143|KGX88444.1
☐	PREDICTED: LOW QUALITY PROTEIN: intercellular adhesion mol	31.6	31.6	80%	13	69%	gi|587012049|XP_003997114.2
☐	chemotaxis motility protein [Rhizobium freirei]	31.6	31.6	95%	14	52%	gi|490216585|WP_004114965.1
☐	YraI [Streptomyces fulvissimus]	31.2	31.2	85%	17	71%	gi|505422209|WP_015609311.1
☐	hypothetical protein [Streptomyces sp. HmicA12]	31.2	31.2	65%	19	69%	gi|648554995|WP_026246746.1
☐	predicted protein [Postia placenta Mad-698-R]	31.2	31.2	70%	19	79%	gi|242211389|XP_002471533.1
☐	translation initiation factor IF-2 [Deinococcus sp. RL]	31.2	31.2	95%	19	63%	gi|656342093|KEF35053.1
☐	translation initiation factor IF-2 [Deinococcus murrayi]	31.2	31.2	95%	19	63%	gi|653256119|WP_027460791.1
☐	NRPS protein [Streptomyces glaucescens]	31.2	31.2	90%	19	46%	gi|692325976|AIS02180.1
☐	PREDICTED: voltage-dependent calcium channel gamma-2 subuni	30.8	30.8	100%	25	60%	gi|488529316|XP_004456445.1
☐	hypothetical protein [Arthrobacter sp. H5]	30.8	30.8	80%	25	65%	gi|654827001|WP_028279809.1
☐	PREDICTED: voltage-dependent calcium channel gamma-2 subuni	30.8	30.8	100%	26	60%	gi|667303694|XP_008582077.1
☐	PREDICTED: voltage-dependent calcium channel gamma-2 subuni	30.8	30.8	100%	26	60%	gi|488529314|XP_004456444.1
☐	ABC transporter [Paenibacillus polymyxa]	30.8	30.8	85%	26	71%	gi|647276067|WP_025721927.1
☐	hypothetical protein [Streptomyces sp. NRRL S-1022]	30.8	30.8	80%	26	71%	gi|663348860|WP_030347846.1
☐	branched-chain alpha-keto acid dehydrogenase subunit E2 [Dyella	30.8	30.8	100%	26	65%	gi|516029995|WP_017460578.1
☐	pyruvate dehydrogenase [Pontibacter actiniarum]	30.8	30.8	55%	26	91%	gi|646878080|WP_025606427.1
☐	envelope glycoprotein [Human immunodeficiency virus 1]	30.8	30.8	50%	26	90%	gi|37682527|AAQ98215.1
☐	hypothetical protein [Sphingomonas sp. KC8]	30.3	30.3	65%	33	69%	gi|657923241|WP_029624715.1
☐	unknown [Saccharomyces cerevisiae]	30.3	30.3	50%	34	90%	gi|899394|CAA90367.1
☐	PREDICTED: intercellular adhesion molecule 2 [Trichechus manatu	30.3	30.3	75%	35	73%	gi|471367485|XP_004374272.1
☐	PREDICTED: LOW QUALITY PROTEIN: intercellular adhesion mol	30.3	30.3	80%	35	69%	gi|591324590|XP_007088336.1

☐	hypothetical protein EAH_00035580 [Eimeria acervulina]	30.3	30.3	55%	35	91%	gi|557123960|CDI78608.1
☐	ABC transporter [Paenibacillus polymyxa]	30.3	30.3	85%	35	71%	gi|670514736|WP_031462258.1
☐	ceuA [Paenibacillus polymyxa SQR-21]	30.3	30.3	85%	35	71%	gi|595635719|AHM67977.1
☐	cellulase (glycosyl hydrolase family 5) subfamily protein [Acanthamo	30.3	30.3	55%	35	82%	gi|470406343|XP_004335946.1
☐	Mkc7p [Saccharomyces cerevisiae x Saccharomyces kudriavzevii V	30.3	30.3	50%	36	90%	gi|365766626|EHN08122.1
☐	Mkc7p [Saccharomyces cerevisiae Lalvin QA23]	30.3	30.3	50%	36	90%	gi|323349313|EGA83540.1
☐	Mkc7p [Saccharomyces cerevisiae EC1118]	30.3	30.3	50%	36	90%	gi|259145385|CAY78649.1
☐	aspartyl protease [Saccharomyces cerevisiae RM11-1a]	30.3	30.3	50%	36	90%	gi|190404898|EDV08165.1
☐	prepro-aspartyl protease [Saccharomyces cerevisiae]	30.3	30.3	50%	36	90%	gi|1063606|AAC49112.1
☐	Mkc7p [Saccharomyces cerevisiae S288c]	30.3	30.3	50%	36	90%	gi|398365835|NP_010428.3
☐	K7_Mkc7p [Saccharomyces cerevisiae Kyokai no. 7]	30.3	30.3	50%	36	90%	gi|349577207|GAA22376.1
☐	Mkc7p [Saccharomyces cerevisiae Vin13]	30.3	30.3	50%	36	90%	gi|323338292|EGA79523.1
☐	Mkc7p [Saccharomyces cerevisiae FostersB]	30.3	30.3	50%	36	90%	gi|323305654|EGA59395.1
☐	aspartyl protease [Saccharomyces cerevisiae YJM789]	30.3	30.3	50%	36	90%	gi|151942128|EDN60484.1
☐	choline transporter [Corynebacterium efficiens]	30.3	30.3	90%	36	67%	gi|493821357|WP_006768864.1
☐	choline transporter [Corynebacterium efficiens]	30.3	30.3	90%	36	67%	gi|499388609|WP_011076076.1
☐	hypothetical protein V501_03344 [Pseudogymnoascus pannorum V	30.3	30.3	55%	36	82%	gi|682456359|KFZ14205.1
☐	PREDICTED: intersectin-1 isoform X4 [Chrysemys picta bellii]	30.3	30.3	75%	36	57%	gi|641801520|XP_008163459.1
☐	PREDICTED: intersectin-1 isoform X3 [Chrysemys picta bellii]	30.3	30.3	75%	36	57%	gi|641801518|XP_008163458.1
☐	PREDICTED: intersectin-1 isoform X2 [Chrysemys picta bellii]	30.3	30.3	75%	36	57%	gi|641801516|XP_008163457.1
☐	PREDICTED: intersectin-1 isoform X1 [Chrysemys picta bellii]	30.3	30.3	75%	36	57%	gi|641801508|XP_008163453.1
☐	RecName: Full=Trans-splicing factor Raa3, chloroplastic; Flags: Pr	30.3	30.3	55%	36	91%	gi|20532239|Q9FEC4.1
☐	psaA mRNA maturation factor 3 [Chlamydomonas reinhardtii]	30.3	30.3	55%	36	91%	gi|159469542|XP_001692922.1
☐	hypothetical protein [cyanobacterium PCC 7702]	29.9	29.9	60%	47	83%	gi|515889762|WP_017320345.1
☐	Glucose-1-phosphate thymidylyltransferase [Haliea rubra DSM 197	29.9	29.9	80%	48	69%	gi|687957758|KGE02858.1
☐	predicted protein [Hordeum vulgare subsp. vulgare]	29.9	29.9	75%	48	65%	gi|326528445|BAJ93411.1
☐	predicted protein [Hordeum vulgare subsp. vulgare]	29.9	29.9	75%	48	65%	gi|326488801|BAJ98012.1

⊟ Alignments

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Chain A, The Crystal Structure Of Icam-2

Sequence ID: gi|157834428|pdb|1ZXQ|A **Length:** 192 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 139 to 158 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	3e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KAAPAPQEATATFNSTADRE  20
            KAAPAPQEATATFNSTADRE
Sbjct  139  KAAPAPQEATATFNSTADRE  158
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous ▲ Descriptions

intercellular adhesion molecule 2, isoform CRA_b [Homo sapiens]

Sequence ID: gi|119614623|gb|EAW94217.1| **Length:** 255 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 163 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	3e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KAAPAPQEATATFNSTADRE  20
            KAAPAPQEATATFNSTADRE
Sbjct  163  KAAPAPQEATATFNSTADRE  182
```

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intercellular adhesion molecule 2 precursor [Homo sapiens]

Sequence ID: gi|153082686|ref|NP_001093256.1| **Length:** 275 **Number of Matches:** 1

See 18 more title(s)

Range 1: 163 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	3e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KAAPAPQEATATFNSTADRE  20
            KAAPAPQEATATFNSTADRE
Sbjct  163  KAAPAPQEATATFNSTADRE  182
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

ICAM-2 preprotein (AA -21 to 254) [Homo sapiens]

Sequence ID: gi|32624|emb|CAA33630.1| **Length:** 275 **Number of Matches:** 1

See 1 more title(s)

Range 1: 163 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	3e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KAAPAPQEATATFNSTADRE  20
            KAAPAPQEATATFNSTADRE
Sbjct  163  KAAPAPQEATATFNSTADRE  182
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: gi|158259681|dbj|BAF85799.1| **Length:** 275 **Number of Matches:** 1

Range 1: 163 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.8 bits(143)	3e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KAAPAPQEATATFNSTADRE  20
            KAAPAPQEATATFNSTADRE
Sbjct  163  KAAPAPQEATATFNSTADRE  182
```

Related Information

Gene - associated gene details

NCBI/ BLAST/ blastp suite/ Formatting Results - BVH2P79P01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download YouTube How to read this page Blast report description

ITGB1_RKEDSSEICSNNGECVCGQCVCRK_Mod

RID BVH2P79P01R (Expires on 01-21 09:58 am)

Query ID	lcl|371267	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	24	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

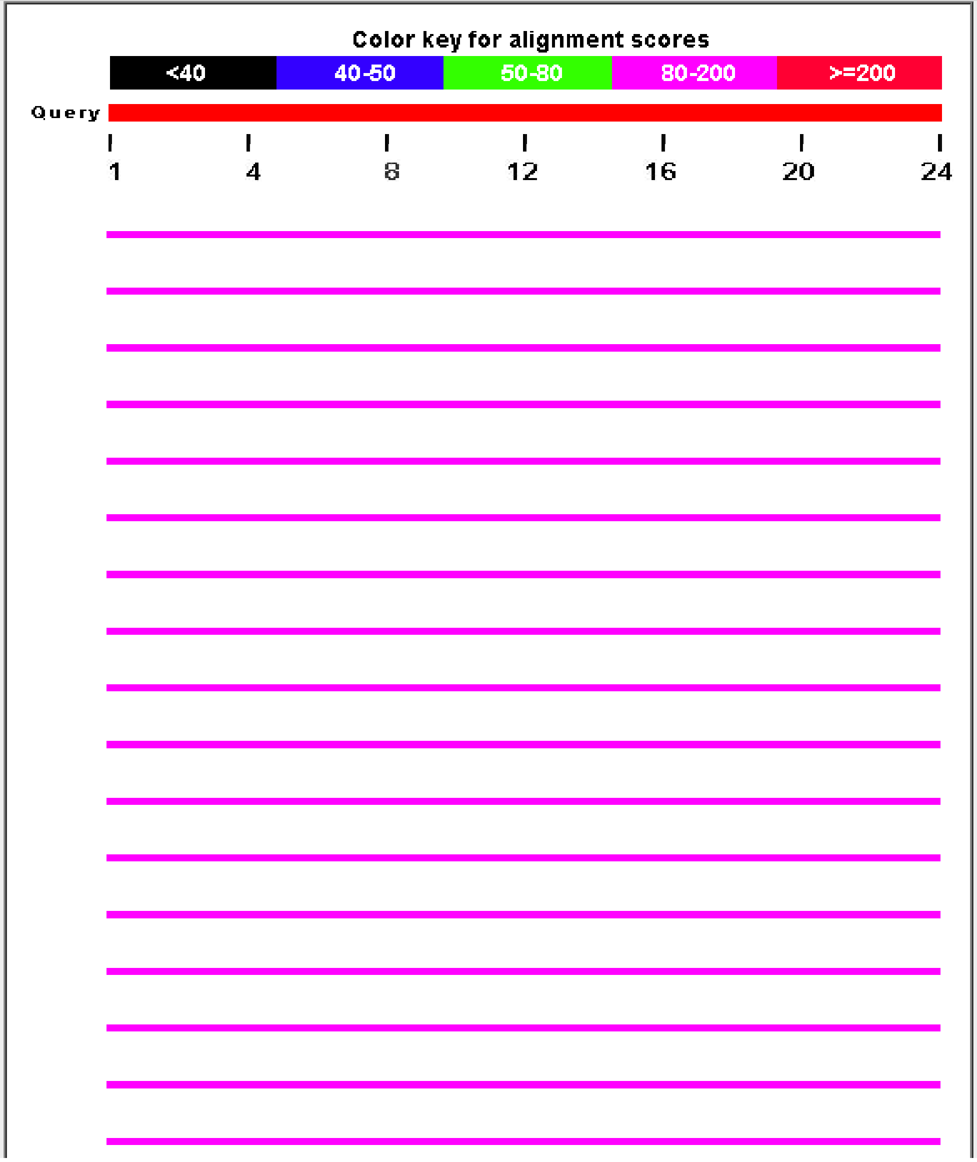
Graphic Summary

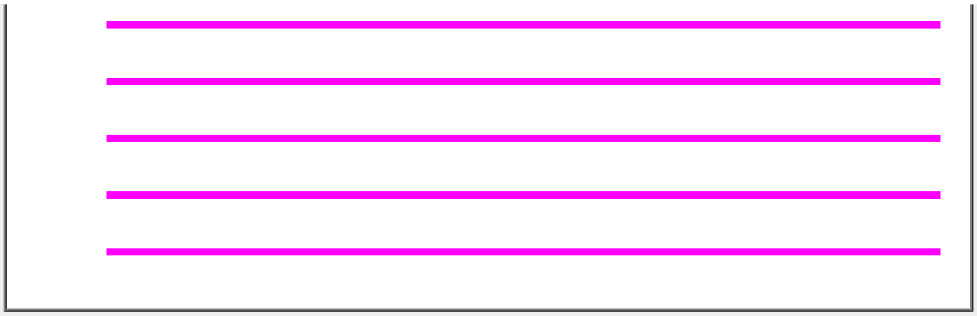
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 103 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	beta1 integrin [Equus caballus]	80.4	80.4	100%	1e-15	96%	BAG06145.1
☐	unnamed protein product [Mus musculus]	80.4	80.4	100%	1e-15	96%	BAC36379.1
☐	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes	80.4	80.4	100%	1e-15	96%	EAW85956.1
☐	PREDICTED: integrin beta-1 [Mesocricetus auratus]	80.4	80.4	100%	1e-15	96%	XP_005083522.1
☐	PREDICTED: integrin beta-1 isoform X2 [Jaculus jaculus]	80.4	80.4	100%	1e-15	96%	XP_004659843.1
☐	integrin beta-1 isoform 1 [Camelus ferus]	80.4	80.4	100%	1e-15	96%	EPY79213.1
☐	PREDICTED: integrin beta-1 [Trichechus manatus latirostris]	80.4	80.4	100%	1e-15	96%	XP_004387928.1
☐	PREDICTED: integrin beta-1 [Eptesicus fuscus]	80.4	80.4	100%	1e-15	96%	XP_008154521.1
☐	Integrin beta-1 [Tupaia chinensis]	80.4	80.4	100%	1e-15	96%	ELW48458.1
☐	Integrin beta-1 [Pteropus alecto]	80.4	80.4	100%	1e-15	96%	ELK19641.1
☐	PREDICTED: integrin beta-1-like [Pteropus alecto]	80.4	80.4	100%	1e-15	96%	XP_006903905.1
☐	PREDICTED: integrin beta-1-like [Dasypus novemcinctus]	80.4	80.4	100%	1e-15	96%	XP_004483041.1
☐	PREDICTED: integrin beta-1 [Sorex araneus]	80.4	80.4	100%	1e-15	96%	XP_004605564.1
☐	PREDICTED: integrin beta-1 [Macaca mulatta]	80.4	80.4	100%	2e-15	96%	XP_002805655.1
☐	hypothetical protein PANDA_013008 [Ailuropoda melanoleuca]	80.4	80.4	100%	2e-15	96%	EFB17666.1
☐	unnamed protein product [Mus musculus]	80.4	80.4	100%	2e-15	96%	BAE35290.1
☐	beta-1 integrin subunit [Bos taurus]	80.4	80.4	100%	2e-15	96%	AAA80571.1
☐	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes	80.4	80.4	100%	2e-15	96%	EAW85960.1
☐	PREDICTED: LOW QUALITY PROTEIN: integrin beta-1 [Erinaceus europaeu	80.4	80.4	100%	2e-15	96%	XP_007536525.1
☐	PREDICTED: integrin beta-1 [Ursus maritimus]	80.4	80.4	100%	2e-15	96%	XP_008682126.1
☐	PREDICTED: integrin beta-1 [Galeopterus variegatus]	80.4	80.4	100%	2e-15	96%	XP_008584293.1
☐	PREDICTED: integrin beta-1 [Tarsius syrichta]	80.4	80.4	100%	2e-15	96%	XP_008063074.1
☐	PREDICTED: integrin beta-1 isoform X2 [Orycteropus afer afer]	80.4	80.4	100%	2e-15	96%	XP_007940645.1
☐	PREDICTED: integrin beta-1 isoform X2 [Oryctolagus cuniculus]	80.4	80.4	100%	2e-15	96%	XP_002721235.1
☐	PREDICTED: integrin beta-1 [Bubalus bubalis]	80.4	80.4	100%	2e-15	96%	XP_006063272.1
☐	integrin beta-1 precursor [Bos taurus]	80.4	80.4	100%	2e-15	96%	NP_776793.1
☐	PREDICTED: integrin beta-1 isoform X3 [Lipotes vexillifer]	80.4	80.4	100%	2e-15	96%	XP_007471382.1
☐	PREDICTED: integrin beta-1 isoform X5 [Balaenoptera acutorostrata scammo	80.4	80.4	100%	2e-15	96%	XP_007189916.1
☐	PREDICTED: integrin beta-1-like isoform X2 [Physeter catodon]	80.4	80.4	100%	2e-15	96%	XP_007115902.1

☐	PREDICTED: integrin beta-1 isoform X1 [Panthera tigris altaica]	80.4	80.4	100%	2e-15	96%	XP_007092823.1
☐	PREDICTED: integrin beta-1 isoform X2 [Peromyscus maniculatus bairdii]	80.4	80.4	100%	2e-15	96%	XP_006982576.1
☐	PREDICTED: integrin beta-1-like isoform X2 [Elephantulus edwardii]	80.4	80.4	100%	2e-15	96%	XP_006889010.1
☐	PREDICTED: integrin beta-1 isoform X2 [Leptonychotes weddellii]	80.4	80.4	100%	2e-15	96%	XP_006737563.1
☐	PREDICTED: integrin beta-1 isoform X2 [Tupaia chinensis]	80.4	80.4	100%	2e-15	96%	XP_006158348.1
☐	PREDICTED: integrin beta-1-like [Camelus ferus]	80.4	80.4	100%	2e-15	96%	XP_006187117.1
☐	PREDICTED: integrin beta-1 isoform X2 [Myotis lucifugus]	80.4	80.4	100%	2e-15	96%	XP_006086741.1
☐	PREDICTED: integrin beta-1 isoform X2 [Pantholops hodgsonii]	80.4	80.4	100%	2e-15	96%	XP_005972136.1
☐	PREDICTED: integrin beta-1 isoform X2 [Bos mutus]	80.4	80.4	100%	2e-15	96%	XP_005890244.1
☐	PREDICTED: integrin beta-1 isoform X2 [Ictidomys tridecemlineatus]	80.4	80.4	100%	2e-15	96%	XP_005330880.1
☐	PREDICTED: integrin beta-1 [Microtus ochrogaster]	80.4	80.4	100%	2e-15	96%	XP_005345987.1
☐	PREDICTED: integrin beta-1 isoform X2 [Mustela putorius furo]	80.4	80.4	100%	2e-15	96%	XP_004774339.1
☐	PREDICTED: integrin beta-1-like [Octodon degus]	80.4	80.4	100%	2e-15	96%	XP_004641911.1
☐	PREDICTED: integrin beta-1 isoform X1 [Jaculus jaculus]	80.4	80.4	100%	2e-15	96%	XP_004659842.1
☐	PREDICTED: integrin beta-1 isoform 2 [Ceratotherium simum simum]	80.4	80.4	100%	2e-15	96%	XP_004425300.1
☐	PREDICTED: integrin beta-1 isoform 2 [Odobenus rosmarus divergens]	80.4	80.4	100%	2e-15	96%	XP_004401882.1
☐	PREDICTED: integrin beta-1 isoform 2 [Orcinus orca]	80.4	80.4	100%	2e-15	96%	XP_004275966.1
☐	integrin beta-1 precursor [Pongo abelii]	80.4	80.4	100%	2e-15	96%	NP_001125324.1
☐	Fn receptor beta prechain [Mus musculus]	80.4	80.4	100%	2e-15	96%	CAA33272.1
☐	integrin beta-1 precursor [Mus musculus]	80.4	80.4	100%	2e-15	96%	NP_034708.1
☐	unnamed protein product [Homo sapiens]	80.4	80.4	100%	2e-15	96%	CAA30790.1
☐	integrin beta-1 precursor [Felis catus]	80.4	80.4	100%	2e-15	96%	NP_001041625.1
☐	integrin subunit beta 1 [Capra hircus]	80.4	80.4	100%	2e-15	96%	AFP87513.1
☐	PREDICTED: integrin beta-1 isoform X2 [Pan paniscus]	80.4	80.4	100%	2e-15	96%	XP_003814839.1
☐	PREDICTED: integrin beta-1 isoform 1 [Otolemur garnettii]	80.4	80.4	100%	2e-15	96%	XP_003786766.1
☐	PREDICTED: integrin beta-1 isoform X2 [Papio anubis]	80.4	80.4	100%	2e-15	96%	XP_003903581.1
☐	PREDICTED: integrin beta-1 [Heterocephalus glaber]	80.4	80.4	100%	2e-15	96%	XP_004861939.1
☐	PREDICTED: integrin beta-1 isoform 1 [Cavia porcellus]	80.4	80.4	100%	2e-15	96%	XP_003468668.1
☐	PREDICTED: integrin beta-1 isoform X2 [Canis lupus familiaris]	80.4	80.4	100%	2e-15	96%	XP_005617006.1
☐	PREDICTED: integrin beta-1 [Loxodonta africana]	80.4	80.4	100%	2e-15	96%	XP_003420767.1
☐	PREDICTED: integrin beta-1 isoform X2 [Cricetulus griseus]	80.4	80.4	100%	2e-15	96%	XP_007621878.1
☐	PREDICTED: integrin beta-1 isoform X2 [Pan troglodytes]	80.4	80.4	100%	2e-15	96%	XP_507735.3
☐	PREDICTED: integrin beta-1 isoform 1 [Nomascus leucogenys]	80.4	80.4	100%	2e-15	96%	XP_003276062.1
☐	PREDICTED: integrin beta-1-like [Ailuropoda melanoleuca]	80.4	80.4	100%	2e-15	96%	XP_002923799.1
☐	integrin beta1 [Camelus dromedarius]	80.4	80.4	100%	2e-15	96%	ACT68325.1
☐	integrin beta1 [Litocranius walleri]	80.4	80.4	100%	2e-15	96%	ACT68324.1
☐	integrin beta-1 precursor [Ovis aries]	80.4	80.4	100%	2e-15	96%	NP_001107242.1
☐	unnamed protein product [Homo sapiens]	80.4	80.4	100%	2e-15	96%	BAF84386.1
☐	RecName: Full=Integrin beta-1; AltName: Full=Fibronectin receptor subunit be	80.4	80.4	100%	2e-15	96%	A5Z1X6.1
☐	integrin beta-1 precursor [Rattus norvegicus]	80.4	80.4	100%	2e-15	96%	NP_058718.2
☐	hypothetical protein [synthetic construct]	80.4	101	100%	2e-15	96%	CAL38075.1
☐	integrin beta 1 [Bos taurus]	80.4	80.4	100%	2e-15	96%	ABH07895.1
☐	unnamed protein product [Mus musculus]	80.4	80.4	100%	2e-15	96%	BAC40532.1
☐	integrin beta-1 isoform 1A precursor [Homo sapiens]	80.4	80.4	100%	2e-15	96%	NP_002202.2
☐	PREDICTED: integrin beta-1 isoform X1 [Bison bison bison]	80.4	80.4	100%	2e-15	96%	XP_010858191.1

☐	PREDICTED: integrin beta-1 [Nannospalax galili]	80.4	80.4	100%	2e-15	96%	XP_008845808.1
☐	RecName: Full=Integrin beta-1; AltName: Full=Beta oligodendroglia; Short=Be	80.4	80.4	100%	2e-15	96%	P49134.1
☐	PREDICTED: integrin beta-1 [Sarcophilus harrisii]	80.4	104	100%	2e-15	96%	XP_003771880.1
☐	PREDICTED: integrin beta-1 [Ornithorhynchus anatinus]	80.4	80.4	100%	2e-15	96%	XP_007666003.1
☐	PREDICTED: integrin beta-1 isoform X1 [Monodelphis domestica]	80.4	104	100%	2e-15	96%	XP_001366567.1
☐	PREDICTED: integrin beta-1 isoform X2 [Camelus dromedarius]	80.4	80.4	100%	2e-15	96%	XP_010991989.1
☐	PREDICTED: integrin beta-1 isoform X1 [Pan troglodytes]	80.4	80.4	100%	2e-15	96%	XP_009456504.1
☐	PREDICTED: integrin beta-1 isoform X1 [Pan paniscus]	80.4	80.4	100%	2e-15	96%	XP_008965875.1
☐	PREDICTED: integrin beta-1 isoform X1 [Oryctolagus cuniculus]	80.4	80.4	100%	2e-15	96%	XP_008272963.1
☐	PREDICTED: integrin beta-1 isoform X1 [Orycteropus afer afer]	80.4	80.4	100%	2e-15	96%	XP_007940644.1
☐	PREDICTED: integrin beta-1 isoform X1 [Bos taurus]	80.4	80.4	100%	2e-15	96%	XP_005214205.1
☐	PREDICTED: integrin beta-1 isoform X2 [Lipotes vexillifer]	80.4	80.4	100%	2e-15	96%	XP_007471381.1
☐	PREDICTED: integrin beta-1 isoform X1 [Balaenoptera acutorostrata scammo	80.4	80.4	100%	2e-15	96%	XP_007189912.1
☐	PREDICTED: integrin beta-1 isoform X1 [Peromyscus maniculatus bairdii]	80.4	80.4	100%	2e-15	96%	XP_006982575.1
☐	PREDICTED: integrin beta-1-like isoform X1 [Elephantulus edwardii]	80.4	80.4	100%	2e-15	96%	XP_006889009.1
☐	PREDICTED: integrin beta-1 isoform X1 [Leptonychotes weddellii]	80.4	80.4	100%	2e-15	96%	XP_006737562.1
☐	PREDICTED: integrin beta-1 isoform X1 [Rattus norvegicus]	80.4	80.4	100%	2e-15	96%	XP_006255886.1
☐	PREDICTED: integrin beta-1 isoform X1 [Tupaia chinensis]	80.4	80.4	100%	2e-15	96%	XP_006158347.1
☐	PREDICTED: integrin beta-1 isoform X1 [Myotis lucifugus]	80.4	80.4	100%	2e-15	96%	XP_006086740.1
☐	PREDICTED: integrin beta-1 isoform X1 [Pantholops hodgsonii]	80.4	80.4	100%	2e-15	96%	XP_005972135.1
☐	PREDICTED: integrin beta-1 isoform X1 [Sus scrofa]	80.4	80.4	100%	2e-15	96%	XP_005668230.1
☐	PREDICTED: integrin beta-1 isoform X1 [Canis lupus familiaris]	80.4	80.4	100%	2e-15	96%	XP_005617005.1
☐	PREDICTED: integrin beta-1 isoform X1 [Macaca fascicularis]	80.4	80.4	100%	2e-15	96%	XP_005564990.1
☐	PREDICTED: integrin beta-1-like isoform X2 [Chinchilla lanigera]	80.4	80.4	100%	2e-15	96%	XP_005398209.1
☐	PREDICTED: integrin beta-1 isoform X1 [Ictidomys tridecemlineatus]	80.4	80.4	100%	2e-15	96%	XP_005330879.1
☐	PREDICTED: integrin beta-1 isoform X1 [Bos mutus]	80.4	80.4	100%	2e-15	96%	XP_005890243.1

Alignments

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beta1 integrin [Equus caballus]

Sequence ID: dbj|BAG06145.1| **Length:** 221 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 19 to 42 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	1e-15	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    RKEDSSEICSNNGECVCGQCVCRK  24
            RKE+SSEICSNNGECVCGQCVCRK
Sbjct  19   RKENSSEICSNNGECVCGQCVCRK  42
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Mus musculus]

Sequence ID: dbj|BAC36379.1| **Length:** 504 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 369 to 392 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	1e-15	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    RKEDSSEICSNNGECVCGQCVCRK  24
            RKE+SSEICSNNGECVCGQCVCRK
Sbjct  369  RKENSSEICSNNGECVCGQCVCRK  392
```

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integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12), isoform CRA_e [Homo sapiens]

Sequence ID: gb|EAW85956.1| **Length:** 682 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 460 to 483 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	1e-15	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    RKEDSSEICSNNGECVCGQCVCRK  24
            RKE+SSEICSNNGECVCGQCVCRK
Sbjct  460  RKENSSEICSNNGECVCGQCVCRK  483
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: integrin beta-1 [Mesocricetus auratus]

Sequence ID: ref|XP_005083522.1| **Length:** 686 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 405 to 428 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	1e-15	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    RKEDSSEICSNNGECVCGQCVCRK  24
            RKE+SSEICSNNGECVCGQCVCRK
Sbjct  405  RKENSSEICSNNGECVCGQCVCRK  428
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: integrin beta-1 isoform X2 [Jaculus jaculus]

Sequence ID: ref|XP_004659843.1| **Length:** 698 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 417 to 440 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
80.4 bits(182)	1e-15	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    RKEDSSEICSNNGECVCGQCVCRK  24
            RKE+SSEICSNNGECVCGQCVCRK
Sbjct  417  RKENSSEICSNNGECVCGQCVCRK  440
```

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - B9FY0F8C01R

Your search parameters were adjusted to search for a short input sequence.

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How to read this page | Blast report description

ITGB1_RKENSSEICSNNGECVCGQCVCRK_NonMod

RID B9FY0F8C01R (Expires on 01-14 13:48 pm)

Query ID lcl|16271
Description None
Molecule type amino acid
Query Length 24

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

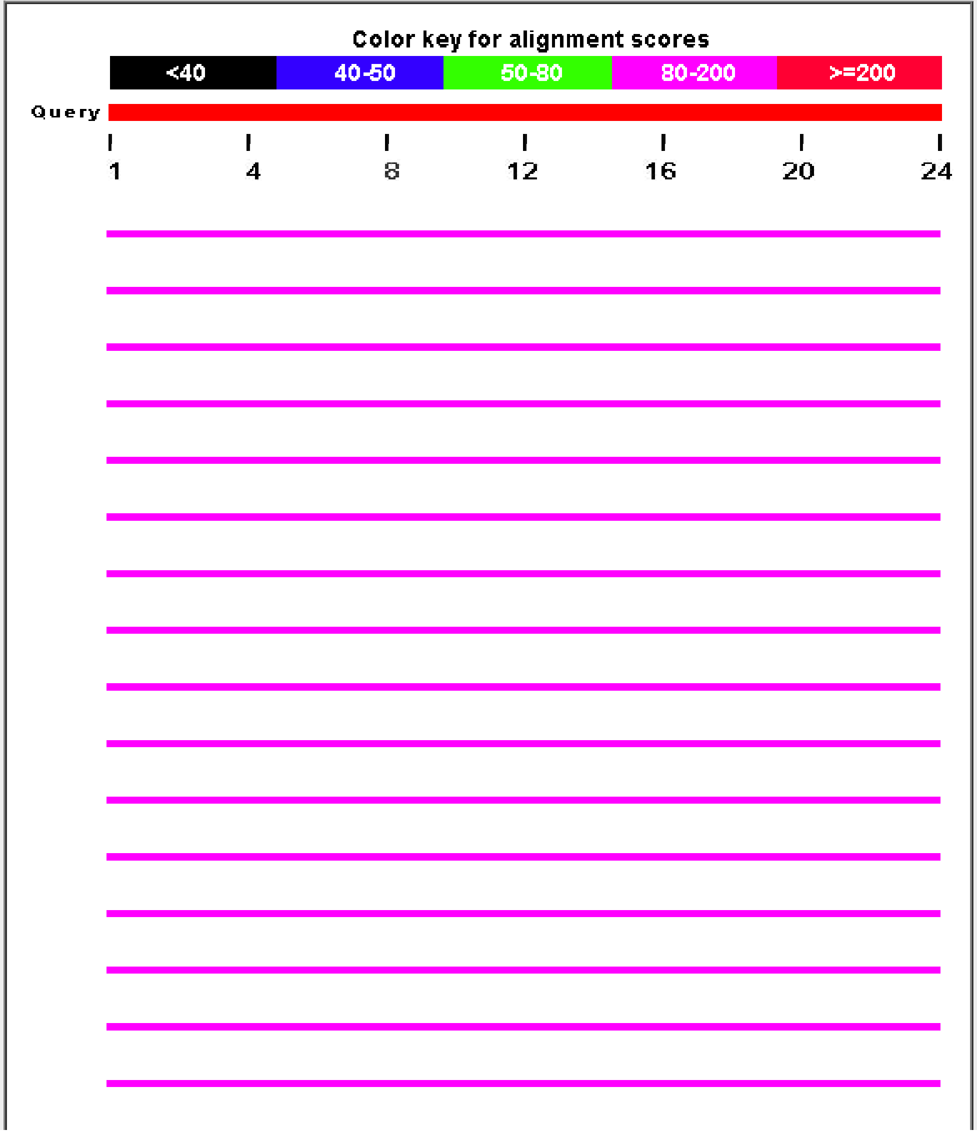
Graphic Summary

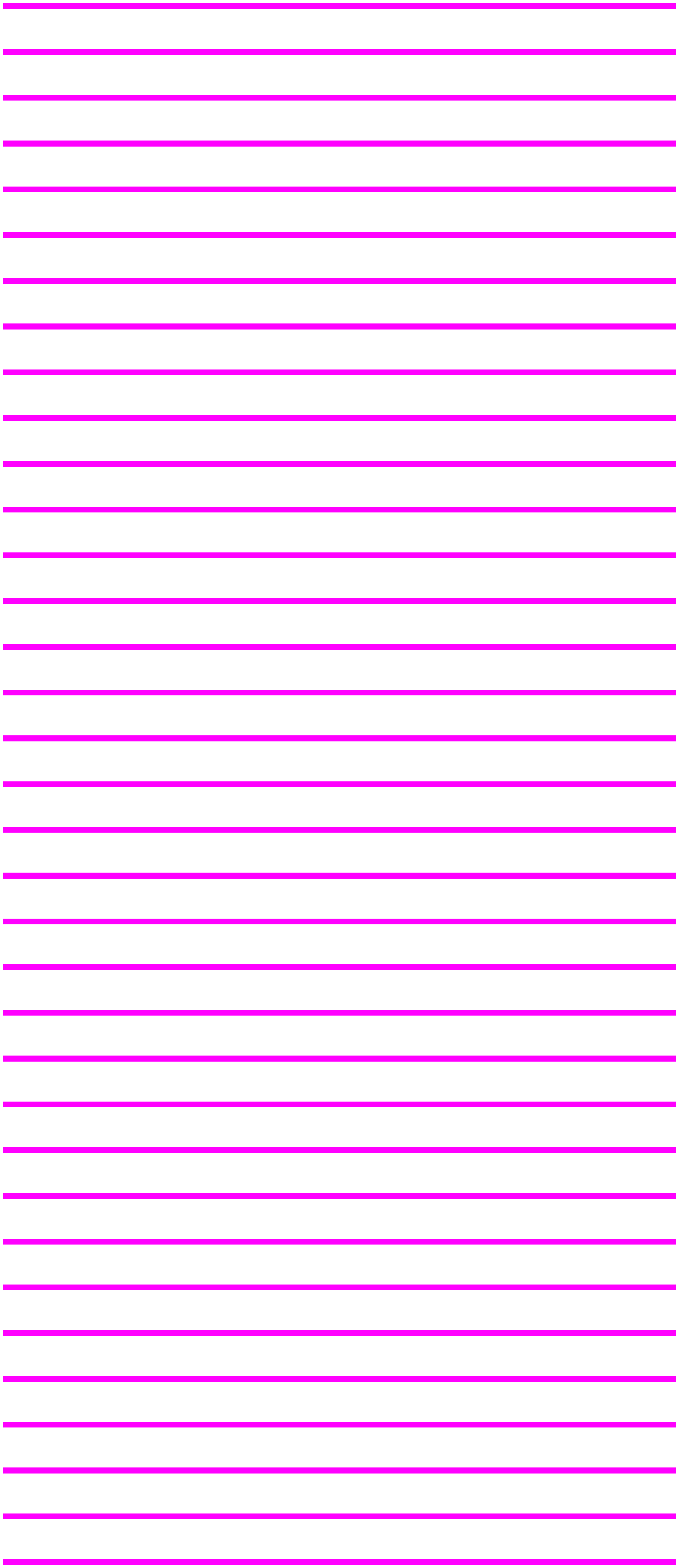
Show Conserved Domains

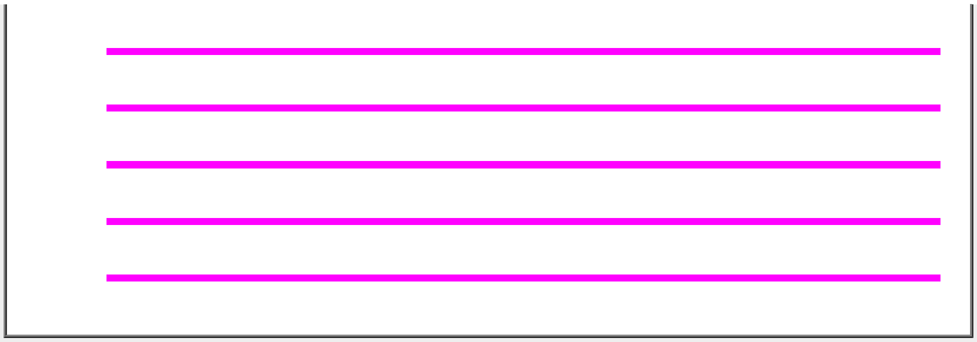
No putative conserved domains have been detected

Distribution of 104 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	beta1 integrin [Equus caballus]	82.9	82.9	100%	1e-16	100%	gi|166157373|BAG06145.1
☐	unnamed protein product [Mus musculus]	82.9	82.9	100%	2e-16	100%	gi|26345456|BAC36379.1
☐	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD2	82.9	82.9	100%	2e-16	100%	gi|119606362|EAW85956.1
☐	PREDICTED: integrin beta-1 [Mesocricetus auratus]	82.9	82.9	100%	2e-16	100%	gi|524967265|XP_005083522.1
☐	PREDICTED: integrin beta-1 isoform X2 [Jaculus jaculus]	82.9	82.9	100%	2e-16	100%	gi|507552093|XP_004659843.1
☐	integrin beta-1 isoform 1 [Camelus ferus]	82.9	82.9	100%	2e-16	100%	gi|528759554|EPY79213.1
☐	PREDICTED: integrin beta-1 [Trichechus manatus latirostris]	82.9	82.9	100%	2e-16	100%	gi|471412758|XP_004387928.1
☐	PREDICTED: integrin beta-1 [Eptesicus fuscus]	82.9	82.9	100%	2e-16	100%	gi|641728728|XP_008154521.1
☐	Integrin beta-1 [Tupaia chinensis]	82.9	82.9	100%	2e-16	100%	gi|444707169|ELW48458.1
☐	Integrin beta-1 [Pteropus alecto]	82.9	82.9	100%	2e-16	100%	gi|431922892|ELK19641.1
☐	PREDICTED: integrin beta-1-like [Pteropus alecto]	82.9	82.9	100%	2e-16	100%	gi|586519049|XP_006903905.1
☐	PREDICTED: integrin beta-1-like [Dasypus novemcinctus]	82.9	103	100%	2e-16	100%	gi|488595691|XP_004483041.1
☐	PREDICTED: integrin beta-1 [Sorex araneus]	82.9	82.9	100%	2e-16	100%	gi|505789884|XP_004605564.1
☐	PREDICTED: integrin beta-1 [Macaca mulatta]	82.9	82.9	100%	2e-16	100%	gi|297300768|XP_002805655.1
☐	hypothetical protein PANDA_013008 [Ailuropoda melanoleuca]	82.9	82.9	100%	2e-16	100%	gi|281342082|EFB17666.1
☐	unnamed protein product [Mus musculus]	82.9	82.9	100%	2e-16	100%	gi|74198239|BAE35290.1
☐	beta-1 integrin subunit [Bos taurus]	82.9	82.9	100%	2e-16	100%	gi|520521|AAA80571.1
☐	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD2	82.9	82.9	100%	2e-16	100%	gi|119606366|EAW85960.1
☐	PREDICTED: LOW QUALITY PROTEIN: integrin beta-1 [Erinaceus	82.9	82.9	100%	2e-16	100%	gi|617658590|XP_007536525.1
☐	PREDICTED: integrin beta-1 [Ursus maritimus]	82.9	82.9	100%	2e-16	100%	gi|671040340|XP_008682126.1
☐	PREDICTED: integrin beta-1 [Galeopterus variegatus]	82.9	82.9	100%	2e-16	100%	gi|667310115|XP_008584293.1
☐	PREDICTED: integrin beta-1 [Tarsius syrichta]	82.9	82.9	100%	2e-16	100%	gi|640812799|XP_008063074.1
☐	PREDICTED: integrin beta-1 isoform X2 [Orycteropus afer afer]	82.9	82.9	100%	2e-16	100%	gi|634852628|XP_007940645.1
☐	PREDICTED: integrin beta-1 isoform X2 [Oryctolagus cuniculus]	82.9	82.9	100%	2e-16	100%	gi|291409905|XP_002721235.1
☐	PREDICTED: integrin beta-1 [Bubalus bubalis]	82.9	82.9	100%	2e-16	100%	gi|594079184|XP_006063272.1
☐	integrin beta-1 precursor [Bos taurus]	82.9	82.9	100%	2e-16	100%	gi|27805959|NP_776793.1
☐	PREDICTED: integrin beta-1 isoform X3 [Lipotes vexillifer]	82.9	82.9	100%	2e-16	100%	gi|602722472|XP_007471382.1
☐	PREDICTED: integrin beta-1 isoform X5 [Balaenoptera acutorostrat	82.9	82.9	100%	2e-16	100%	gi|594684797|XP_007189916.1
☐							

	PREDICTED: integrin beta-1-like isoform X2 [Physeter catodon]	82.9	82.9	100%	2e-16	100%	gi|593754014|XP_007115902.1
☐	PREDICTED: integrin beta-1 isoform X1 [Panthera tigris altaica]	82.9	82.9	100%	2e-16	100%	gi|591334243|XP_007092823.1
☐	PREDICTED: integrin beta-1 isoform X2 [Peromyscus maniculatus	82.9	82.9	100%	2e-16	100%	gi|589939670|XP_006982576.1
☐	PREDICTED: integrin beta-1-like isoform X2 [Elephantulus edwardi	82.9	82.9	100%	2e-16	100%	gi|585670442|XP_006889010.1
☐	PREDICTED: integrin beta-1 isoform X2 [Leptonychotes weddellii]	82.9	82.9	100%	2e-16	100%	gi|585171151|XP_006737563.1
☐	PREDICTED: integrin beta-1 isoform X2 [Tupaia chinensis]	82.9	82.9	100%	2e-16	100%	gi|562859888|XP_006158348.1
☐	PREDICTED: integrin beta-1-like [Camelus ferus]	82.9	82.9	100%	2e-16	100%	gi|560921824|XP_006187117.1
☐	PREDICTED: integrin beta-1 isoform X2 [Myotis lucifugus]	82.9	82.9	100%	2e-16	100%	gi|558115793|XP_006086741.1
☐	PREDICTED: integrin beta-1 isoform X2 [Pantholops hodgsonii]	82.9	82.9	100%	2e-16	100%	gi|556753520|XP_005972136.1
☐	PREDICTED: integrin beta-1 isoform X2 [Bos mutus]	82.9	82.9	100%	2e-16	100%	gi|555956189|XP_005890244.1
☐	PREDICTED: integrin beta-1 isoform X2 [Ictidomys tridecemlineatu	82.9	82.9	100%	2e-16	100%	gi|532090374|XP_005330880.1
☐	PREDICTED: integrin beta-1 [Microtus ochrogaster]	82.9	82.9	100%	2e-16	100%	gi|532003510|XP_005345987.1
☐	PREDICTED: integrin beta-1 isoform X2 [Mustela putorius furo]	82.9	82.9	100%	2e-16	100%	gi|511909857|XP_004774339.1
☐	PREDICTED: integrin beta-1-like [Octodon degus]	82.9	82.9	100%	2e-16	100%	gi|507691051|XP_004641911.1
☐	PREDICTED: integrin beta-1 isoform X1 [Jaculus jaculus]	82.9	82.9	100%	2e-16	100%	gi|507552091|XP_004659842.1
☐	PREDICTED: integrin beta-1 isoform 2 [Ceratotherium simum simu	82.9	82.9	100%	2e-16	100%	gi|478501978|XP_004425300.1
☐	PREDICTED: integrin beta-1 isoform 2 [Odobenus rosmarus diverg	82.9	82.9	100%	2e-16	100%	gi|472364641|XP_004401882.1
☐	PREDICTED: integrin beta-1 isoform 2 [Orcinus orca]	82.9	82.9	100%	2e-16	100%	gi|466039204|XP_004275966.1
☐	integrin beta-1 precursor [Pongo abelii]	82.9	82.9	100%	2e-16	100%	gi|197098822|NP_001125324.1
☐	Fn receptor beta prechain [Mus musculus]	82.9	82.9	100%	2e-16	100%	gi|762977|CAA33272.1
☐	integrin beta-1 precursor [Mus musculus]	82.9	82.9	100%	2e-16	100%	gi|45504394|NP_034708.1
☐	unnamed protein product [Homo sapiens]	82.9	82.9	100%	2e-16	100%	gi|31442|CAA30790.1
☐	integrin beta-1 precursor [Felis catus]	82.9	82.9	100%	2e-16	100%	gi|114326428|NP_001041625.1
☐	integrin subunit beta 1 [Capra hircus]	82.9	82.9	100%	2e-16	100%	gi|400653598|AFP87513.1
☐	PREDICTED: integrin beta-1 isoform X2 [Pan paniscus]	82.9	82.9	100%	2e-16	100%	gi|397487507|XP_003814839.1
☐	PREDICTED: integrin beta-1 isoform 1 [Otolemur garnettii]	82.9	82.9	100%	2e-16	100%	gi|395827144|XP_003786766.1
☐	PREDICTED: integrin beta-1 isoform X2 [Papio anubis]	82.9	82.9	100%	2e-16	100%	gi|402879948|XP_003903581.1
☐	PREDICTED: integrin beta-1 [Heterocephalus glaber]	82.9	82.9	100%	2e-16	100%	gi|513000828|XP_004861939.1
☐	PREDICTED: integrin beta-1 isoform 1 [Cavia porcellus]	82.9	82.9	100%	2e-16	100%	gi|348565755|XP_003468668.1
☐	PREDICTED: integrin beta-1 isoform X2 [Canis lupus familiaris]	82.9	82.9	100%	2e-16	100%	gi|545489482|XP_005617006.1
☐	PREDICTED: integrin beta-1 [Loxodonta africana]	82.9	82.9	100%	2e-16	100%	gi|344298170|XP_003420767.1
☐	PREDICTED: integrin beta-1 isoform X2 [Cricetulus griseus]	82.9	82.9	100%	2e-16	100%	gi|625260885|XP_007621878.1
☐	PREDICTED: integrin beta-1 isoform X2 [Pan troglodytes]	82.9	82.9	100%	2e-16	100%	gi|332833907|XP_507735.3
☐	PREDICTED: integrin beta-1 isoform 1 [Nomascus leucogenys]	82.9	82.9	100%	2e-16	100%	gi|332253882|XP_003276062.1
☐	PREDICTED: integrin beta-1-like [Ailuropoda melanoleuca]	82.9	82.9	100%	2e-16	100%	gi|301776761|XP_002923799.1
☐	integrin beta1 [Camelus dromedarius]	82.9	82.9	100%	2e-16	100%	gi|254575655|ACT68325.1
☐	integrin beta1 [Litocranius walleri]	82.9	82.9	100%	2e-16	100%	gi|254575653|ACT68324.1
☐	integrin beta-1 precursor [Ovis aries]	82.9	82.9	100%	2e-16	100%	gi|166157504|NP_001107242.1
☐	unnamed protein product [Homo sapiens]	82.9	82.9	100%	2e-16	100%	gi|158256826|BAF84386.1
☐	RecName: Full=Integrin beta-1; AltName: Full=Fibronectin receptor	82.9	82.9	100%	2e-16	100%	gi|215275341|A5Z1X6.1
☐	integrin beta-1 precursor [Rattus norvegicus]	82.9	82.9	100%	2e-16	100%	gi|158303324|NP_058718.2
☐	hypothetical protein [synthetic construct]	82.9	103	100%	2e-16	100%	gi|117645218|CAL38075.1
☐	integrin beta 1 [Bos taurus]	82.9	82.9	100%	2e-16	100%	gi|111183155|ABH07895.1
☐	unnamed protein product [Mus musculus]	82.9	82.9	100%	2e-16	100%	gi|26353804|BAC40532.1
☐	integrin beta-1 isoform 1A precursor [Homo sapiens]	82.9	82.9	100%	2e-16	100%	gi|19743813|NP_002202.2

☐	PREDICTED: integrin beta-1 [Nannospalax galili]	82.9	82.9	100%	2e-16	100%	gi|674076844|XP_008845808.1
☐	RecName: Full=Integrin beta-1; AltName: Full=Beta oligodendroglia	82.9	82.9	100%	2e-16	100%	gi|1352494|P49134.1
☐	PREDICTED: integrin beta-1 [Sarcophilus harrisii]	82.9	107	100%	2e-16	100%	gi|395539855|XP_003771880.1
☐	PREDICTED: integrin beta-1 [Ornithorhynchus anatinus]	82.9	82.9	100%	2e-16	100%	gi|620962569|XP_007666003.1
☐	PREDICTED: integrin beta-1 isoform X1 [Monodelphis domestica]	82.9	106	100%	2e-16	100%	gi|126341188|XP_001366567.1
☐	PREDICTED: integrin beta-1 isoform X1 [Pan troglodytes]	82.9	82.9	100%	2e-16	100%	gi|694939321|XP_009456504.1
☐	PREDICTED: integrin beta-1 isoform X1 [Pan paniscus]	82.9	82.9	100%	2e-16	100%	gi|675729741|XP_008965875.1
☐	PREDICTED: integrin beta-1 isoform X1 [Oryctolagus cuniculus]	82.9	82.9	100%	2e-16	100%	gi|655883134|XP_008272963.1
☐	PREDICTED: integrin beta-1 isoform X1 [Orycteropus afer afer]	82.9	82.9	100%	2e-16	100%	gi|634852625|XP_007940644.1
☐	PREDICTED: integrin beta-1 isoform X1 [Bos taurus]	82.9	82.9	100%	2e-16	100%	gi|528972462|XP_005214205.1
☐	PREDICTED: integrin beta-1 isoform X2 [Lipotes vexillifer]	82.9	82.9	100%	2e-16	100%	gi|602722470|XP_007471381.1
☐	PREDICTED: integrin beta-1 isoform X1 [Balaenoptera acutorostrat	82.9	82.9	100%	2e-16	100%	gi|594684789|XP_007189912.1
☐	PREDICTED: integrin beta-1 isoform X1 [Peromyscus maniculatus	82.9	82.9	100%	2e-16	100%	gi|589939668|XP_006982575.1
☐	PREDICTED: integrin beta-1-like isoform X1 [Elephantulus edwardi	82.9	82.9	100%	2e-16	100%	gi|585670438|XP_006889009.1
☐	PREDICTED: integrin beta-1 isoform X1 [Leptonychotes weddellii]	82.9	82.9	100%	2e-16	100%	gi|585171149|XP_006737562.1
☐	PREDICTED: integrin beta-1 isoform X1 [Rattus norvegicus]	82.9	82.9	100%	2e-16	100%	gi|564396374|XP_006255886.1
☐	PREDICTED: integrin beta-1 isoform X1 [Tupaia chinensis]	82.9	82.9	100%	2e-16	100%	gi|562859886|XP_006158347.1
☐	PREDICTED: integrin beta-1 isoform X1 [Myotis lucifugus]	82.9	82.9	100%	2e-16	100%	gi|558115789|XP_006086740.1
☐	PREDICTED: integrin beta-1 isoform X1 [Pantholops hodgsonii]	82.9	82.9	100%	2e-16	100%	gi|556753518|XP_005972135.1
☐	PREDICTED: integrin beta-1 isoform X1 [Sus scrofa]	82.9	82.9	100%	2e-16	100%	gi|545853818|XP_005668230.1
☐	PREDICTED: integrin beta-1 isoform X1 [Canis lupus familiaris]	82.9	82.9	100%	2e-16	100%	gi|545489480|XP_005617005.1
☐	PREDICTED: integrin beta-1 isoform X1 [Macaca fascicularis]	82.9	82.9	100%	2e-16	100%	gi|544456576|XP_005564990.1
☐	PREDICTED: integrin beta-1-like isoform X2 [Chinchilla lanigera]	82.9	82.9	100%	2e-16	100%	gi|533169242|XP_005398209.1
☐	PREDICTED: integrin beta-1 isoform X1 [Ictidomys tridecemlineatus	82.9	82.9	100%	2e-16	100%	gi|532090372|XP_005330879.1
☐	PREDICTED: integrin beta-1 isoform X1 [Mustela putorius furo]	82.9	82.9	100%	2e-16	100%	gi|511909855|XP_004774338.1
☐	PREDICTED: integrin beta-1 isoform 1 [Ceratotherium simum simu	82.9	82.9	100%	2e-16	100%	gi|478501976|XP_004425299.1
☐	PREDICTED: integrin beta-1 isoform X1 [Bos mutus]	82.9	82.9	100%	2e-16	100%	gi|555956187|XP_005890243.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

beta1 integrin [Equus caballus]

Sequence ID: gi|166157373|dbj|BAG06145.1| **Length:** 221 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 19 to 42 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.9 bits(188)	1e-16	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    RKENSSEICSNNGECVCGQCVCRK  24
           RKENSSEICSNNGECVCGQCVCRK
Sbjct  19   RKENSSEICSNNGECVCGQCVCRK  42
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Mus musculus]

Sequence ID: gi|26345456|dbj|BAC36379.1| **Length:** 504 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 369 to 392 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.9 bits(188)	2e-16	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1     RKENSSEICSNNGECVCGQCVCRK  24
```

```
                RKENSSEICSNNGECVCGQCVCRK
Sbjct  369  RKENSSEICSNNGECVCGQCVCRK  392
```

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integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12), isoform CRA_e [Homo sapiens]

Sequence ID: gi|119606362|gb|EAW85956.1| **Length:** 682 **Number of Matches:** 1

Range 1: 460 to 483 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.9 bits(188)	2e-16	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    RKENSSEICSNNGECVCGQCVCRK  24
            RKENSSEICSNNGECVCGQCVCRK
Sbjct  460  RKENSSEICSNNGECVCGQCVCRK  483
```

Related Information

Gene - associated gene details

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: integrin beta-1 [Mesocricetus auratus]

Sequence ID: gi|524967265|ref|XP_005083522.1| **Length:** 686 **Number of Matches:** 1

Range 1: 405 to 428 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.9 bits(188)	2e-16	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    RKENSSEICSNNGECVCGQCVCRK  24
            RKENSSEICSNNGECVCGQCVCRK
Sbjct  405  RKENSSEICSNNGECVCGQCVCRK  428
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: integrin beta-1 isoform X2 [Jaculus jaculus]

Sequence ID: gi|507552093|ref|XP_004659843.1| **Length:** 698 **Number of Matches:** 1

Range 1: 417 to 440 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.9 bits(188)	2e-16	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    RKENSSEICSNNGECVCGQCVCRK  24
            RKENSSEICSNNGECVCGQCVCRK
Sbjct  417  RKENSSEICSNNGECVCGQCVCRK  440
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download YouTube How to read this page Blast report description

LAMP2_KVASVININPDTTHSTGSCRS_Mod

RID BVHXA0HZ01R (Expires on 01-21 10:12 am)

Query ID	lcl|290063	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	21		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

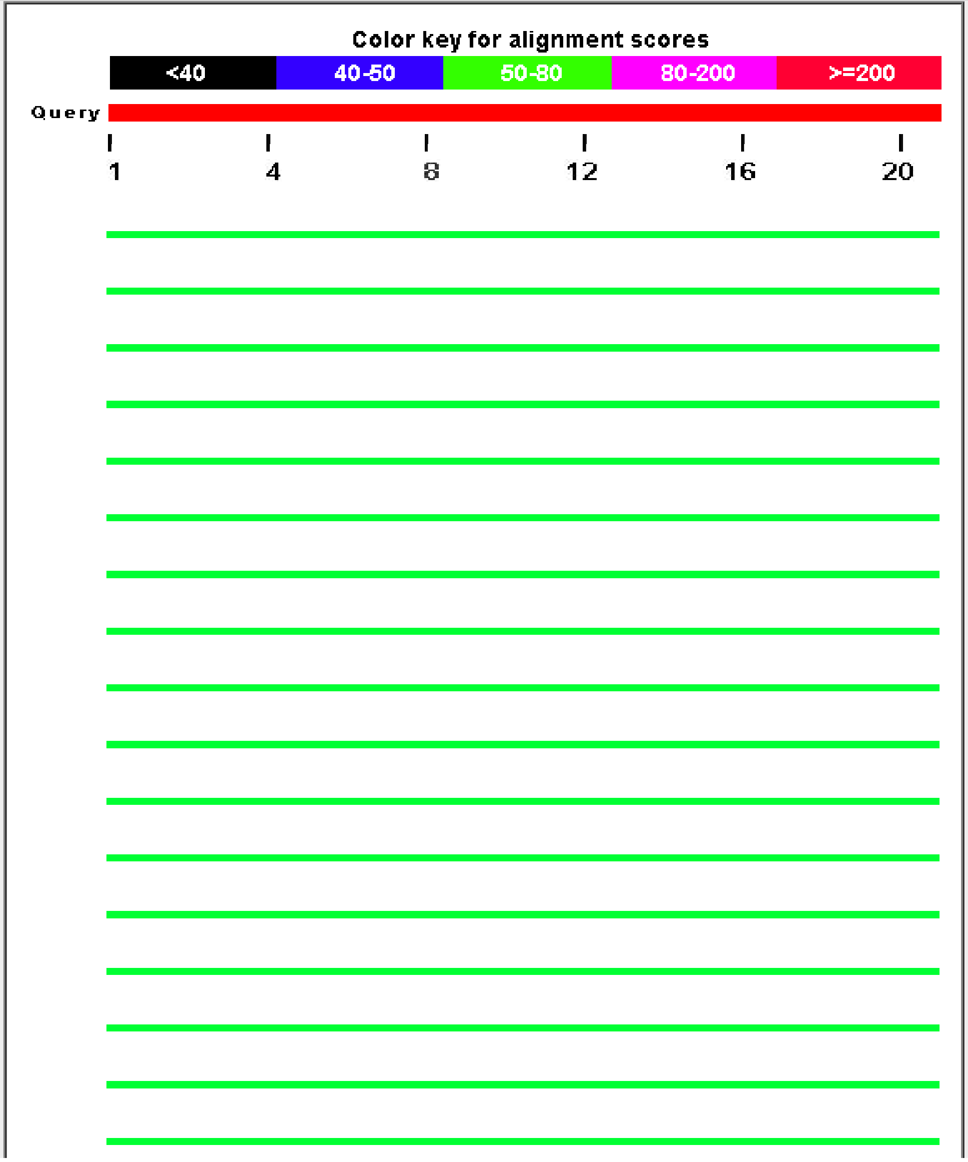
⊟Graphic Summary

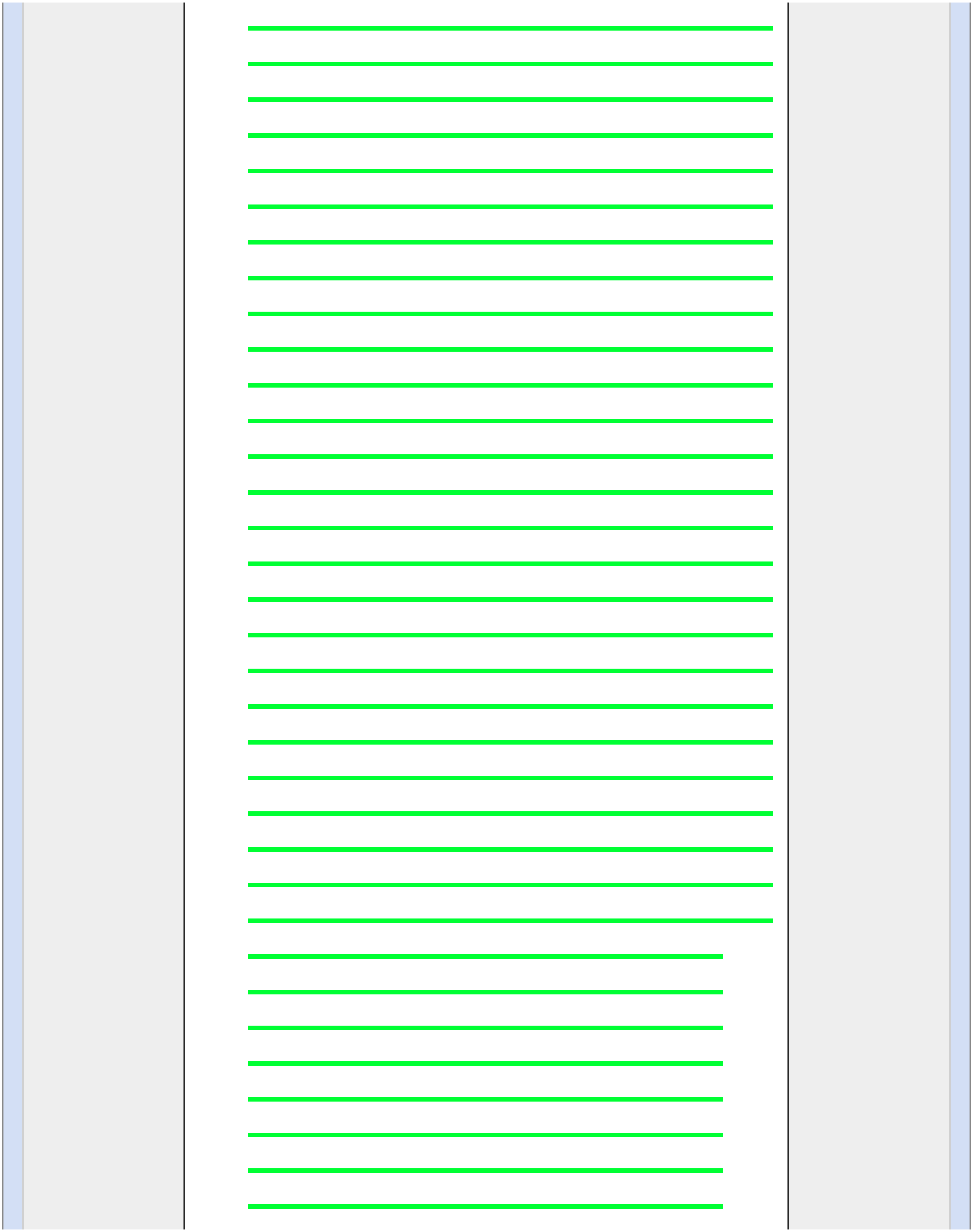
⊟Show Conserved Domains

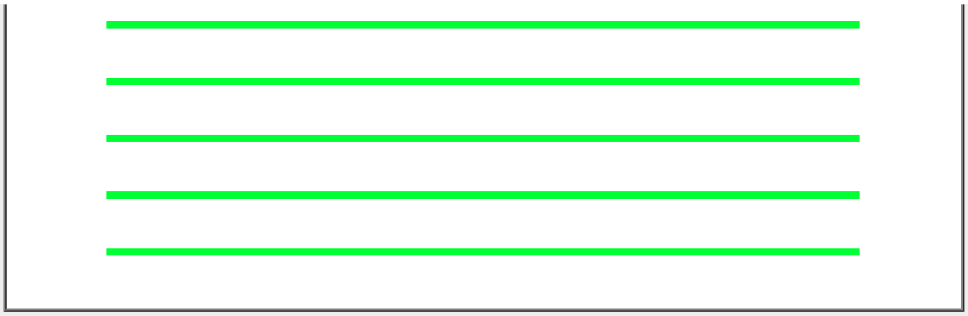
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Macaca fascicularis]	65.5	65.5	100%	8e-11	95%	BAE87445.1
☐	lysosome-associated membrane protein 2 [Homo sapiens]	65.5	65.5	100%	1e-10	95%	2106261A
☐	unnamed protein product [Homo sapiens]	65.5	65.5	100%	1e-10	95%	BAH11955.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 [Pan troglodyte	65.5	65.5	100%	1e-10	95%	XP_009437861.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 [Gorilla gorilla g	65.5	65.5	100%	1e-10	95%	XP_004064857.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X3 [Rhi	65.5	65.5	100%	1e-10	95%	XP_010353039.1
☐	unnamed protein product [Homo sapiens]	65.5	65.5	100%	1e-10	95%	BAG65239.1
☐	lysosomal membrane glycoprotein-2 [Homo sapiens]	65.5	65.5	100%	1e-10	95%	AAA60383.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Rhi	65.5	65.5	100%	1e-10	95%	XP_010353037.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Rhi	65.5	65.5	100%	1e-10	95%	XP_010353036.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X3 [Paı	65.5	65.5	100%	1e-10	95%	XP_009196467.1
☐	LAMP2 [synthetic construct]	65.5	65.5	100%	1e-10	95%	AIC54689.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X3 [Chl	65.5	65.5	100%	1e-10	95%	XP_008017647.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Chl	65.5	65.5	100%	1e-10	95%	XP_008017646.1
☐	lysosomal membrane glycoprotein-2 [Homo sapiens]	65.5	65.5	100%	1e-10	95%	AAB41647.1
☐	lysosome-associated membrane glycoprotein 2 isoform B precursor [Homo sa	65.5	65.5	100%	1e-10	95%	NP_054701.1
☐	hypothetical protein [Pongo abelii]	65.5	65.5	100%	1e-10	95%	CAH92900.1
☐	lysosome-associated membrane glycoprotein 2 isoform A precursor [Homo sa	65.5	65.5	100%	1e-10	95%	NP_002285.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Paı	65.5	65.5	100%	1e-10	95%	XP_003918269.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Par	65.5	65.5	100%	1e-10	95%	XP_003823188.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X3 [Par	65.5	65.5	100%	1e-10	95%	XP_003823187.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Por	65.5	65.5	100%	1e-10	95%	XP_003779762.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform 1 [Nom	65.5	65.5	100%	1e-10	95%	XP_003262323.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X3 [Por	65.5	65.5	100%	1e-10	95%	XP_002832104.1
☐	lysosome-associated membrane glycoprotein 2 precursor [Macaca mulatta]	65.5	65.5	100%	1e-10	95%	NP_001247737.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Ma	65.5	65.5	100%	1e-10	95%	XP_005594543.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X4 [Rhi	65.5	65.5	100%	1e-10	95%	XP_010353040.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Chl	65.5	65.5	100%	1e-10	95%	XP_008017645.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Paı	65.5	65.5	100%	1e-10	95%	XP_003918270.1

☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Par	65.5	65.5	100%	1e-10	95%	XP_003823189.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Por	65.5	65.5	100%	1e-10	95%	XP_003779763.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform 3 [Nom	65.5	65.5	100%	1e-10	95%	XP_003262325.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Ma	65.5	65.5	100%	1e-10	95%	XP_005594542.1
☐	lysosome-associated membrane glycoprotein 2 isoform C precursor [Homo sa	65.5	65.5	100%	1e-10	95%	NP_001116078.1
☐	unnamed protein product [Homo sapiens]	63.4	63.4	100%	5e-10	90%	BAG57310.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X3 [Sai	61.3	61.3	100%	3e-09	90%	XP_010340007.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X3 [Cal	61.3	61.3	100%	3e-09	90%	XP_002763275.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Cal	61.3	61.3	100%	3e-09	90%	XP_002763274.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Sai	61.3	61.3	100%	3e-09	90%	XP_003931138.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Cal	61.3	61.3	100%	3e-09	90%	XP_008988091.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Sai	61.3	61.3	100%	3e-09	90%	XP_003931139.1
☐	lysosome-associated membrane glycoprotein 2 isoform 1 precursor [Sus scro	52.4	52.4	100%	3e-06	76%	NP_001231184.1
☐	lysosome-associated membrane glycoprotein 2 isoform 2 precursor [Sus scro	52.0	52.0	100%	4e-06	76%	NP_001231185.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2-like [Tursiops tr	50.7	50.7	90%	1e-05	84%	XP_004322447.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X5 [Lip	50.7	50.7	90%	1e-05	84%	XP_007464492.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X4 [Lip	50.7	50.7	90%	1e-05	84%	XP_007464491.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X3 [Lip	50.7	50.7	90%	1e-05	84%	XP_007464490.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Lip	50.7	50.7	90%	1e-05	84%	XP_007464489.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Phy	50.7	50.7	90%	1e-05	84%	XP_007116126.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Phy	50.7	50.7	90%	1e-05	84%	XP_007116125.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform 3 [Orci	50.7	50.7	90%	1e-05	84%	XP_004285633.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform 2 [Orci	50.7	50.7	90%	1e-05	84%	XP_004285632.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Lip	50.7	50.7	90%	1e-05	84%	XP_007464488.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Bal	50.7	50.7	90%	1e-05	84%	XP_007178670.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Bal	50.7	50.7	90%	1e-05	84%	XP_007178669.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform 1 [Orci	50.7	50.7	90%	1e-05	84%	XP_004285631.1
☐	lysosomal membrane glycoprotein lamp-2 homolog [Homo sapiens]	50.3	50.3	76%	2e-05	94%	AAB28483.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Bis	49.0	49.0	90%	4e-05	79%	XP_010830554.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Bis	49.0	49.0	90%	4e-05	79%	XP_010830553.1
☐	Lysosome-associated membrane glycoprotein 2 [Bos mutus]	49.0	49.0	90%	4e-05	79%	ELR59401.1
☐	lysosome-associated membrane glycoprotein 2 isoform 2 precursor [Bos taur	49.0	49.0	90%	4e-05	79%	NP_001029742.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Bos	49.0	49.0	90%	4e-05	79%	XP_005891592.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Bos	49.0	49.0	90%	4e-05	79%	XP_005891591.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform 2 [Ovis	49.0	49.0	90%	4e-05	79%	XP_004022400.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform 1 [Ovis	49.0	49.0	90%	4e-05	79%	XP_004022399.1
☐	lysosome-associated membrane glycoprotein 2 isoform 1 precursor [Bos taur	49.0	49.0	90%	4e-05	79%	NP_001106715.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Ca	49.0	49.0	90%	4e-05	84%	XP_003465647.2
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform 3 [Ovis	49.0	49.0	90%	4e-05	79%	XP_004022401.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Ca	49.0	49.0	90%	4e-05	84%	XP_005001877.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoformX4 [Can	49.0	49.0	90%	4e-05	84%	XP_864590.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X6 [Ca	49.0	49.0	90%	4e-05	84%	XP_005641822.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X5 [Ca	49.0	49.0	90%	4e-05	84%	XP_005641821.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X3 [Bu	49.0	49.0	90%	4e-05	79%	XP_006048863.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Bu	49.0	49.0	90%	4e-05	79%	XP_006048862.1

☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Par	49.0	49.0	90%	4e-05	79%	XP_005954005.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Par	49.0	49.0	90%	4e-05	79%	XP_005954004.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Ca	49.0	49.0	90%	4e-05	79%	XP_005700397.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Ca	49.0	49.0	90%	4e-05	79%	XP_005700396.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Bu	49.0	49.0	90%	4e-05	79%	XP_006048861.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Bos	49.0	49.0	90%	4e-05	79%	XP_005227520.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 [Octodon degus	46.9	46.9	90%	2e-04	84%	XP_004647723.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X3 [Ory	46.9	46.9	90%	2e-04	74%	XP_008271378.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Ory	46.9	46.9	90%	2e-04	74%	XP_008271377.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Ory	46.9	46.9	90%	2e-04	74%	XP_008271376.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Tu	46.4	46.4	90%	3e-04	79%	XP_006165272.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Tu	46.4	46.4	90%	3e-04	79%	XP_006165271.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X3 [My	46.4	46.4	100%	3e-04	71%	XP_006082216.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [My	46.4	46.4	100%	3e-04	71%	XP_006082215.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X3 [My	46.4	46.4	100%	3e-04	71%	XP_005884738.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [My	46.4	46.4	100%	3e-04	71%	XP_005884737.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X3 [Tu	46.4	46.4	90%	3e-04	79%	XP_006165273.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [My	46.4	46.4	100%	3e-04	71%	XP_006082214.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [My	46.4	46.4	100%	3e-04	71%	XP_005884736.1
☐	Lysosome-associated membrane glycoprotein 2 [Tupaia chinensis]	46.4	46.4	90%	3e-04	79%	ELV12237.1
☐	Lysosome-associated membrane glycoprotein 2 [Myotis brandtii]	46.4	46.4	100%	3e-04	71%	EPQ19198.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X3 [Gal	46.0	46.0	90%	4e-04	79%	XP_008585587.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Gal	46.0	46.0	90%	4e-04	79%	XP_008585586.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X1 [Gal	46.0	46.0	90%	4e-04	79%	XP_008585585.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 [Leptonychotes	45.6	45.6	90%	5e-04	79%	XP_006746269.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isoform X2 [Ory	45.6	45.6	90%	5e-04	79%	XP_007951511.1

⊟ Alignments

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unnamed protein product [Macaca fascicularis]

Sequence ID: dbj|BAE87445.1| **Length:** 174 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 11 to 31 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	8e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1   KVASVININPDTTHSTGSCRS  21
           KVASVININP+TTHSTGSCRS
Sbjct  11  KVASVININPNTTHSTGSCRS  31
```

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lysosome-associated membrane protein 2

Sequence ID: prf||2106261A **Length:** 268 **Number of Matches:** 1

Related Information

Range 1: 105 to 125 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	1e-10	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KVASVININPDTTHSTGSCRS  21
            KVASVININP+TTHSTGSCRS
Sbjct  105  KVASVININPNTTHSTGSCRS  125
```

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unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAH11955.1| **Length:** 300 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 136 to 156 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	1e-10	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KVASVININPDTTHSTGSCRS  21
            KVASVININP+TTHSTGSCRS
Sbjct  136  KVASVININPNTTHSTGSCRS  156
```

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PREDICTED: lysosome-associated membrane glycoprotein 2 [Pan troglodytes]

Sequence ID: ref|XP_009437861.1| **Length:** 337 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 173 to 193 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	1e-10	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KVASVININPDTTHSTGSCRS  21
            KVASVININP+TTHSTGSCRS
Sbjct  173  KVASVININPNTTHSTGSCRS  193
```

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PREDICTED: lysosome-associated membrane glycoprotein 2 [Gorilla gorilla gorilla]

Sequence ID: ref|XP_004064857.1| **Length:** 346 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 211 to 231 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	1e-10	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KVASVININPDTTHSTGSCRS  21
            KVASVININP+TTHSTGSCRS
Sbjct  211  KVASVININPNTTHSTGSCRS  231
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download

How to read this page Blast report description

LAMP2_KVASVININPNTTHSTGSCRS_NonMod

RID B9HMRNH201R (Expires on 01-14 14:17 pm)

Query ID	lcl|98360	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	21		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

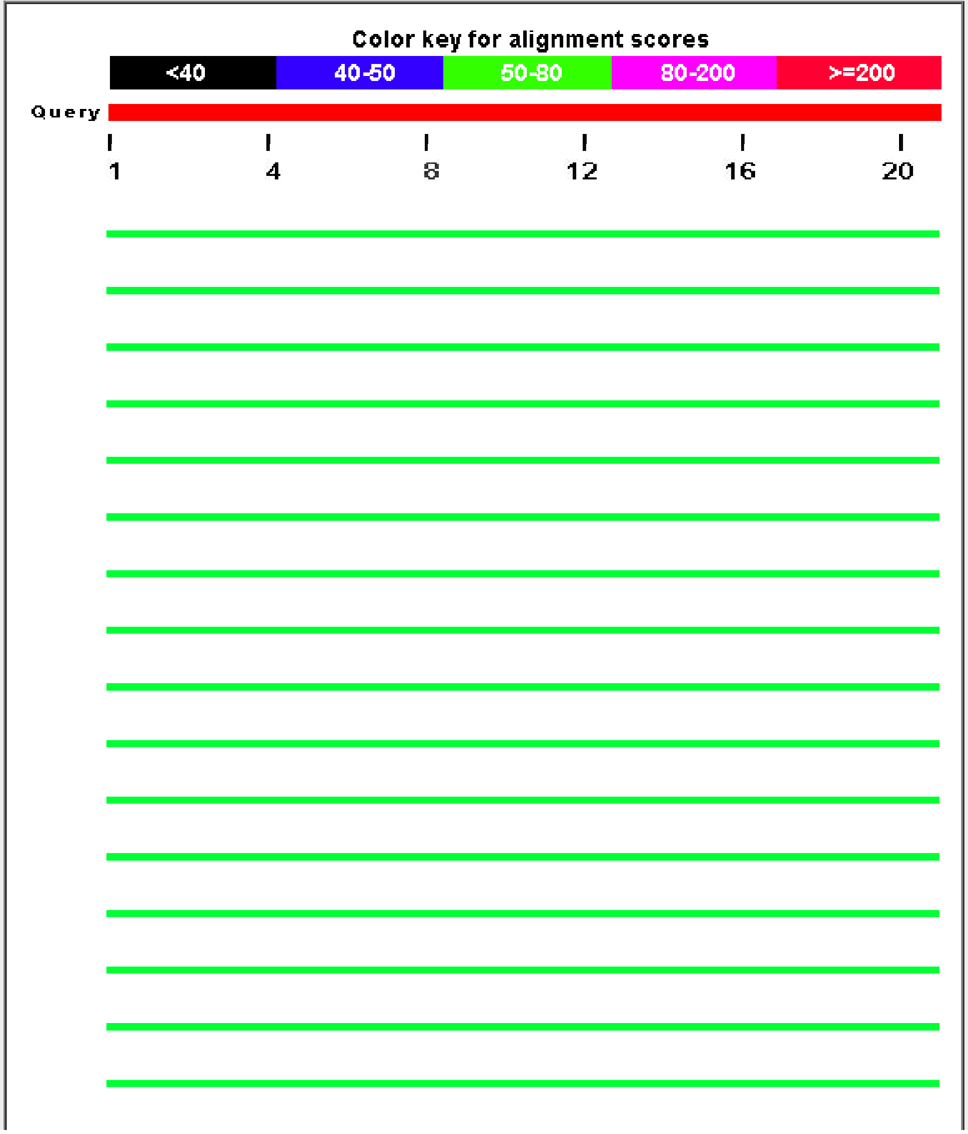
Graphic Summary

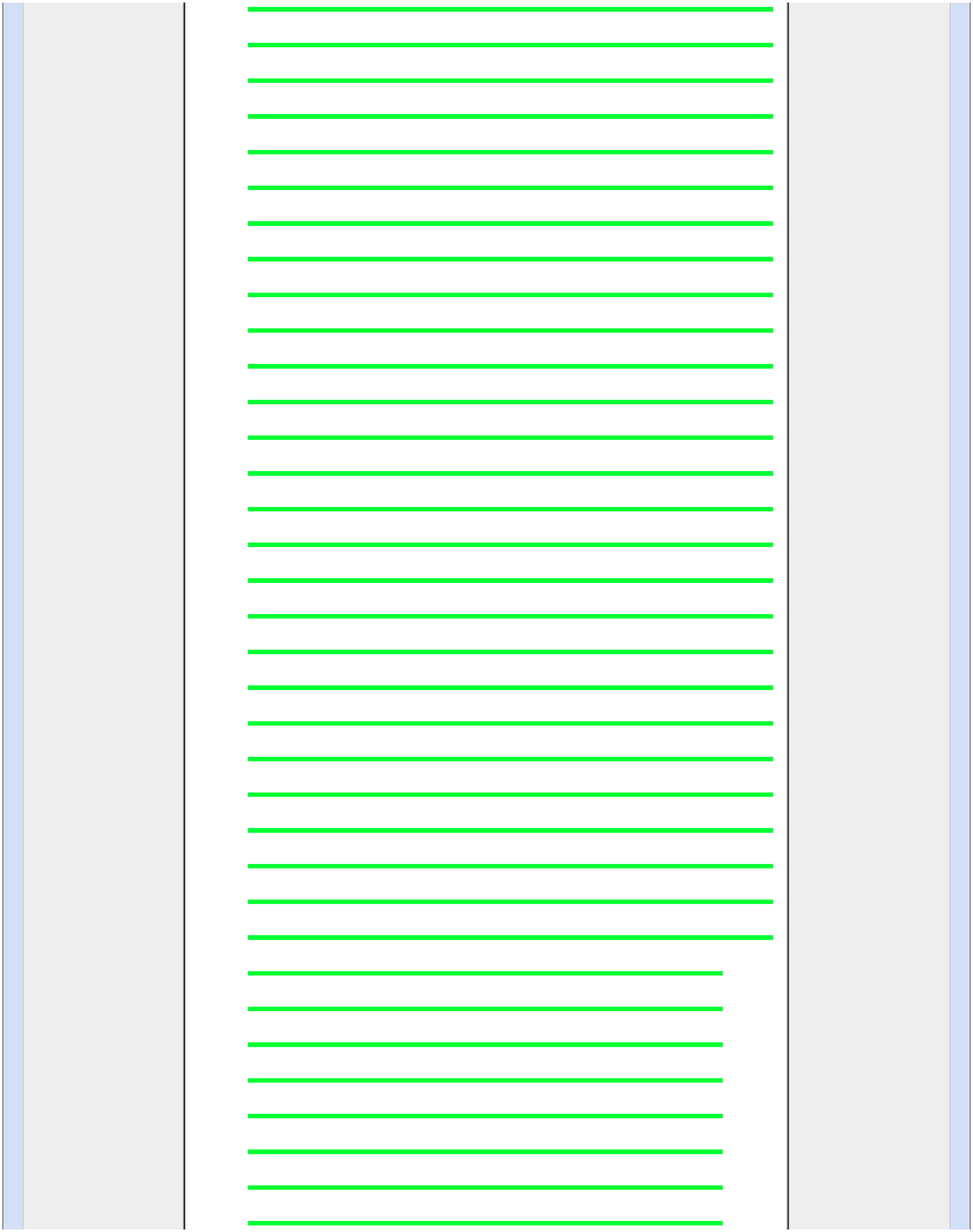
Show Conserved Domains

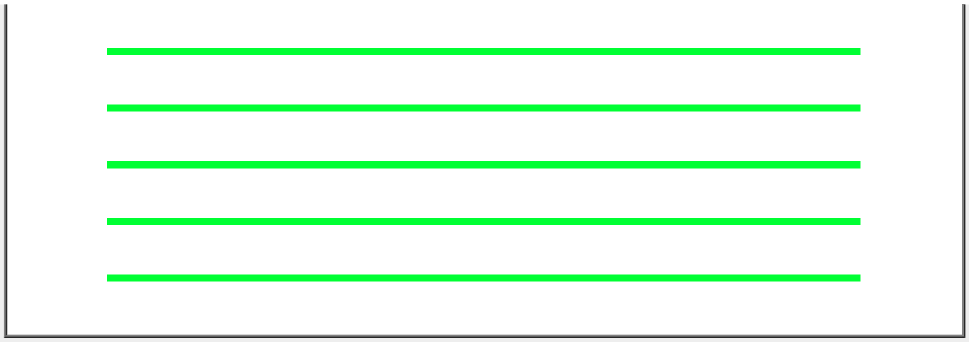
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊖ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Macaca fascicularis]	68.1	68.1	100%	1e-11	100%	gi|90075530|BAE87445.1
☐	lysosome-associated membrane protein 2 [Homo sapiens]	68.1	68.1	100%	1e-11	100%	gi|1094569|2106261A
☐	unnamed protein product [Homo sapiens]	68.1	68.1	100%	1e-11	100%	gi|221040556|BAH11955.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 [Pan	68.1	68.1	100%	1e-11	100%	gi|694986114|XP_009437861.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 [Goril	68.1	68.1	100%	1e-11	100%	gi|426397293|XP_004064857.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|724955883|XP_010353039.1
☐	unnamed protein product [Homo sapiens]	68.1	68.1	100%	1e-11	100%	gi|194385728|BAG65239.1
☐	lysosomal membrane glycoprotein-2 [Homo sapiens]	68.1	68.1	100%	1e-11	100%	gi|307110|AAA60383.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|724955880|XP_010353037.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|724955878|XP_010353036.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|685617844|XP_009196467.1
☐	LAMP2 [synthetic construct]	68.1	68.1	100%	1e-11	100%	gi|649119698|AIC54689.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|635147704|XP_008017647.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|635147702|XP_008017646.1
☐	lysosomal membrane glycoprotein-2 [Homo sapiens]	68.1	68.1	100%	1e-11	100%	gi|1809215|AAB41647.1
☐	lysosome-associated membrane glycoprotein 2 isoform B precursor	68.1	68.1	100%	1e-11	100%	gi|7669503|NP_054701.1
☐	hypothetical protein [Pongo abelii]	68.1	68.1	100%	1e-11	100%	gi|55732398|CAH92900.1
☐	lysosome-associated membrane glycoprotein 2 isoform A precursor	68.1	68.1	100%	1e-11	100%	gi|4504957|NP_002285.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|402911290|XP_003918269.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|397505262|XP_003823188.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|397505260|XP_003823187.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|395754380|XP_003779762.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|332226294|XP_003262323.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|297710915|XP_002832104.1
☐	lysosome-associated membrane glycoprotein 2 precursor [Macaca	68.1	68.1	100%	1e-11	100%	gi|386782257|NP_001247737.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|544522660|XP_005594543.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|724955885|XP_010353040.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|635147700|XP_008017645.1
☐							

	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|402911292|XP_003918270.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|397505264|XP_003823189.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|395754382|XP_003779763.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|332226298|XP_003262325.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	68.1	68.1	100%	1e-11	100%	gi|544522658|XP_005594542.1
☐	lysosome-associated membrane glycoprotein 2 isoform C precursor	68.1	68.1	100%	1e-11	100%	gi|169790833|NP_001116078.1
☐	unnamed protein product [Homo sapiens]	66.0	66.0	100%	7e-11	95%	gi|194375932|BAG57310.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	63.8	63.8	100%	4e-10	95%	gi|725575673|XP_010340007.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	63.8	63.8	100%	4e-10	95%	gi|296236307|XP_002763275.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	63.8	63.8	100%	4e-10	95%	gi|296236305|XP_002763274.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	63.8	63.8	100%	4e-10	95%	gi|403279171|XP_003931138.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	63.8	63.8	100%	4e-10	95%	gi|675769593|XP_008988091.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	63.8	63.8	100%	4e-10	95%	gi|403279173|XP_003931139.1
☐	lysosome-associated membrane glycoprotein 2 isoform 1 precursor	54.9	54.9	100%	4e-07	81%	gi|346716335|NP_001231184.1
☐	lysosome-associated membrane glycoprotein 2 isoform 2 precursor	54.5	54.5	100%	5e-07	81%	gi|346716337|NP_001231185.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2-like [	53.2	53.2	90%	1e-06	89%	gi|470632997|XP_004322447.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	53.2	53.2	90%	1e-06	89%	gi|602708463|XP_007464492.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	53.2	53.2	90%	1e-06	89%	gi|602708461|XP_007464491.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	53.2	53.2	90%	1e-06	89%	gi|602708459|XP_007464490.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	53.2	53.2	90%	1e-06	89%	gi|602708457|XP_007464489.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	53.2	53.2	90%	1e-06	89%	gi|593754480|XP_007116126.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	53.2	53.2	90%	1e-06	89%	gi|593754478|XP_007116125.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	53.2	53.2	90%	1e-06	89%	gi|466085768|XP_004285633.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	53.2	53.2	90%	1e-06	89%	gi|466085764|XP_004285632.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	53.2	53.2	90%	1e-06	89%	gi|602708455|XP_007464488.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	53.2	53.2	90%	1e-06	89%	gi|594660829|XP_007178670.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	53.2	53.2	90%	1e-06	89%	gi|594660827|XP_007178669.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	53.2	53.2	90%	1e-06	89%	gi|466085762|XP_004285631.1
☐	lysosomal membrane glycoprotein lamp-2 homolog [Homo sapiens]	52.8	52.8	76%	2e-06	100%	gi|435756|AAB28483.1
☐	Lysosome-associated membrane glycoprotein 2 [Bos mutus]	51.5	51.5	90%	5e-06	84%	gi|440909498|ELR59401.1
☐	lysosome-associated membrane glycoprotein 2 isoform 2 precursor	51.5	51.5	90%	5e-06	84%	gi|77736087|NP_001029742.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	84%	gi|555958958|XP_005891592.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	84%	gi|555958956|XP_005891591.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	84%	gi|426257572|XP_004022400.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	84%	gi|426257570|XP_004022399.1
☐	lysosome-associated membrane glycoprotein 2 isoform 1 precursor	51.5	51.5	90%	5e-06	84%	gi|164420738|NP_001106715.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	89%	gi|514453030|XP_003465647.2
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	84%	gi|426257574|XP_004022401.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	89%	gi|514453028|XP_005001877.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	89%	gi|74008247|XP_864590.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	89%	gi|545559229|XP_005641822.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	89%	gi|545559226|XP_005641821.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	84%	gi|594048957|XP_006048863.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	84%	gi|594048955|XP_006048862.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	84%	gi|556716158|XP_005954005.1

☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	84%	gi|556716156|XP_005954004.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	84%	gi|548529771|XP_005700397.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	84%	gi|548529766|XP_005700396.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	84%	gi|594048953|XP_006048861.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	51.5	51.5	90%	5e-06	84%	gi|529013535|XP_005227520.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 [Octo	49.4	49.4	90%	3e-05	89%	gi|507713360|XP_004647723.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	49.4	49.4	90%	3e-05	79%	gi|655877736|XP_008271378.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	49.4	49.4	90%	3e-05	79%	gi|655877734|XP_008271377.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	49.4	49.4	90%	3e-05	79%	gi|655877732|XP_008271376.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	49.0	49.0	90%	4e-05	84%	gi|562874873|XP_006165272.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	49.0	49.0	90%	4e-05	84%	gi|562874871|XP_006165271.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	49.0	49.0	100%	4e-05	76%	gi|558099063|XP_006082216.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	49.0	49.0	100%	4e-05	76%	gi|558099061|XP_006082215.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	49.0	49.0	100%	4e-05	76%	gi|554586647|XP_005884738.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	49.0	49.0	100%	4e-05	76%	gi|554586645|XP_005884737.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	49.0	49.0	90%	4e-05	84%	gi|562874875|XP_006165273.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	49.0	49.0	100%	4e-05	76%	gi|558099059|XP_006082214.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	49.0	49.0	100%	4e-05	76%	gi|554586643|XP_005884736.1
☐	Lysosome-associated membrane glycoprotein 2 [Tupaia chinensis]	49.0	49.0	90%	4e-05	84%	gi|444518571|ELV12237.1
☐	Lysosome-associated membrane glycoprotein 2 [Myotis brandtii]	49.0	49.0	100%	4e-05	76%	gi|521037420|EPQ19198.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	48.6	48.6	90%	5e-05	84%	gi|667313899|XP_008585587.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	48.6	48.6	90%	5e-05	84%	gi|667313896|XP_008585586.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	48.6	48.6	90%	5e-05	84%	gi|667313892|XP_008585585.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 [Lept	48.1	48.1	90%	7e-05	84%	gi|585189937|XP_006746269.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	48.1	48.1	90%	7e-05	84%	gi|634883039|XP_007951511.1
☐	PREDICTED: lysosome-associated membrane glycoprotein 2 isofor	48.1	48.1	90%	7e-05	84%	gi|472375054|XP_004406977.1
☐	hypothetical protein PANDA_011592 [Ailuropoda melanoleuca]	48.1	48.1	90%	7e-05	84%	gi|281340908|EFB16492.1

⊟ Alignments

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unnamed protein product [Macaca fascicularis]

Sequence ID: gi|90075530|dbj|BAE87445.1| **Length:** 174 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 11 to 31 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	1e-11	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KVASVININPNTTHSTGSCRS  21
            KVASVININPNTTHSTGSCRS
Sbjct  11   KVASVININPNTTHSTGSCRS  31
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

lysosome-associated membrane protein 2

Sequence ID: gi|1094569|prf||2106261A **Length:** 268 **Number of Matches:** 1

Related Information

Range 1: 105 to 125 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	1e-11	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KVASVININPNTTHSTGSCRS  21
```

```
           KVASVININPNTTHSTGSCRS
Sbjct  105  KVASVININPNTTHSTGSCRS  125
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221040556|dbj|BAH11955.1| **Length:** 300 **Number of Matches:** 1

Range 1: 136 to 156 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	1e-11	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KVASVININPNTTHSTGSCRS  21
           KVASVININPNTTHSTGSCRS
Sbjct  136  KVASVININPNTTHSTGSCRS  156
```

Related Information

Gene - associated gene details

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PREDICTED: lysosome-associated membrane glycoprotein 2 [Pan troglodytes]

Sequence ID: gi|694986114|ref|XP_009437861.1| **Length:** 337 **Number of Matches:** 1

Range 1: 173 to 193 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	1e-11	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KVASVININPNTTHSTGSCRS  21
           KVASVININPNTTHSTGSCRS
Sbjct  173  KVASVININPNTTHSTGSCRS  193
```

Related Information

Gene - associated gene details

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PREDICTED: lysosome-associated membrane glycoprotein 2 [Gorilla gorilla gorilla]

Sequence ID: gi|426397293|ref|XP_004064857.1| **Length:** 346 **Number of Matches:** 1

Range 1: 211 to 231 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	1e-11	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KVASVININPNTTHSTGSCRS  21
           KVASVININPNTTHSTGSCRS
Sbjct  211  KVASVININPNTTHSTGSCRS  231
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVHYXTMA01R

Your search parameters were adjusted to search for a short input sequence.

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LCAT_KAELSDHTRPVILVPGCLGNQLEAKL_Mod

RID BVHYXTMA01R (Expires on 01-21 10:13 am)

Query ID	lcl|307745	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	26	**Program**	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

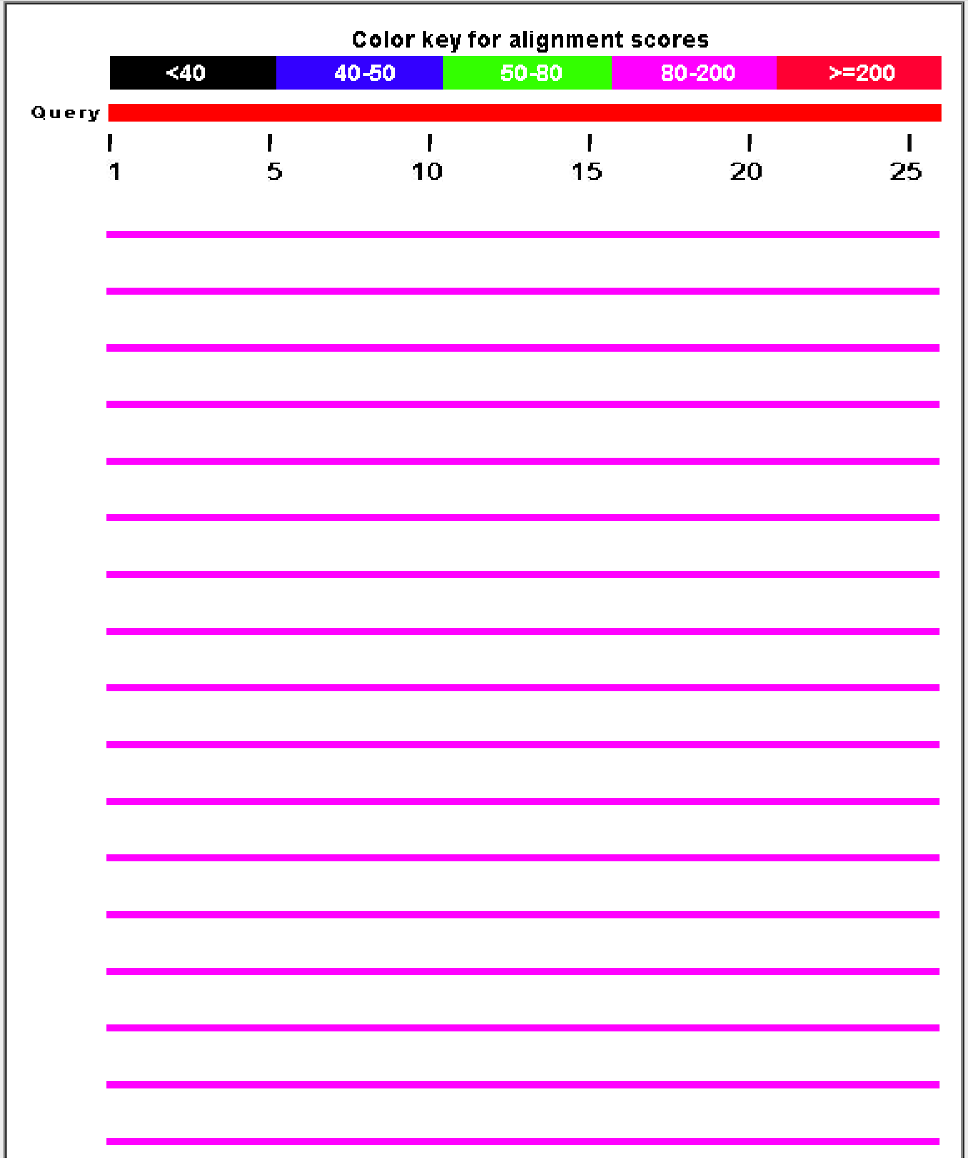
Graphic Summary

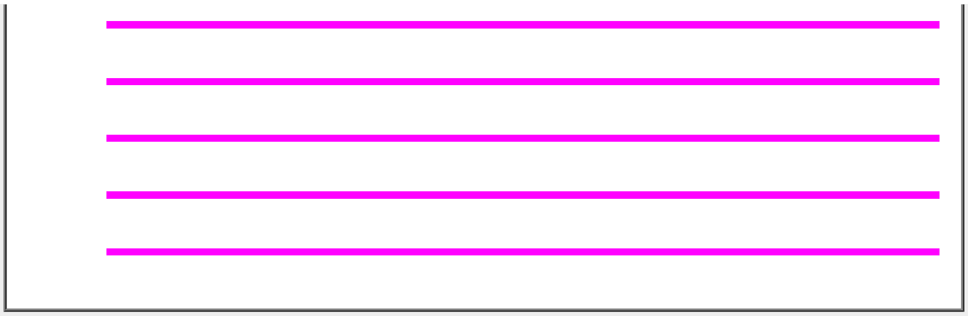
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





⊖Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	lecithin cholesterol acyltransferase [Macaca sp.]	81.7	81.7	100%	5e-16	96%	AAM76621.1
☐	lecithin cholesterol acyltransferase [Pongo pygmaeus]	81.7	81.7	100%	5e-16	96%	AAM76620.1
☐	lecithin cholesterol acyltransferase [Gorilla gorilla]	81.7	81.7	100%	5e-16	96%	AAM76619.1
☐	lecithin cholesterol acyltransferase [Saguinus oedipus]	81.7	81.7	100%	5e-16	96%	AAM76622.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Mesocricetus auratu	81.7	81.7	100%	6e-16	96%	XP_005076409.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase-like [Macaca mulatta	81.7	81.7	100%	6e-16	96%	XP_001090154.2
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Pongo abelii]	81.7	81.7	100%	6e-16	96%	XP_009249145.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2 [Pan trog	81.7	81.7	100%	6e-16	96%	XP_009429355.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X3 [Galeopte	81.7	81.7	100%	6e-16	96%	XP_008565520.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X3 [Equus pr	81.7	81.7	100%	7e-16	96%	XP_008516437.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X3 [Equus ca	81.7	81.7	100%	7e-16	96%	XP_005608407.1
☐	lecithin:cholesterol acyltransferase, LCAT [Homo sapiens]	81.7	81.7	100%	7e-16	96%	AAB34898.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2 [Panthera	81.7	81.7	100%	7e-16	96%	XP_007090383.1
☐	lecithin:cholesterol acyltransferase precursor [Homo sapiens]	81.7	81.7	100%	7e-16	96%	AAA59499.1
☐	Phosphatidylcholine-sterol acyltransferase [Macaca fascicularis]	81.7	81.7	100%	7e-16	96%	EHH60494.1
☐	lecithin-cholesterol acyltransferase precursor (EC 2.3.1.43) [Homo sapiens]	81.7	81.7	100%	7e-16	96%	AAA59500.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Loxodonta africana]	81.7	81.7	100%	7e-16	96%	XP_003417179.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Fukomys damarens	81.7	81.7	100%	7e-16	96%	XP_010610588.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform 2 [Canis lupu	81.7	81.7	100%	7e-16	96%	XP_851673.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Chinchilla lanigera]	81.7	81.7	100%	7e-16	96%	XP_005403659.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Heterocephalus glab	81.7	81.7	100%	7e-16	96%	XP_004843055.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1 [Heteroce	81.7	81.7	100%	7e-16	96%	XP_004907111.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Orycteropus afer afe	81.7	81.7	100%	7e-16	96%	XP_007938473.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Chrysochloris asiatic	81.7	81.7	100%	7e-16	96%	XP_006860289.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Elephantulus edwar	81.7	81.7	100%	7e-16	96%	XP_006878737.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Trichechus manatus	81.7	81.7	100%	7e-16	96%	XP_004371526.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Bison bison bison]	81.7	81.7	100%	7e-16	96%	XP_010849309.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Rhinopithecus roxel	81.7	81.7	100%	7e-16	96%	XP_010353366.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2 [Galeopte	81.7	81.7	100%	7e-16	96%	XP_008565513.1

☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2 [Equus pr	81.7	81.7	100%	7e-16	96%	XP_008516436.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Tarsius syrichta]	81.7	81.7	100%	7e-16	96%	XP_008063935.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Chlorocebus sabaeu	81.7	81.7	100%	7e-16	96%	XP_007992092.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2 [Tupaia c	81.7	81.7	100%	7e-16	96%	XP_006156948.1
☐	phosphatidylcholine-sterol acyltransferase precursor [Bos taurus]	81.7	81.7	100%	7e-16	96%	NP_001039534.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Lipotes vexillifer]	81.7	81.7	100%	7e-16	96%	XP_007457320.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Balaenoptera acutor	81.7	81.7	100%	7e-16	96%	XP_007198213.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1 [Bubalus	81.7	81.7	100%	7e-16	96%	XP_006041058.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1 [Panthera	81.7	81.7	100%	7e-16	96%	XP_007090382.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Peromyscus manicu	81.7	81.7	100%	7e-16	96%	XP_006986895.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2 [Leptonyc	81.7	81.7	100%	7e-16	96%	XP_006730154.1
☐	phosphatidylcholine-sterol acyltransferase precursor [Papio anubis]	81.7	81.7	100%	7e-16	96%	NP_001106083.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X3 [Tupaia c	81.7	81.7	100%	7e-16	96%	XP_006156949.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Vicugna pacos]	81.7	81.7	100%	7e-16	96%	XP_006203780.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Camelus ferus]	81.7	81.7	100%	7e-16	96%	XP_006180662.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Pantholops hodgsor	81.7	81.7	100%	7e-16	96%	XP_005956897.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1 [Macaca	81.7	81.7	100%	7e-16	96%	XP_005592370.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Ictidomys tridecemli	81.7	81.7	100%	7e-16	96%	XP_005318397.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Condylura cristata]	81.7	81.7	100%	7e-16	96%	XP_004690509.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Jaculus jaculus]	81.7	81.7	100%	7e-16	96%	XP_004661727.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Sorex araneus]	81.7	81.7	100%	7e-16	96%	XP_004600640.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform 2 [Ceratothe	81.7	81.7	100%	7e-16	96%	XP_004431810.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Tursiops truncatus]	81.7	81.7	100%	7e-16	96%	XP_004330924.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Orcinus orca]	81.7	81.7	100%	7e-16	96%	XP_004273232.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Bos mutus]	81.7	81.7	100%	7e-16	96%	XP_005896591.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Pteropus alecto]	81.7	81.7	100%	7e-16	96%	XP_006909849.1
☐	phosphatidylcholine-sterol acyltransferase precursor [Oryctolagus cuniculus]	81.7	81.7	100%	7e-16	96%	NP_001075659.1
☐	phosphatidylcholine-sterol acyltransferase precursor [Homo sapiens]	81.7	81.7	100%	7e-16	96%	NP_000220.1
☐	Phosphatidylcholine-sterol acyltransferase [Macaca mulatta]	81.7	81.7	100%	7e-16	96%	EHH31776.1
☐	phosphatidylcholine-sterol acyltransferase precursor [Ovis aries]	81.7	81.7	100%	7e-16	96%	NP_001156040.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1 [Equus ca	81.7	81.7	100%	7e-16	96%	XP_001498513.1
☐	lecithin-cholesterol acyltransferase [synthetic construct]	81.7	81.7	100%	7e-16	96%	AAP88749.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Cavia porcellus]	81.7	81.7	100%	7e-16	96%	XP_003472190.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1 [Callithrix	81.7	81.7	100%	7e-16	96%	XP_002761124.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Otolemur garnettii]	81.7	81.7	100%	7e-16	96%	XP_003799423.1
☐	lecithin cholesterol acyltransferase [Meriones unguiculatus]	81.7	81.7	100%	7e-16	96%	AGH06057.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Felis catus]	81.7	81.7	100%	7e-16	96%	XP_003998196.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1 [Tupaia c	81.7	81.7	100%	7e-16	96%	XP_006156947.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Ochotona princeps]	81.7	81.7	100%	7e-16	96%	XP_004584021.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1 [Galeopte	81.7	81.7	100%	7e-16	96%	XP_008565507.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1 [Leptonyc	81.7	81.7	100%	7e-16	96%	XP_006730153.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1 [Equus pr	81.7	81.7	100%	7e-16	96%	XP_008516435.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2 [Equus ca	81.7	81.7	100%	7e-16	96%	XP_005608406.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform 1 [Ceratothe	81.7	81.7	100%	7e-16	96%	XP_004431809.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Octodon degus]	81.7	81.7	100%	7e-16	96%	XP_004625900.1

☐	PREDICTED: phosphatidylcholine-sterol acyltransferase-like isoform X3 [Phys	81.7	81.7	100%	7e-16	96%	XP_007120847.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase-like isoform X2 [Phys	81.7	81.7	100%	7e-16	96%	XP_007120846.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase-like isoform X1 [Phys	81.7	81.7	100%	7e-16	96%	XP_007120845.1
☐	solute carrier family 12 member 4-like isoform 4 [Camelus ferus]	81.7	81.7	100%	8e-16	96%	EPY84185.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Myotis lucifugus]	79.5	79.5	100%	4e-15	92%	XP_006099517.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Myotis brandtii]	79.5	79.5	100%	4e-15	92%	XP_005876489.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Myotis davidii]	79.5	79.5	100%	4e-15	92%	XP_006769815.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Eptesicus fuscus]	79.5	79.5	100%	4e-15	92%	XP_008138152.1
☐	hypothetical protein PANDA_006959 [Ailuropoda melanoleuca]	79.1	79.1	100%	5e-15	92%	EFB15890.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2 [Ursus m	79.1	79.1	100%	5e-15	92%	XP_008700662.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X4 [Mustela	79.1	79.1	100%	5e-15	92%	XP_004744543.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase-like [Ailuropoda mela	79.1	79.1	100%	5e-15	92%	XP_002918480.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X3 [Mustela	79.1	79.1	100%	5e-15	92%	XP_004744542.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2 [Mustela	79.1	79.1	100%	5e-15	92%	XP_004744541.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1 [Mustela	79.1	79.1	100%	5e-15	92%	XP_004744540.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1 [Saimiri b	78.7	78.7	96%	7e-15	96%	XP_010345110.1
☐	lecithin cholesterol acyltransferase, isoform CRA_b [Mus musculus]	77.4	77.4	100%	2e-14	92%	EDL11335.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X3 [Cricetulu	77.4	77.4	100%	2e-14	92%	XP_007610057.1
☐	cholesterol acyltransferase [Mus musculus]	77.4	77.4	100%	2e-14	92%	AAA39419.1
☐	phosphatidylcholine-sterol acyltransferase precursor [Mus musculus]	77.4	77.4	100%	2e-14	92%	NP_032516.2
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Microtus ochrogaste	77.4	77.4	100%	2e-14	92%	XP_005345498.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform 1 [Dasypus r	77.4	77.4	100%	2e-14	92%	XP_004459692.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2 [Cricetulu	77.4	77.4	100%	2e-14	92%	XP_003504331.1
☐	unnamed protein product [Mus musculus]	77.4	77.4	100%	2e-14	92%	BAB23665.1
☐	lecithin cholesterol acyltransferase [Sus scrofa]	75.3	75.3	100%	1e-13	92%	ACV21076.1
☐	phosphatidylcholine-sterol acyltransferase precursor [Sus scrofa]	75.3	75.3	100%	1e-13	92%	NP_001158328.1

Alignments

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lecithin cholesterol acyltransferase [Macaca sp.]

Sequence ID: gb|AAM76621.1| **Length:** 209 **Number of Matches:** 1

Related Information

Range 1: 9 to 34 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	5e-16	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1   KAELSDHTRPVILVPGCLGNQLEAKL  26
           KAELS+HTRPVILVPGCLGNQLEAKL
Sbjct  9   KAELSNHTRPVILVPGCLGNQLEAKL  34
```

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lecithin cholesterol acyltransferase [Pongo pygmaeus]

Sequence ID: gb|AAM76620.1| **Length:** 209 **Number of Matches:** 1

Related Information

Range 1: 9 to 34 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	5e-16	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    KAELSDHTRPVILVPGCLGNQLEAKL  26
            KAELS+HTRPVILVPGCLGNQLEAKL
Sbjct  9    KAELSNHTRPVILVPGCLGNQLEAKL  34
```

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lecithin cholesterol acyltransferase [Gorilla gorilla]

Sequence ID: gb|AAM76619.1| **Length:** 209 **Number of Matches:** 1

Related Information

Range 1: 9 to 34 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	5e-16	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    KAELSDHTRPVILVPGCLGNQLEAKL  26
            KAELS+HTRPVILVPGCLGNQLEAKL
Sbjct  9    KAELSNHTRPVILVPGCLGNQLEAKL  34
```

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lecithin cholesterol acyltransferase [Saguinus oedipus]

Sequence ID: gb|AAM76622.1| **Length:** 210 **Number of Matches:** 1

Related Information

Range 1: 9 to 34 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	5e-16	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    KAELSDHTRPVILVPGCLGNQLEAKL  26
            KAELS+HTRPVILVPGCLGNQLEAKL
Sbjct  9    KAELSNHTRPVILVPGCLGNQLEAKL  34
```

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PREDICTED: phosphatidylcholine-sterol acyltransferase [Mesocricetus auratus]

Sequence ID: ref|XP_005076409.1| **Length:** 308 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 38 to 63 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	6e-16	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    KAELSDHTRPVILVPGCLGNQLEAKL  26
            KAELS+HTRPVILVPGCLGNQLEAKL
Sbjct  38   KAELSNHTRPVILVPGCLGNQLEAKL  63
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - B9HPATHC01R

Your search parameters were adjusted to search for a short input sequence.

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How to read this page | Blast report description

LCAT_KAELSNHTRPVILVPGCLGNQLEAKL_NonMod

RID B9HPATHC01R (Expires on 01-14 14:18 pm)

Query ID	lcl|120449	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	26		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

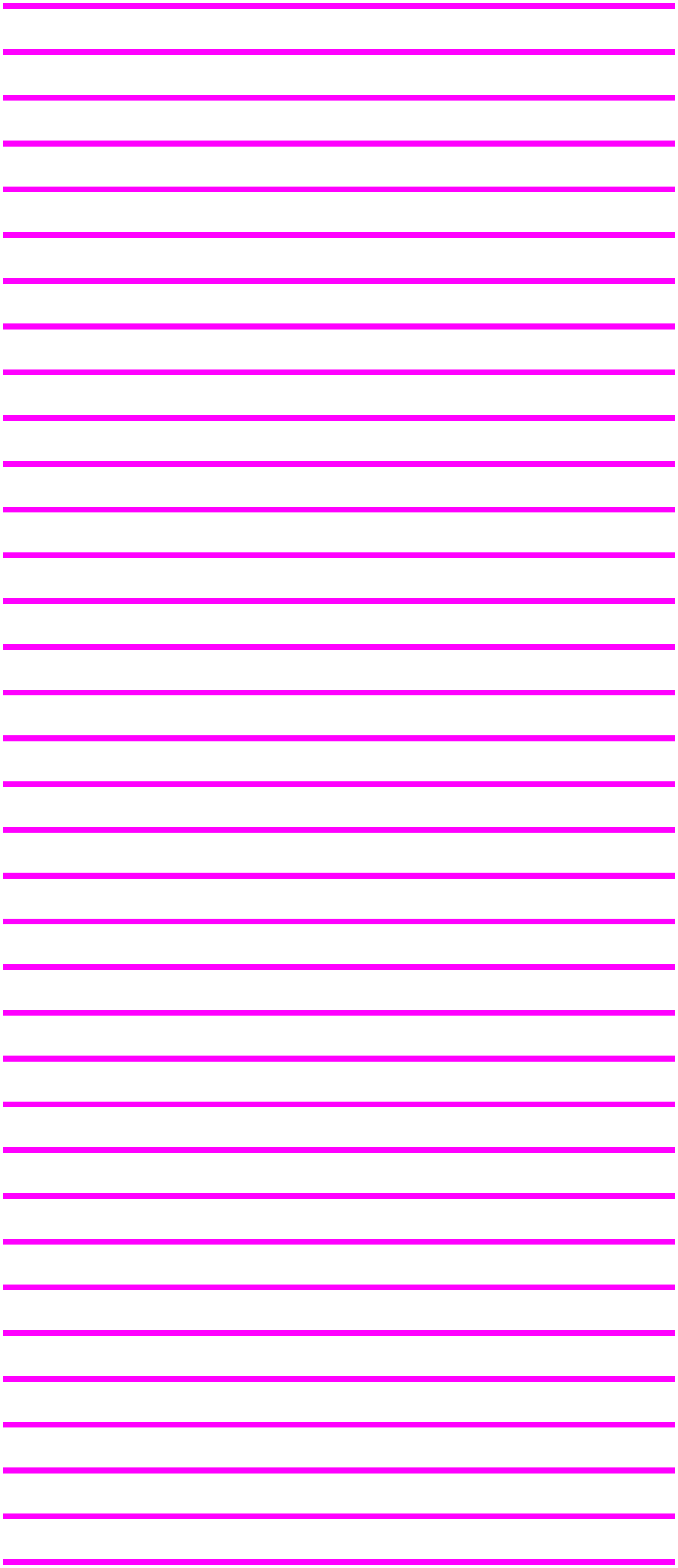
Graphic Summary

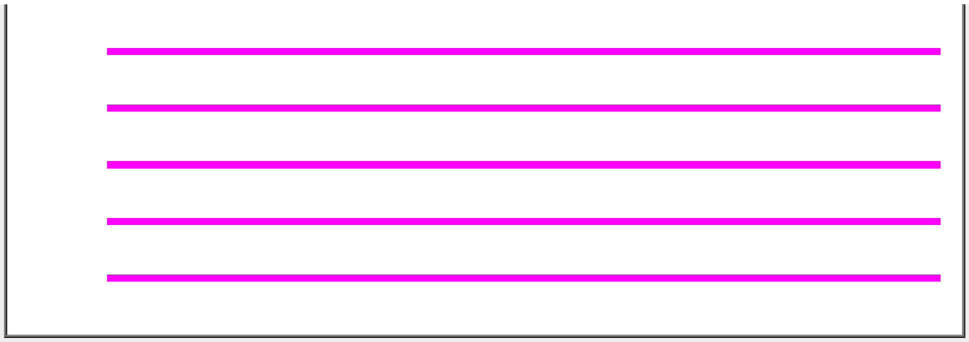
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	lecithin cholesterol acyltransferase [Macaca sp.]	84.2	84.2	100%	6e-17	100%	gi|23379758|AAM76621.1
☐	lecithin cholesterol acyltransferase [Pongo pygmaeus]	84.2	84.2	100%	6e-17	100%	gi|23379756|AAM76620.1
☐	lecithin cholesterol acyltransferase [Gorilla gorilla]	84.2	84.2	100%	6e-17	100%	gi|23379754|AAM76619.1
☐	lecithin cholesterol acyltransferase [Saguinus oedipus]	84.2	84.2	100%	6e-17	100%	gi|23379760|AAM76622.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Mesocrice	84.2	84.2	100%	7e-17	100%	gi|524952837|XP_005076409.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase-like [Maca	84.2	84.2	100%	8e-17	100%	gi|297284280|XP_001090154.2
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Pongo ab	84.2	84.2	100%	8e-17	100%	gi|686751128|XP_009249145.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2	84.2	84.2	100%	8e-17	100%	gi|694964284|XP_009429355.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X3	84.2	84.2	100%	8e-17	100%	gi|667240883|XP_008565520.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X3	84.2	84.2	100%	8e-17	100%	gi|664718824|XP_008516437.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X3	84.2	84.2	100%	8e-17	100%	gi|545211579|XP_005608407.1
☐	lecithin:cholesterol acyltransferase, LCAT [Homo sapiens]	84.2	84.2	100%	8e-17	100%	gi|998999|AAB34898.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2	84.2	84.2	100%	8e-17	100%	gi|591328993|XP_007090383.1
☐	lecithin:cholesterol acyltransferase precursor [Homo sapiens]	84.2	84.2	100%	8e-17	100%	gi|187025|AAA59499.1
☐	Phosphatidylcholine-sterol acyltransferase [Macaca fascicularis]	84.2	84.2	100%	8e-17	100%	gi|355756886|EHH60494.1
☐	lecithin-cholesterol acyltransferase precursor (EC 2.3.1.43) [Homo s	84.2	84.2	100%	8e-17	100%	gi|386858|AAA59500.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Loxodonta	84.2	84.2	100%	8e-17	100%	gi|344290909|XP_003417179.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Fukomys	84.2	84.2	100%	8e-17	100%	gi|731284193|XP_010610588.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform 2 [	84.2	84.2	100%	8e-17	100%	gi|73957241|XP_851673.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Chinchilla	84.2	84.2	100%	8e-17	100%	gi|533180990|XP_005403659.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Heterocep	84.2	84.2	100%	8e-17	100%	gi|512961581|XP_004843055.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1	84.2	84.2	100%	8e-17	100%	gi|512932199|XP_004907111.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Orycterop	84.2	84.2	100%	8e-17	100%	gi|634846635|XP_007938473.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Chrysochl	84.2	84.2	100%	8e-17	100%	gi|586459252|XP_006860289.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Elephantu	84.2	84.2	100%	8e-17	100%	gi|585637009|XP_006878737.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Trichechu	84.2	84.2	100%	8e-17	100%	gi|471361928|XP_004371526.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Rhinopith	84.2	84.2	100%	8e-17	100%	gi|724956501|XP_010353366.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2	84.2	84.2	100%	8e-17	100%	gi|667240880|XP_008565513.1
☐							

	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2	84.2	84.2	100%	8e-17	100%	gi|664718822|XP_008516436.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Tarsius sy	84.2	84.2	100%	8e-17	100%	gi|640814419|XP_008063935.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Chloroce	84.2	84.2	100%	8e-17	100%	gi|635033522|XP_007992092.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2	84.2	84.2	100%	8e-17	100%	gi|562856857|XP_006156948.1
☐	phosphatidylcholine-sterol acyltransferase precursor [Bos taurus]	84.2	84.2	100%	8e-17	100%	gi|114051546|NP_001039534.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Lipotes ve	84.2	84.2	100%	8e-17	100%	gi|602690230|XP_007457320.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Balaenop	84.2	84.2	100%	8e-17	100%	gi|594627205|XP_007198213.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1	84.2	84.2	100%	8e-17	100%	gi|594032594|XP_006041058.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1	84.2	84.2	100%	8e-17	100%	gi|591328991|XP_007090382.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Peromysc	84.2	84.2	100%	8e-17	100%	gi|589948468|XP_006986895.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2	84.2	84.2	100%	8e-17	100%	gi|585155641|XP_006730154.1
☐	phosphatidylcholine-sterol acyltransferase precursor [Papio anubis]	84.2	84.2	100%	8e-17	100%	gi|162951952|NP_001106083.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X3	84.2	84.2	100%	8e-17	100%	gi|562856859|XP_006156949.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Vicugna p	84.2	84.2	100%	8e-17	100%	gi|560962696|XP_006203780.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Camelus	84.2	84.2	100%	8e-17	100%	gi|560908696|XP_006180662.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Panthol	84.2	84.2	100%	8e-17	100%	gi|556722113|XP_005956897.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1	84.2	84.2	100%	8e-17	100%	gi|544517956|XP_005592370.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Ictidomys	84.2	84.2	100%	8e-17	100%	gi|532065072|XP_005318397.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Condylura	84.2	84.2	100%	8e-17	100%	gi|507970839|XP_004690509.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Jaculus ja	84.2	84.2	100%	8e-17	100%	gi|507555923|XP_004661727.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Sorex ara	84.2	84.2	100%	8e-17	100%	gi|505769153|XP_004600640.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform 2 [	84.2	84.2	100%	8e-17	100%	gi|478515124|XP_004431810.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Tursiops t	84.2	84.2	100%	8e-17	100%	gi|470657693|XP_004330924.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Orcinus o	84.2	84.2	100%	8e-17	100%	gi|466026005|XP_004273232.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Bos mutu	84.2	84.2	100%	8e-17	100%	gi|555969128|XP_005896591.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Pteropus	84.2	84.2	100%	8e-17	100%	gi|586549557|XP_006909849.1
☐	phosphatidylcholine-sterol acyltransferase precursor [Oryctolagus c	84.2	84.2	100%	8e-17	100%	gi|126722618|NP_001075659.1
☐	phosphatidylcholine-sterol acyltransferase precursor [Homo sapiens	84.2	84.2	100%	8e-17	100%	gi|4557892|NP_000220.1
☐	Phosphatidylcholine-sterol acyltransferase [Macaca mulatta]	84.2	84.2	100%	8e-17	100%	gi|355710312|EHH31776.1
☐	phosphatidylcholine-sterol acyltransferase precursor [Ovis aries]	84.2	84.2	100%	8e-17	100%	gi|242247443|NP_001156040.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1	84.2	84.2	100%	8e-17	100%	gi|149699252|XP_001498513.1
☐	lecithin-cholesterol acyltransferase [synthetic construct]	84.2	84.2	100%	8e-17	100%	gi|32879837|AAP88749.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Cavia por	84.2	84.2	100%	8e-17	100%	gi|348572820|XP_003472190.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1	84.2	84.2	100%	8e-17	100%	gi|296231379|XP_002761124.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Otolemur	84.2	84.2	100%	8e-17	100%	gi|395853873|XP_003799423.1
☐	lecithin cholesterol acyltransferase [Meriones unguiculatus]	84.2	84.2	100%	8e-17	100%	gi|459996769|AGH06057.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Felis catu	84.2	84.2	100%	8e-17	100%	gi|410983741|XP_003998196.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1	84.2	84.2	100%	8e-17	100%	gi|562856855|XP_006156947.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Ochotona	84.2	84.2	100%	8e-17	100%	gi|504143175|XP_004584021.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1	84.2	84.2	100%	8e-17	100%	gi|667240877|XP_008565507.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1	84.2	84.2	100%	8e-17	100%	gi|585155639|XP_006730153.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1	84.2	84.2	100%	9e-17	100%	gi|664718820|XP_008516435.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2	84.2	84.2	100%	9e-17	100%	gi|545211576|XP_005608406.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform 1 [	84.2	84.2	100%	9e-17	100%	gi|478515122|XP_004431809.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Octodon c	84.2	84.2	100%	9e-17	100%	gi|507623413|XP_004625900.1

☐	PREDICTED: phosphatidylcholine-sterol acyltransferase-like isoforr	84.2	84.2	100%	9e-17	100%	gi|593764538|XP_007120847.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase-like isoforr	84.2	84.2	100%	9e-17	100%	gi|593764535|XP_007120846.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase-like isoforr	84.2	84.2	100%	9e-17	100%	gi|593764533|XP_007120845.1
☐	solute carrier family 12 member 4-like isoform 4 [Camelus ferus]	84.2	84.2	100%	1e-16	100%	gi|528764526|EPY84185.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Myotis luc	82.1	82.1	100%	4e-16	96%	gi|558173082|XP_006099517.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Myotis bra	82.1	82.1	100%	4e-16	96%	gi|554564342|XP_005876489.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Myotis da	82.1	82.1	100%	4e-16	96%	gi|584050215|XP_006769815.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Eptesicus	82.1	82.1	100%	4e-16	96%	gi|641699319|XP_008138152.1
☐	hypothetical protein PANDA_006959 [Ailuropoda melanoleuca]	81.7	81.7	100%	6e-16	96%	gi|281340306|EFB15890.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2	81.7	81.7	100%	6e-16	96%	gi|671019677|XP_008700662.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X4	81.7	81.7	100%	6e-16	96%	gi|511840073|XP_004744543.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase-like [Ailurc	81.7	81.7	100%	6e-16	96%	gi|301766160|XP_002918480.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X3	81.7	81.7	100%	6e-16	96%	gi|511840071|XP_004744542.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2	81.7	81.7	100%	6e-16	96%	gi|511840069|XP_004744541.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1	81.7	81.7	100%	6e-16	96%	gi|511840067|XP_004744540.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X1	81.2	81.2	96%	9e-16	100%	gi|725588121|XP_010345110.1
☐	lecithin cholesterol acyltransferase, isoform CRA_b [Mus musculus]	80.0	80.0	100%	2e-15	96%	gi|148679388|EDL11335.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X3	80.0	80.0	100%	2e-15	96%	gi|625237667|XP_007610057.1
☐	cholesterol acyltransferase [Mus musculus]	80.0	80.0	100%	2e-15	96%	gi|293697|AAA39419.1
☐	phosphatidylcholine-sterol acyltransferase precursor [Mus musculus	80.0	80.0	100%	2e-15	96%	gi|244791354|NP_032516.2
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase [Microtus c	80.0	80.0	100%	2e-15	96%	gi|532002485|XP_005345498.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform 1 [	80.0	80.0	100%	2e-15	96%	gi|488536006|XP_004459692.1
☐	PREDICTED: phosphatidylcholine-sterol acyltransferase isoform X2	80.0	80.0	100%	2e-15	96%	gi|354484309|XP_003504331.1
☐	unnamed protein product [Mus musculus]	80.0	80.0	100%	2e-15	96%	gi|12836459|BAB23665.1
☐	lecithin cholesterol acyltransferase [Sus scrofa]	77.8	77.8	100%	1e-14	96%	gi|256790402|ACV21076.1
☐	phosphatidylcholine-sterol acyltransferase precursor [Sus scrofa]	77.8	77.8	100%	1e-14	96%	gi|258690251|NP_001158328.1
☐	lecithin cholesterol acyltransferase, isoform CRA_a [Rattus norvegi	77.4	77.4	100%	2e-14	92%	gi|149038063|EDL92423.1

⊟ Alignments

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lecithin cholesterol acyltransferase [Macaca sp.]

Sequence ID: gi|23379758|gb|AAM76621.1| **Length:** 209 **Number of Matches:** 1

Related Information

Range 1: 9 to 34 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.2 bits(191)	6e-17	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KAELSNHTRPVILVPGCLGNQLEAKL  26
            KAELSNHTRPVILVPGCLGNQLEAKL
Sbjct  9    KAELSNHTRPVILVPGCLGNQLEAKL  34
```

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lecithin cholesterol acyltransferase [Pongo pygmaeus]

Sequence ID: gi|23379756|gb|AAM76620.1| **Length:** 209 **Number of Matches:** 1

Related Information

Range 1: 9 to 34 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.2 bits(191)	6e-17	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KAELSNHTRPVILVPGCLGNQLEAKL  26
```

```
             KAELSNHTRPVILVPGCLGNQLEAKL
Sbjct  9    KAELSNHTRPVILVPGCLGNQLEAKL  34
```

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lecithin cholesterol acyltransferase [Gorilla gorilla]

Sequence ID: gi|23379754|gb|AAM76619.1| **Length:** 209 **Number of Matches:** 1

Related Information

Range 1: 9 to 34 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.2 bits(191)	6e-17	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KAELSNHTRPVILVPGCLGNQLEAKL  26
             KAELSNHTRPVILVPGCLGNQLEAKL
Sbjct  9    KAELSNHTRPVILVPGCLGNQLEAKL  34
```

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lecithin cholesterol acyltransferase [Saguinus oedipus]

Sequence ID: gi|23379760|gb|AAM76622.1| **Length:** 210 **Number of Matches:** 1

Related Information

Range 1: 9 to 34 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.2 bits(191)	6e-17	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KAELSNHTRPVILVPGCLGNQLEAKL  26
             KAELSNHTRPVILVPGCLGNQLEAKL
Sbjct  9    KAELSNHTRPVILVPGCLGNQLEAKL  34
```

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PREDICTED: phosphatidylcholine-sterol acyltransferase [Mesocricetus auratus]

Sequence ID: gi|524952837|ref|XP_005076409.1| **Length:** 308 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 38 to 63 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.2 bits(191)	7e-17	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KAELSNHTRPVILVPGCLGNQLEAKL  26
             KAELSNHTRPVILVPGCLGNQLEAKL
Sbjct  38   KAELSNHTRPVILVPGCLGNQLEAKL  63
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

LGALS3BP_RALGFEDATQALGRA_Mod

RID BVH4K6SH01R (Expires on 01-21 09:59 am)

Query ID	lcl|62054	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	15		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

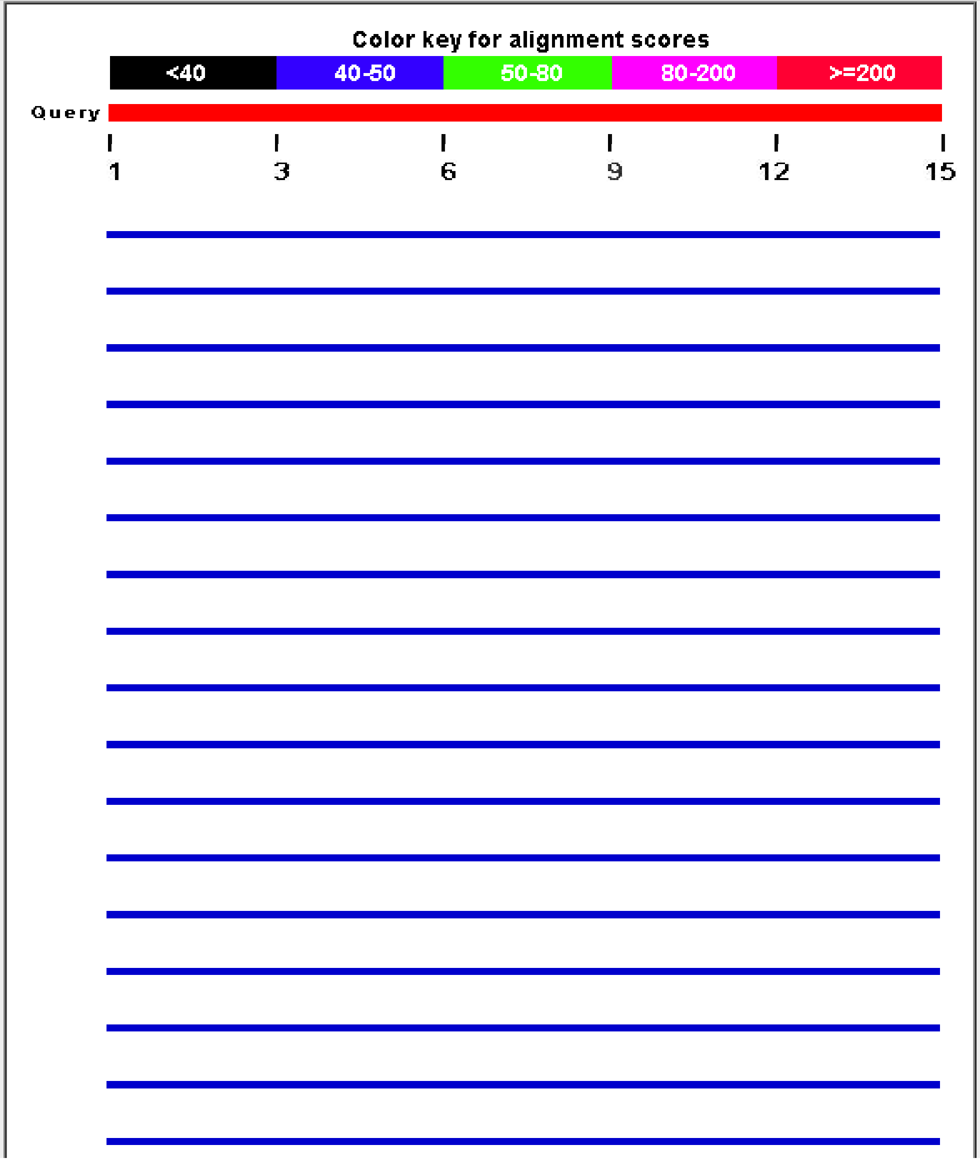
Graphic Summary

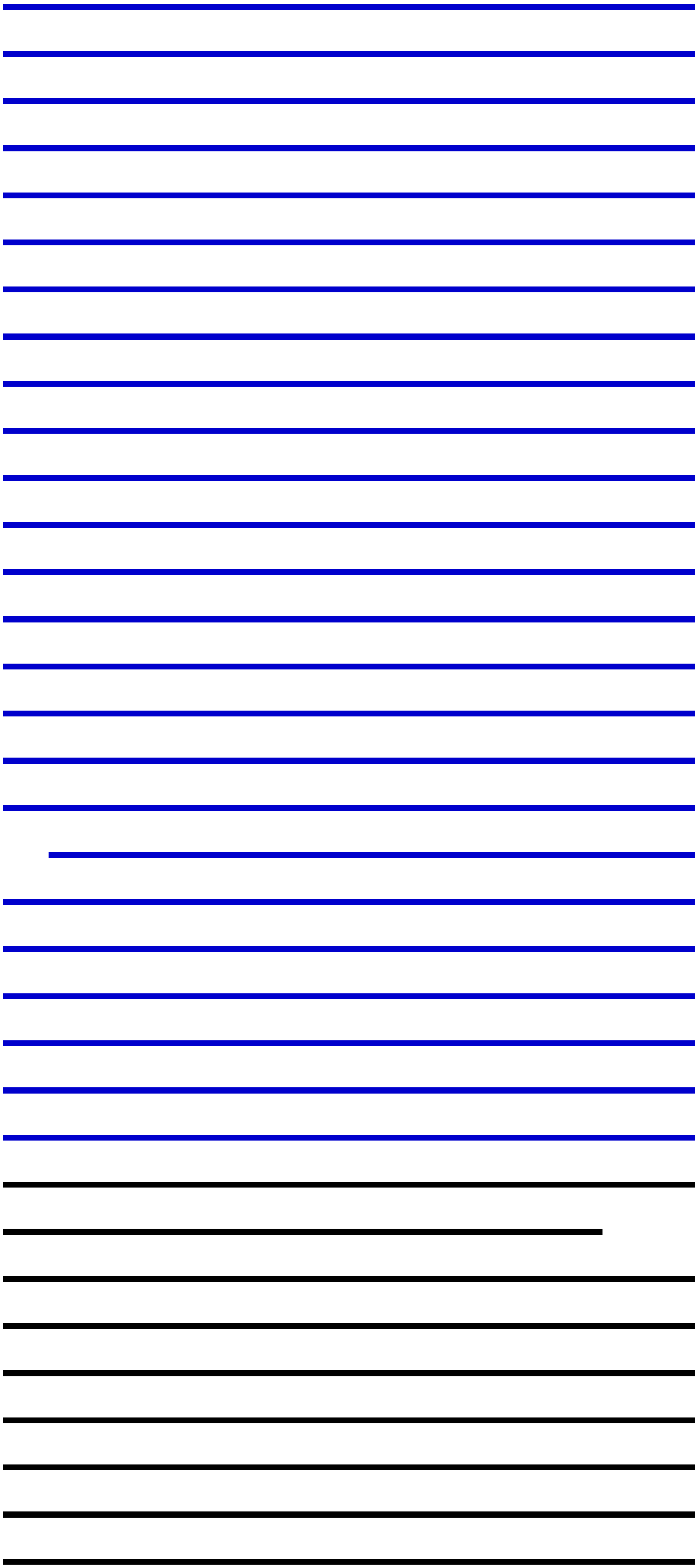
Show Conserved Domains

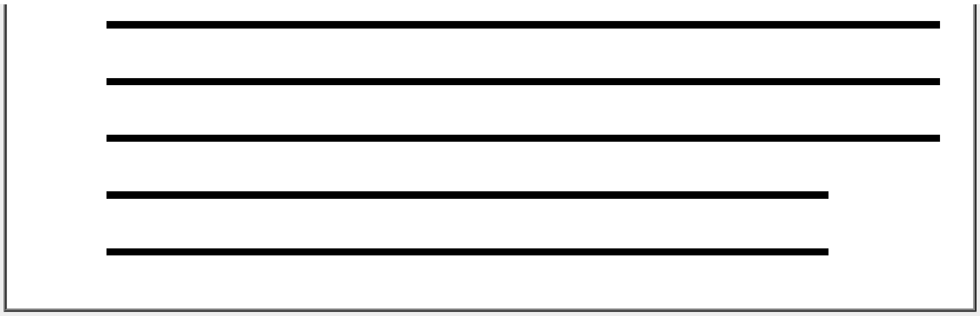
No putative conserved domains have been detected

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Structure Of M2bp Scavenger Receptor Cysteine-rich Domain [Homo	45.6	45.6	100%	2e-04	93%	1BY2_A
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_c [Homo s	45.6	45.6	100%	2e-04	93%	EAW89545.1
☐	unnamed protein product [Homo sapiens]	45.6	45.6	100%	3e-04	93%	BAG58382.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein [Rhinopith	45.6	45.6	100%	3e-04	93%	XP_010380238.1
☐	unnamed protein product [Homo sapiens]	45.6	45.6	100%	3e-04	93%	BAG62653.1
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_a [Homo s	45.6	45.6	100%	3e-04	93%	EAW89543.1
☐	PREDICTED: galectin-3-binding protein [Chlorocebus sabaeus]	45.6	45.6	100%	3e-04	93%	XP_008011313.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Macaca fascicularis]	45.6	45.6	100%	3e-04	93%	XP_005585203.1
☐	RecName: Full=Galectin-3-binding protein; AltName: Full=Lectin galactoside-b	45.6	45.6	100%	3e-04	93%	Q5RDA4.1
☐	PREDICTED: galectin-3-binding protein [Papio anubis]	45.6	45.6	100%	3e-04	93%	XP_003913572.1
☐	PREDICTED: galectin-3-binding protein [Pan troglodytes]	45.6	45.6	100%	3e-04	93%	XP_511716.1
☐	galectin-3-binding protein precursor [Homo sapiens]	45.6	45.6	100%	3e-04	93%	NP_005558.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Gorilla gorilla gorilla]	45.6	45.6	100%	3e-04	93%	XP_004040917.1
☐	PREDICTED: galectin-3-binding protein [Pan paniscus]	45.6	45.6	100%	3e-04	93%	XP_003818311.1
☐	PREDICTED: galectin-3-binding protein isoform 2 [Nomascus leucogenys]	45.6	45.6	100%	3e-04	93%	XP_003278481.1
☐	lectin, galactoside-binding, soluble, 3 binding protein [synthetic construct]	45.6	45.6	100%	3e-04	93%	ABM86350.1
☐	hypothetical protein EGK_09048 [Macaca mulatta]	45.6	45.6	100%	3e-04	93%	EHH25259.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Macaca mulatta]	45.6	45.6	100%	3e-04	93%	XP_001109047.1
☐	PREDICTED: galectin-3-binding protein [Callithrix jacchus]	45.6	45.6	100%	3e-04	93%	XP_002748850.2
☐	hypothetical protein EGM_08232 [Macaca fascicularis]	45.6	45.6	100%	3e-04	93%	EHH58393.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Macaca fascicularis]	45.6	45.6	100%	3e-04	93%	XP_005585202.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Nomascus leucogenys]	45.6	45.6	100%	3e-04	93%	XP_003278480.2
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein [Myotis luc	42.6	42.6	100%	0.003	87%	XP_006108225.1
☐	cyclophilin C-associated protein [Mus musculus domesticus]	42.6	42.6	100%	0.003	87%	AAA37499.1
☐	PREDICTED: galectin-3-binding protein [Eptesicus fuscus]	42.6	42.6	100%	0.003	87%	XP_008153225.1
☐	PREDICTED: galectin-3-binding protein [Ceratotherium simum simum]	42.6	42.6	100%	0.003	87%	XP_004432888.1
☐	PREDICTED: galectin-3-binding protein [Peromyscus maniculatus bairdii]	42.6	42.6	100%	0.003	87%	XP_006990333.1
☐	unnamed protein product [Mus musculus]	42.6	42.6	100%	0.003	87%	BAE31013.1
☐	unnamed protein product [Mus musculus]	42.6	42.6	100%	0.003	87%	BAE29246.1

☐	unnamed protein product [Mus musculus]	42.6	42.6	100%	0.003	87%	BAE31894.1
☐	galectin-3-binding protein precursor [Mus musculus]	42.6	42.6	100%	0.003	87%	NP_035280.1
☐	galectin-3-binding protein precursor [Mesocricetus auratus]	42.6	42.6	100%	0.003	87%	NP_001268610.1
☐	PREDICTED: galectin-3-binding protein [Otolemur garnettii]	42.6	42.6	100%	0.003	87%	XP_003786610.1
☐	PREDICTED: galectin-3-binding protein [Tarsius syrichta]	42.6	42.6	100%	0.003	87%	XP_008046502.1
☐	PREDICTED: galectin-3-binding protein [Nannospalax galili]	42.2	42.2	100%	0.004	87%	XP_008847879.1
☐	PREDICTED: galectin-3-binding protein [Erinaceus europaeus]	42.2	42.2	93%	0.004	93%	XP_007533029.1
☐	PREDICTED: putative scavenger receptor cysteine-rich domain-containing pr	40.9	40.9	100%	0.009	87%	XP_007091541.1
☐	PREDICTED: galectin-3-binding protein [Trichechus manatus latirostris]	40.9	40.9	100%	0.010	87%	XP_004374429.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Felis catus]	40.9	40.9	100%	0.010	87%	XP_003997300.1
☐	PREDICTED: galectin-3-binding protein [Equus caballus]	40.9	40.9	100%	0.010	87%	XP_001491000.1
☐	PREDICTED: galectin-3-binding protein [Jaculus jaculus]	40.9	40.9	100%	0.010	87%	XP_004655763.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Felis catus]	40.9	40.9	100%	0.010	87%	XP_006940706.1
☐	PREDICTED: galectin-3-binding protein [Oryctolagus cuniculus]	39.7	39.7	100%	0.027	80%	XP_002724384.1
☐	PREDICTED: galectin-3-binding protein [Ochotona princeps]	39.7	39.7	86%	0.027	92%	XP_004593086.1
☐	PREDICTED: galectin-3-binding protein [Saimiri boliviensis boliviensis]	39.7	39.7	100%	0.027	87%	XP_010340649.1
☐	galectin-3-binding protein precursor [Rattus norvegicus]	39.2	39.2	100%	0.037	80%	NP_620796.1
☐	RecName: Full=Galectin-3-binding protein; AltName: Full=Cyp-C-associated p	39.2	39.2	100%	0.037	80%	O70513.2
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_a [Rattus	39.2	39.2	100%	0.037	80%	EDM06755.1
☐	galectin-3-binding protein [Cricetulus griseus]	38.4	38.4	100%	0.069	80%	ERE69017.1
☐	PREDICTED: galectin-3-binding protein [Cricetulus griseus]	38.4	38.4	100%	0.070	80%	XP_007620278.1
☐	PREDICTED: galectin-3-binding protein [Cricetulus griseus]	38.4	38.4	100%	0.070	80%	XP_003498865.1
☐	PREDICTED: galectin-3-binding protein [Microtus ochrogaster]	38.4	38.4	100%	0.070	80%	XP_005350871.1
☐	PREDICTED: galectin-3-binding protein [Balaenoptera acutorostrata scammo	37.5	37.5	100%	0.13	80%	XP_007185856.1
☐	PREDICTED: galectin-3-binding protein [Lipotes vexillifer]	37.5	37.5	100%	0.13	80%	XP_007462419.1
☐	PREDICTED: galectin-3-binding protein [Tursiops truncatus]	36.7	36.7	86%	0.25	85%	XP_004323016.1
☐	PREDICTED: galectin-3-binding protein [Orcinus orca]	36.7	36.7	86%	0.25	85%	XP_004275584.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1 isoform X5 [Canis lupu	36.7	36.7	86%	0.25	85%	XP_540464.2
☐	PREDICTED: galectin-3-binding protein [Chrysochloris asiatica]	36.7	36.7	86%	0.25	85%	XP_006869713.1
☐	PREDICTED: galectin-3-binding protein [Octodon degus]	36.7	36.7	86%	0.25	85%	XP_004639582.1
☐	PREDICTED: galectin-3-binding protein [Fukomys damarensis]	36.7	36.7	86%	0.25	85%	XP_010616820.1
☐	PREDICTED: galectin-3-binding protein [Chinchilla lanigera]	36.7	36.7	86%	0.25	85%	XP_005407410.1
☐	Galectin-3-binding protein [Tupaia chinensis]	36.7	36.7	86%	0.25	85%	ELW68246.1
☐	PREDICTED: galectin-3-binding protein [Cavia porcellus]	36.7	36.7	100%	0.25	80%	XP_003464931.2
☐	PREDICTED: galectin-3-binding protein [Tupaia chinensis]	36.7	36.7	86%	0.25	85%	XP_006145764.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1 isoform X1 [Canis lupu	36.7	36.7	86%	0.25	85%	XP_005624092.1
☐	Galectin-3-binding protein [Fukomys damarensis]	36.7	36.7	86%	0.26	85%	KFO35672.1
☐	PREDICTED: galectin-3-binding protein [Camelus dromedarius]	35.4	35.4	100%	0.64	80%	XP_010997923.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Physeter catodon]	35.4	35.4	100%	0.64	80%	XP_007106758.1
☐	PREDICTED: galectin-3-binding protein [Vicugna pacos]	35.4	35.4	100%	0.64	80%	XP_006199496.1
☐	PREDICTED: galectin-3-binding protein-like [Camelus ferus]	35.4	35.4	100%	0.64	80%	XP_006182736.1
☐	galectin-3-binding protein precursor [Camelus ferus]	35.4	35.4	100%	0.64	80%	EPY80953.1
☐	PREDICTED: galectin-3-binding protein [Camelus bactrianus]	35.4	35.4	100%	0.64	80%	XP_010948995.1
☐	galectin-3-binding protein precursor [Camelus ferus]	35.4	35.4	100%	0.64	80%	EPY82790.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Physeter catodon]	35.4	35.4	100%	0.64	80%	XP_007106757.1

☐	PREDICTED: galectin-3-binding protein [Echinops telfairi]	35.0	35.0	100%	0.88	80%	XP_004709313.1
☐	PREDICTED: galectin-3-binding protein [Ictidomys tridecemlineatus]	34.1	34.1	80%	1.6	83%	XP_005332681.1
☐	PREDICTED: galectin-3-binding protein [Elephantulus edwardii]	34.1	34.1	80%	1.6	83%	XP_006886403.1
☐	PREDICTED: galectin-3-binding protein [Loxodonta africana]	33.7	33.7	80%	1.9	83%	XP_010595362.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Bison bison bison]	33.7	33.7	86%	2.2	77%	XP_010854576.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Bos taurus]	33.7	33.7	86%	2.2	77%	XP_005221293.1
☐	galectin-3-binding protein precursor [Bos taurus]	33.7	33.7	86%	2.2	77%	NP_001039781.1
☐	PREDICTED: galectin-3-binding protein [Bos mutus]	33.7	33.7	86%	2.2	77%	XP_005910379.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Bison bison bison]	33.7	33.7	86%	2.2	77%	XP_010854575.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Bos taurus]	33.7	33.7	86%	2.2	77%	XP_005221292.1
☐	PREDICTED: galectin-3-binding protein [Heterocephalus glaber]	33.7	33.7	86%	2.2	77%	XP_004860896.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Heterocephalus glaber]	33.7	33.7	86%	2.2	77%	XP_004881532.1
☐	chromosome segregation protein SMC [Psychrobacter sp. PAMC 21119]	33.7	33.7	73%	2.3	91%	WP_010196556.1
☐	Galectin-3-binding protein [Heterocephalus glaber]	33.7	62.8	86%	2.3	77%	EHB01017.1
☐	hypothetical protein [Thioalkalivibrio sp. ALMg11]	33.7	33.7	93%	2.3	79%	WP_018948689.1
☐	PREDICTED: galectin-3-binding protein [Myotis davidii]	32.9	32.9	86%	4.1	77%	XP_006753504.1
☐	xanthine dehydrogenase [alpha proteobacterium BAL199]	32.5	32.5	93%	5.4	79%	WP_007673419.1
☐	methyl-accepting chemotaxis sensory transducer [Stenotrophomonas maltoph	32.5	32.5	86%	5.5	86%	CCP16517.1
☐	chemotaxis protein [Stenotrophomonas maltophilia]	32.5	32.5	86%	5.5	86%	WP_032970136.1
☐	chemotaxis protein [Stenotrophomonas maltophilia]	32.5	32.5	86%	5.6	86%	WP_033835503.1
☐	chemotaxis protein [Stenotrophomonas maltophilia]	32.5	32.5	86%	5.6	86%	WP_032127364.1
☐	chemotaxis protein [Pseudoxanthomonas sp. J35]	32.5	32.5	86%	5.6	86%	WP_028917099.1
☐	chemotaxis protein [Stenotrophomonas maltophilia]	32.5	32.5	86%	5.6	86%	WP_024958753.1
☐	chemotaxis protein [Stenotrophomonas rhizophila]	32.5	32.5	86%	5.6	86%	WP_038688404.1
☐	MULTISPECIES: chemotaxis protein [Stenotrophomonas]	32.5	32.5	86%	5.6	86%	WP_025879122.1
☐	chemotaxis protein [Stenotrophomonas maltophilia]	32.5	32.5	86%	5.6	86%	WP_017354425.1

⊟ Alignments

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Chain A, Structure Of M2bp Scavenger Receptor Cysteine-rich Domain

Sequence ID: pdb|1BY2|A **Length:** 119 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 49 to 63 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.6 bits(100)	2e-04	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1   RALGFEDATQALGRA  15
           RALGFE+ATQALGRA
Sbjct  49  RALGFENATQALGRA  63
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_c, partial [Homo sapiens]

Sequence ID: gb|EAW89545.1| **Length:** 165 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 63 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.6 bits(100)	2e-04	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1   RALGFEDATQALGRA  15
           RALGFE+ATQALGRA
Sbjct  63  RALGFENATQALGRA  77
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG58382.1| **Length:** 413 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 63 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.6 bits(100)	3e-04	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1   RALGFEDATQALGRA  15
           RALGFE+ATQALGRA
Sbjct  63  RALGFENATQALGRA  77
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein [Rhinopithecus roxellana]

Sequence ID: ref|XP_010380238.1| **Length:** 567 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 45 to 59 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.6 bits(100)	3e-04	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1   RALGFEDATQALGRA  15
           RALGFE+ATQALGRA
Sbjct  45  RALGFENATQALGRA  59
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG62653.1| **Length:** 573 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 63 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
45.6 bits(100)	3e-04	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1   RALGFEDATQALGRA  15
           RALGFE+ATQALGRA
Sbjct  63  RALGFENATQALGRA  77
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download

How to read this page Blast report description

LGALS3BP_RALGFENATQALGRA_NonMod

RID B9HPN2C501R (Expires on 01-14 14:18 pm)

Query ID	lcl|124499	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	15		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

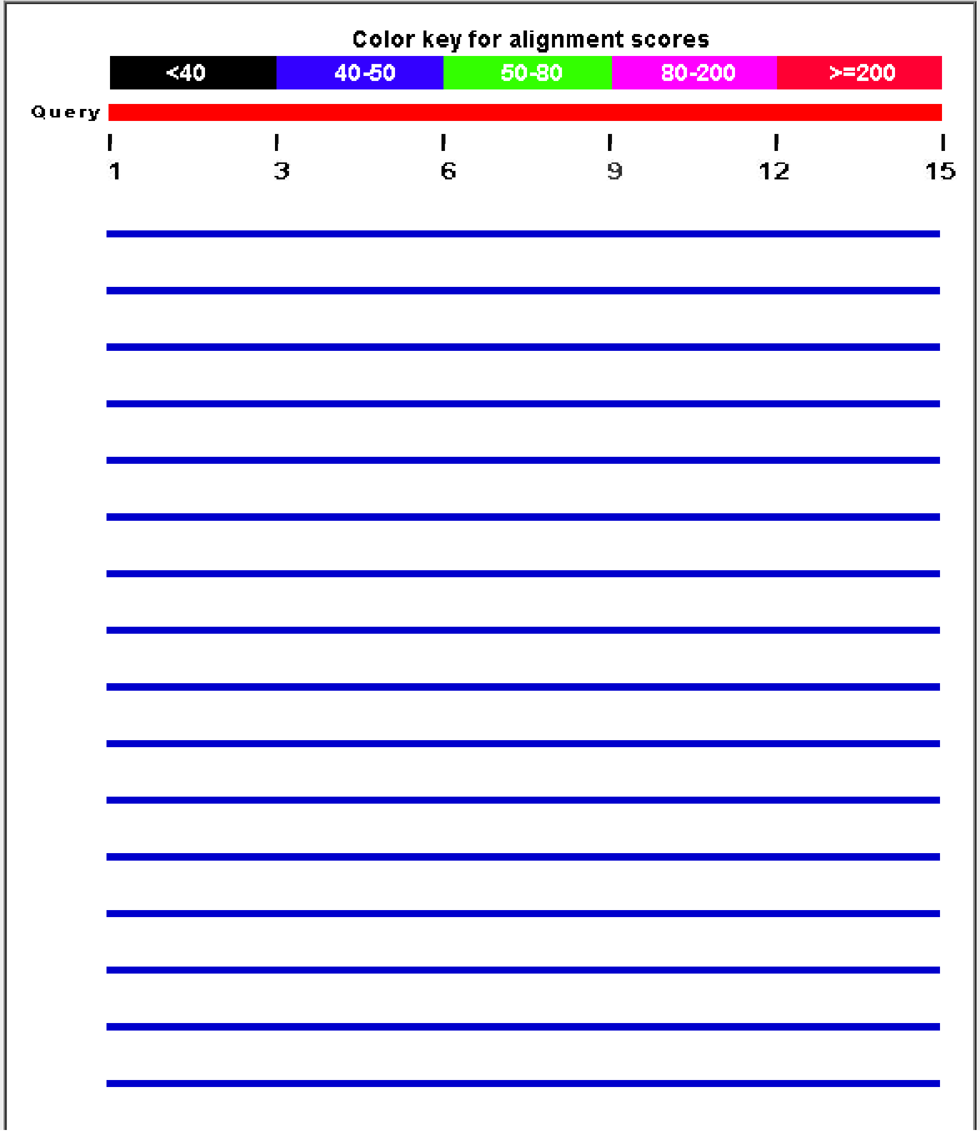
Graphic Summary

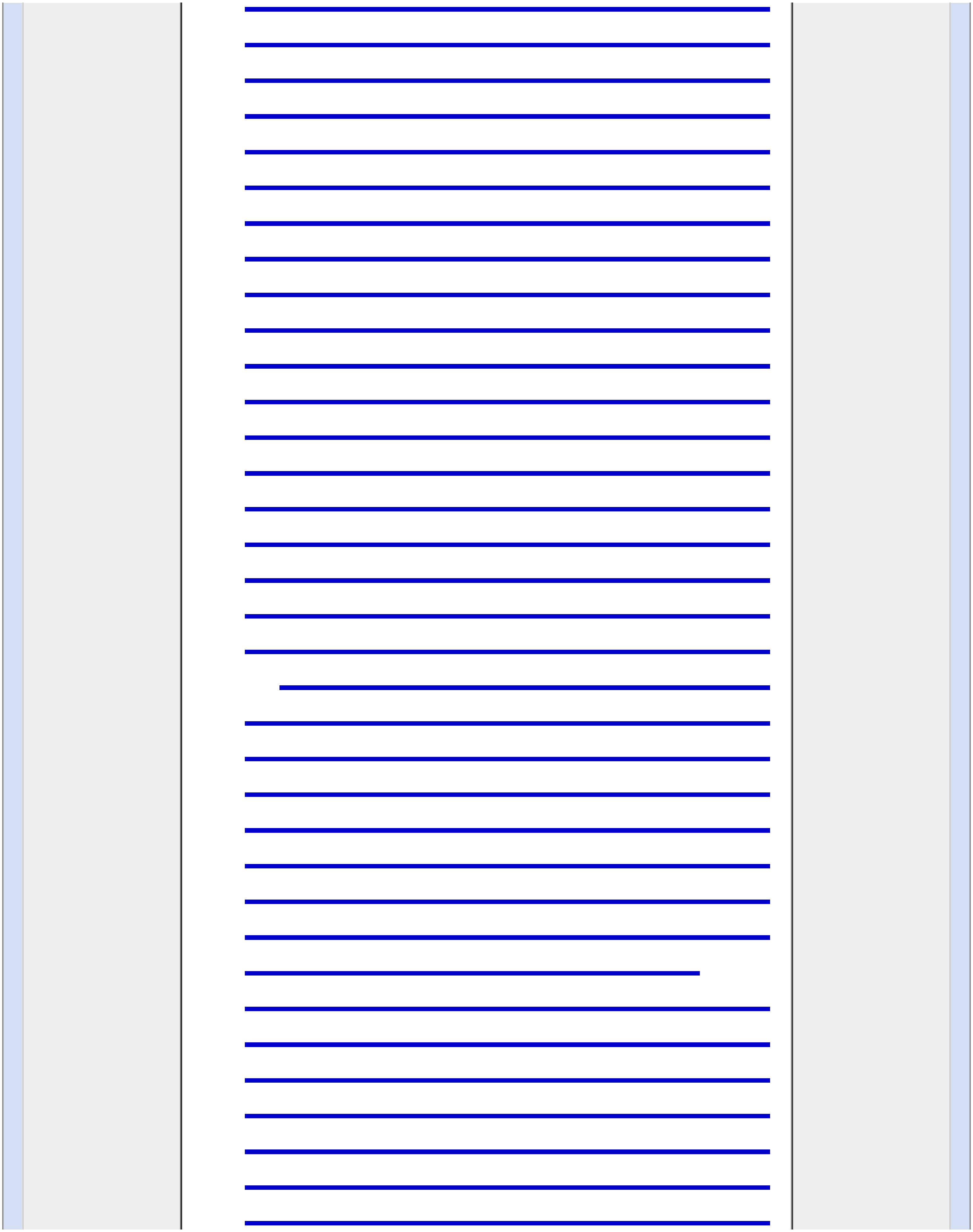
Show Conserved Domains

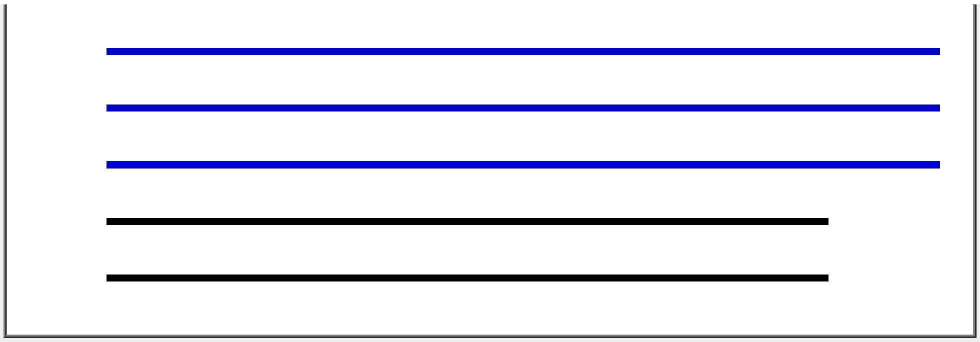
No putative conserved domains have been detected

Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Structure Of M2bp Scavenger Receptor Cysteine-rich Don	48.1	48.1	100%	3e-05	100%	gi|157830494|1BY2_A
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_	48.1	48.1	100%	3e-05	100%	gi|119609951|EAW89545.1
☐	unnamed protein product [Homo sapiens]	48.1	48.1	100%	4e-05	100%	gi|194380458|BAG58382.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein	48.1	48.1	100%	4e-05	100%	gi|724915028|XP_010380238.1
☐	unnamed protein product [Homo sapiens]	48.1	48.1	100%	4e-05	100%	gi|194375081|BAG62653.1
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_	48.1	48.1	100%	4e-05	100%	gi|119609949|EAW89543.1
☐	PREDICTED: galectin-3-binding protein [Chlorocebus sabaeus]	48.1	48.1	100%	4e-05	100%	gi|635093239|XP_008011313.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Macaca fascicu	48.1	48.1	100%	4e-05	100%	gi|544502104|XP_005585203.1
☐	RecName: Full=Galectin-3-binding protein; AltName: Full=Lectin ga	48.1	48.1	100%	4e-05	100%	gi|75042301|Q5RDA4.1
☐	PREDICTED: galectin-3-binding protein [Papio anubis]	48.1	48.1	100%	4e-05	100%	gi|402901262|XP_003913572.1
☐	PREDICTED: galectin-3-binding protein [Pan troglodytes]	48.1	48.1	100%	4e-05	100%	gi|55646067|XP_511716.1
☐	galectin-3-binding protein precursor [Homo sapiens]	48.1	48.1	100%	4e-05	100%	gi|5031863|NP_005558.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Gorilla gorilla go	48.1	48.1	100%	4e-05	100%	gi|426346505|XP_004040917.1
☐	PREDICTED: galectin-3-binding protein [Pan paniscus]	48.1	48.1	100%	4e-05	100%	gi|397494909|XP_003818311.1
☐	PREDICTED: galectin-3-binding protein isoform 2 [Nomascus leucc	48.1	48.1	100%	4e-05	100%	gi|332258797|XP_003278481.1
☐	lectin, galactoside-binding, soluble, 3 binding protein [synthetic cons	48.1	48.1	100%	4e-05	100%	gi|123997497|ABM86350.1
☐	hypothetical protein EGK_09048 [Macaca mulatta]	48.1	48.1	100%	4e-05	100%	gi|355568978|EHH25259.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Macaca mulatta]	48.1	48.1	100%	4e-05	100%	gi|109118737|XP_001109047.1
☐	PREDICTED: galectin-3-binding protein [Callithrix jacchus]	48.1	48.1	100%	4e-05	100%	gi|675661532|XP_002748850.2
☐	hypothetical protein EGM_08232 [Macaca fascicularis]	48.1	48.1	100%	4e-05	100%	gi|355754428|EHH58393.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Macaca fascicu	48.1	48.1	100%	4e-05	100%	gi|544502102|XP_005585202.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Nomascus leucc	48.1	48.1	100%	4e-05	100%	gi|441643566|XP_003278480.2
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein	45.2	45.2	100%	4e-04	93%	gi|558213798|XP_006108225.1
☐	cyclophilin C-associated protein [Mus musculus domesticus]	45.2	45.2	100%	4e-04	93%	gi|397800|AAA37499.1
☐	PREDICTED: galectin-3-binding protein [Eptesicus fuscus]	45.2	45.2	100%	4e-04	93%	gi|641726407|XP_008153225.1
☐	PREDICTED: galectin-3-binding protein [Ceratotherium simum simu	45.2	45.2	100%	4e-04	93%	gi|478517307|XP_004432888.1
☐	PREDICTED: galectin-3-binding protein [Peromyscus maniculatus b	45.2	45.2	100%	4e-04	93%	gi|589955428|XP_006990333.1
☐	unnamed protein product [Mus musculus]	45.2	45.2	100%	4e-04	93%	gi|74212546|BAE31013.1
☐							

	unnamed protein product [Mus musculus]	45.2	45.2	100%	4e-04	93%	gi|74211789|BAE29246.1
☐	unnamed protein product [Mus musculus]	45.2	45.2	100%	4e-04	93%	gi|74142260|BAE31894.1
☐	galectin-3-binding protein precursor [Mus musculus]	45.2	45.2	100%	4e-04	93%	gi|6755144|NP_035280.1
☐	galectin-3-binding protein precursor [Mesocricetus auratus]	45.2	45.2	100%	4e-04	93%	gi|528078247|NP_001268610.1
☐	PREDICTED: galectin-3-binding protein [Otolemur garnettii]	45.2	45.2	100%	4e-04	93%	gi|395826815|XP_003786610.1
☐	PREDICTED: galectin-3-binding protein [Tarsius syrichta]	45.2	45.2	100%	4e-04	93%	gi|640781767|XP_008046502.1
☐	PREDICTED: galectin-3-binding protein [Nannospalax galili]	44.8	44.8	100%	5e-04	93%	gi|674080617|XP_008847879.1
☐	PREDICTED: galectin-3-binding protein [Erinaceus europaeus]	44.8	44.8	93%	5e-04	100%	gi|617646710|XP_007533029.1
☐	PREDICTED: putative scavenger receptor cysteine-rich domain-co	43.5	43.5	100%	0.001	93%	gi|591331486|XP_007091541.1
☐	PREDICTED: galectin-3-binding protein [Trichechus manatus latiro	43.5	43.5	100%	0.001	93%	gi|471367801|XP_004374429.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Felis catus]	43.5	43.5	100%	0.001	93%	gi|410981896|XP_003997300.1
☐	PREDICTED: galectin-3-binding protein [Equus caballus]	43.5	43.5	100%	0.001	93%	gi|149723277|XP_001491000.1
☐	PREDICTED: galectin-3-binding protein [Jaculus jaculus]	43.5	43.5	100%	0.001	93%	gi|507543547|XP_004655763.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Felis catus]	43.5	43.5	100%	0.001	93%	gi|587012494|XP_006940706.1
☐	PREDICTED: galectin-3-binding protein [Oryctolagus cuniculus]	42.2	42.2	100%	0.004	87%	gi|291416302|XP_002724384.1
☐	PREDICTED: galectin-3-binding protein [Ochotona princeps]	42.2	42.2	86%	0.004	100%	gi|504166431|XP_004593086.1
☐	PREDICTED: galectin-3-binding protein [Saimiri boliviensis bolivien	42.2	42.2	100%	0.004	93%	gi|725577242|XP_010340649.1
☐	galectin-3-binding protein precursor [Rattus norvegicus]	41.8	41.8	100%	0.005	87%	gi|20806135|NP_620796.1
☐	RecName: Full=Galectin-3-binding protein; AltName: Full=Cyp-C-a	41.8	41.8	100%	0.005	87%	gi|218526547|O70513.2
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_	41.8	41.8	100%	0.005	87%	gi|149054938|EDM06755.1
☐	galectin-3-binding protein [Cricetulus griseus]	40.9	40.9	100%	0.010	87%	gi|537143564|ERE69017.1
☐	PREDICTED: galectin-3-binding protein [Cricetulus griseus]	40.9	40.9	100%	0.010	87%	gi|625257783|XP_007620278.1
☐	PREDICTED: galectin-3-binding protein [Cricetulus griseus]	40.9	40.9	100%	0.010	87%	gi|354473282|XP_003498865.1
☐	PREDICTED: galectin-3-binding protein [Microtus ochrogaster]	40.9	40.9	100%	0.010	87%	gi|532014189|XP_005350871.1
☐	PREDICTED: galectin-3-binding protein [Balaenoptera acutorostrat	40.1	40.1	100%	0.018	87%	gi|594676074|XP_007185856.1
☐	PREDICTED: galectin-3-binding protein [Lipotes vexillifer]	40.1	40.1	100%	0.018	87%	gi|602701011|XP_007462419.1
☐	PREDICTED: galectin-3-binding protein [Tursiops truncatus]	39.2	39.2	86%	0.035	92%	gi|470634961|XP_004323016.1
☐	PREDICTED: galectin-3-binding protein [Orcinus orca]	39.2	39.2	86%	0.035	92%	gi|466037200|XP_004275584.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1 isoform X5 [	39.2	39.2	86%	0.035	92%	gi|73964953|XP_540464.2
☐	PREDICTED: galectin-3-binding protein [Chrysochloris asiatica]	39.2	39.2	86%	0.035	92%	gi|586478358|XP_006869713.1
☐	PREDICTED: galectin-3-binding protein [Octodon degus]	39.2	39.2	86%	0.035	92%	gi|507681576|XP_004639582.1
☐	PREDICTED: galectin-3-binding protein [Fukomys damarensis]	39.2	39.2	86%	0.035	92%	gi|731203892|XP_010616820.1
☐	PREDICTED: galectin-3-binding protein [Chinchilla lanigera]	39.2	39.2	86%	0.035	92%	gi|533188976|XP_005407410.1
☐	Galectin-3-binding protein [Tupaia chinensis]	39.2	39.2	86%	0.035	92%	gi|444727768|ELW68246.1
☐	PREDICTED: galectin-3-binding protein [Cavia porcellus]	39.2	39.2	100%	0.035	87%	gi|514451490|XP_003464931.2
☐	PREDICTED: galectin-3-binding protein [Tupaia chinensis]	39.2	39.2	86%	0.035	92%	gi|562832654|XP_006145764.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1 isoform X1 [	39.2	39.2	86%	0.035	92%	gi|545509197|XP_005624092.1
☐	Galectin-3-binding protein [Fukomys damarensis]	39.2	39.2	86%	0.036	92%	gi|676282129|KFO35672.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Physeter catod	38.0	38.0	100%	0.090	87%	gi|593720930|XP_007106758.1
☐	PREDICTED: galectin-3-binding protein [Vicugna pacos]	38.0	38.0	100%	0.090	87%	gi|560953982|XP_006199496.1
☐	PREDICTED: galectin-3-binding protein-like [Camelus ferus]	38.0	38.0	100%	0.090	87%	gi|560912913|XP_006182736.1
☐	galectin-3-binding protein precursor [Camelus ferus]	38.0	38.0	100%	0.090	87%	gi|528761294|EPY80953.1
☐	galectin-3-binding protein precursor [Camelus ferus]	38.0	38.0	100%	0.090	87%	gi|528763131|EPY82790.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Physeter catod	38.0	38.0	100%	0.091	87%	gi|593720928|XP_007106757.1
☐	PREDICTED: galectin-3-binding protein [Echinops telfairi]	37.5	37.5	100%	0.12	87%	gi|507673535|XP_004709313.1

☐	PREDICTED: galectin-3-binding protein [Ictidomys tridecemlineatus	36.7	36.7	80%	0.23	92%	gi|532094003|XP_005332681.1
☐	PREDICTED: galectin-3-binding protein [Elephantulus edwardii]	36.7	36.7	80%	0.24	92%	gi|585660824|XP_006886403.1
☐	PREDICTED: galectin-3-binding protein [Loxodonta africana]	36.3	36.3	80%	0.27	92%	gi|731502681|XP_010595362.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Bos taurus]	36.3	36.3	86%	0.32	85%	gi|528997315|XP_005221293.1
☐	galectin-3-binding protein precursor [Bos taurus]	36.3	36.3	86%	0.32	85%	gi|114052595|NP_001039781.1
☐	PREDICTED: galectin-3-binding protein [Bos mutus]	36.3	36.3	86%	0.32	85%	gi|555997305|XP_005910379.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Bos taurus]	36.3	36.3	86%	0.32	85%	gi|528997313|XP_005221292.1
☐	PREDICTED: galectin-3-binding protein [Heterocephalus glaber]	36.3	36.3	86%	0.32	85%	gi|512998688|XP_004860896.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Heterocephalus	36.3	36.3	86%	0.32	85%	gi|512828899|XP_004881532.1
☐	Galectin-3-binding protein [Heterocephalus glaber]	36.3	67.9	86%	0.32	85%	gi|351698098|EHB01017.1
☐	PREDICTED: galectin-3-binding protein [Myotis davidii]	35.4	35.4	86%	0.60	85%	gi|584038281|XP_006753504.1
☐	hypothetical protein PANDA_006893 [Ailuropoda melanoleuca]	35.0	35.0	86%	0.82	85%	gi|281342805|EFB18389.1
☐	PREDICTED: galectin-3-binding protein [Odobenus rosmarus diver	35.0	35.0	86%	0.82	85%	gi|472394090|XP_004416304.1
☐	PREDICTED: galectin-3-binding protein isoform X3 [Ursus maritimu	35.0	35.0	86%	0.82	85%	gi|671002383|XP_008692049.1
☐	PREDICTED: galectin-3-binding protein-like [Ailuropoda melanoleu	35.0	35.0	86%	0.82	85%	gi|301766034|XP_002918426.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Ursus maritimu	35.0	35.0	86%	0.84	85%	gi|671002381|XP_008692048.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Ursus maritimu	35.0	35.0	86%	0.84	85%	gi|671002379|XP_008692047.1
☐	PREDICTED: galectin-3-binding protein isoform X3 [Galeopterus va	33.7	33.7	86%	2.1	85%	gi|667281302|XP_008574380.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Galeopterus va	33.7	33.7	86%	2.1	85%	gi|667281299|XP_008574379.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Galeopterus va	33.7	33.7	86%	2.1	85%	gi|667281296|XP_008574378.1
☐	PREDICTED: galectin-3-binding protein [Leptonychotes weddellii]	33.3	33.3	86%	2.9	85%	gi|585188403|XP_006745574.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	33.3	33.3	86%	2.9	85%	gi|511848965|XP_004748843.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	33.3	33.3	86%	2.9	85%	gi|511848961|XP_004748841.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	33.3	33.3	86%	2.9	85%	gi|511848959|XP_004748840.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	33.3	33.3	86%	2.9	85%	gi|511848957|XP_004748839.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	33.3	33.3	86%	2.9	85%	gi|511848955|XP_004748838.1
☐	Dtr system oriT relaxase [Ensifer adhaerens]	32.9	32.9	66%	4.0	100%	gi|645057598|WP_025428878.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Structure Of M2bp Scavenger Receptor Cysteine-rich Domain

Sequence ID: gi|157830494|pdb|1BY2|A **Length:** 119 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 49 to 63 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.1 bits(106)	3e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    RALGFENATQALGRA  15
            RALGFENATQALGRA
Sbjct  49   RALGFENATQALGRA  63
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_c, partial [Homo sapiens]

Sequence ID: gi|119609951|gb|EAW89545.1| **Length:** 165 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 63 to 77 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.1 bits(106)	3e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    RALGFENATQALGRA  15
```

```
               RALGFENATQALGRA
Sbjct  63   RALGFENATQALGRA  77
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: gi|194380458|dbj|BAG58382.1| **Length:** 413 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 63 to 77 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.1 bits(106)	4e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    RALGFENATQALGRA  15
            RALGFENATQALGRA
Sbjct  63   RALGFENATQALGRA  77
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein [Rhinopithecus roxellana]

Sequence ID: gi|724915028|ref|XP_010380238.1| **Length:** 567 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 45 to 59 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.1 bits(106)	4e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    RALGFENATQALGRA  15
            RALGFENATQALGRA
Sbjct  45   RALGFENATQALGRA  59
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: gi|194375081|dbj|BAG62653.1| **Length:** 573 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 63 to 77 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
48.1 bits(106)	4e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    RALGFENATQALGRA  15
            RALGFENATQALGRA
Sbjct  63   RALGFENATQALGRA  77
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVH5FPKY01R

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LGALS3BP_RTVIRPFYLTDSSGVD_Mod

RID BVH5FPKY01R (Expires on 01-21 09:59 am)

Query ID lcl|8051
Description None
Molecule type amino acid
Query Length 16

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

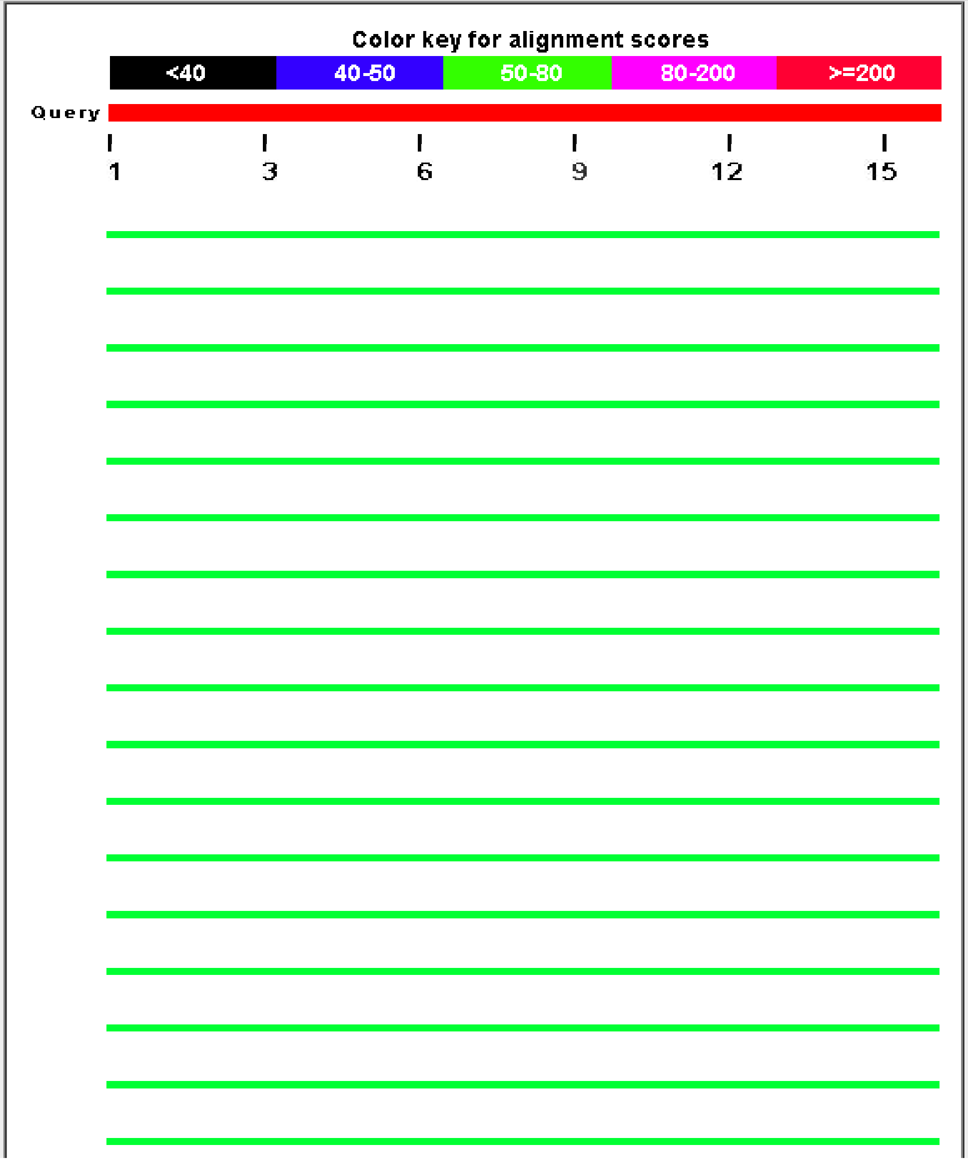
Graphic Summary

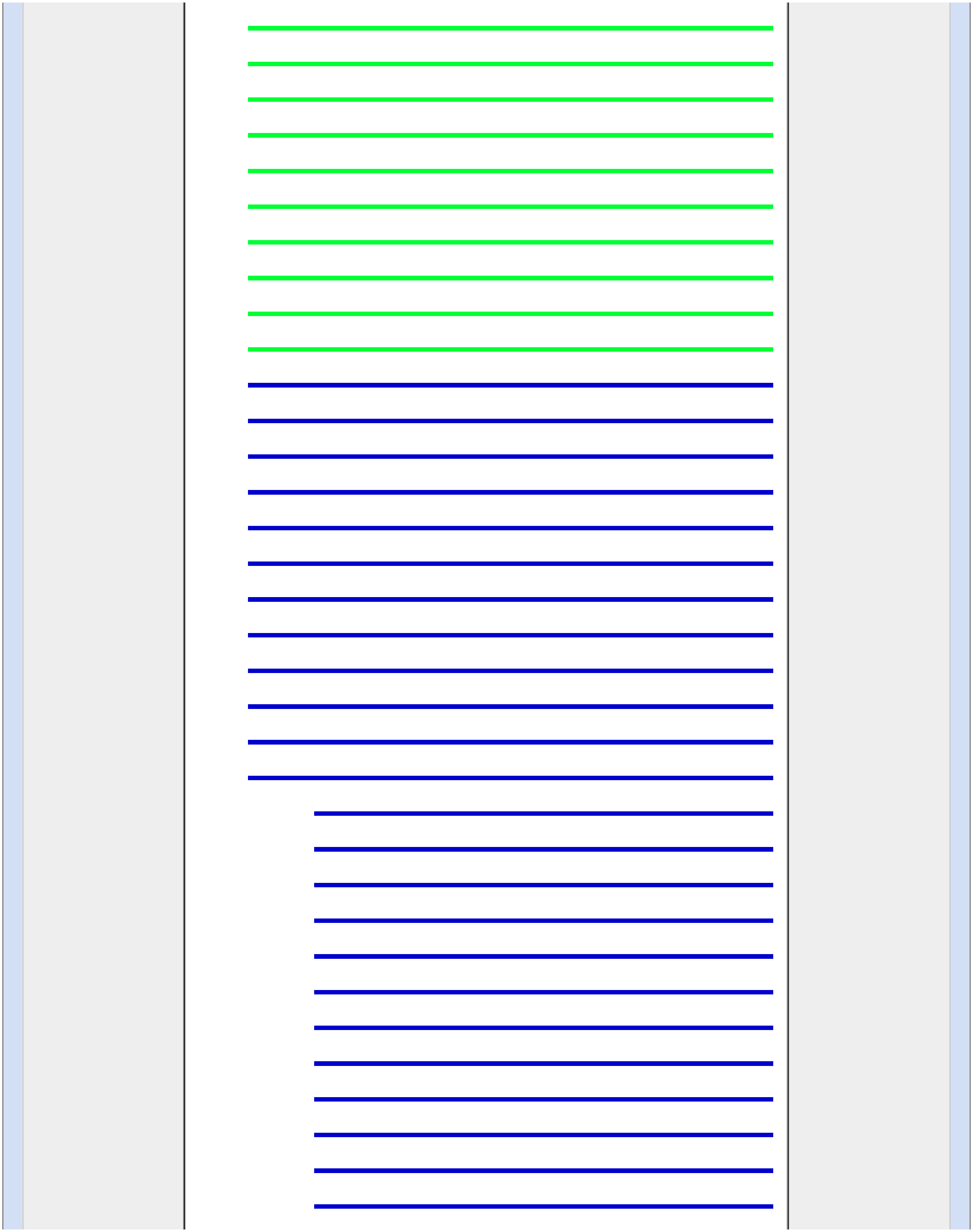
Show Conserved Domains

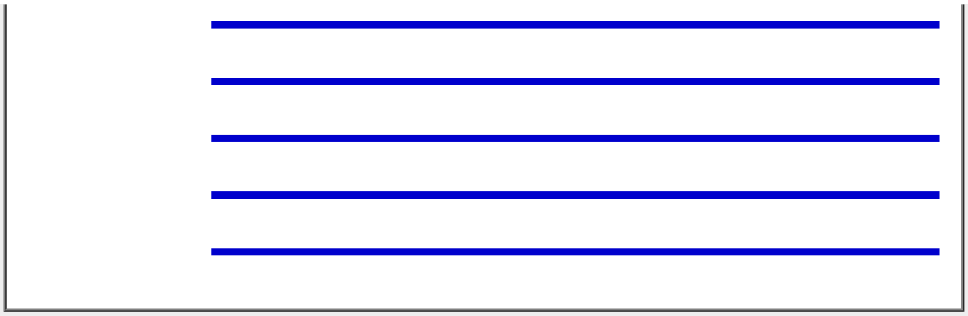
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	galectin-3-binding precursor-like protein [Callithrix jacchus]	51.5	51.5	100%	2e-06	94%	ABQ22691.1
☐	galectin-3-binding precursor-like protein [Callithrix jacchus]	51.5	51.5	100%	2e-06	94%	ABQ22355.1
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_b [Homo s	51.5	51.5	100%	3e-06	94%	EAW89544.1
☐	unnamed protein product [Homo sapiens]	51.5	51.5	100%	3e-06	94%	BAG58382.1
☐	unnamed protein product [Homo sapiens]	51.5	51.5	100%	3e-06	94%	BAG62970.1
☐	PREDICTED: galectin-3-binding protein isoform 3 [Macaca mulatta]	51.5	51.5	100%	3e-06	94%	XP_002800676.1
☐	unnamed protein product [Homo sapiens]	51.5	51.5	100%	3e-06	94%	BAG51600.1
☐	unnamed protein product [Homo sapiens]	51.5	51.5	100%	3e-06	94%	BAG56725.1
☐	PREDICTED: galectin-3-binding protein isoform 2 [Macaca mulatta]	51.5	51.5	100%	3e-06	94%	XP_002800675.1
☐	unnamed protein product [Homo sapiens]	51.5	51.5	100%	3e-06	94%	BAG62653.1
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_a [Homo s	51.5	51.5	100%	3e-06	94%	EAW89543.1
☐	PREDICTED: galectin-3-binding protein [Chlorocebus sabaeus]	51.5	51.5	100%	3e-06	94%	XP_008011313.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Macaca fascicularis]	51.5	51.5	100%	3e-06	94%	XP_005585203.1
☐	RecName: Full=Galectin-3-binding protein; AltName: Full=Lectin galactoside-l	51.5	51.5	100%	3e-06	94%	Q5RDA4.1
☐	PREDICTED: galectin-3-binding protein [Papio anubis]	51.5	51.5	100%	3e-06	94%	XP_003913572.1
☐	PREDICTED: galectin-3-binding protein [Pan troglodytes]	51.5	51.5	100%	3e-06	94%	XP_511716.1
☐	galectin-3-binding protein precursor [Homo sapiens]	51.5	51.5	100%	3e-06	94%	NP_005558.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Gorilla gorilla gorilla]	51.5	51.5	100%	3e-06	94%	XP_004040917.1
☐	PREDICTED: galectin-3-binding protein [Pan paniscus]	51.5	51.5	100%	3e-06	94%	XP_003818311.1
☐	PREDICTED: galectin-3-binding protein isoform 2 [Nomascus leucogenys]	51.5	51.5	100%	3e-06	94%	XP_003278481.1
☐	PREDICTED: galectin-3-binding protein [Saimiri boliviensis boliviensis]	51.5	51.5	100%	3e-06	94%	XP_010340649.1
☐	hypothetical protein EGK_09048 [Macaca mulatta]	51.5	51.5	100%	3e-06	94%	EHH25259.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Macaca mulatta]	51.5	51.5	100%	3e-06	94%	XP_001109047.1
☐	PREDICTED: galectin-3-binding protein [Callithrix jacchus]	51.5	51.5	100%	3e-06	94%	XP_002748850.2
☐	hypothetical protein EGM_08232 [Macaca fascicularis]	51.5	51.5	100%	3e-06	94%	EHH58393.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Macaca fascicularis]	51.5	51.5	100%	3e-06	94%	XP_005585202.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Nomascus leucogenys]	51.5	51.5	100%	3e-06	94%	XP_003278480.2
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein-like [Pong	49.0	49.0	100%	2e-05	88%	XP_009234739.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein [Pongo ab	49.0	49.0	100%	2e-05	88%	XP_003778963.1

☐	Galectin-3-binding protein [Pteropus alecto]	48.1	48.1	100%	4e-05	88%	ELK12298.1
☐	PREDICTED: galectin-3-binding protein [Pteropus alecto]	48.1	48.1	100%	5e-05	88%	XP_006912443.1
☐	lectin, galactoside-binding, soluble, 3 binding protein [synthetic construct]	48.1	48.1	100%	5e-05	88%	ABM86350.1
☐	Galectin-3-binding protein [Myotis brandtii]	46.0	46.0	100%	2e-04	88%	EPQ18923.1
☐	PREDICTED: galectin-3-binding protein [Myotis brandtii]	46.0	46.0	100%	2e-04	88%	XP_005884378.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein [Myotis lu	46.0	46.0	100%	2e-04	88%	XP_006108225.1
☐	PREDICTED: galectin-3-binding protein [Eptesicus fuscus]	46.0	46.0	100%	2e-04	88%	XP_008153225.1
☐	PREDICTED: galectin-3-binding protein isoform X3 [Galeopterus variegatus]	45.6	45.6	100%	3e-04	81%	XP_008574380.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Galeopterus variegatus]	45.6	45.6	100%	3e-04	81%	XP_008574379.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Galeopterus variegatus]	45.6	45.6	100%	3e-04	81%	XP_008574378.1
☐	hypothetical protein PANDA_006893 [Ailuropoda melanoleuca]	45.2	45.2	87%	4e-04	93%	EFB18389.1
☐	PREDICTED: galectin-3-binding protein [Camelus dromedarius]	45.2	45.2	87%	4e-04	93%	XP_010997923.1
☐	PREDICTED: galectin-3-binding protein [Vicugna pacos]	45.2	45.2	87%	4e-04	93%	XP_006199496.1
☐	PREDICTED: galectin-3-binding protein-like [Camelus ferus]	45.2	45.2	87%	4e-04	93%	XP_006182736.1
☐	galectin-3-binding protein precursor [Camelus ferus]	45.2	45.2	87%	4e-04	93%	EPY80953.1
☐	PREDICTED: galectin-3-binding protein [Odobenus rosmarus divergens]	45.2	45.2	87%	4e-04	93%	XP_004416304.1
☐	PREDICTED: galectin-3-binding protein [Camelus bactrianus]	45.2	45.2	87%	4e-04	93%	XP_010948995.1
☐	PREDICTED: galectin-3-binding protein isoform X3 [Ursus maritimus]	45.2	45.2	87%	4e-04	93%	XP_008692049.1
☐	PREDICTED: galectin-3-binding protein [Leptonychotes weddellii]	45.2	45.2	87%	4e-04	93%	XP_006745574.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform X6 [Muste	45.2	45.2	87%	4e-04	93%	XP_004748843.1
☐	PREDICTED: galectin-3-binding protein-like [Ailuropoda melanoleuca]	45.2	45.2	87%	4e-04	93%	XP_002918426.1
☐	galectin-3-binding protein precursor [Camelus ferus]	45.2	45.2	87%	4e-04	93%	EPY82790.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform X4 [Muste	45.2	45.2	87%	4e-04	93%	XP_004748841.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform X3 [Muste	45.2	45.2	87%	5e-04	93%	XP_004748840.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Ursus maritimus]	45.2	45.2	87%	5e-04	93%	XP_008692048.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform X2 [Muste	45.2	45.2	87%	5e-04	93%	XP_004748839.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Ursus maritimus]	45.2	45.2	87%	5e-04	93%	XP_008692047.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform X1 [Muste	45.2	45.2	87%	5e-04	93%	XP_004748838.1
☐	Galectin-3-binding protein [Myotis davidii]	43.5	43.5	100%	0.002	81%	ELK38015.1
☐	PREDICTED: galectin-3-binding protein [Myotis davidii]	43.5	43.5	100%	0.002	81%	XP_006753504.1
☐	PREDICTED: galectin-3-binding protein [Tursiops truncatus]	42.6	42.6	87%	0.003	86%	XP_004323016.1
☐	PREDICTED: galectin-3-binding protein [Orcinus orca]	42.6	42.6	87%	0.003	86%	XP_004275584.1
☐	PREDICTED: galectin-3-binding protein [Lipotes vexillifer]	42.6	42.6	87%	0.003	86%	XP_007462419.1
☐	PREDICTED: galectin-3-binding protein [Trichechus manatus latirostris]	41.8	41.8	81%	0.006	92%	XP_004374429.1
☐	PREDICTED: galectin-3-binding protein [Ceratotherium simum simum]	41.8	41.8	87%	0.006	86%	XP_004432888.1
☐	PREDICTED: galectin-3-binding protein [Orycteropus afer afer]	41.8	41.8	81%	0.006	92%	XP_007958025.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1 isoform X5 [Canis lupu	41.4	41.4	87%	0.008	86%	XP_540464.2
☐	PREDICTED: soluble calcium-activated nucleotidase 1 isoform X1 [Canis lupu	41.4	41.4	87%	0.008	86%	XP_005624092.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein [Rhinopith	40.1	40.1	100%	0.021	81%	XP_010380238.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Physeter catodon]	39.7	39.7	81%	0.029	85%	XP_007106758.1
☐	PREDICTED: galectin-3-binding protein [Balaenoptera acutorostrata scammo	39.7	39.7	81%	0.029	85%	XP_007185856.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Physeter catodon]	39.7	39.7	81%	0.030	85%	XP_007106757.1
☐	PREDICTED: galectin-3-binding protein [Ovis aries]	39.2	39.2	87%	0.040	79%	XP_004013518.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein [Pantholo	39.2	39.2	87%	0.040	79%	XP_005958671.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Capra hircus]	39.2	39.2	87%	0.040	79%	XP_005694143.1

☐	PREDICTED: galectin-3-binding protein isoform X1 [Bubalus bubalis]	39.2	39.2	87%	0.040	79%	XP_006064180.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Capra hircus]	39.2	39.2	87%	0.040	79%	XP_005694142.1
☐	PREDICTED: galectin-3-binding protein [Tarsius syrichta]	39.2	39.2	87%	0.041	79%	XP_008046502.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Felis catus]	38.8	38.8	87%	0.056	79%	XP_003997300.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Felis catus]	38.8	38.8	87%	0.056	79%	XP_006940706.1
☐	galectin-3-binding protein [Cricetulus griseus]	37.1	37.1	100%	0.20	69%	ERE69017.1
☐	PREDICTED: galectin-3-binding protein [Cricetulus griseus]	37.1	37.1	100%	0.20	69%	XP_007620278.1
☐	PREDICTED: galectin-3-binding protein [Cricetulus griseus]	37.1	37.1	100%	0.20	69%	XP_003498865.1
☐	galectin-3-binding protein precursor [Mesocricetus auratus]	37.1	37.1	100%	0.20	69%	NP_001268610.1
☐	PREDICTED: galectin-3-binding protein [Panthera tigris altaica]	36.3	36.3	68%	0.37	91%	XP_007091540.1
☐	PREDICTED: galectin-3-binding protein [Echinops telfairi]	36.3	36.3	68%	0.37	91%	XP_004709313.1
☐	RecName: Full=Galectin-3-binding protein; AltName: Full=Cyp-C-associated	35.8	35.8	75%	0.51	83%	O70513.2
☐	90K protein precursor [Rattus norvegicus]	35.8	35.8	75%	0.51	83%	AAS58489.1
☐	unnamed protein product [Mus musculus]	35.8	35.8	75%	0.51	83%	BAE31013.1
☐	unnamed protein product [Mus musculus]	35.8	35.8	75%	0.51	83%	BAE29246.1
☐	unnamed protein product [Mus musculus]	35.8	35.8	75%	0.51	83%	BAE31894.1
☐	galectin-3-binding protein precursor [Mus musculus]	35.8	35.8	75%	0.51	83%	NP_035280.1
☐	PREDICTED: galectin-3-binding protein [Otolemur garnettii]	35.8	35.8	87%	0.51	71%	XP_003786610.1
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_a [Rattus	35.8	35.8	75%	0.51	83%	EDM06755.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Bison bison bison]	35.4	35.4	87%	0.69	71%	XP_010854576.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Bos taurus]	35.4	35.4	87%	0.69	71%	XP_005221293.1
☐	galectin-3-binding protein precursor [Bos taurus]	35.4	35.4	87%	0.69	71%	NP_001039781.1
☐	PREDICTED: galectin-3-binding protein [Bos mutus]	35.4	35.4	87%	0.69	71%	XP_005910379.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Bison bison bison]	35.4	35.4	87%	0.69	71%	XP_010854575.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Bos taurus]	35.4	35.4	87%	0.69	71%	XP_005221292.1
☐	PREDICTED: galectin-3-binding protein [Chrysochloris asiatica]	35.4	35.4	81%	0.69	77%	XP_006869713.1

⊟ Alignments

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galectin-3-binding precursor-like protein [Callithrix jacchus]

Sequence ID: gb|ABQ22691.1| **Length:** 125 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 110 to 125 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	2e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RTVIRPFYLTDSSGVD  16
            RTVIRPFYLT+SSGVD
Sbjct  110  RTVIRPFYLTNSSGVD  125
```

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galectin-3-binding precursor-like protein [Callithrix jacchus]

Sequence ID: gb|ABQ22355.1| **Length:** 125 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 110 to 125 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	2e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RTVIRPFYLTDSSGVD  16
            RTVIRPFYLT+SSGVD
Sbjct  110  RTVIRPFYLTNSSGVD  125
```

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lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_b [Homo sapiens]

Sequence ID: gb|EAW89544.1| **Length:** 391 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 376 to 391 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	3e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RTVIRPFYLTDSSGVD  16
            RTVIRPFYLT+SSGVD
Sbjct  376  RTVIRPFYLTNSSGVD  391
```

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unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG58382.1| **Length:** 413 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 398 to 413 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	3e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RTVIRPFYLTDSSGVD  16
            RTVIRPFYLT+SSGVD
Sbjct  398  RTVIRPFYLTNSSGVD  413
```

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unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG62970.1| **Length:** 466 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 451 to 466 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	3e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RTVIRPFYLTDSSGVD  16
            RTVIRPFYLT+SSGVD
Sbjct  451  RTVIRPFYLTNSSGVD  466
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - B9G1FU5S01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

LGALS3BP_RTVIRPFYLTNSSGVD_NonMod

RID	B9G1FU5S01R (Expires on 01-14 13:50 pm)
Query ID	lcl|378470
Description	None
Molecule type	amino acid
Query Length	16

Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

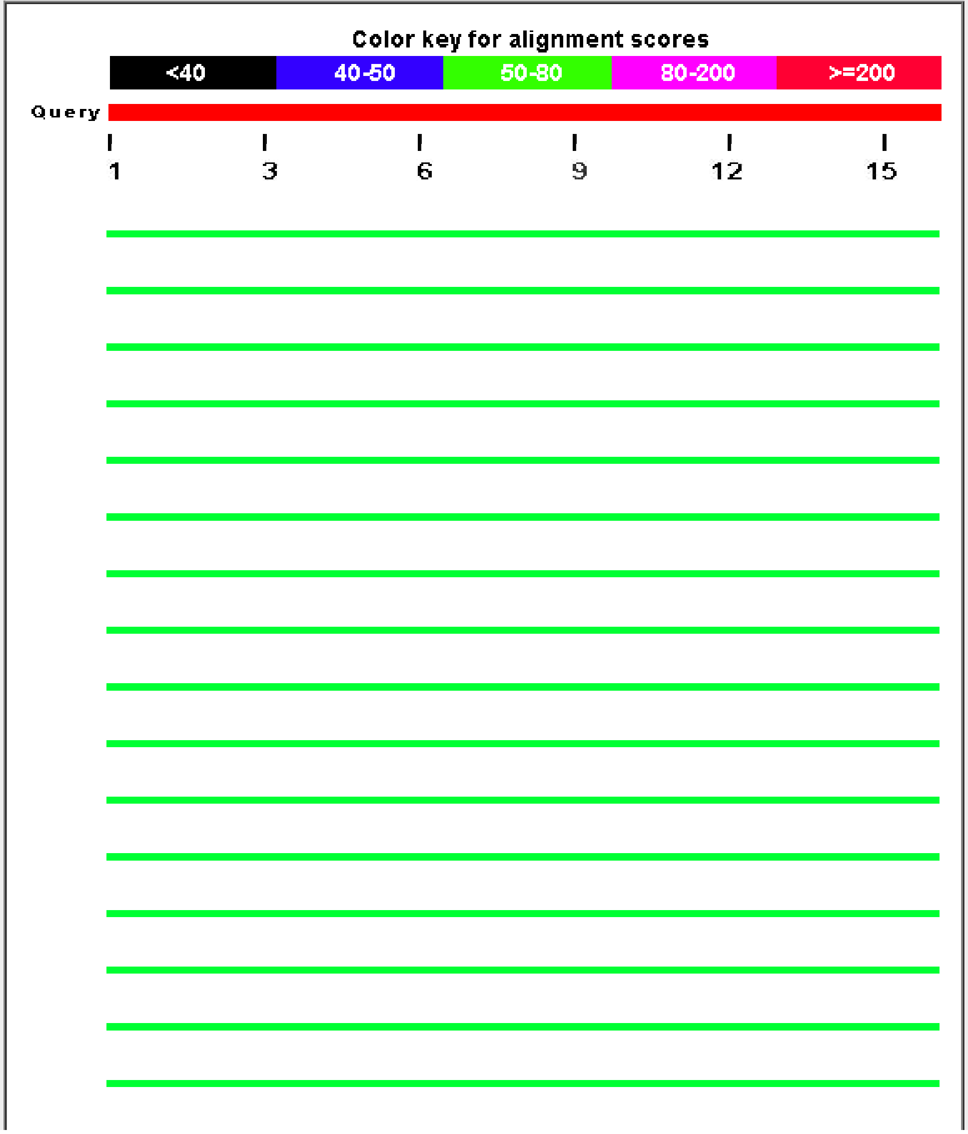
Graphic Summary

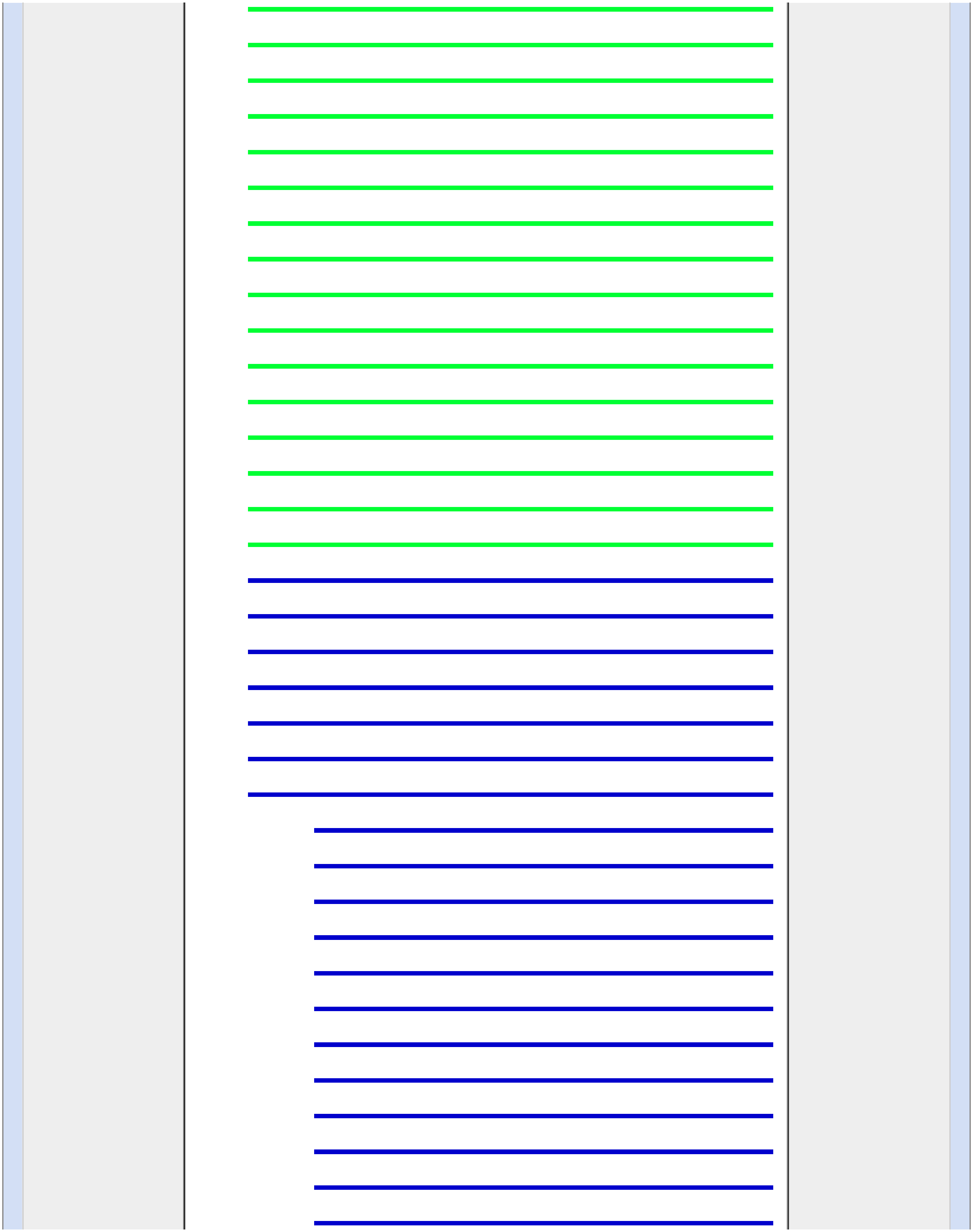
Show Conserved Domains

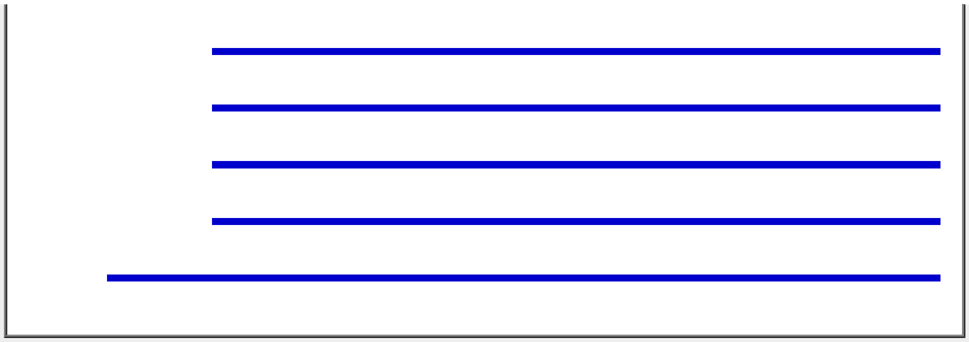
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	galectin-3-binding precursor-like protein [Callithrix jacchus]	54.1	54.1	100%	3e-07	100%	gi|146332371|ABQ22691.1
☐	galectin-3-binding precursor-like protein [Callithrix jacchus]	54.1	54.1	100%	3e-07	100%	gi|146331698|ABQ22355.1
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_	54.1	54.1	100%	4e-07	100%	gi|119609950|EAW89544.1
☐	unnamed protein product [Homo sapiens]	54.1	54.1	100%	4e-07	100%	gi|194380458|BAG58382.1
☐	unnamed protein product [Homo sapiens]	54.1	54.1	100%	4e-07	100%	gi|194376422|BAG62970.1
☐	PREDICTED: galectin-3-binding protein isoform 3 [Macaca mulatta]	54.1	54.1	100%	4e-07	100%	gi|297273768|XP_002800676.1
☐	unnamed protein product [Homo sapiens]	54.1	54.1	100%	4e-07	100%	gi|193786317|BAG51600.1
☐	unnamed protein product [Homo sapiens]	54.1	54.1	100%	4e-07	100%	gi|194375560|BAG56725.1
☐	PREDICTED: galectin-3-binding protein isoform 2 [Macaca mulatta]	54.1	54.1	100%	4e-07	100%	gi|297273766|XP_002800675.1
☐	unnamed protein product [Homo sapiens]	54.1	54.1	100%	4e-07	100%	gi|194375081|BAG62653.1
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_	54.1	54.1	100%	4e-07	100%	gi|119609949|EAW89543.1
☐	PREDICTED: galectin-3-binding protein [Chlorocebus sabaeus]	54.1	54.1	100%	4e-07	100%	gi|635093239|XP_008011313.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Macaca fascicu	54.1	54.1	100%	4e-07	100%	gi|544502104|XP_005585203.1
☐	RecName: Full=Galectin-3-binding protein; AltName: Full=Lectin ga	54.1	54.1	100%	4e-07	100%	gi|75042301|Q5RDA4.1
☐	PREDICTED: galectin-3-binding protein [Papio anubis]	54.1	54.1	100%	4e-07	100%	gi|402901262|XP_003913572.1
☐	PREDICTED: galectin-3-binding protein [Pan troglodytes]	54.1	54.1	100%	4e-07	100%	gi|55646067|XP_511716.1
☐	galectin-3-binding protein precursor [Homo sapiens]	54.1	54.1	100%	4e-07	100%	gi|5031863|NP_005558.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Gorilla gorilla go	54.1	54.1	100%	4e-07	100%	gi|426346505|XP_004040917.1
☐	PREDICTED: galectin-3-binding protein [Pan paniscus]	54.1	54.1	100%	4e-07	100%	gi|397494909|XP_003818311.1
☐	PREDICTED: galectin-3-binding protein isoform 2 [Nomascus leucc	54.1	54.1	100%	4e-07	100%	gi|332258797|XP_003278481.1
☐	PREDICTED: galectin-3-binding protein [Saimiri boliviensis bolivien	54.1	54.1	100%	4e-07	100%	gi|725577242|XP_010340649.1
☐	hypothetical protein EGK_09048 [Macaca mulatta]	54.1	54.1	100%	4e-07	100%	gi|355568978|EHH25259.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Macaca mulatta]	54.1	54.1	100%	4e-07	100%	gi|109118737|XP_001109047.1
☐	PREDICTED: galectin-3-binding protein [Callithrix jacchus]	54.1	54.1	100%	4e-07	100%	gi|675661532|XP_002748850.2
☐	hypothetical protein EGM_08232 [Macaca fascicularis]	54.1	54.1	100%	4e-07	100%	gi|355754428|EHH58393.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Macaca fascicu	54.1	54.1	100%	4e-07	100%	gi|544502102|XP_005585202.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Nomascus leucc	54.1	54.1	100%	4e-07	100%	gi|441643566|XP_003278480.2
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein-	51.5	51.5	100%	3e-06	94%	gi|686772908|XP_009234739.1
☐							

	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein	51.5	51.5	100%	3e-06	94%	gi|395749542|XP_003778963.1
☐	Galectin-3-binding protein [Pteropus alecto]	50.7	50.7	100%	6e-06	94%	gi|431908706|ELK12298.1
☐	PREDICTED: galectin-3-binding protein [Pteropus alecto]	50.7	50.7	100%	6e-06	94%	gi|586558304|XP_006912443.1
☐	lectin, galactoside-binding, soluble, 3 binding protein [synthetic cons	50.7	50.7	100%	6e-06	94%	gi|123997497|ABM86350.1
☐	Galectin-3-binding protein [Myotis brandtii]	48.6	48.6	100%	3e-05	94%	gi|521037145|EPQ18923.1
☐	PREDICTED: galectin-3-binding protein [Myotis brandtii]	48.6	48.6	100%	3e-05	94%	gi|554585904|XP_005884378.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein	48.6	48.6	100%	3e-05	94%	gi|558213798|XP_006108225.1
☐	PREDICTED: galectin-3-binding protein [Eptesicus fuscus]	48.6	48.6	100%	3e-05	94%	gi|641726407|XP_008153225.1
☐	PREDICTED: galectin-3-binding protein isoform X3 [Galeopterus va	48.1	48.1	100%	4e-05	88%	gi|667281302|XP_008574380.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Galeopterus va	48.1	48.1	100%	4e-05	88%	gi|667281299|XP_008574379.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Galeopterus va	48.1	48.1	100%	4e-05	88%	gi|667281296|XP_008574378.1
☐	hypothetical protein PANDA_006893 [Ailuropoda melanoleuca]	47.7	47.7	87%	6e-05	100%	gi|281342805|EFB18389.1
☐	PREDICTED: galectin-3-binding protein [Vicugna pacos]	47.7	47.7	87%	6e-05	100%	gi|560953982|XP_006199496.1
☐	PREDICTED: galectin-3-binding protein-like [Camelus ferus]	47.7	47.7	87%	6e-05	100%	gi|560912913|XP_006182736.1
☐	galectin-3-binding protein precursor [Camelus ferus]	47.7	47.7	87%	6e-05	100%	gi|528761294|EPY80953.1
☐	PREDICTED: galectin-3-binding protein [Odobenus rosmarus diverg	47.7	47.7	87%	6e-05	100%	gi|472394090|XP_004416304.1
☐	PREDICTED: galectin-3-binding protein isoform X3 [Ursus maritimu	47.7	47.7	87%	6e-05	100%	gi|671002383|XP_008692049.1
☐	PREDICTED: galectin-3-binding protein [Leptonychotes weddellii]	47.7	47.7	87%	6e-05	100%	gi|585188403|XP_006745574.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	47.7	47.7	87%	6e-05	100%	gi|511848965|XP_004748843.1
☐	PREDICTED: galectin-3-binding protein-like [Ailuropoda melanoleu	47.7	47.7	87%	6e-05	100%	gi|301766034|XP_002918426.1
☐	galectin-3-binding protein precursor [Camelus ferus]	47.7	47.7	87%	6e-05	100%	gi|528763131|EPY82790.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	47.7	47.7	87%	6e-05	100%	gi|511848961|XP_004748841.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	47.7	47.7	87%	6e-05	100%	gi|511848959|XP_004748840.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Ursus maritimu	47.7	47.7	87%	6e-05	100%	gi|671002381|XP_008692048.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	47.7	47.7	87%	6e-05	100%	gi|511848957|XP_004748839.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Ursus maritimu	47.7	47.7	87%	6e-05	100%	gi|671002379|XP_008692047.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	47.7	47.7	87%	6e-05	100%	gi|511848955|XP_004748838.1
☐	Galectin-3-binding protein [Myotis davidii]	46.0	46.0	100%	2e-04	88%	gi|432118125|ELK38015.1
☐	PREDICTED: galectin-3-binding protein [Myotis davidii]	46.0	46.0	100%	2e-04	88%	gi|584038281|XP_006753504.1
☐	PREDICTED: galectin-3-binding protein [Tursiops truncatus]	45.2	45.2	87%	4e-04	93%	gi|470634961|XP_004323016.1
☐	PREDICTED: galectin-3-binding protein [Orcinus orca]	45.2	45.2	87%	4e-04	93%	gi|466037200|XP_004275584.1
☐	PREDICTED: galectin-3-binding protein [Lipotes vexillifer]	45.2	45.2	87%	4e-04	93%	gi|602701011|XP_007462419.1
☐	PREDICTED: galectin-3-binding protein [Trichechus manatus latiros	44.3	44.3	81%	8e-04	100%	gi|471367801|XP_004374429.1
☐	PREDICTED: galectin-3-binding protein [Ceratotherium simum simu	44.3	44.3	87%	8e-04	93%	gi|478517307|XP_004432888.1
☐	PREDICTED: galectin-3-binding protein [Orycteropus afer afer]	44.3	44.3	81%	8e-04	100%	gi|634830004|XP_007958025.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1 isoform X5 [	43.9	43.9	87%	0.001	93%	gi|73964953|XP_540464.2
☐	PREDICTED: soluble calcium-activated nucleotidase 1 isoform X1 [	43.9	43.9	87%	0.001	93%	gi|545509197|XP_005624092.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein	42.6	42.6	100%	0.003	88%	gi|724915028|XP_010380238.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Physeter catod	42.2	42.2	81%	0.004	92%	gi|593720930|XP_007106758.1
☐	PREDICTED: galectin-3-binding protein [Balaenoptera acutorostrata	42.2	42.2	81%	0.004	92%	gi|594676074|XP_007185856.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Physeter catod	42.2	42.2	81%	0.004	92%	gi|593720928|XP_007106757.1
☐	PREDICTED: galectin-3-binding protein [Ovis aries]	41.8	41.8	87%	0.006	86%	gi|426239209|XP_004013518.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein	41.8	41.8	87%	0.006	86%	gi|556725783|XP_005958671.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Capra hircus]	41.8	41.8	87%	0.006	86%	gi|548509918|XP_005694143.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Bubalus bubali	41.8	41.8	87%	0.006	86%	gi|594081110|XP_006064180.1

☐	PREDICTED: galectin-3-binding protein isoform X1 [Capra hircus]	41.8	41.8	87%	0.006	86%	gi|548509916|XP_005694142.1
☐	PREDICTED: galectin-3-binding protein [Tarsius syrichta]	41.8	41.8	87%	0.006	86%	gi|640781767|XP_008046502.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Felis catus]	41.4	41.4	87%	0.008	86%	gi|410981896|XP_003997300.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Felis catus]	41.4	41.4	87%	0.008	86%	gi|587012494|XP_006940706.1
☐	galectin-3-binding protein [Cricetulus griseus]	39.7	39.7	100%	0.028	75%	gi|537143564|ERE69017.1
☐	PREDICTED: galectin-3-binding protein [Cricetulus griseus]	39.7	39.7	100%	0.028	75%	gi|625257783|XP_007620278.1
☐	PREDICTED: galectin-3-binding protein [Cricetulus griseus]	39.7	39.7	100%	0.028	75%	gi|354473282|XP_003498865.1
☐	galectin-3-binding protein precursor [Mesocricetus auratus]	39.7	39.7	100%	0.028	75%	gi|528078247|NP_001268610.1
☐	PREDICTED: galectin-3-binding protein [Panthera tigris altaica]	38.8	38.8	68%	0.052	100%	gi|591331484|XP_007091540.1
☐	PREDICTED: galectin-3-binding protein [Echinops telfairi]	38.8	38.8	68%	0.053	100%	gi|507673535|XP_004709313.1
☐	RecName: Full=Galectin-3-binding protein; AltName: Full=Cyp-C-as	38.4	38.4	75%	0.072	92%	gi|218526547|O70513.2
☐	90K protein precursor [Rattus norvegicus]	38.4	38.4	75%	0.072	92%	gi|45357062|AAS58489.1
☐	unnamed protein product [Mus musculus]	38.4	38.4	75%	0.072	92%	gi|74212546|BAE31013.1
☐	unnamed protein product [Mus musculus]	38.4	38.4	75%	0.072	92%	gi|74211789|BAE29246.1
☐	unnamed protein product [Mus musculus]	38.4	38.4	75%	0.072	92%	gi|74142260|BAE31894.1
☐	galectin-3-binding protein precursor [Mus musculus]	38.4	38.4	75%	0.072	92%	gi|6755144|NP_035280.1
☐	PREDICTED: galectin-3-binding protein [Otolemur garnettii]	38.4	38.4	87%	0.072	79%	gi|395826815|XP_003786610.1
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_	38.4	38.4	75%	0.072	92%	gi|149054938|EDM06755.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Bos taurus]	38.0	38.0	87%	0.099	79%	gi|528997315|XP_005221293.1
☐	galectin-3-binding protein precursor [Bos taurus]	38.0	38.0	87%	0.099	79%	gi|114052595|NP_001039781.1
☐	PREDICTED: galectin-3-binding protein [Bos mutus]	38.0	38.0	87%	0.099	79%	gi|555997305|XP_005910379.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Bos taurus]	38.0	38.0	87%	0.099	79%	gi|528997313|XP_005221292.1
☐	PREDICTED: galectin-3-binding protein [Chrysochloris asiatica]	38.0	38.0	81%	0.099	85%	gi|586478358|XP_006869713.1
☐	PREDICTED: galectin-3-binding protein [Erinaceus europaeus]	38.0	38.0	75%	0.099	92%	gi|617646710|XP_007533029.1
☐	PREDICTED: galectin-3-binding protein [Nannospalax galili]	37.5	37.5	100%	0.14	69%	gi|674080617|XP_008847879.1
☐	galectin-3-binding protein precursor [Rattus norvegicus]	37.1	37.1	75%	0.19	92%	gi|20806135|NP_620796.1
☐	PREDICTED: galectin-3-binding protein [Jaculus jaculus]	37.1	37.1	87%	0.19	79%	gi|507543547|XP_004655763.1

⊟ Alignments

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galectin-3-binding precursor-like protein [Callithrix jacchus]

Sequence ID: gi|146332371|gb|ABQ22691.1| **Length:** 125 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 110 to 125 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	3e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RTVIRPFYLTNSSGVD  16
            RTVIRPFYLTNSSGVD
Sbjct  110  RTVIRPFYLTNSSGVD  125
```

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galectin-3-binding precursor-like protein [Callithrix jacchus]

Sequence ID: gi|146331698|gb|ABQ22355.1| **Length:** 125 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 110 to 125 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	3e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RTVIRPFYLTNSSGVD  16
```

```
               RTVIRPFYLTNSSGVD
Sbjct  110  RTVIRPFYLTNSSGVD  125
```

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lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_b [Homo sapiens]

Sequence ID: gi|119609950|gb|EAW89544.1| **Length:** 391 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 376 to 391 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	4e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RTVIRPFYLTNSSGVD  16
            RTVIRPFYLTNSSGVD
Sbjct  376  RTVIRPFYLTNSSGVD  391
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194380458|dbj|BAG58382.1| **Length:** 413 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 398 to 413 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	4e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RTVIRPFYLTNSSGVD  16
            RTVIRPFYLTNSSGVD
Sbjct  398  RTVIRPFYLTNSSGVD  413
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194376422|dbj|BAG62970.1| **Length:** 466 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 451 to 466 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	4e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RTVIRPFYLTNSSGVD  16
            RTVIRPFYLTNSSGVD
Sbjct  451  RTVIRPFYLTNSSGVD  466
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVH6EW9B01R

Your search parameters were adjusted to search for a short input sequence.

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LGALS3BP_RYKGLDLTEDTYKPRI_Mod

RID	BVH6EW9B01R (Expires on 01-21 10:00 am)		
Query ID	lcl|26651	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	16	**Program**	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

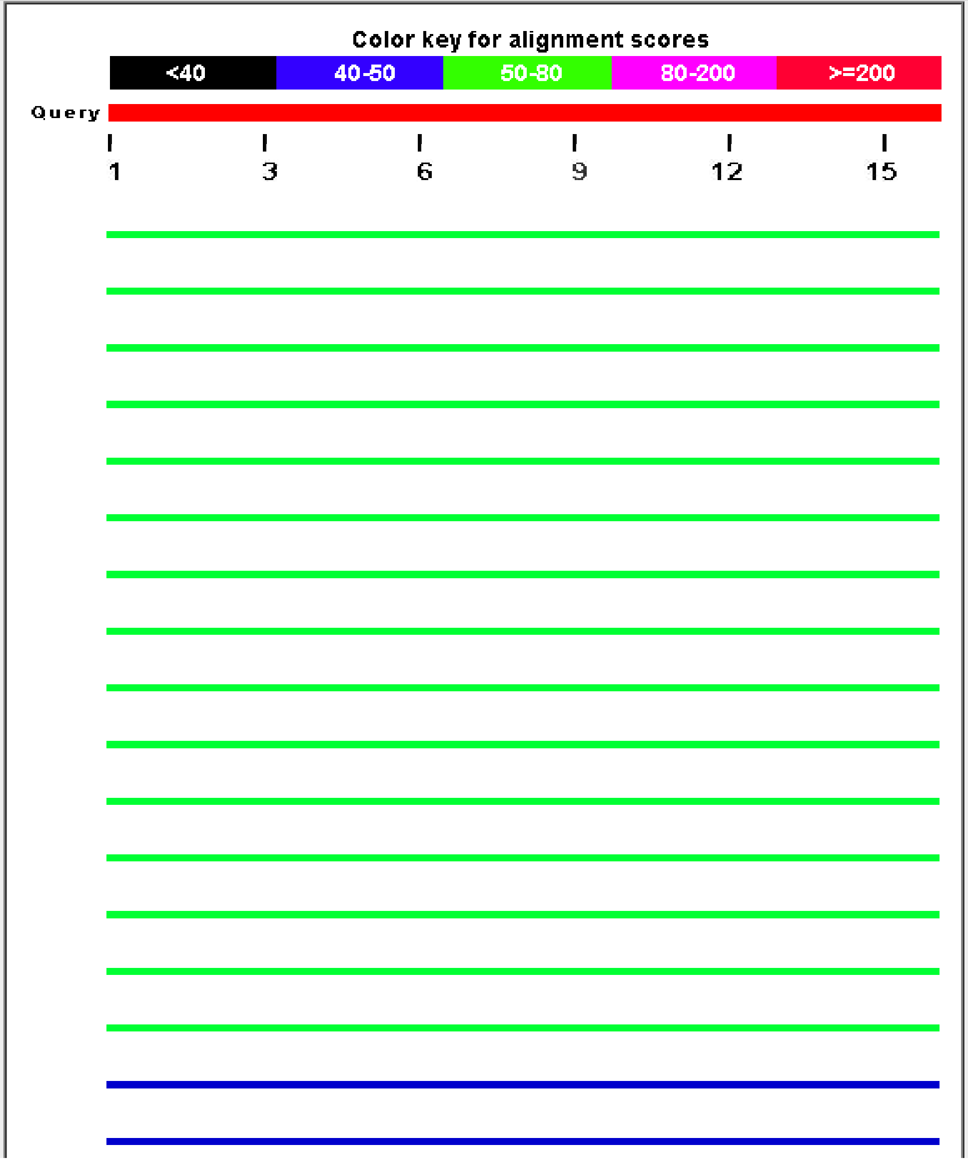
Graphic Summary

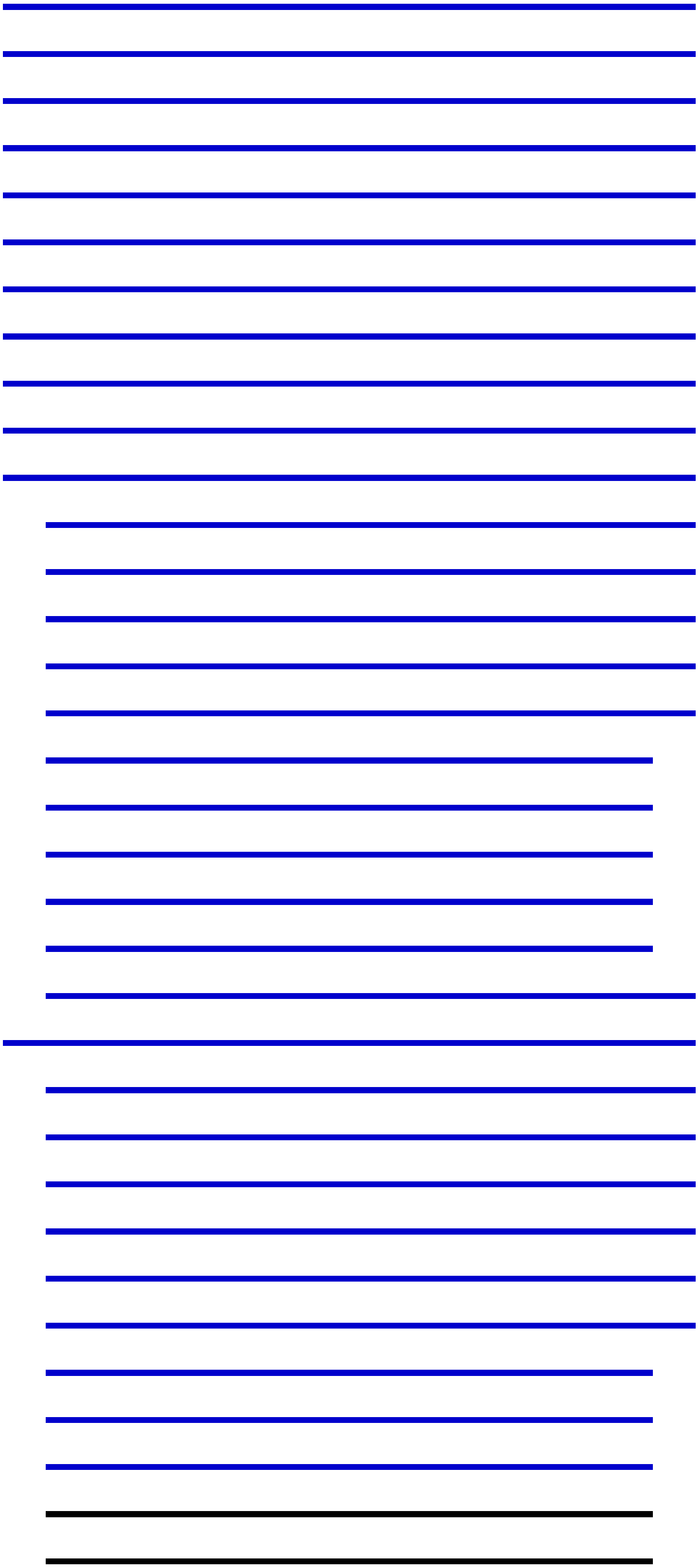
Show Conserved Domains

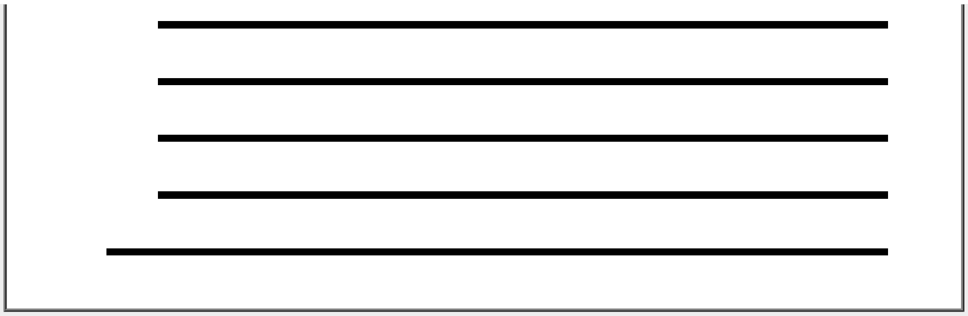
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein-like [Pong	53.2	53.2	100%	8e-07	94%	XP_009234739.1
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_b [Homo s	53.2	53.2	100%	8e-07	94%	EAW89544.1
☐	unnamed protein product [Homo sapiens]	53.2	53.2	100%	8e-07	94%	BAG58382.1
☐	unnamed protein product [Homo sapiens]	53.2	53.2	100%	9e-07	94%	BAG62970.1
☐	unnamed protein product [Homo sapiens]	53.2	53.2	100%	9e-07	94%	BAG51600.1
☐	unnamed protein product [Homo sapiens]	53.2	53.2	100%	9e-07	94%	BAG56725.1
☐	unnamed protein product [Homo sapiens]	53.2	53.2	100%	9e-07	94%	BAG62653.1
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_a [Homo s	53.2	53.2	100%	9e-07	94%	EAW89543.1
☐	RecName: Full=Galectin-3-binding protein; AltName: Full=Lectin galactoside-l	53.2	53.2	100%	9e-07	94%	Q5RDA4.1
☐	PREDICTED: galectin-3-binding protein [Pan troglodytes]	53.2	53.2	100%	9e-07	94%	XP_511716.1
☐	galectin-3-binding protein precursor [Homo sapiens]	53.2	53.2	100%	9e-07	94%	NP_005558.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Gorilla gorilla gorilla]	53.2	53.2	100%	9e-07	94%	XP_004040917.1
☐	PREDICTED: galectin-3-binding protein [Pan paniscus]	53.2	53.2	100%	9e-07	94%	XP_003818311.1
☐	lectin, galactoside-binding, soluble, 3 binding protein [synthetic construct]	53.2	53.2	100%	9e-07	94%	ABM86350.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein [Pongo ab	53.2	53.2	100%	9e-07	94%	XP_003778963.1
☐	PREDICTED: galectin-3-binding protein isoform 3 [Macaca mulatta]	49.8	49.8	100%	1e-05	88%	XP_002800676.1
☐	PREDICTED: galectin-3-binding protein isoform 2 [Macaca mulatta]	49.8	49.8	100%	1e-05	88%	XP_002800675.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Macaca fascicularis]	49.8	49.8	100%	1e-05	88%	XP_005585203.1
☐	PREDICTED: galectin-3-binding protein [Papio anubis]	49.8	49.8	100%	1e-05	88%	XP_003913572.1
☐	PREDICTED: galectin-3-binding protein isoform 2 [Nomascus leucogenys]	49.8	49.8	100%	1e-05	88%	XP_003278481.1
☐	PREDICTED: galectin-3-binding protein [Saimiri boliviensis boliviensis]	49.8	49.8	100%	1e-05	88%	XP_010340649.1
☐	hypothetical protein EGK_09048 [Macaca mulatta]	49.8	49.8	100%	1e-05	88%	EHH25259.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Macaca mulatta]	49.8	49.8	100%	1e-05	88%	XP_001109047.1
☐	PREDICTED: galectin-3-binding protein [Callithrix jacchus]	49.8	49.8	100%	1e-05	88%	XP_002748850.2
☐	hypothetical protein EGM_08232 [Macaca fascicularis]	49.8	49.8	100%	1e-05	88%	EHH58393.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Macaca fascicularis]	49.8	49.8	100%	1e-05	88%	XP_005585202.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Nomascus leucogenys]	49.8	49.8	100%	1e-05	88%	XP_003278480.2
☐	PREDICTED: galectin-3-binding protein [Jaculus jaculus]	47.7	47.7	100%	6e-05	88%	XP_004655763.1
☐	PREDICTED: galectin-3-binding protein isoform X3 [Galeopterus variegatus]	46.9	46.9	93%	1e-04	87%	XP_008574380.1

☐	PREDICTED: galectin-3-binding protein isoform X2 [Galeopterus variegatus]	46.9	46.9	93%	1e-04	87%	XP_008574379.1
☐	PREDICTED: galectin-3-binding protein [Nannospalax galili]	46.9	46.9	93%	1e-04	87%	XP_008847879.1
☐	PREDICTED: galectin-3-binding protein [Tarsius syrichta]	46.9	46.9	93%	1e-04	87%	XP_008046502.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Galeopterus variegatus]	46.9	46.9	93%	1e-04	87%	XP_008574378.1
☐	cyclophilin C-associated protein [Mus musculus domesticus]	46.4	46.4	87%	2e-04	93%	AAA37499.1
☐	unnamed protein product [Mus musculus]	46.4	46.4	87%	2e-04	93%	BAE31013.1
☐	unnamed protein product [Mus musculus]	46.4	46.4	87%	2e-04	93%	BAE29246.1
☐	unnamed protein product [Mus musculus]	46.4	46.4	87%	2e-04	93%	BAE31894.1
☐	galectin-3-binding protein precursor [Mus musculus]	46.4	46.4	87%	2e-04	93%	NP_035280.1
☐	PREDICTED: galectin-3-binding protein [Chlorocebus sabaeus]	46.4	46.4	93%	2e-04	87%	XP_008011313.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein [Rhinopith	45.2	45.2	100%	4e-04	81%	XP_010380238.1
☐	PREDICTED: galectin-3-binding protein [Heterocephalus glaber]	42.2	42.2	93%	0.004	80%	XP_004860896.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Heterocephalus glaber]	42.2	42.2	93%	0.004	80%	XP_004881532.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Heterocephalus glaber]	42.2	42.2	93%	0.004	80%	XP_004881531.1
☐	PREDICTED: galectin-3-binding protein [Fukomys damarensis]	42.2	42.2	93%	0.004	80%	XP_010616820.1
☐	Galectin-3-binding protein [Heterocephalus glaber]	42.2	42.2	93%	0.004	80%	EHB01017.1
☐	Galectin-3-binding protein [Fukomys damarensis]	42.2	42.2	93%	0.004	80%	KFO35672.1
☐	galectin-3-binding protein [Cricetulus griseus]	40.9	40.9	87%	0.011	79%	ERE69017.1
☐	PREDICTED: galectin-3-binding protein [Cricetulus griseus]	40.9	40.9	87%	0.011	79%	XP_007620278.1
☐	PREDICTED: galectin-3-binding protein [Cricetulus griseus]	40.9	40.9	87%	0.011	79%	XP_003498865.1
☐	PREDICTED: galectin-3-binding protein [Ictidomys tridecemlineatus]	39.7	39.7	87%	0.030	79%	XP_005332681.1
☐	PREDICTED: galectin-3-binding protein [Tursiops truncatus]	39.2	39.2	87%	0.040	79%	XP_004323016.1
☐	PREDICTED: galectin-3-binding protein [Orcinus orca]	39.2	39.2	87%	0.040	79%	XP_004275584.1
☐	PREDICTED: galectin-3-binding protein [Balaenoptera acutorostrata scammo	39.2	39.2	87%	0.040	79%	XP_007185856.1
☐	galectin-3-binding protein precursor [Mesocricetus auratus]	39.2	39.2	87%	0.041	79%	NP_001268610.1
☐	PREDICTED: galectin-3-binding protein [Lipotes vexillifer]	39.2	39.2	87%	0.041	79%	XP_007462419.1
☐	PREDICTED: galectin-3-binding protein [Microtus ochrogaster]	38.8	38.8	93%	0.056	73%	XP_005350871.1
☐	PREDICTED: galectin-3-binding protein [Odobenus rosmarus divergens]	37.1	37.1	87%	0.20	71%	XP_004416304.1
☐	PREDICTED: galectin-3-binding protein [Peromyscus maniculatus bairdii]	37.1	37.1	87%	0.20	71%	XP_006990333.1
☐	PREDICTED: galectin-3-binding protein [Equus caballus]	36.7	36.7	93%	0.27	67%	XP_001491000.1
☐	PREDICTED: galectin-3-binding protein [Ceratotherium simum simum]	36.7	36.7	87%	0.27	71%	XP_004432888.1
☐	Galectin-3-binding protein [Tupaia chinensis]	36.7	36.7	93%	0.27	67%	ELW68246.1
☐	PREDICTED: galectin-3-binding protein [Tupaia chinensis]	36.7	36.7	93%	0.27	67%	XP_006145764.1
☐	hypothetical protein PANDA_006893 [Ailuropoda melanoleuca]	35.8	35.8	87%	0.51	71%	EFB18389.1
☐	PREDICTED: galectin-3-binding protein isoform X3 [Ursus maritimus]	35.8	35.8	87%	0.51	71%	XP_008692049.1
☐	PREDICTED: galectin-3-binding protein [Leptonychotes weddellii]	35.8	35.8	87%	0.51	71%	XP_006745574.1
☐	PREDICTED: galectin-3-binding protein-like [Ailuropoda melanoleuca]	35.8	35.8	87%	0.51	71%	XP_002918426.1
☐	galectin-3-binding protein precursor [Rattus norvegicus]	35.8	35.8	87%	0.51	71%	NP_620796.1
☐	RecName: Full=Galectin-3-binding protein; AltName: Full=Cyp-C-associated p	35.8	35.8	87%	0.51	71%	O70513.2
☐	90K protein precursor [Rattus norvegicus]	35.8	35.8	87%	0.51	71%	AAS58489.1
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_a [Rattus	35.8	35.8	87%	0.51	71%	EDM06755.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Ursus maritimus]	35.8	35.8	87%	0.51	71%	XP_008692048.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Ursus maritimus]	35.8	35.8	87%	0.51	71%	XP_008692047.1
☐	PREDICTED: galectin-3-binding protein [Camelus dromedarius]	35.4	35.4	87%	0.69	71%	XP_010997923.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Physeter catodon]	35.4	35.4	87%	0.69	71%	XP_007106758.1

☐	PREDICTED: galectin-3-binding protein-like [Camelus ferus]	35.4	35.4	87%	0.69	71%	XP_006182736.1
☐	galectin-3-binding protein precursor [Camelus ferus]	35.4	35.4	87%	0.69	71%	EPY80953.1
☐	PREDICTED: galectin-3-binding protein [Camelus bactrianus]	35.4	35.4	87%	0.69	71%	XP_010948995.1
☐	galectin-3-binding protein precursor [Camelus ferus]	35.4	35.4	87%	0.69	71%	EPY82790.1
☐	PREDICTED: galectin-3-binding protein [Otolemur garnettii]	35.4	35.4	87%	0.69	71%	XP_003786610.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Physeter catodon]	35.4	35.4	87%	0.69	71%	XP_007106757.1
☐	PREDICTED: galectin-3-binding protein [Cavia porcellus]	35.4	35.4	100%	0.69	63%	XP_003464931.2
☐	PREDICTED: galectin-3-binding protein [Oryctolagus cuniculus]	35.0	35.0	93%	0.95	67%	XP_002724384.1
☐	PREDICTED: galectin-3-binding protein [Chinchilla lanigera]	35.0	35.0	93%	0.95	67%	XP_005407410.1
☐	PREDICTED: serine-rich adhesin for platelets-like [Ceratitis capitata]	34.1	34.1	75%	1.8	79%	XP_004526329.1
☐	Galectin-3-binding protein [Pteropus alecto]	33.7	33.7	93%	2.4	67%	ELK12298.1
☐	PREDICTED: galectin-3-binding protein [Pteropus alecto]	33.7	33.7	93%	2.4	67%	XP_006912443.1
☐	PREDICTED: galectin-3-binding protein [Trichechus manatus latirostris]	33.3	33.3	87%	3.3	64%	XP_004374429.1
☐	malate dehydrogenase [Sutterella wadsworthensis]	32.9	32.9	87%	4.3	79%	WP_005434869.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform X6 [Muste	32.9	32.9	87%	4.5	64%	XP_004748843.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform X4 [Muste	32.9	32.9	87%	4.5	64%	XP_004748841.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform X3 [Muste	32.9	32.9	87%	4.5	64%	XP_004748840.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform X2 [Muste	32.9	32.9	87%	4.5	64%	XP_004748839.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform X1 [Muste	32.9	32.9	87%	4.5	64%	XP_004748838.1
☐	PREDICTED: galectin-3-binding protein [Ovis aries]	31.6	31.6	75%	11	75%	XP_004013518.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein [Panthol	31.6	31.6	75%	11	75%	XP_005958671.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Capra hircus]	31.6	31.6	75%	11	75%	XP_005694143.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Capra hircus]	31.6	31.6	75%	11	75%	XP_005694142.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1 isoform X5 [Canis lupu	31.6	31.6	75%	11	75%	XP_540464.2
☐	PREDICTED: galectin-3-binding protein [Erinaceus europaeus]	31.6	31.6	87%	11	71%	XP_007533029.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1 isoform X1 [Canis lupu	31.6	31.6	75%	11	75%	XP_005624092.1

Alignments

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PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein-like, partial [Pongo abelii]

Sequence ID: ref|XP_009234739.1| **Length:** 341 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 149 to 164 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
53.2 bits(118)	8e-07	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RYKGLDLTEDTYKPRI  16
            RYKGL+LTEDTYKPRI
Sbjct  149  RYKGLNLTEDTYKPRI  164
```

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lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_b [Homo sapiens]

Sequence ID: gb|EAW89544.1| **Length:** 391 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 199 to 214 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
53.2 bits(118)	8e-07	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RYKGLDLTEDTYKPRI  16
            RYKGL+LTEDTYKPRI
Sbjct  199  RYKGLNLTEDTYKPRI  214
```

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unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG58382.1| **Length:** 413 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 221 to 236 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
53.2 bits(118)	8e-07	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RYKGLDLTEDTYKPRI  16
            RYKGL+LTEDTYKPRI
Sbjct  221  RYKGLNLTEDTYKPRI  236
```

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unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG62970.1| **Length:** 466 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 274 to 289 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
53.2 bits(118)	9e-07	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RYKGLDLTEDTYKPRI  16
            RYKGL+LTEDTYKPRI
Sbjct  274  RYKGLNLTEDTYKPRI  289
```

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unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG51600.1| **Length:** 481 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 289 to 304 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
53.2 bits(118)	9e-07	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RYKGLDLTEDTYKPRI  16
            RYKGL+LTEDTYKPRI
Sbjct  289  RYKGLNLTEDTYKPRI  304
```

BLAST ®

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NCBI/ BLAST/ blastp suite/ Formatting Results - B9HSY82101R

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How to read this page Blast report description

LGALS3BP_RYKGLNLTEDTYKPRI_NonMod

RID B9HSY82101R (Expires on 01-14 14:19 pm)

Query ID	lcl|147197	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	16		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

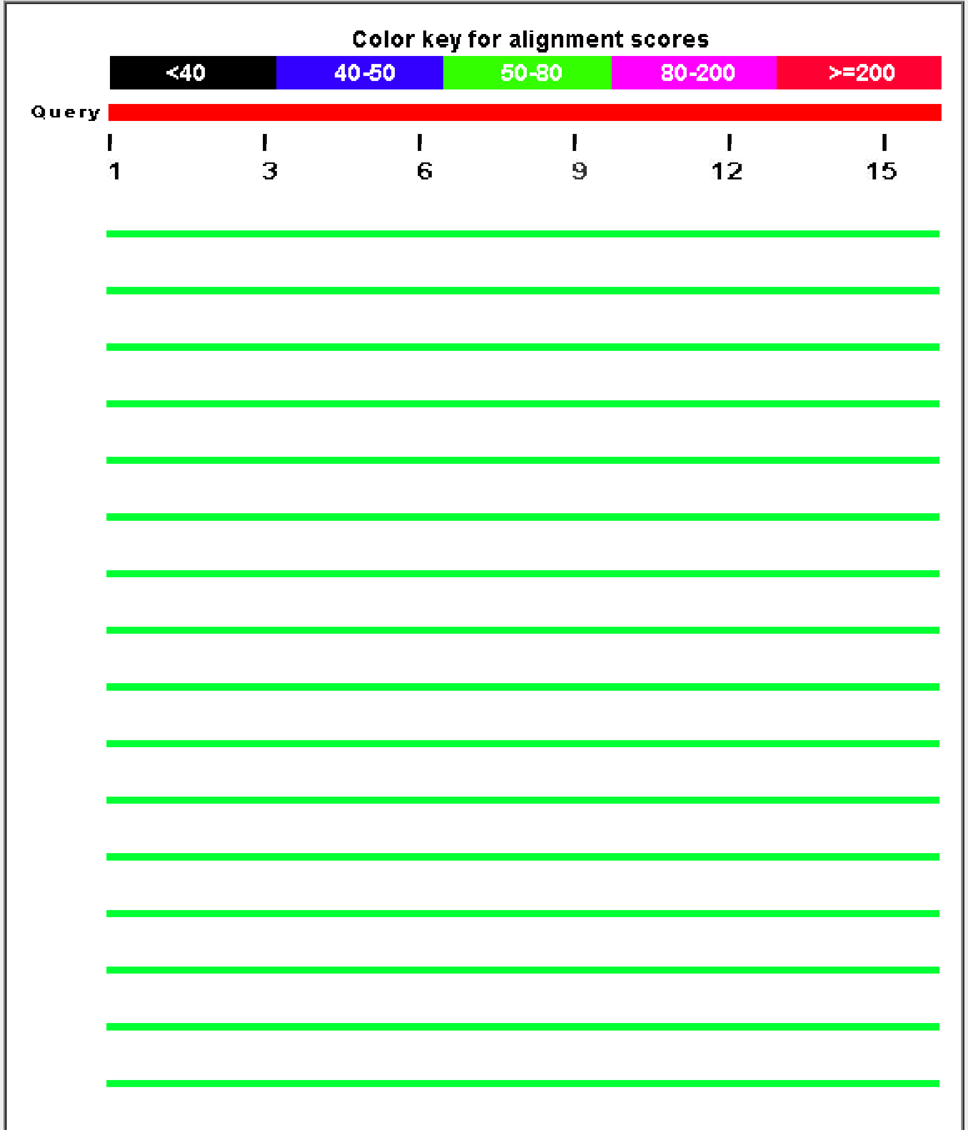
Graphic Summary

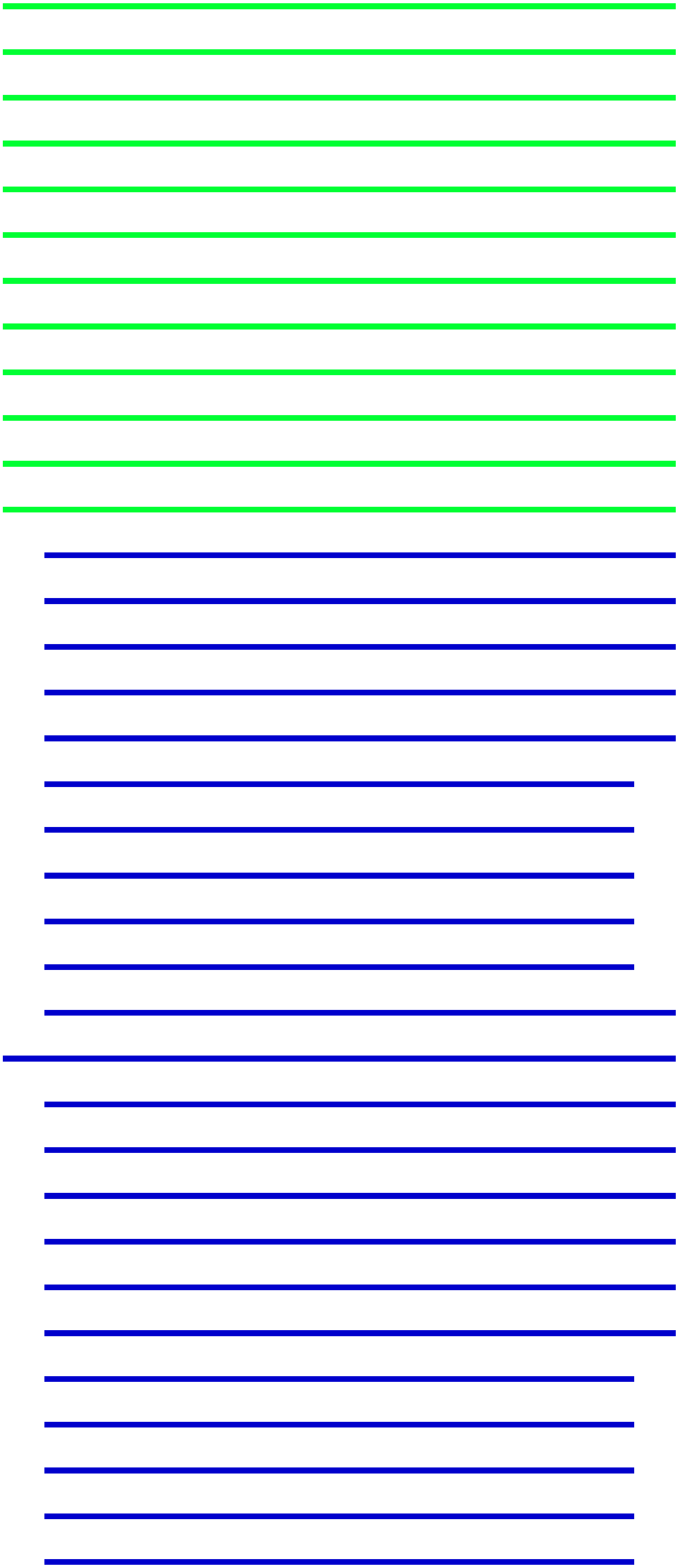
Show Conserved Domains

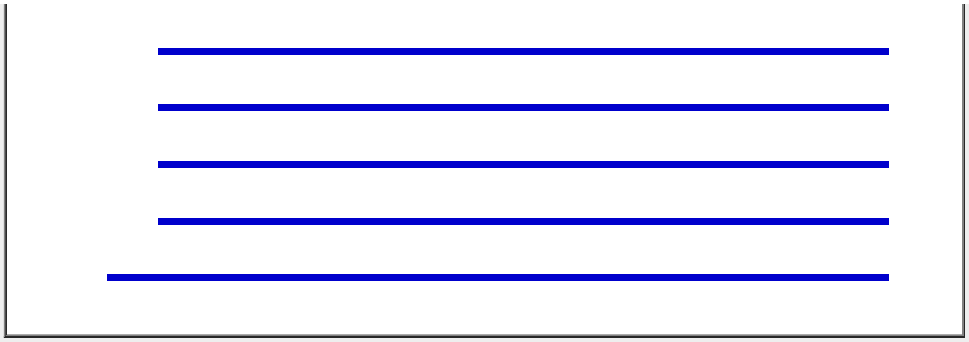
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein	55.8	55.8	100%	1e-07	100%	gi|686772908|XP_009234739.1
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_	55.8	55.8	100%	1e-07	100%	gi|119609950|EAW89544.1
☐	unnamed protein product [Homo sapiens]	55.8	55.8	100%	1e-07	100%	gi|194380458|BAG58382.1
☐	unnamed protein product [Homo sapiens]	55.8	55.8	100%	1e-07	100%	gi|194376422|BAG62970.1
☐	unnamed protein product [Homo sapiens]	55.8	55.8	100%	1e-07	100%	gi|193786317|BAG51600.1
☐	unnamed protein product [Homo sapiens]	55.8	55.8	100%	1e-07	100%	gi|194375560|BAG56725.1
☐	unnamed protein product [Homo sapiens]	55.8	55.8	100%	1e-07	100%	gi|194375081|BAG62653.1
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_	55.8	55.8	100%	1e-07	100%	gi|119609949|EAW89543.1
☐	RecName: Full=Galectin-3-binding protein; AltName: Full=Lectin ga	55.8	55.8	100%	1e-07	100%	gi|75042301|Q5RDA4.1
☐	PREDICTED: galectin-3-binding protein [Pan troglodytes]	55.8	55.8	100%	1e-07	100%	gi|55646067|XP_511716.1
☐	galectin-3-binding protein precursor [Homo sapiens]	55.8	55.8	100%	1e-07	100%	gi|5031863|NP_005558.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Gorilla gorilla go	55.8	55.8	100%	1e-07	100%	gi|426346505|XP_004040917.1
☐	PREDICTED: galectin-3-binding protein [Pan paniscus]	55.8	55.8	100%	1e-07	100%	gi|397494909|XP_003818311.1
☐	lectin, galactoside-binding, soluble, 3 binding protein [synthetic cons	55.8	55.8	100%	1e-07	100%	gi|123997497|ABM86350.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein	55.8	55.8	100%	1e-07	100%	gi|395749542|XP_003778963.1
☐	PREDICTED: galectin-3-binding protein isoform 3 [Macaca mulatta]	52.4	52.4	100%	2e-06	94%	gi|297273768|XP_002800676.1
☐	PREDICTED: galectin-3-binding protein isoform 2 [Macaca mulatta]	52.4	52.4	100%	2e-06	94%	gi|297273766|XP_002800675.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Macaca fascicu	52.4	52.4	100%	2e-06	94%	gi|544502104|XP_005585203.1
☐	PREDICTED: galectin-3-binding protein [Papio anubis]	52.4	52.4	100%	2e-06	94%	gi|402901262|XP_003913572.1
☐	PREDICTED: galectin-3-binding protein isoform 2 [Nomascus leucc	52.4	52.4	100%	2e-06	94%	gi|332258797|XP_003278481.1
☐	PREDICTED: galectin-3-binding protein [Saimiri boliviensis bolivien	52.4	52.4	100%	2e-06	94%	gi|725577242|XP_010340649.1
☐	hypothetical protein EGK_09048 [Macaca mulatta]	52.4	52.4	100%	2e-06	94%	gi|355568978|EHH25259.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Macaca mulatta]	52.4	52.4	100%	2e-06	94%	gi|109118737|XP_001109047.1
☐	PREDICTED: galectin-3-binding protein [Callithrix jacchus]	52.4	52.4	100%	2e-06	94%	gi|675661532|XP_002748850.2
☐	hypothetical protein EGM_08232 [Macaca fascicularis]	52.4	52.4	100%	2e-06	94%	gi|355754428|EHH58393.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Macaca fascicu	52.4	52.4	100%	2e-06	94%	gi|544502102|XP_005585202.1
☐	PREDICTED: galectin-3-binding protein isoform 1 [Nomascus leucc	52.4	52.4	100%	2e-06	94%	gi|441643566|XP_003278480.2
☐	PREDICTED: galectin-3-binding protein [Jaculus jaculus]	50.3	50.3	100%	8e-06	94%	gi|507543547|XP_004655763.1
☐							

	PREDICTED: galectin-3-binding protein isoform X3 [Galeopterus va	49.4	49.4	93%	2e-05	93%	gi|667281302|XP_008574380.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Galeopterus va	49.4	49.4	93%	2e-05	93%	gi|667281299|XP_008574379.1
☐	PREDICTED: galectin-3-binding protein [Nannospalax galili]	49.4	49.4	93%	2e-05	93%	gi|674080617|XP_008847879.1
☐	PREDICTED: galectin-3-binding protein [Tarsius syrichta]	49.4	49.4	93%	2e-05	93%	gi|640781767|XP_008046502.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Galeopterus va	49.4	49.4	93%	2e-05	93%	gi|667281296|XP_008574378.1
☐	cyclophilin C-associated protein [Mus musculus domesticus]	49.0	49.0	87%	2e-05	100%	gi|397800|AAA37499.1
☐	unnamed protein product [Mus musculus]	49.0	49.0	87%	2e-05	100%	gi|74212546|BAE31013.1
☐	unnamed protein product [Mus musculus]	49.0	49.0	87%	2e-05	100%	gi|74211789|BAE29246.1
☐	unnamed protein product [Mus musculus]	49.0	49.0	87%	2e-05	100%	gi|74142260|BAE31894.1
☐	galectin-3-binding protein precursor [Mus musculus]	49.0	49.0	87%	2e-05	100%	gi|6755144|NP_035280.1
☐	PREDICTED: galectin-3-binding protein [Chlorocebus sabaeus]	49.0	49.0	93%	2e-05	93%	gi|635093239|XP_008011313.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein	47.7	47.7	100%	6e-05	88%	gi|724915028|XP_010380238.1
☐	PREDICTED: galectin-3-binding protein [Heterocephalus glaber]	44.8	44.8	93%	6e-04	87%	gi|512998688|XP_004860896.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Heterocephalus	44.8	44.8	93%	6e-04	87%	gi|512828899|XP_004881532.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Heterocephalus	44.8	44.8	93%	6e-04	87%	gi|512828896|XP_004881531.1
☐	PREDICTED: galectin-3-binding protein [Fukomys damarensis]	44.8	44.8	93%	6e-04	87%	gi|731203892|XP_010616820.1
☐	Galectin-3-binding protein [Heterocephalus glaber]	44.8	44.8	93%	6e-04	87%	gi|351698098|EHB01017.1
☐	Galectin-3-binding protein [Fukomys damarensis]	44.8	44.8	93%	6e-04	87%	gi|676282129|KFO35672.1
☐	galectin-3-binding protein [Cricetulus griseus]	43.5	43.5	87%	0.002	86%	gi|537143564|ERE69017.1
☐	PREDICTED: galectin-3-binding protein [Cricetulus griseus]	43.5	43.5	87%	0.002	86%	gi|625257783|XP_007620278.1
☐	PREDICTED: galectin-3-binding protein [Cricetulus griseus]	43.5	43.5	87%	0.002	86%	gi|354473282|XP_003498865.1
☐	PREDICTED: galectin-3-binding protein [Ictidomys tridecemlineatus	42.2	42.2	87%	0.004	86%	gi|532094003|XP_005332681.1
☐	PREDICTED: galectin-3-binding protein [Tursiops truncatus]	41.8	41.8	87%	0.006	86%	gi|470634961|XP_004323016.1
☐	PREDICTED: galectin-3-binding protein [Orcinus orca]	41.8	41.8	87%	0.006	86%	gi|466037200|XP_004275584.1
☐	PREDICTED: galectin-3-binding protein [Balaenoptera acutorostrata	41.8	41.8	87%	0.006	86%	gi|594676074|XP_007185856.1
☐	galectin-3-binding protein precursor [Mesocricetus auratus]	41.8	41.8	87%	0.006	86%	gi|528078247|NP_001268610.1
☐	PREDICTED: galectin-3-binding protein [Lipotes vexillifer]	41.8	41.8	87%	0.006	86%	gi|602701011|XP_007462419.1
☐	PREDICTED: galectin-3-binding protein [Microtus ochrogaster]	41.4	41.4	93%	0.008	80%	gi|532014189|XP_005350871.1
☐	PREDICTED: galectin-3-binding protein [Odobenus rosmarus diverg	39.7	39.7	87%	0.028	79%	gi|472394090|XP_004416304.1
☐	PREDICTED: galectin-3-binding protein [Peromyscus maniculatus b	39.7	39.7	87%	0.028	79%	gi|589955428|XP_006990333.1
☐	PREDICTED: galectin-3-binding protein [Equus caballus]	39.2	39.2	93%	0.038	73%	gi|149723277|XP_001491000.1
☐	PREDICTED: galectin-3-binding protein [Ceratotherium simum simu	39.2	39.2	87%	0.038	79%	gi|478517307|XP_004432888.1
☐	Galectin-3-binding protein [Tupaia chinensis]	39.2	39.2	93%	0.038	73%	gi|444727768|ELW68246.1
☐	PREDICTED: galectin-3-binding protein [Tupaia chinensis]	39.2	39.2	93%	0.038	73%	gi|562832654|XP_006145764.1
☐	hypothetical protein PANDA_006893 [Ailuropoda melanoleuca]	38.4	38.4	87%	0.072	79%	gi|281342805|EFB18389.1
☐	PREDICTED: galectin-3-binding protein isoform X3 [Ursus maritimu	38.4	38.4	87%	0.072	79%	gi|671002383|XP_008692049.1
☐	PREDICTED: galectin-3-binding protein [Leptonychotes weddellii]	38.4	38.4	87%	0.072	79%	gi|585188403|XP_006745574.1
☐	PREDICTED: galectin-3-binding protein-like [Ailuropoda melanoleu	38.4	38.4	87%	0.072	79%	gi|301766034|XP_002918426.1
☐	galectin-3-binding protein precursor [Rattus norvegicus]	38.4	38.4	87%	0.072	79%	gi|20806135|NP_620796.1
☐	RecName: Full=Galectin-3-binding protein; AltName: Full=Cyp-C-as	38.4	38.4	87%	0.072	79%	gi|218526547|O70513.2
☐	90K protein precursor [Rattus norvegicus]	38.4	38.4	87%	0.072	79%	gi|45357062|AAS58489.1
☐	lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_	38.4	38.4	87%	0.072	79%	gi|149054938|EDM06755.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Ursus maritimu	38.4	38.4	87%	0.073	79%	gi|671002381|XP_008692048.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Ursus maritimu	38.4	38.4	87%	0.073	79%	gi|671002379|XP_008692047.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Physeter catod	38.0	38.0	87%	0.099	79%	gi|593720930|XP_007106758.1

☐	PREDICTED: galectin-3-binding protein-like [Camelus ferus]	38.0	38.0	87%	0.099	79%	gi|560912913|XP_006182736.1
☐	galectin-3-binding protein precursor [Camelus ferus]	38.0	38.0	87%	0.099	79%	gi|528761294|EPY80953.1
☐	galectin-3-binding protein precursor [Camelus ferus]	38.0	38.0	87%	0.099	79%	gi|528763131|EPY82790.1
☐	PREDICTED: galectin-3-binding protein [Otolemur garnettii]	38.0	38.0	87%	0.099	79%	gi|395826815|XP_003786610.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Physeter catod	38.0	38.0	87%	0.099	79%	gi|593720928|XP_007106757.1
☐	PREDICTED: galectin-3-binding protein [Cavia porcellus]	38.0	38.0	100%	0.099	69%	gi|514451490|XP_003464931.2
☐	PREDICTED: galectin-3-binding protein [Oryctolagus cuniculus]	37.5	37.5	93%	0.14	73%	gi|291416302|XP_002724384.1
☐	PREDICTED: galectin-3-binding protein [Chinchilla lanigera]	37.5	37.5	93%	0.14	73%	gi|533188976|XP_005407410.1
☐	Galectin-3-binding protein [Pteropus alecto]	36.3	36.3	93%	0.34	73%	gi|431908706|ELK12298.1
☐	PREDICTED: galectin-3-binding protein [Pteropus alecto]	36.3	36.3	93%	0.35	73%	gi|586558304|XP_006912443.1
☐	PREDICTED: galectin-3-binding protein [Trichechus manatus latiros	35.8	35.8	87%	0.47	71%	gi|471367801|XP_004374429.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	35.4	35.4	87%	0.65	71%	gi|511848965|XP_004748843.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	35.4	35.4	87%	0.65	71%	gi|511848961|XP_004748841.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	35.4	35.4	87%	0.66	71%	gi|511848959|XP_004748840.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	35.4	35.4	87%	0.66	71%	gi|511848957|XP_004748839.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1-like isoform	35.4	35.4	87%	0.66	71%	gi|511848955|XP_004748838.1
☐	PREDICTED: galectin-3-binding protein [Ovis aries]	34.1	34.1	75%	1.7	83%	gi|426239209|XP_004013518.1
☐	PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein	34.1	34.1	75%	1.7	83%	gi|556725783|XP_005958671.1
☐	PREDICTED: galectin-3-binding protein isoform X2 [Capra hircus]	34.1	34.1	75%	1.7	83%	gi|548509918|XP_005694143.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Capra hircus]	34.1	34.1	75%	1.7	83%	gi|548509916|XP_005694142.1
☐	PREDICTED: soluble calcium-activated nucleotidase 1 isoform X5 [	34.1	34.1	75%	1.7	83%	gi|73964953|XP_540464.2
☐	PREDICTED: soluble calcium-activated nucleotidase 1 isoform X1 [	34.1	34.1	75%	1.7	83%	gi|545509197|XP_005624092.1
☐	PREDICTED: galectin-3-binding protein [Echinops telfairi]	33.7	33.7	93%	2.3	73%	gi|507673535|XP_004709313.1
☐	PREDICTED: galectin-3-binding protein [Octodon degus]	33.7	33.7	93%	2.3	69%	gi|507681576|XP_004639582.1
☐	PREDICTED: galectin-3-binding protein [Panthera tigris altaica]	32.9	32.9	87%	4.2	64%	gi|591331484|XP_007091540.1
☐	PREDICTED: galectin-3-binding protein [Vicugna pacos]	32.9	32.9	87%	4.2	71%	gi|560953982|XP_006199496.1
☐	PREDICTED: galectin-3-binding protein isoform X1 [Bubalus bubali:	32.9	32.9	75%	4.2	83%	gi|594081110|XP_006064180.1

Alignments

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PREDICTED: LOW QUALITY PROTEIN: galectin-3-binding protein-like, partial [Pongo abelii]

Sequence ID: gi|686772908|ref|XP_009234739.1| **Length:** 341 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 149 to 164 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.8 bits(124)	1e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RYKGLNLTEDTYKPRI  16
            RYKGLNLTEDTYKPRI
Sbjct  149  RYKGLNLTEDTYKPRI  164
```

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lectin, galactoside-binding, soluble, 3 binding protein, isoform CRA_b [Homo sapiens]

Sequence ID: gi|119609950|gb|EAW89544.1| **Length:** 391 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 199 to 214 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.8 bits(124)	1e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RYKGLNLTEDTYKPRI  16
```

```
                RYKGLNLTEDTYKPRI
Sbjct  199  RYKGLNLTEDTYKPRI  214
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194380458|dbj|BAG58382.1| **Length:** 413 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 221 to 236 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.8 bits(124)	1e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RYKGLNLTEDTYKPRI  16
            RYKGLNLTEDTYKPRI
Sbjct  221  RYKGLNLTEDTYKPRI  236
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194376422|dbj|BAG62970.1| **Length:** 466 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 274 to 289 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.8 bits(124)	1e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RYKGLNLTEDTYKPRI  16
            RYKGLNLTEDTYKPRI
Sbjct  274  RYKGLNLTEDTYKPRI  289
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|193786317|dbj|BAG51600.1| **Length:** 481 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 289 to 304 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.8 bits(124)	1e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RYKGLNLTEDTYKPRI  16
            RYKGLNLTEDTYKPRI
Sbjct  289  RYKGLNLTEDTYKPRI  304
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

LRP1_KLTSCATDASICGDEARC_Mod

RID BVH6YN4001R (Expires on 01-21 10:00 am)

Query ID lcl|36986
Description None
Molecule type amino acid
Query Length 18

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

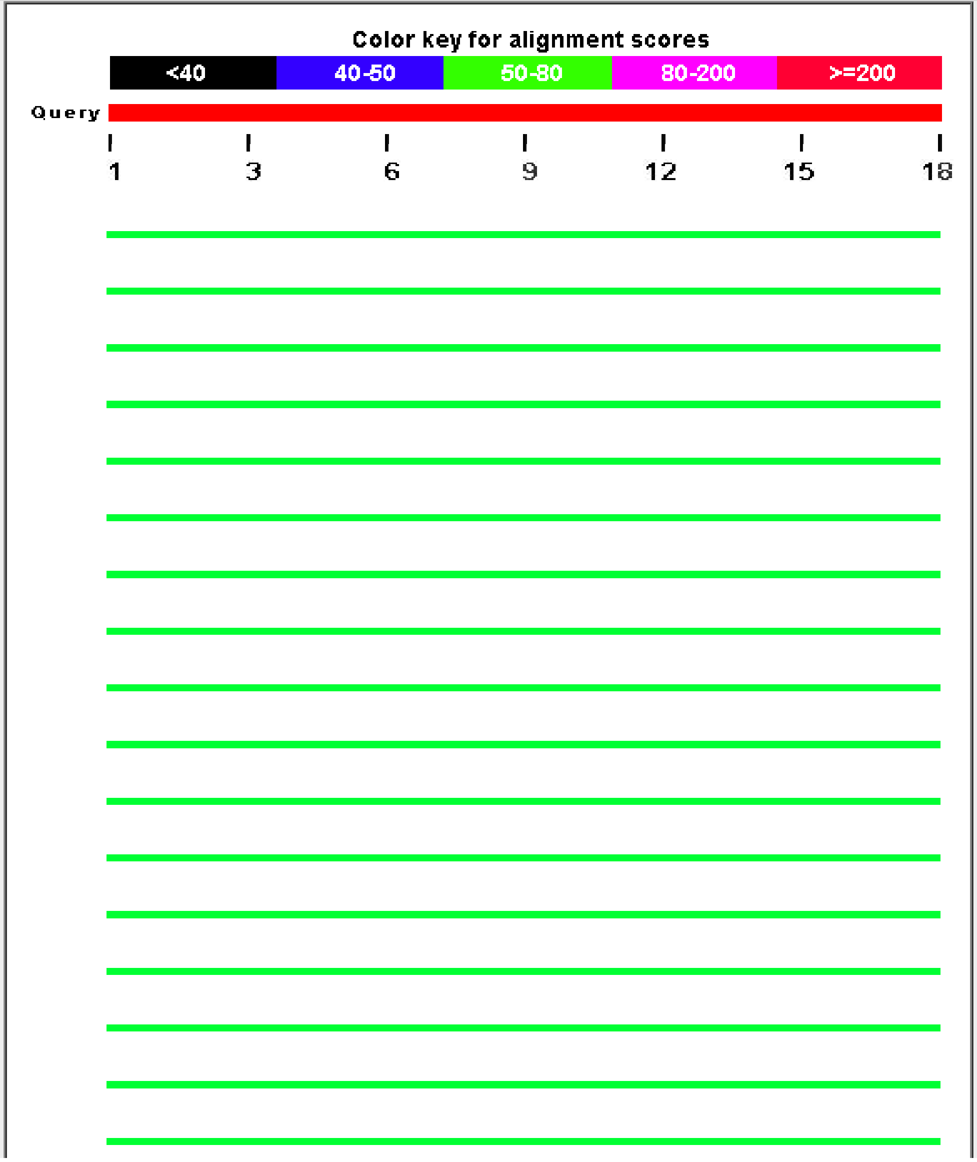
Graphic Summary

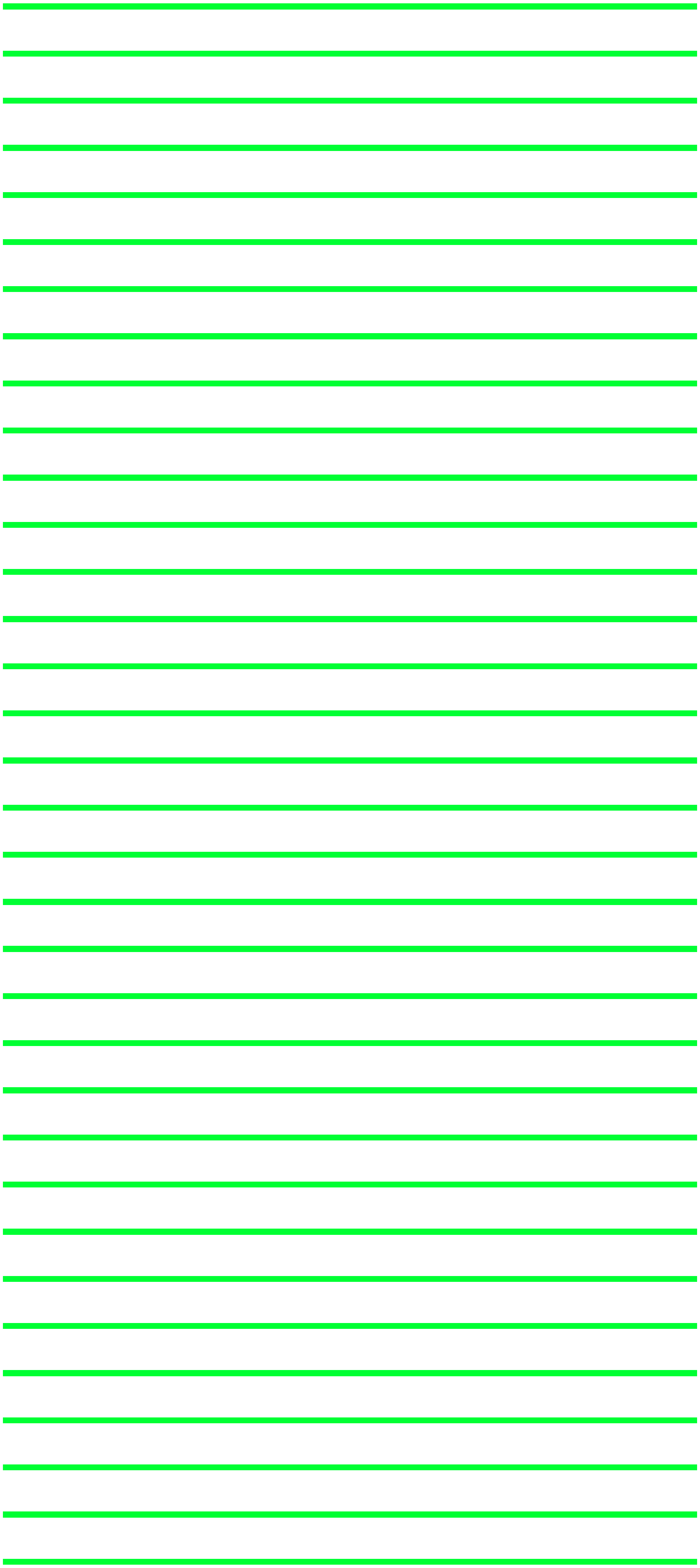
Show Conserved Domains

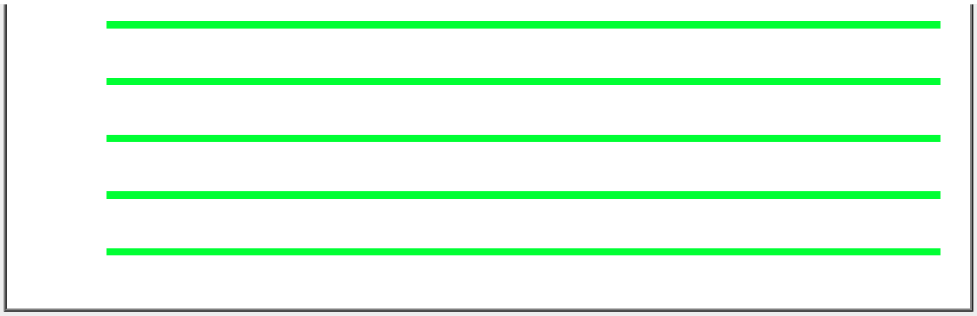
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Galeopteru	60.0	60.0	100%	6e-09	100%	XP_008577888.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1-like [Gorilla	57.5	57.5	100%	3e-08	94%	XP_004053466.1
☐	alpha-2 macroglobulin receptor [Homo sapiens]	57.5	57.5	100%	4e-08	94%	CAA38905.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Macaca m	57.5	57.5	100%	4e-08	94%	XP_001099776.2
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1-like [Sus sc	57.5	57.5	100%	4e-08	94%	XP_005663981.1
☐	Prolow-density lipoprotein receptor-related protein 1 [Cricetulus griseus]	57.5	57.5	100%	4e-08	94%	EGW02265.1
☐	low density lipoprotein-related protein 1 variant [Homo sapiens]	57.5	57.5	100%	4e-08	94%	BAD92735.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_005663982.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1-like [Leptor	57.5	57.5	100%	5e-08	94%	XP_006740139.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 isoform X6	57.5	57.5	100%	5e-08	94%	XP_004861314.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_005079884.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_005680480.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_010837673.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_004089687.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_009246220.1
☐	prolow-density lipoprotein receptor-related protein 1 [Cricetulus griseus]	57.5	57.5	100%	5e-08	94%	ERE90595.1
☐	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor), isof	57.5	57.5	100%	5e-08	94%	EAW96991.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Papio anu	57.5	57.5	100%	5e-08	94%	XP_009179348.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_006171989.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_004007507.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 isoform X2	57.5	57.5	100%	5e-08	94%	XP_005571350.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Nannospa	57.5	57.5	100%	5e-08	94%	XP_008842311.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Eptesicus	57.5	57.5	100%	5e-08	94%	XP_008146901.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Chloroceb	57.5	57.5	100%	5e-08	94%	XP_008001930.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_006077921.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Peromyscu	57.5	57.5	100%	5e-08	94%	XP_006973336.1
☐	LDL-receptor related precursor (AA -19 to 4525) [Homo sapiens]	57.5	57.5	100%	5e-08	94%	CAA32112.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_005970658.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 isoform X1	57.5	57.5	100%	5e-08	94%	XP_005571349.1

☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Ictidomys t	57.5	57.5	100%	5e-08	94%	XP_005335719.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Microtus o	57.5	57.5	100%	5e-08	94%	XP_005358067.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 isoform X2	57.5	57.5	100%	5e-08	94%	XP_004773232.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Ochotona	57.5	57.5	100%	5e-08	94%	XP_004582988.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Ceratother	57.5	57.5	100%	5e-08	94%	XP_004429344.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Odobenus	57.5	57.5	100%	5e-08	94%	XP_004401759.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Pteropus a	57.5	57.5	100%	5e-08	94%	XP_006908994.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Gorilla gor	57.5	57.5	100%	5e-08	94%	XP_004053457.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Felis catus	57.5	57.5	100%	5e-08	94%	XP_003988980.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Pan panis	57.5	57.5	100%	5e-08	94%	XP_003824931.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Otolemur	57.5	57.5	100%	5e-08	94%	XP_003790595.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Canis lupu	57.5	57.5	100%	5e-08	94%	XP_538245.4
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_003586126.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_003582266.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 isoform X1	57.5	57.5	100%	5e-08	94%	XP_003507539.1
☐	Prolow-density lipoprotein receptor-related protein 1 [Heterocephalus glaber]	57.5	57.5	100%	5e-08	94%	EHB07654.1
☐	prolow-density lipoprotein receptor-related protein 1 precursor [Homo sapiens	57.5	57.5	100%	5e-08	94%	NP_002323.2
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Heterocep	57.5	57.5	100%	5e-08	94%	XP_004892003.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 isoform X3	57.5	57.5	100%	5e-08	94%	XP_007631248.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_005901764.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_005006453.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 isoform X5	57.5	57.5	100%	5e-08	94%	XP_004861313.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_002916050.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Rhinopithe	57.5	57.5	100%	5e-08	94%	XP_010387314.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 isoform X1	57.5	57.5	100%	5e-08	94%	XP_004773231.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Panthera t	57.5	57.5	100%	5e-08	94%	XP_007081658.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Orycteropu	57.5	57.5	100%	5e-08	94%	XP_007948203.1
☐	Prolow-density lipoprotein receptor-related protein 1 [Tupaia chinensis]	57.5	57.5	100%	5e-08	94%	ELV09244.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 isoform X4	57.5	57.5	100%	5e-08	94%	XP_004861312.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 isoform X3	57.5	57.5	100%	5e-08	94%	XP_004861311.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 isoform X2	57.5	57.5	100%	5e-08	94%	XP_004861310.1
☐	Prolow-density lipoprotein receptor-related protein 1 [Macaca mulatta]	57.5	57.5	100%	5e-08	94%	EHH20885.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 isoform X1	57.5	57.5	100%	5e-08	94%	XP_004861309.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	57.5	57.5	100%	5e-08	94%	XP_009423492.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Saimiri bol	54.5	54.5	100%	5e-07	89%	XP_003926506.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Fukomys	54.5	54.5	100%	5e-07	89%	XP_010642934.1
☐	prolow-density lipoprotein receptor-related protein 1 precursor [Camelus ferus	54.1	54.1	100%	6e-07	89%	EPY83079.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	54.1	54.1	100%	6e-07	89%	XP_004319899.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Equus prz	54.1	54.1	100%	6e-07	89%	XP_008538795.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	54.1	54.1	100%	6e-07	89%	XP_001916726.3
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Dasypus n	54.1	54.1	100%	6e-07	89%	XP_004466256.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	54.1	54.1	100%	6e-07	89%	XP_006182311.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Physeter c	54.1	54.1	100%	6e-07	89%	XP_007103970.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	54.1	54.1	100%	6e-07	89%	XP_010944587.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Tarsius sy	54.1	54.1	100%	6e-07	89%	XP_008063421.1

☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Lipotes ve	54.1	54.1	100%	6e-07	89%	XP_007467748.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Balaenopt	54.1	54.1	100%	6e-07	89%	XP_007179703.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Orcinus or	54.1	54.1	100%	6e-07	89%	XP_004276566.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Vicugna pa	54.1	54.1	100%	6e-07	89%	XP_006217992.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	54.1	54.1	100%	6e-07	89%	XP_010989287.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Trichechus	54.1	54.1	100%	6e-07	89%	XP_004379953.1
☐	Prolow-density lipoprotein receptor-related protein 1 [Myotis brandtii]	53.7	53.7	100%	9e-07	89%	EPQ15635.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Condylura	53.7	53.7	100%	9e-07	89%	XP_004692481.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	53.7	53.7	100%	9e-07	89%	XP_005879129.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Jaculus ja	53.7	53.7	100%	9e-07	89%	XP_004650057.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	53.7	53.7	100%	9e-07	89%	XP_002720990.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Octodon d	53.7	53.7	100%	9e-07	89%	XP_004647047.1
☐	prolow-density lipoprotein receptor-related protein 1 precursor [Rattus norvegi	53.7	53.7	100%	9e-07	89%	NP_001123962.1
☐	RecName: Full=Prolow-density lipoprotein receptor-related protein 1; Short=LI	53.7	53.7	100%	9e-07	89%	Q91ZX7.1
☐	AM2 receptor [Mus musculus]	53.7	53.7	100%	9e-07	89%	CAA47817.1
☐	prolow-density lipoprotein receptor-related protein 1 precursor [Mus musculus]	53.7	53.7	100%	9e-07	89%	NP_032538.2
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Chinchilla	53.7	53.7	100%	9e-07	89%	XP_005397405.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 isoform X1	53.7	53.7	100%	9e-07	89%	XP_008763615.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Sorex arar	52.8	52.8	100%	2e-06	89%	XP_004602001.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Chrysochlo	51.5	51.5	100%	5e-06	83%	XP_006859524.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Callithrix ja	51.1	51.1	100%	6e-06	83%	XP_009002393.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	51.1	51.1	100%	6e-06	83%	XP_010599559.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-r	51.1	51.1	100%	6e-06	83%	XP_009002304.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Echinops t	50.7	50.7	100%	9e-06	83%	XP_004700589.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Elephantul	50.3	50.3	100%	1e-05	83%	XP_006897663.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Erinaceus	44.8	44.8	100%	8e-04	72%	XP_007535029.1

⊟ Alignments

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PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Galeopterus variegatus]

Sequence ID: ref|XP_008577888.1| **Length:** 4544 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 3781 to 3798 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	6e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1     KLTSCATDASICGDEARC  18
             KLTSCATDASICGDEARC
Sbjct  3781  KLTSCATDASICGDEARC  3798
```

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PREDICTED: prolow-density lipoprotein receptor-related protein 1-like [Gorilla gorilla gorilla]

Sequence ID: ref|XP_004053466.1| **Length:** 216 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 92 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.5 bits(128)	3e-08	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KLTSCATDASICGDEARC  18
            KLTSCAT+ASICGDEARC
Sbjct  92   KLTSCATNASICGDEARC  109
```

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alpha-2 macroglobulin receptor, partial [Homo sapiens]

Sequence ID: emb|CAA38905.1| **Length:** 591 **Number of Matches:** 1

Range 1: 507 to 524 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.5 bits(128)	4e-08	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KLTSCATDASICGDEARC  18
            KLTSCAT+ASICGDEARC
Sbjct  507  KLTSCATNASICGDEARC  524
```

Related Information

Gene - associated gene details

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PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Macaca mulatta]

Sequence ID: ref|XP_001099776.2| **Length:** 1682 **Number of Matches:** 1

Range 1: 919 to 936 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.5 bits(128)	4e-08	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KLTSCATDASICGDEARC  18
            KLTSCAT+ASICGDEARC
Sbjct  919  KLTSCATNASICGDEARC  936
```

Related Information

Gene - associated gene details
UniGene - clustered expressed sequence tags
Map Viewer - aligned genomic context

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PREDICTED: prolow-density lipoprotein receptor-related protein 1-like [Sus scrofa]

Sequence ID: ref|XP_005663981.1| **Length:** 1689 **Number of Matches:** 1

Range 1: 926 to 943 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.5 bits(128)	4e-08	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KLTSCATDASICGDEARC  18
            KLTSCAT+ASICGDEARC
Sbjct  926  KLTSCATNASICGDEARC  943
```

Related Information

Gene - associated gene details

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NCBI/ BLAST/ blastp suite/ Formatting Results - B9G227V901R

Your search parameters were adjusted to search for a short input sequence.

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LRP1_KLTSCATNASICGDEARC_NonMod

RID B9G227V901R (Expires on 01-14 13:50 pm)

Query ID	lcl|55787	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	18		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

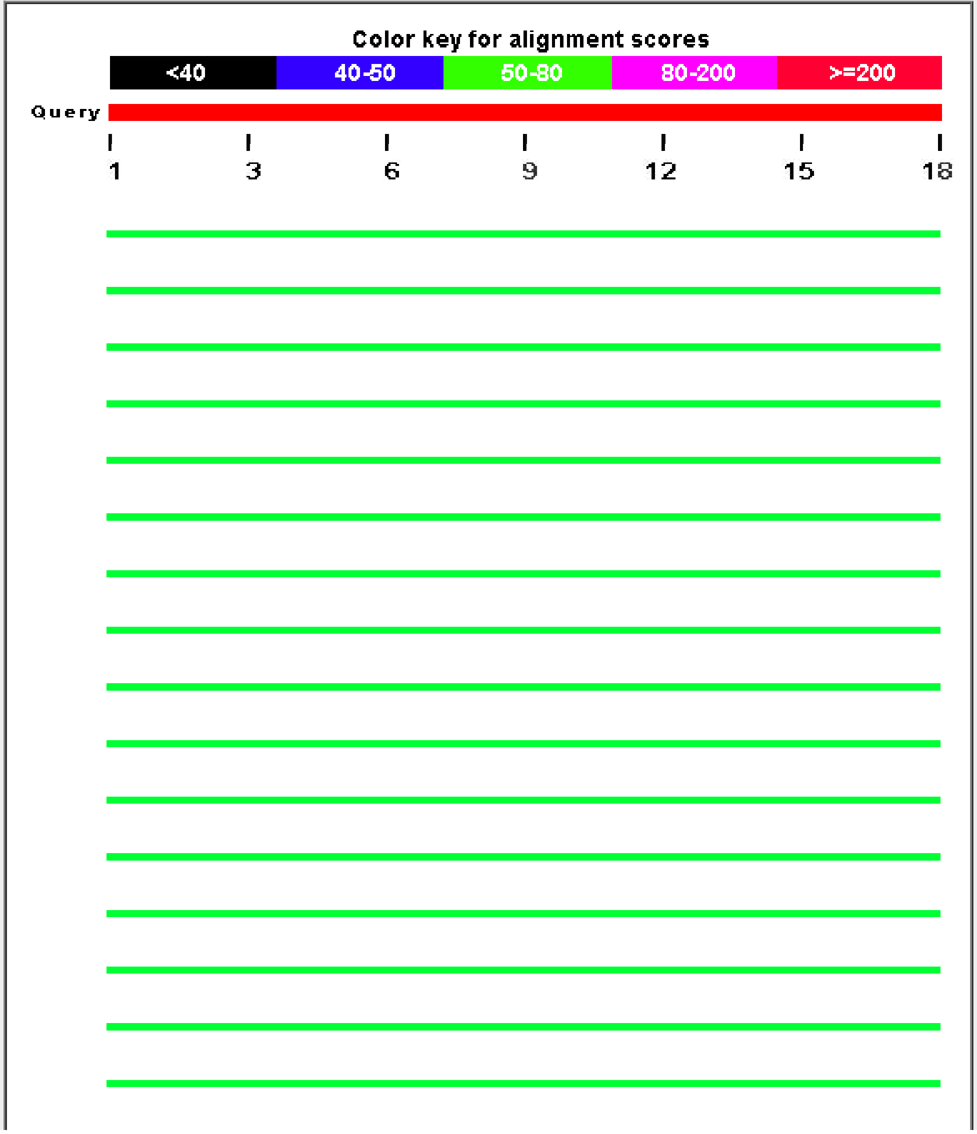
Graphic Summary

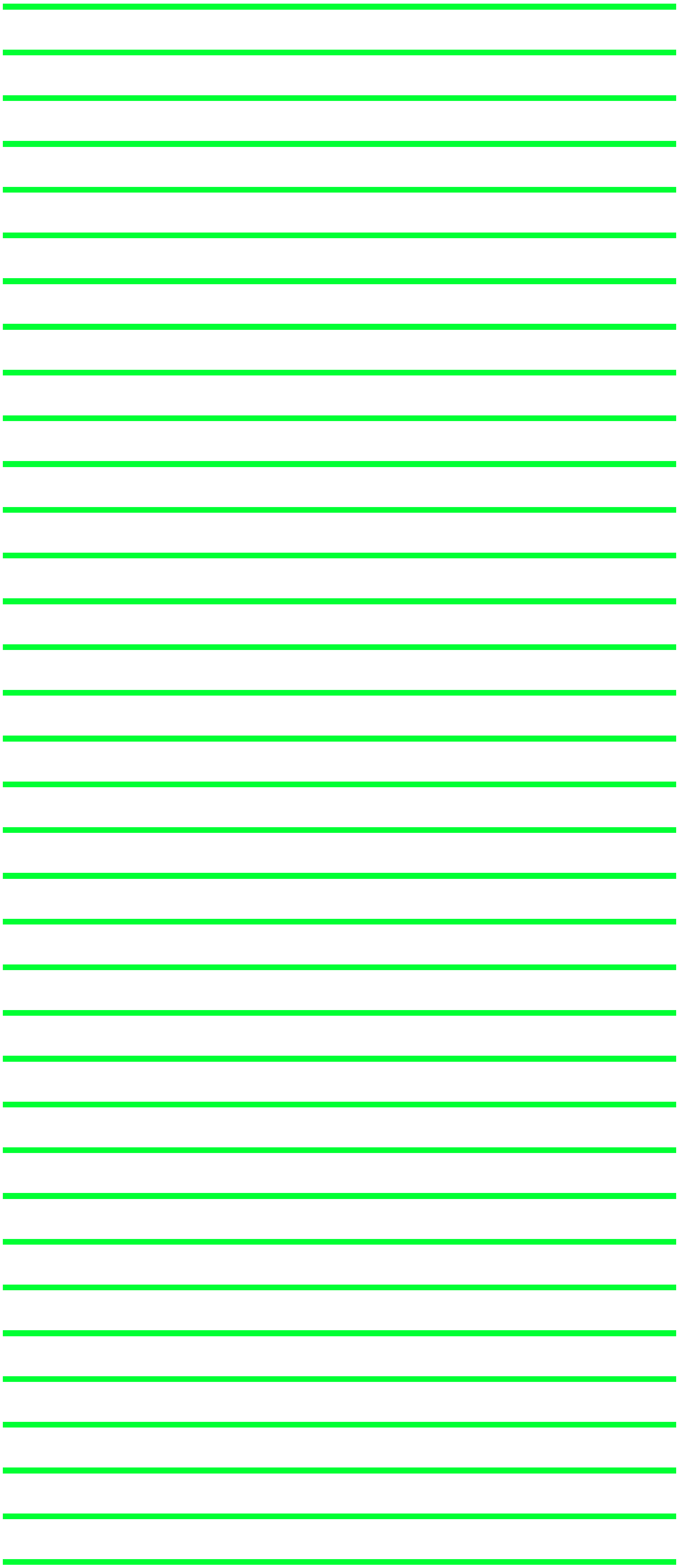
Show Conserved Domains

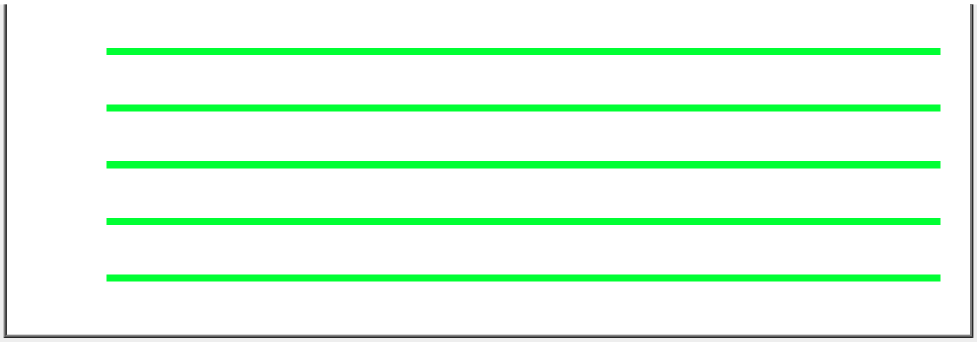
No putative conserved domains have been detected

Distribution of 185 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1-l	60.0	60.0	100%	4e-09	100%	gi|426373132|XP_004053466.1
☐	alpha-2 macroglobulin receptor [Homo sapiens]	60.0	60.0	100%	5e-09	100%	gi|24763|CAA38905.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	60.0	100%	6e-09	100%	gi|297262740|XP_001099776.2
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1-l	60.0	60.0	100%	6e-09	100%	gi|545826194|XP_005663981.1
☐	Prolow-density lipoprotein receptor-related protein 1 [Cricetulus gris	60.0	60.0	100%	6e-09	100%	gi|344246161|EGW02265.1
☐	low density lipoprotein-related protein 1 variant [Homo sapiens]	60.0	60.0	100%	6e-09	100%	gi|62088576|BAD92735.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|545826198|XP_005663982.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1-l	60.0	79.7	100%	6e-09	100%	gi|585176792|XP_006740139.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 i	60.0	79.7	100%	6e-09	100%	gi|512999545|XP_004861314.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|524959879|XP_005079884.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|548466622|XP_005680480.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|441632367|XP_004089687.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|686741357|XP_009246220.1
☐	prolow-density lipoprotein receptor-related protein 1 [Cricetulus gris	60.0	79.7	100%	6e-09	100%	gi|537264203|ERE90595.1
☐	low density lipoprotein-related protein 1 (alpha-2-macroglobulin rec	60.0	79.7	100%	6e-09	100%	gi|119617397|EAW96991.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|685573313|XP_009179348.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|562889304|XP_006171989.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|426226765|XP_004007507.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 i	60.0	79.7	100%	6e-09	100%	gi|544470778|XP_005571350.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|674070409|XP_008842311.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|641715077|XP_008146901.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|635066271|XP_008001930.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|594110160|XP_006077921.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|589920548|XP_006973336.1
☐	LDL-receptor related precursor (AA -19 to 4525) [Homo sapiens]	60.0	79.7	100%	6e-09	100%	gi|34339|CAA32112.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|556750484|XP_005970658.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 i	60.0	79.7	100%	6e-09	100%	gi|544470776|XP_005571349.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|532100180|XP_005335719.1
☐							

	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|532030242|XP_005358067.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 i	60.0	79.7	100%	6e-09	100%	gi|511907565|XP_004773232.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|504141085|XP_004582988.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|478510137|XP_004429344.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|472364394|XP_004401759.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|586547805|XP_006908994.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|426373114|XP_004053457.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|410964879|XP_003988980.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|397509011|XP_003824931.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|395835250|XP_003790595.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|359320553|XP_538245.4
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|359065534|XP_003586126.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|358412256|XP_003582266.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 i	60.0	79.7	100%	6e-09	100%	gi|354490790|XP_003507539.1
☐	Prolow-density lipoprotein receptor-related protein 1 [Heterocephalu	60.0	79.7	100%	6e-09	100%	gi|351704735|EHB07654.1
☐	prolow-density lipoprotein receptor-related protein 1 precursor [Hom	60.0	79.7	100%	6e-09	100%	gi|126012562|NP_002323.2
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|512869594|XP_004892003.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 i	60.0	79.7	100%	6e-09	100%	gi|625279203|XP_007631248.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|555979667|XP_005901764.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|514472752|XP_005006453.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 i	60.0	79.7	100%	6e-09	100%	gi|512999543|XP_004861313.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|301761302|XP_002916050.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|724946197|XP_010387314.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 i	60.0	79.7	100%	6e-09	100%	gi|511907563|XP_004773231.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|591310166|XP_007081658.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	60.0	79.7	100%	6e-09	100%	gi|634873719|XP_007948203.1
☐	Prolow-density lipoprotein receptor-related protein 1 [Tupaia chinen	60.0	79.7	100%	6e-09	100%	gi|444509407|ELV09244.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 i	60.0	79.7	100%	6e-09	100%	gi|512999541|XP_004861312.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 i	60.0	79.7	100%	6e-09	100%	gi|512999539|XP_004861311.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 i	60.0	79.7	100%	6e-09	100%	gi|512999537|XP_004861310.1
☐	Prolow-density lipoprotein receptor-related protein 1 [Macaca mulat	60.0	79.7	100%	6e-09	100%	gi|355564385|EHH20885.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 i	60.0	79.7	100%	6e-09	100%	gi|512999535|XP_004861309.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	60.0	79.7	100%	6e-09	100%	gi|694949713|XP_009423492.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	57.5	77.2	100%	4e-08	94%	gi|667291496|XP_008577888.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	57.1	76.8	100%	6e-08	94%	gi|403268915|XP_003926506.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	57.1	76.8	100%	6e-08	94%	gi|731261055|XP_010642934.1
☐	prolow-density lipoprotein receptor-related protein 1 precursor [Cam	56.6	76.4	100%	8e-08	94%	gi|528763420|EPY83079.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	56.6	56.6	100%	8e-08	94%	gi|470625014|XP_004319899.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	56.6	76.4	100%	8e-08	94%	gi|664762329|XP_008538795.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	56.6	76.4	100%	8e-08	94%	gi|545220722|XP_001916726.3
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	56.6	76.4	100%	8e-08	94%	gi|488549570|XP_004466256.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	56.6	76.4	100%	8e-08	94%	gi|560912045|XP_006182311.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	56.6	76.4	100%	8e-08	94%	gi|593714981|XP_007103970.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	56.6	76.4	100%	8e-08	94%	gi|640813454|XP_008063421.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	56.6	76.4	100%	8e-08	94%	gi|602715078|XP_007467748.1

☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	56.6	76.4	100%	8e-08	94%	gi|594663045|XP_007179703.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	56.6	76.4	100%	8e-08	94%	gi|466042191|XP_004276566.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	56.6	76.4	100%	8e-08	94%	gi|560991701|XP_006217992.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	56.6	76.4	100%	8e-08	94%	gi|471390420|XP_004379953.1
☐	Prolow-density lipoprotein receptor-related protein 1 [Myotis brandti	56.2	56.2	100%	1e-07	94%	gi|521033850|EPQ15635.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	56.2	56.2	100%	1e-07	94%	gi|507976614|XP_004692481.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	56.2	75.9	100%	1e-07	94%	gi|554569741|XP_005879129.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	56.2	75.9	100%	1e-07	94%	gi|507531962|XP_004650057.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	56.2	75.9	100%	1e-07	94%	gi|291409329|XP_002720990.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	56.2	75.9	100%	1e-07	94%	gi|507710973|XP_004647047.1
☐	prolow-density lipoprotein receptor-related protein 1 precursor [Ratt	56.2	75.9	100%	1e-07	94%	gi|283837871|NP_001123962.1
☐	RecName: Full=Prolow-density lipoprotein receptor-related protein 1	56.2	75.9	100%	1e-07	94%	gi|81867523|Q91ZX7.1
☐	AM2 receptor [Mus musculus]	56.2	75.9	100%	1e-07	94%	gi|49942|CAA47817.1
☐	prolow-density lipoprotein receptor-related protein 1 precursor [Mus	56.2	75.9	100%	1e-07	94%	gi|124494256|NP_032538.2
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	56.2	56.2	100%	1e-07	94%	gi|533167518|XP_005397405.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 i	56.2	75.9	100%	1e-07	94%	gi|672058769|XP_008763615.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	55.4	55.4	100%	2e-07	94%	gi|505774707|XP_004602001.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	54.1	73.8	100%	6e-07	89%	gi|586457594|XP_006859524.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	53.7	53.7	100%	8e-07	89%	gi|675680855|XP_009002393.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	53.7	73.4	100%	8e-07	89%	gi|731457843|XP_010599559.1
☐	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein	53.7	73.4	100%	8e-07	89%	gi|675680438|XP_009002304.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	53.2	53.2	100%	1e-06	89%	gi|507637104|XP_004700589.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	52.8	72.5	100%	2e-06	89%	gi|585702292|XP_006897663.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1 [	47.3	67.0	100%	1e-04	78%	gi|617654244|XP_007535029.1
☐	PREDICTED: prolow-density lipoprotein receptor-related protein 1-l	45.6	45.6	100%	4e-04	78%	gi|395540761|XP_003772319.1
☐	PREDICTED: LOW QUALITY PROTEIN: low density lipoprotein rec	45.6	65.3	100%	4e-04	78%	gi|612062387|XP_007508013.1
☐	integrin-like protein [Candidatus Koribacter versatilis]	33.7	33.7	83%	2.6	80%	gi|499843048|WP_011523782.1

Alignments

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PREDICTED: prolow-density lipoprotein receptor-related protein 1-like [Gorilla gorilla gorilla]

Sequence ID: gi|426373132|ref|XP_004053466.1| **Length:** 216 **Number of Matches:** 1

Range 1: 92 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	4e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    KLTSCATNASICGDEARC  18
            KLTSCATNASICGDEARC
Sbjct  92   KLTSCATNASICGDEARC  109
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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alpha-2 macroglobulin receptor, partial [Homo sapiens]

Sequence ID: gi|24763|emb|CAA38905.1| **Length:** 591 **Number of Matches:** 1

Range 1: 507 to 524 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	5e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    KLTSCATNASICGDEARC  18
```

Related Information

Gene - associated gene details

```
                KLTSCATNASICGDEARC
Sbjct  507  KLTSCATNASICGDEARC  524
```

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PREDICTED: prolow-density lipoprotein receptor-related protein 1 [Macaca mulatta]

Sequence ID: gi|297262740|ref|XP_001099776.2| **Length:** 1682 **Number of Matches:** 1

Range 1: 919 to 936 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	6e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    KLTSCATNASICGDEARC  18
            KLTSCATNASICGDEARC
Sbjct  919  KLTSCATNASICGDEARC  936
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

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PREDICTED: prolow-density lipoprotein receptor-related protein 1-like [Sus scrofa]

Sequence ID: gi|545826194|ref|XP_005663981.1| **Length:** 1689 **Number of Matches:** 1

Range 1: 926 to 943 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	6e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    KLTSCATNASICGDEARC  18
            KLTSCATNASICGDEARC
Sbjct  926  KLTSCATNASICGDEARC  943
```

Related Information

Gene - associated gene details

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Prolow-density lipoprotein receptor-related protein 1 [Cricetulus griseus]

Sequence ID: gi|344246161|gb|EGW02265.1| **Length:** 2217 **Number of Matches:** 1

Range 1: 1454 to 1471 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	6e-09	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1     KLTSCATNASICGDEARC  18
             KLTSCATNASICGDEARC
Sbjct  1454  KLTSCATNASICGDEARC  1471
```

Related Information

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVH83S2201R

Your search parameters were adjusted to search for a short input sequence.

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LYVE1_KANQQLDFTEAKE_Mod

RID	BVH83S2201R (Expires on 01-21 10:01 am)		
Query ID	lcl|52364	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	13	**Program**	BLASTP 2.2.30+ ▹Citation

Other reports: ▹Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

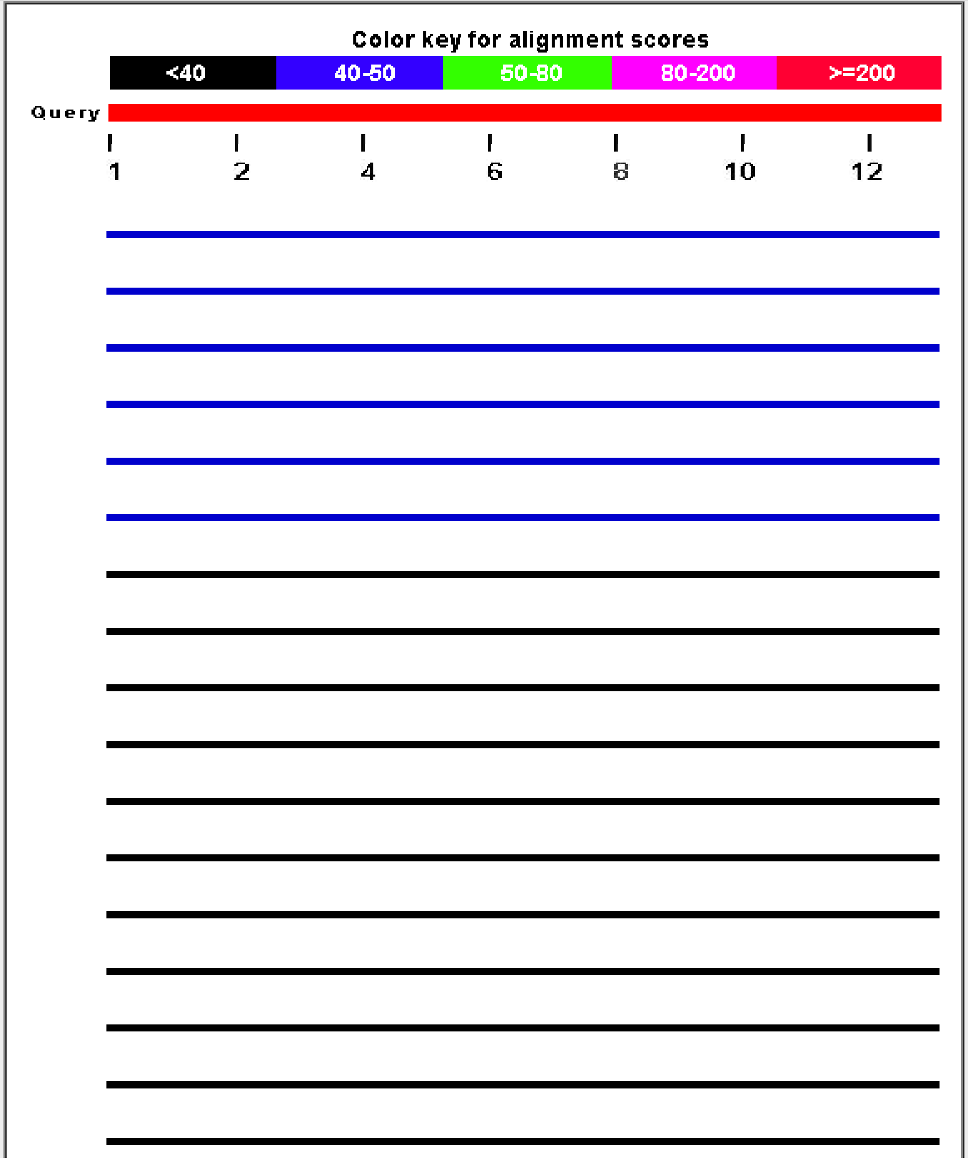
Graphic Summary

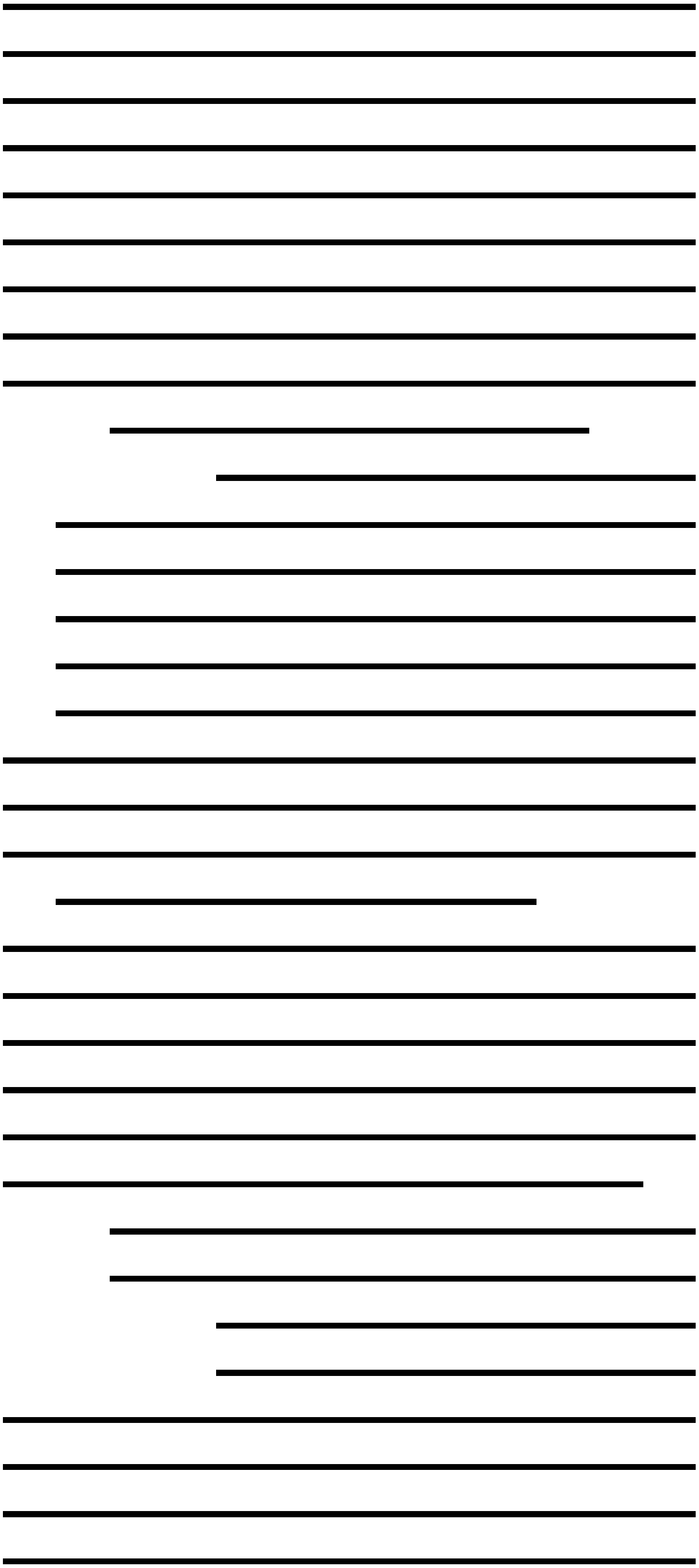
Show Conserved Domains

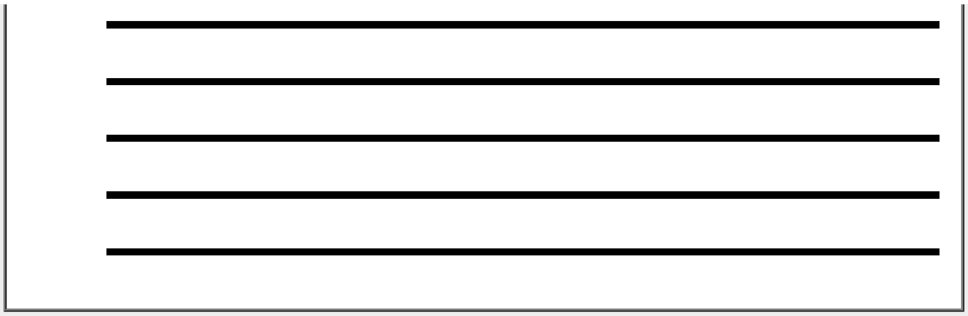
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	lymphatic vessel endothelial hyaluronic acid receptor 1 precursor [Homo sapie	41.8	41.8	100%	0.004	92%	NP_006682.2
☐	lymphatic endothelium-specific hyaluronan receptor LYVE-1 [Homo sapiens]	41.8	41.8	100%	0.004	92%	AAD42764.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Pan pa	41.8	41.8	100%	0.004	92%	XP_003818206.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Pan tro	41.8	41.8	100%	0.004	92%	XP_508283.2
☐	Lymphatic vessel endothelial hyaluronan receptor 1 [Homo sapiens]	41.8	41.8	100%	0.004	92%	AAH26231.1
☐	extracellular link domain containing 1 [synthetic construct]	41.8	41.8	100%	0.004	92%	AAX36112.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Rhinopi	37.1	37.1	100%	0.14	85%	XP_010383112.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Chloroc	37.1	37.1	100%	0.14	85%	XP_008004966.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Papio a	37.1	37.1	100%	0.14	85%	XP_003910275.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Macaca	37.1	37.1	100%	0.14	85%	XP_005578681.1
☐	Lymphatic vessel endothelial hyaluronic acid receptor 1 [Macaca mulatta]	37.1	37.1	100%	0.14	85%	EHH23103.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 isoform	37.1	37.1	100%	0.14	85%	XP_001100103.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Saimiri	37.1	37.1	100%	0.14	85%	XP_003919881.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Pongo a	36.3	36.3	100%	0.26	85%	XP_009244896.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Gorilla g	36.3	36.3	100%	0.27	85%	XP_004050750.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Nomasc	36.3	36.3	100%	0.27	85%	XP_003254985.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Galeop	35.8	35.8	100%	0.37	77%	XP_008584943.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Eptesic	35.8	35.8	100%	0.37	77%	XP_008149260.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Orycter	35.0	35.0	100%	0.71	77%	XP_007953340.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Mesocr	34.6	34.6	100%	0.97	77%	XP_005075737.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 isoform	34.1	34.1	100%	1.3	85%	XP_002755091.2
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 isoform	34.1	34.1	100%	1.3	85%	XP_009005908.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Tarsius	33.7	33.7	100%	1.8	77%	XP_008067473.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Myotis l	32.5	32.5	100%	4.7	77%	XP_006089678.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Myotis l	32.5	32.5	100%	4.7	77%	XP_005874034.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Myotis d	32.5	32.5	100%	4.7	77%	XP_006763529.1
☐	hypothetical protein [Devosia sp. 17-2-E-8]	32.5	32.5	69%	4.9	100%	WP_035095607.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Chryso	32.0	32.0	69%	6.4	100%	XP_006873070.1
☐	nucleoside-diphosphate-sugar epimerase [Xanthomonas vesicatoria]	31.2	31.2	92%	12	83%	WP_005998050.1

☐	NmrA family protein [Xanthomonas vesicatoria]	31.2	31.2	92%	12	83%	WP_039425432.1
☐	NmrA family protein [Xanthomonas arboricola]	31.2	31.2	92%	12	83%	WP_039517947.1
☐	NmrA family protein [Xanthomonas arboricola]	31.2	31.2	92%	12	83%	WP_024940476.1
☐	hypothetical protein [Mucispirillum schaedleri]	31.2	31.2	92%	12	85%	WP_023275572.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Trichec	30.8	30.8	100%	16	69%	XP_004369701.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Panthe	30.3	30.3	100%	23	69%	XP_007083276.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Felis ca	30.3	30.3	100%	23	69%	XP_003993039.1
☐	aminoglycoside adenylyltransferase [Streptomyces sp. CNS654]	29.9	29.9	69%	28	89%	WP_032764358.1
☐	lymphatic vessel endothelial hyaluronic acid receptor 1 [Camelus ferus]	29.9	29.9	100%	30	69%	EPY74693.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Vicugna	29.9	29.9	100%	31	69%	XP_006203587.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Camelu	29.9	29.9	100%	31	69%	XP_006192969.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Camelu	29.9	29.9	100%	31	69%	XP_010975450.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Camelu	29.9	29.9	100%	31	69%	XP_010963177.1
☐	hypothetical protein [Vibrio proteolyticus]	29.9	29.9	92%	32	63%	WP_021706437.1
☐	hypothetical protein TTHERM_00780670 [Tetrahymena thermophila SB210]	29.9	29.9	84%	33	82%	EAS05978.2
☐	hypothetical protein TTHERM_00780670 [Tetrahymena thermophila]	29.9	29.9	84%	33	82%	XP_001026223.1
☐	PREDICTED: LOW QUALITY PROTEIN: lymphatic vessel endothelial hyaluro	29.5	29.5	69%	42	89%	XP_003465744.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Ochoto	29.5	29.5	69%	42	89%	XP_004593845.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 isoform	29.5	29.5	100%	42	69%	XP_004453453.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_038812945.1
☐	MULTISPECIES: excinuclease ABC subunit C [Staphylococcus]	29.5	29.5	100%	43	69%	WP_002456231.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_017464291.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_001830175.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_002486269.1
☐	UvrABC system protein C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_002476607.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_002503092.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_002498400.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_002495462.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_002493762.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_002489759.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_002485780.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_002473256.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_002470770.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_002469571.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_002457416.1
☐	excinuclease ABC, C subunit [Staphylococcus epidermidis M23864:W2(grey)]	29.5	29.5	100%	43	69%	EFE59543.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis]	29.5	29.5	100%	43	69%	WP_011082657.1
☐	excinuclease ABC, C subunit [Staphylococcus epidermidis BCM-HMP0060]	29.5	29.5	100%	43	69%	EES58411.1
☐	excinuclease ABC, C subunit [Staphylococcus epidermidis W23144]	29.5	29.5	100%	43	69%	EES36408.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis Scl25]	29.5	29.5	100%	43	69%	EST99885.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis CIM28]	29.5	29.5	100%	43	69%	ESR05177.1
☐	excinuclease ABC subunit C [Staphylococcus epidermidis Scl31]	29.5	29.5	100%	43	69%	EST95350.1
☐	hypothetical protein [Geminicoccus roseus]	29.5	29.5	76%	43	71%	WP_035485321.1
☐	hypothetical protein OsJ_31277 [Oryza sativa Japonica Group]	29.1	29.1	61%	49	100%	EAZ15858.1
☐	Os10g0371100 [Oryza sativa Japonica Group]	29.1	29.1	61%	56	100%	NP_001176119.1

☐	Putative AP2 domain transcriptional regulator [Oryza sativa Japonica Group]	29.1	29.1	61%	57	100%	AAM08622.1
☐	hypothetical protein OsI_33276 [Oryza sativa Indica Group]	29.1	29.1	61%	57	100%	EAY78232.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Canis l	29.1	29.1	100%	57	69%	XP_003639831.1
☐	lymphatic vessel endothelial hyaluronic acid receptor 1 [Rattus norvegicus]	29.1	29.1	92%	57	67%	NP_001099756.1
☐	kinase domain protein [Tetrahymena thermophila SB210]	29.1	29.1	84%	59	82%	EWS72078.1
☐	ATPase P [Prevotella timonensis]	29.1	29.1	69%	59	89%	WP_028900777.1
☐	ATPase P [Prevotella timonensis]	29.1	29.1	69%	59	89%	WP_036926311.1
☐	copper-exporting ATPase [Prevotella timonensis]	29.1	29.1	69%	59	89%	WP_008123083.1
☐	PREDICTED: uncharacterized protein LOC100900376 [Metaseiulus occidenta	29.1	29.1	69%	59	89%	XP_003737880.1
☐	hypothetical protein [Flavobacterium daejeonense]	29.1	29.1	61%	59	100%	WP_026715491.1
☐	hypothetical protein [candidate division WWE1 bacterium JGI OTU-2]	28.6	28.6	76%	76	80%	WP_029949874.1
☐	Lymphatic vessel endothelial hyaluronic acid receptor 1 [Cricetulus griseus]	28.6	28.6	100%	77	69%	EGV97003.1
☐	NmrA family protein [Xanthomonas arboricola]	28.6	28.6	92%	78	75%	WP_039529329.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Equus	28.6	28.6	100%	78	69%	XP_008531961.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Cricetul	28.6	28.6	100%	78	69%	XP_007647074.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Octodo	28.6	28.6	100%	78	62%	XP_004634930.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Oryctol	28.6	28.6	100%	78	62%	XP_002708858.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Jaculus	28.6	28.6	84%	78	73%	XP_004650927.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Equus	28.6	28.6	100%	78	69%	XP_001504970.1
☐	chorismate mutase [Exiguobacterium undae]	28.6	28.6	69%	78	89%	WP_026832308.1
☐	chorismate mutase [Exiguobacterium sibiricum]	28.6	28.6	69%	78	89%	WP_026827712.1
☐	3-deoxy-7-phosphoheptulonate synthase [Exiguobacterium sibiricum]	28.6	28.6	69%	78	89%	WP_012371112.1
☐	3-deoxy-7-phosphoheptulonate synthase [Exiguobacterium antarcticum]	28.6	28.6	69%	78	89%	WP_014971028.1
☐	anthranilate synthase [Acaryochloris marina]	28.6	28.6	92%	79	60%	WP_012166745.1
☐	putative acid phosphatase [Metarhizium anisopliae]	28.6	28.6	69%	79	89%	KFG83838.1
☐	multidrug transporter [Bacillus sp. L1(2012)]	28.6	28.6	76%	79	80%	WP_017729016.1

⊟ Alignments

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lymphatic vessel endothelial hyaluronic acid receptor 1 precursor [Homo sapiens]

Sequence ID: ref|NP_006682.2| **Length:** 322 **Number of Matches:** 1

▷ See 6 more title(s)

Range 1: 47 to 59 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.8 bits(91)	0.004	12/13(92%)	13/13(100%)	0/13(0%)

```
Query  1   KANQQLDFTEAKE  13
           KANQQL+FTEAKE
Sbjct  47  KANQQLNFTEAKE  59
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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lymphatic endothelium-specific hyaluronan receptor LYVE-1 [Homo sapiens]

Sequence ID: gb|AAD42764.1|AF118108_1 **Length:** 322 **Number of Matches:** 1

Range 1: 47 to 59 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.8 bits(91)	0.004	12/13(92%)	13/13(100%)	0/13(0%)

Related Information

Gene - associated gene details

```
Query  1   KANQQLDFTEAKE  13
           KANQQL+FTEAKE
Sbjct  47  KANQQLNFTEAKE  59
```

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PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Pan paniscus]

Sequence ID: ref|XP_003818206.1| **Length:** 322 **Number of Matches:** 1

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

Range 1: 47 to 59 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.8 bits(91)	0.004	12/13(92%)	13/13(100%)	0/13(0%)

```
Query  1   KANQQLDFTEAKE  13
           KANQQL+FTEAKE
Sbjct  47  KANQQLNFTEAKE  59
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Pan troglodytes]

Sequence ID: ref|XP_508283.2| **Length:** 322 **Number of Matches:** 1

Related Information

Gene - associated gene details
UniGene - clustered expressed sequence tags
Map Viewer - aligned genomic context

Range 1: 47 to 59 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.8 bits(91)	0.004	12/13(92%)	13/13(100%)	0/13(0%)

```
Query  1   KANQQLDFTEAKE  13
           KANQQL+FTEAKE
Sbjct  47  KANQQLNFTEAKE  59
```

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Lymphatic vessel endothelial hyaluronan receptor 1 [Homo sapiens]

Sequence ID: gb|AAH26231.1| **Length:** 322 **Number of Matches:** 1

▷ See 3 more title(s)

Related Information

Gene - associated gene details
Identical Proteins - Proteins identical to the subject

Range 1: 47 to 59 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.8 bits(91)	0.004	12/13(92%)	13/13(100%)	0/13(0%)

```
Query  1   KANQQLDFTEAKE  13
           KANQQL+FTEAKE
Sbjct  47  KANQQLNFTEAKE  59
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

LYVE1_KANQQLNFTEAKE_NonMod

RID B9G2BV3N01R (Expires on 01-14 13:50 pm)

Query ID	lcl|58052	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	13		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

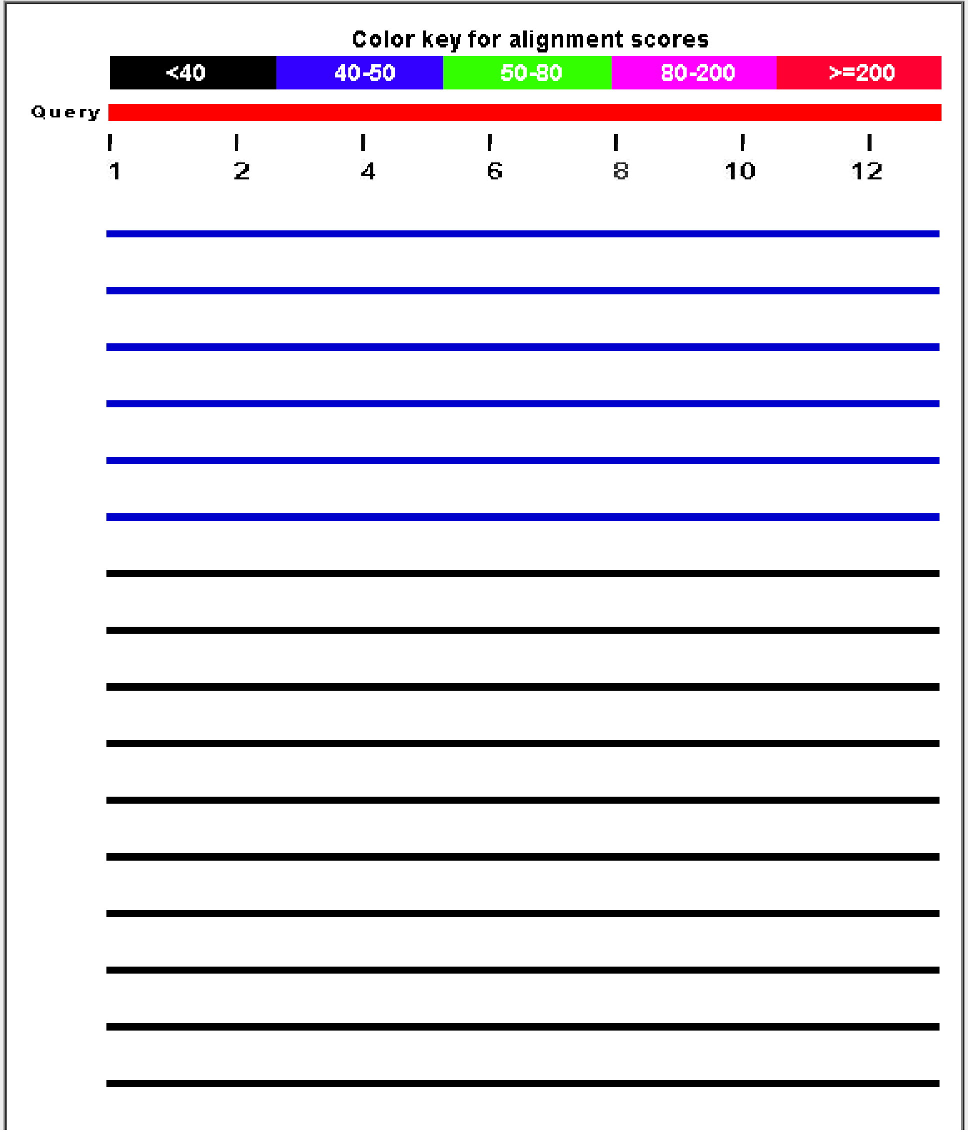
Graphic Summary

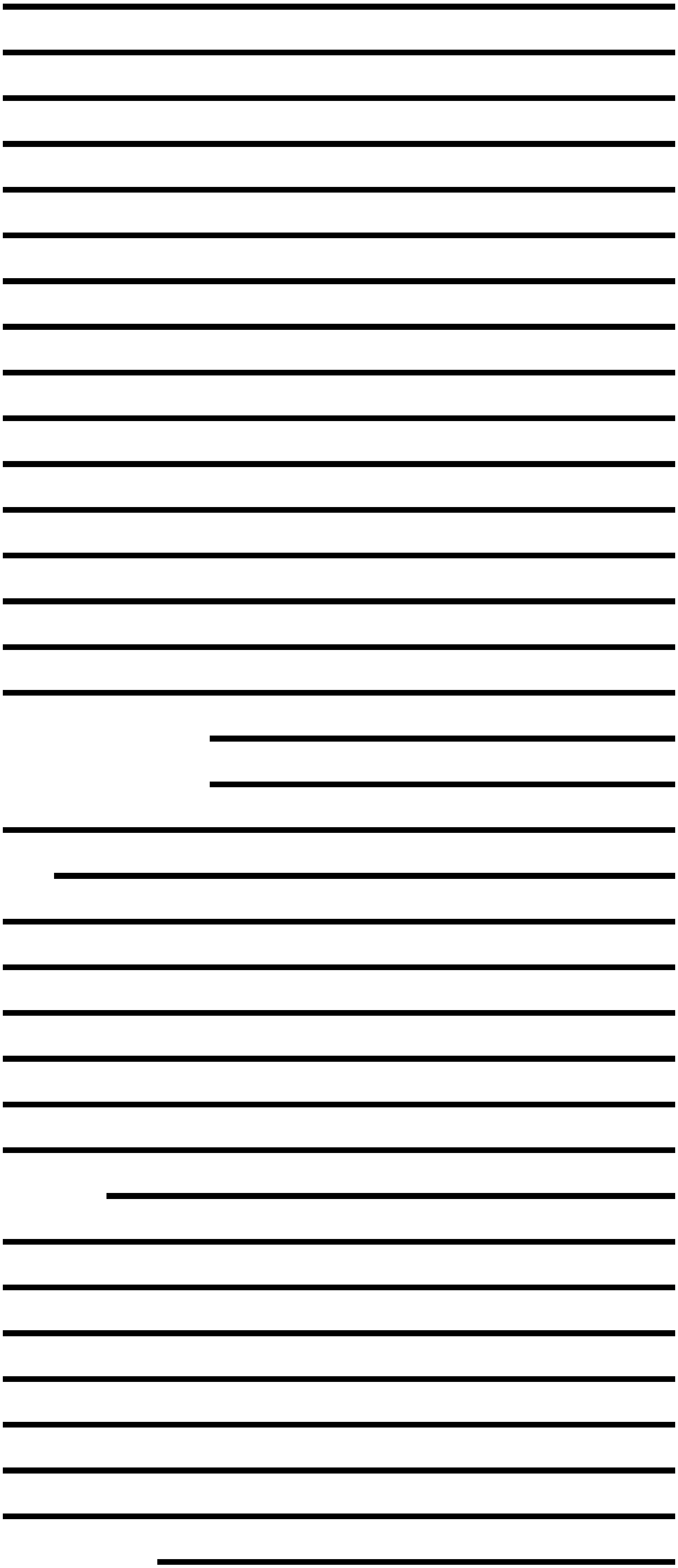
Show Conserved Domains

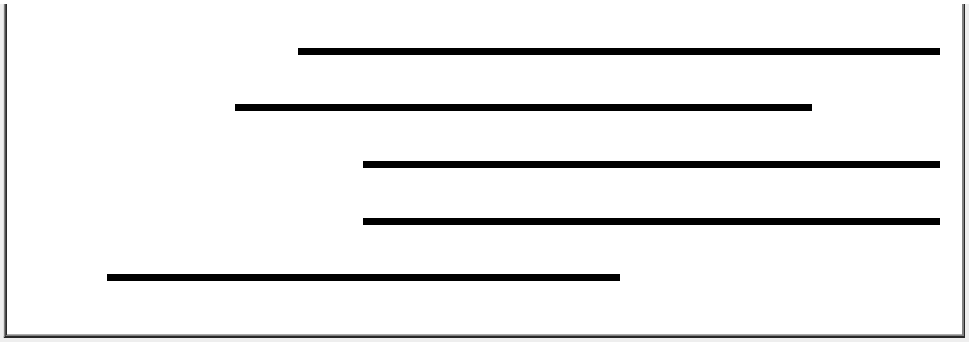
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	lymphatic vessel endothelial hyaluronic acid receptor 1 precursor [H	44.3	44.3	100%	5e-04	100%	gi|40549451|NP_006682.2
☐	lymphatic endothelium-specific hyaluronan receptor LYVE-1 [Homo	44.3	44.3	100%	5e-04	100%	gi|5359673|AAD42764.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	44.3	44.3	100%	5e-04	100%	gi|397494690|XP_003818206.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	44.3	44.3	100%	5e-04	100%	gi|114636135|XP_508283.2
☐	Lymphatic vessel endothelial hyaluronan receptor 1 [Homo sapiens	44.3	44.3	100%	5e-04	100%	gi|20070755|AAH26231.1
☐	extracellular link domain containing 1 [synthetic construct]	44.3	44.3	100%	5e-04	100%	gi|60810113|AAX36112.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	39.7	39.7	100%	0.019	92%	gi|724929569|XP_010383112.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	39.7	39.7	100%	0.019	92%	gi|635015188|XP_008004966.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	39.7	39.7	100%	0.019	92%	gi|402894236|XP_003910275.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	39.7	39.7	100%	0.019	92%	gi|544487485|XP_005578681.1
☐	Lymphatic vessel endothelial hyaluronic acid receptor 1 [Macaca m	39.7	39.7	100%	0.019	92%	gi|355566724|EHH23103.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	39.7	39.7	100%	0.019	92%	gi|109107317|XP_001100103.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	39.7	39.7	100%	0.019	92%	gi|403254235|XP_003919881.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	38.8	38.8	100%	0.035	92%	gi|686737191|XP_009244896.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	38.8	38.8	100%	0.037	92%	gi|426367460|XP_004050750.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	38.8	38.8	100%	0.037	92%	gi|332211767|XP_003254985.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	38.4	38.4	100%	0.051	85%	gi|667312009|XP_008584943.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	38.4	38.4	100%	0.051	85%	gi|641719315|XP_008149260.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	37.5	37.5	100%	0.097	85%	gi|634827344|XP_007953340.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	37.1	37.1	100%	0.13	85%	gi|524951459|XP_005075737.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	36.3	36.3	100%	0.25	85%	gi|640821058|XP_008067473.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	35.4	35.4	100%	0.48	85%	gi|675698236|XP_002755091.2
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	35.4	35.4	100%	0.49	85%	gi|675698233|XP_009005908.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	35.0	35.0	100%	0.66	85%	gi|558128872|XP_006089678.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	35.0	35.0	100%	0.66	85%	gi|554559276|XP_005874034.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	35.0	35.0	100%	0.66	85%	gi|584087727|XP_006763529.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	33.3	33.3	100%	2.4	77%	gi|471358234|XP_004369701.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	32.9	32.9	100%	3.2	77%	gi|591313664|XP_007083276.1
☐							

	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	32.9	32.9	100%	3.2	77%	gi|410973193|XP_003993039.1
☐	lymphatic vessel endothelial hyaluronic acid receptor 1 [Camelus fe	32.5	32.5	100%	4.3	77%	gi|528755034|EPY74693.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	32.5	32.5	100%	4.4	77%	gi|560962305|XP_006203587.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	32.5	32.5	100%	4.4	77%	gi|560933731|XP_006192969.1
☐	PREDICTED: LOW QUALITY PROTEIN: lymphatic vessel endothel	32.0	32.0	69%	6.1	100%	gi|348559882|XP_003465744.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	32.0	32.0	69%	6.1	100%	gi|504168401|XP_004593845.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	31.6	31.6	100%	8.3	77%	gi|359322327|XP_003639831.1
☐	lymphatic vessel endothelial hyaluronic acid receptor 1 [Rattus norv	31.6	31.6	92%	8.4	75%	gi|157820637|NP_001099756.1
☐	Lymphatic vessel endothelial hyaluronic acid receptor 1 [Cricetulus	31.2	31.2	100%	11	77%	gi|344240900|EGV97003.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	31.2	31.2	100%	11	77%	gi|664749112|XP_008531961.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	31.2	31.2	100%	11	77%	gi|625212759|XP_007647074.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	31.2	31.2	100%	11	69%	gi|507658988|XP_004634930.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	31.2	31.2	100%	11	69%	gi|291384633|XP_002708858.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	31.2	31.2	100%	11	69%	gi|488523123|XP_004453453.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	31.2	31.2	84%	11	82%	gi|507533735|XP_004650927.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	31.2	31.2	100%	11	77%	gi|149719443|XP_001504970.1
☐	protein MRVI1-like protein [Cricetulus griseus]	31.2	31.2	100%	12	77%	gi|537207244|ERE80129.1
☐	protein MRVI1-like protein [Cricetulus griseus]	31.2	31.2	100%	12	77%	gi|537207245|ERE80130.1
☐	protein MRVI1-like protein [Cricetulus griseus]	31.2	31.2	100%	12	77%	gi|537207243|ERE80128.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	30.8	30.8	100%	15	69%	gi|344280563|XP_003412052.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	30.8	30.8	100%	16	69%	gi|532082227|XP_005326862.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	30.3	30.3	100%	21	69%	gi|478488200|XP_004418488.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	30.3	30.3	76%	21	90%	gi|617593622|XP_007521220.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	29.9	29.9	76%	29	80%	gi|395543482|XP_003773646.1
☐	hypothetical protein JP74_21765 [Devosia sp. 17-2-E-8]	29.9	29.9	69%	30	89%	gi|674759722|KFL24995.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	29.5	29.5	69%	39	89%	gi|586485154|XP_006873070.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	29.5	29.5	69%	39	89%	gi|507685057|XP_004711592.1
☐	PTS maltose transporter subunit IIBC [Staphylococcus pettenkoferi	29.1	29.1	61%	52	100%	gi|488401911|WP_002471296.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	29.1	29.1	100%	54	69%	gi|593753137|XP_007115477.1
☐	hypothetical protein Q664_06280 [Cystobacter violaceus Cb vi76]	28.6	28.6	69%	69	89%	gi|667804508|KFA93874.1
☐	nucleoside-diphosphate-sugar epimerase [Xanthomonas vesicatori	28.6	28.6	92%	73	75%	gi|492844096|WP_005998050.1
☐	NmrA family protein [Xanthomonas vesicatoria]	28.6	28.6	92%	73	75%	gi|734006070|KHM91708.1
☐	NmrA family protein [Xanthomonas arboricola pv. celebensis]	28.6	28.6	92%	73	75%	gi|663494148|KER88267.1
☐	NmrA family protein [Xanthomonas arboricola]	28.6	28.6	92%	73	75%	gi|640503525|WP_024940476.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	28.6	28.6	92%	73	75%	gi|511857195|XP_004752037.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	28.6	28.6	100%	73	69%	gi|585152326|XP_006728583.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	28.6	28.6	100%	73	69%	gi|472349885|XP_004394637.1
☐	secretion protein HylD [Gramella forsetii]	28.6	28.6	76%	74	80%	gi|500027261|WP_011707979.1
☐	hypothetical protein [Mucispirillum schaedleri]	28.6	28.6	92%	74	77%	gi|555545456|WP_023275572.1
☐	histidine kinase [Myroides odoratimimus]	28.6	28.6	76%	74	80%	gi|640700956|WP_025124556.1
☐	hypothetical protein [Myroides odoratimimus]	28.6	28.6	76%	74	80%	gi|514961695|WP_016650279.1
☐	hypothetical protein [Myroides odoratimimus]	28.6	28.6	76%	74	80%	gi|493309248|WP_006266752.1
☐	hypothetical protein [Myroides odoratimimus]	28.6	28.6	76%	74	80%	gi|493302210|WP_006259803.1
☐	hypothetical protein [Myroides odoratimimus]	28.6	28.6	76%	74	80%	gi|493307022|WP_006264558.1
☐	hypothetical protein [Myroides odoratimimus]	28.6	28.6	76%	74	80%	gi|493304767|WP_006262325.1

☐	Anthranilate synthase [Pseudanabaena biceps]	28.6	28.6	84%	74	64%	gi|497313899|WP_009628116.1
☐	conserved domain protein [Bacteroides fluxus]	28.6	28.6	76%	75	90%	gi|496417113|WP_009125960.1
☐	hypothetical protein [Flavobacterium chungangense]	28.2	28.2	69%	99	89%	gi|670505903|WP_031453726.1
☐	lymphatic vessel endothelial hyaluronic acid receptor 1 precursor [M	28.2	28.2	84%	100	73%	gi|31560771|NP_444477.2
☐	hyaluronan receptor [Mus musculus]	28.2	28.2	84%	100	73%	gi|13162223|CAC33082.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	28.2	28.2	100%	100	69%	gi|589931814|XP_006978709.1
☐	hypothetical protein [Helcococcus sueciensis]	28.2	28.2	69%	101	89%	gi|653097184|WP_027347349.1
☐	unnamed protein product [Oikopleura dioica]	28.2	28.2	92%	102	75%	gi|313220375|CBY31230.1
☐	unnamed protein product [Oikopleura dioica]	28.2	28.2	92%	102	75%	gi|313234209|CBY10277.1
☐	GM20358 [Drosophila sechellia]	28.2	28.2	100%	102	79%	gi|195333784|XP_002033566.1
☐	dim gamma-tubulin 5, isoform A [Drosophila melanogaster]	28.2	28.2	100%	103	79%	gi|20129915|NP_610785.1
☐	MULTISPECIES: hypothetical protein [Parabacteroides]	28.2	28.2	69%	104	89%	gi|498502074|WP_010802776.1
☐	membrane protein [Parabacteroides goldsteinii]	28.2	28.2	69%	104	89%	gi|494932066|WP_007658100.1
☐	hypothetical protein [Photobacterium sp. SKA34]	27.8	27.8	69%	134	90%	gi|493695244|WP_006645113.1
☐	amino acid ABC transporter substrate-binding protein [Streptococcu	27.8	27.8	69%	135	90%	gi|489177246|WP_003086763.1
☐	MULTISPECIES: LysR family transcriptional regulator [Myroides]	27.8	27.8	100%	135	71%	gi|489076611|WP_002986559.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	27.8	27.8	69%	136	89%	gi|602722618|XP_007471455.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	27.8	27.8	69%	136	89%	gi|594653120|XP_007174994.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	27.8	27.8	100%	136	62%	gi|562879636|XP_006167495.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	27.8	27.8	69%	136	89%	gi|470637957|XP_004324243.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	27.8	27.8	69%	136	89%	gi|466055424|XP_004279241.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	27.8	27.8	69%	136	89%	gi|350580301|XP_003480784.1
☐	PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor	27.8	27.8	69%	136	89%	gi|545808430|XP_005661187.1
☐	hypothetical protein [Mycoplasma crocodyli]	27.8	27.8	92%	137	75%	gi|502819168|WP_013054144.1
☐	hypothetical protein [Paramecium tetraurelia strain d4-2]	27.8	27.8	69%	138	90%	gi|145515361|XP_001443580.1
☐	ATP-dependent protease ATP-binding subunit HslU [Lactobacillus e	27.8	27.8	69%	138	89%	gi|564809203|WP_023859436.1
☐	hypothetical protein [Pseudoalteromonas haloplanktis]	27.8	27.8	76%	139	75%	gi|515078162|WP_016707948.1

Alignments

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lymphatic vessel endothelial hyaluronic acid receptor 1 precursor [Homo sapiens]

Sequence ID: gi|40549451|ref|NP_006682.2| **Length:** 322 **Number of Matches:** 1

▷ See 6 more title(s)

Range 1: 47 to 59 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	5e-04	13/13(100%)	13/13(100%)	0/13(0%)

```
Query  1    KANQQLNFTEAKE  13
            KANQQLNFTEAKE
Sbjct  47   KANQQLNFTEAKE  59
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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lymphatic endothelium-specific hyaluronan receptor LYVE-1 [Homo sapiens]

Sequence ID: gi|5359673|gb|AAD42764.1|AF118108_1 **Length:** 322 **Number of Matches:** 1

Range 1: 47 to 59 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	5e-04	13/13(100%)	13/13(100%)	0/13(0%)

Related Information

Gene - associated gene details

```
Query  1    KANQQLNFTEAKE  13
           KANQQLNFTEAKE
Sbjct  47   KANQQLNFTEAKE  59
```

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PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Pan paniscus]

Sequence ID: gi|397494690|ref|XP_003818206.1| **Length:** 322 **Number of Matches:** 1

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

Range 1: 47 to 59 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	5e-04	13/13(100%)	13/13(100%)	0/13(0%)

```
Query  1    KANQQLNFTEAKE  13
           KANQQLNFTEAKE
Sbjct  47   KANQQLNFTEAKE  59
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: lymphatic vessel endothelial hyaluronic acid receptor 1 [Pan troglodytes]

Sequence ID: gi|114636135|ref|XP_508283.2| **Length:** 322 **Number of Matches:** 1

Related Information

Gene - associated gene details
UniGene - clustered expressed sequence tags
Map Viewer - aligned genomic context

Range 1: 47 to 59 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	5e-04	13/13(100%)	13/13(100%)	0/13(0%)

```
Query  1    KANQQLNFTEAKE  13
           KANQQLNFTEAKE
Sbjct  47   KANQQLNFTEAKE  59
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Lymphatic vessel endothelial hyaluronan receptor 1 [Homo sapiens]

Sequence ID: gi|20070755|gb|AAH26231.1| **Length:** 322 **Number of Matches:** 1

▶ See 3 more title(s)

Related Information

Gene - associated gene details
Identical Proteins - Proteins identical to the subject

Range 1: 47 to 59 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	5e-04	13/13(100%)	13/13(100%)	0/13(0%)

```
Query  1    KANQQLNFTEAKE  13
           KANQQLNFTEAKE
Sbjct  47   KANQQLNFTEAKE  59
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVJ1G39001R

Your search parameters were adjusted to search for a short input sequence.

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MASP1_RFGYILHTDDRT_Mod

RID	BVJ1G39001R (Expires on 01-21 10:14 am)		
Query ID	lcl|347621	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	12	**Program**	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

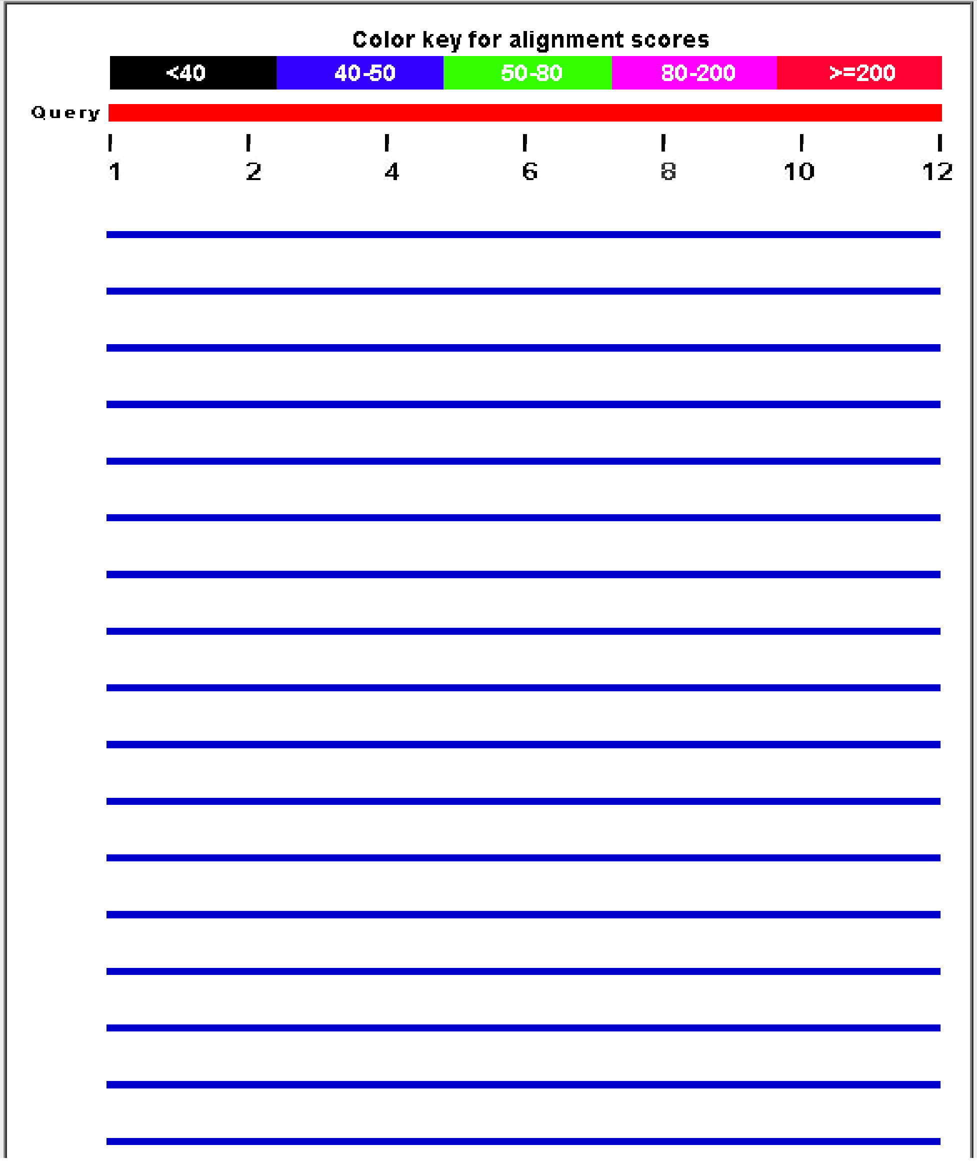
Graphic Summary

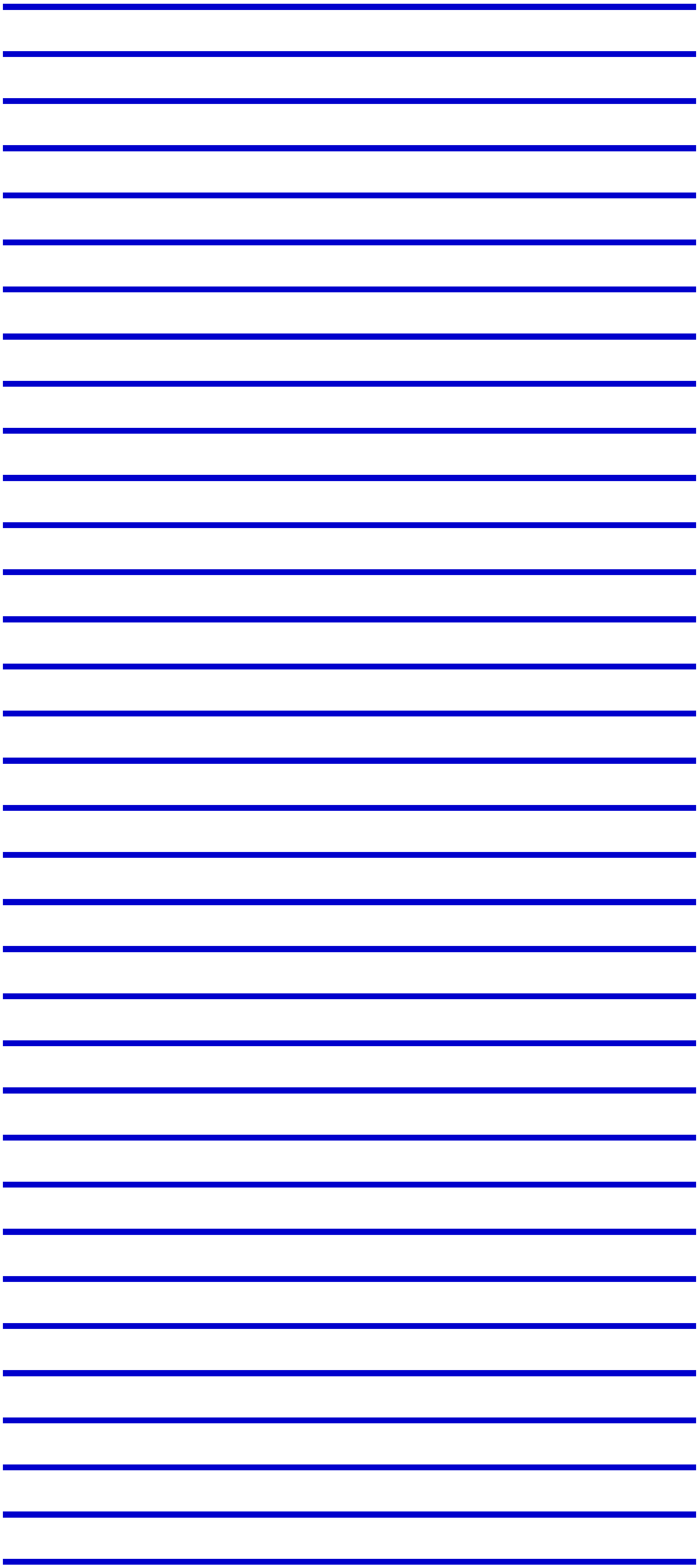
Show Conserved Domains

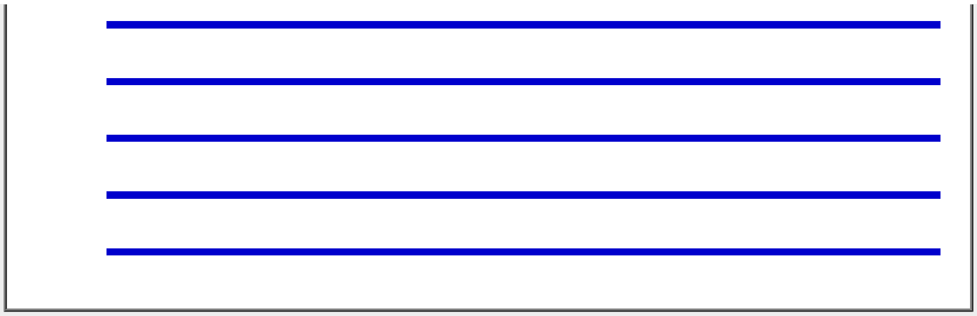
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Ra-reactive factor serine protease p100 [Rattus norvegicus]	40.9	40.9	100%	0.006	92%	AAB65832.1
☐	Chain A, Cub1-egf-cub2 Domain Of Human Masp-1/3 [Homo sapiens]	40.9	40.9	100%	0.007	92%	3DEM_A
☐	unnamed protein product [Homo sapiens]	40.9	40.9	100%	0.007	92%	BAG62349.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Homo sap	40.9	40.9	100%	0.007	92%	XP_006713764.1
☐	Chain A, Mbl-Ficolin Associated Protein-1, Map-1 Aka Map44 [Homo sapiens]	40.9	40.9	100%	0.007	92%	4AQB_A
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Jaculus ja	40.9	40.9	100%	0.007	92%	XP_004654346.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [Oryctolagu	40.9	40.9	100%	0.007	92%	XP_008264861.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Bison biso	40.9	40.9	100%	0.007	92%	XP_010852220.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X7 [Saimiri bol	40.9	40.9	100%	0.007	92%	XP_010336013.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X7 [Callithrix ja	40.9	40.9	100%	0.007	92%	XP_008979623.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Nannospa	40.9	40.9	100%	0.007	92%	XP_008851360.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X5 [Eptesicus	40.9	40.9	100%	0.007	92%	XP_008149800.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [Tarsius sy	40.9	40.9	100%	0.007	92%	XP_008054567.1
☐	mannan-binding lectin serine protease 1 isoform 3 precursor [Homo sapiens]	40.9	40.9	100%	0.007	92%	NP_001027019.1
☐	PREDICTED: mannan-binding lectin serine protease 1-like isoform X3 [Bubalu	40.9	40.9	100%	0.007	92%	XP_006042840.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Peromyscu	40.9	40.9	100%	0.007	92%	XP_006985135.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Pteropus a	40.9	40.9	100%	0.007	92%	XP_006925890.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [Myotis dav	40.9	40.9	100%	0.007	92%	XP_006765915.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Tupaia chi	40.9	40.9	100%	0.007	92%	XP_006156800.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Vicugna pa	40.9	40.9	100%	0.007	92%	XP_006201041.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Camelus f	40.9	40.9	100%	0.007	92%	XP_006188912.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Myotis luci	40.9	40.9	100%	0.007	92%	XP_006084855.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Pantholop	40.9	40.9	100%	0.007	92%	XP_005969146.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Bos mutus	40.9	40.9	100%	0.007	92%	XP_005899711.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Myotis bra	40.9	40.9	100%	0.007	92%	XP_005876336.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Capra hirc	40.9	40.9	100%	0.007	92%	XP_005675200.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Sus scrofa	40.9	40.9	100%	0.007	92%	XP_005657168.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Equus cab	40.9	40.9	100%	0.007	92%	XP_005601937.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Macaca fa	40.9	40.9	100%	0.007	92%	XP_005545503.1

☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Bos taurus	40.9	40.9	100%	0.007	92%	XP_005201546.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 4 [Ceratotheriu	40.9	40.9	100%	0.007	92%	XP_004424648.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 3 [Orcinus orc	40.9	40.9	100%	0.007	92%	XP_004278527.1
☐	hypothetical protein [Homo sapiens]	40.9	40.9	100%	0.007	92%	CAH18409.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [Pan troglo	40.9	40.9	100%	0.007	92%	XP_003310212.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 2 [Nomascus l	40.9	40.9	100%	0.007	92%	XP_003256677.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Fukomys	40.9	40.9	100%	0.007	92%	XP_010622449.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Cavia porc	40.9	40.9	100%	0.007	92%	XP_005006929.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Heterocep	40.9	40.9	100%	0.007	92%	XP_004899716.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Rhinopithe	40.9	40.9	100%	0.007	92%	XP_010350856.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Chloroceb	40.9	40.9	100%	0.007	92%	XP_008007690.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Macaca fa	40.9	40.9	100%	0.007	92%	XP_005545502.1
☐	unnamed protein product [Macaca fascicularis]	40.9	40.9	100%	0.007	92%	BAE90048.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Rattus nor	40.9	40.9	100%	0.007	92%	XP_008767026.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Ictidomys	40.9	40.9	100%	0.007	92%	XP_005331047.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Mus musc	40.9	40.9	100%	0.007	92%	XP_006521892.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [Chinchilla	40.9	40.9	100%	0.007	92%	XP_005383312.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Pan troglo	40.9	40.9	100%	0.007	92%	XP_009445263.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Papio anu	40.9	40.9	100%	0.007	92%	XP_009200178.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X6 [Saimiri bol	40.9	40.9	100%	0.007	92%	XP_010336012.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 5 [Nomascus l	40.9	40.9	100%	0.007	92%	XP_003256680.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X6 [Callithrix ja	40.9	40.9	100%	0.007	92%	XP_008979622.1
☐	rCG36729, isoform CRA_b [Rattus norvegicus]	40.9	40.9	100%	0.007	92%	EDL78090.1
☐	hypothetical protein CB1_001118022 [Camelus ferus]	40.9	40.9	100%	0.007	92%	EPY78128.1
☐	hypothetical protein [Homo sapiens]	40.9	40.9	100%	0.007	92%	CAI46037.1
☐	MASP1 protein [Homo sapiens]	40.9	40.9	100%	0.007	92%	AAH39724.1
☐	PREDICTED: mannan-binding lectin serine protease 1-like isoform X2 [Bubalu	40.9	40.9	100%	0.007	92%	XP_006042839.1
☐	PREDICTED: mannan-binding lectin serine protease 1-like isoform X1 [Bubalu	40.9	40.9	100%	0.007	92%	XP_006042838.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Bos taurus	40.9	40.9	100%	0.007	92%	XP_005201545.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X5 [Saimiri bol	40.9	40.9	100%	0.007	92%	XP_010336011.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Erinaceus	40.9	40.9	100%	0.007	92%	XP_007532796.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X6 [Pongo abe	40.9	40.9	100%	0.007	92%	XP_009237913.1
☐	PREDICTED: mannan-binding lectin serine protease 1 [Galeopterus variegatu	40.9	40.9	100%	0.007	92%	XP_008589455.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Tarsius sy	40.9	40.9	100%	0.007	92%	XP_008054566.1
☐	unnamed protein product [Homo sapiens]	40.9	40.9	100%	0.007	92%	BAG65179.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Pteropus	40.9	40.9	100%	0.007	92%	XP_006925889.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Vicugna pa	40.9	40.9	100%	0.007	92%	XP_006201040.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Camelus f	40.9	40.9	100%	0.007	92%	XP_006188911.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Bos mutus	40.9	40.9	100%	0.007	92%	XP_005899710.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Condylura	40.9	40.9	100%	0.007	92%	XP_004675138.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Sorex ara	40.9	40.9	100%	0.007	92%	XP_004603078.1
☐	rCG36729, isoform CRA_a [Rattus norvegicus]	40.9	40.9	100%	0.007	92%	EDL78089.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [Eptesicus	40.9	40.9	100%	0.007	92%	XP_008149799.1
☐	PREDICTED: mannan-binding lectin serine protease 1-like [Python bivittatus]	40.9	40.9	100%	0.007	92%	XP_007442121.1
☐	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-	40.9	40.9	100%	0.007	92%	EAW78150.1

☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Jaculus ja	40.9	40.9	100%	0.007	92%	XP_004654345.1
☐	PREDICTED: LOW QUALITY PROTEIN: mannan-binding lectin serine protea	40.9	40.9	100%	0.007	92%	XP_002808386.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X5 [Pongo abe	40.9	40.9	100%	0.007	92%	XP_009237912.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Pan panis	40.9	40.9	100%	0.007	92%	XP_008954144.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Chinchilla	40.9	40.9	100%	0.007	92%	XP_005383311.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 4 [Gorilla gorill	40.9	40.9	100%	0.007	92%	XP_004038230.1
☐	PREDICTED: LOW QUALITY PROTEIN: mannan-binding lectin serine protea	40.9	40.9	100%	0.007	92%	XP_003804164.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 4 [Nomascus l	40.9	40.9	100%	0.007	92%	XP_003256679.1
☐	MASP-3 protein [Rattus norvegicus]	40.9	40.9	100%	0.007	92%	CAD32171.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Camelus	40.9	40.9	100%	0.007	92%	XP_010974431.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Camelus b	40.9	40.9	100%	0.007	92%	XP_010957528.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Bison biso	40.9	40.9	100%	0.007	92%	XP_010852216.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Fukomys	40.9	40.9	100%	0.007	92%	XP_010622448.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [Rhinopithe	40.9	40.9	100%	0.007	92%	XP_010350848.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [Nannospa	40.9	40.9	100%	0.007	92%	XP_008851350.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Equus prz	40.9	40.9	100%	0.007	92%	XP_008532698.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Eptesicus	40.9	40.9	100%	0.007	92%	XP_008149798.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Tarsius sy	40.9	40.9	100%	0.007	92%	XP_008054564.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [Chloroceb	40.9	40.9	100%	0.007	92%	XP_008007689.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Lipotes ve	40.9	40.9	100%	0.007	92%	XP_007448486.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Physeter c	40.9	40.9	100%	0.007	92%	XP_007111601.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [Peromysc	40.9	40.9	100%	0.007	92%	XP_006985134.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Myotis dav	40.9	40.9	100%	0.007	92%	XP_006765916.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Tupaia chi	40.9	40.9	100%	0.007	92%	XP_006156799.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Myotis luci	40.9	40.9	100%	0.007	92%	XP_006084854.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Myotis bra	40.9	40.9	100%	0.007	92%	XP_005876335.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Ra-reactive factor serine protease p100 [Rattus norvegicus]

Sequence ID: gb|AAB65832.1| **Length:** 212 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 163 to 174 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
40.9 bits(89)	0.006	11/12(92%)	12/12(100%)	0/12(0%)

```
Query  1    RFGYILHTDDRT  12
            RFGYILHTD+RT
Sbjct  163  RFGYILHTDNRT  174
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Cub1-egf-cub2 Domain Of Human Masp-1/3

Sequence ID: pdb|3DEM|A **Length:** 278 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins

Range 1: 150 to 161 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
40.9 bits(89)	0.007	11/12(92%)	12/12(100%)	0/12(0%)

identical to the subject

```
Query  1    RFGYILHTDDRT  12
            RFGYILHTD+RT
Sbjct  150  RFGYILHTDNRT  161
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG62349.1| **Length:** 354 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 143 to 154 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
40.9 bits(89)	0.007	11/12(92%)	12/12(100%)	0/12(0%)

```
Query  1    RFGYILHTDDRT  12
            RFGYILHTD+RT
Sbjct  143  RFGYILHTDNRT  154
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Homo sapiens]

Sequence ID: ref|XP_006713764.1| **Length:** 354 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 143 to 154 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
40.9 bits(89)	0.007	11/12(92%)	12/12(100%)	0/12(0%)

```
Query  1    RFGYILHTDDRT  12
            RFGYILHTD+RT
Sbjct  143  RFGYILHTDNRT  154
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Mbl-Ficolin Associated Protein-1, Map-1 Aka Map44

Sequence ID: pdb|4AQB|A **Length:** 361 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 150 to 161 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
40.9 bits(89)	0.007	11/12(92%)	12/12(100%)	0/12(0%)

```
Query  1    RFGYILHTDDRT  12
            RFGYILHTD+RT
Sbjct  150  RFGYILHTDNRT  161
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVJ2FYVD01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download   You Tube How to read this page   Blast report description

MASP1_RFGYILHTDDRTCRV_Mod

RID	BVJ2FYVD01R (Expires on 01-21 10:15 am)		
Query ID	lcl|355772	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	15	**Program**	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

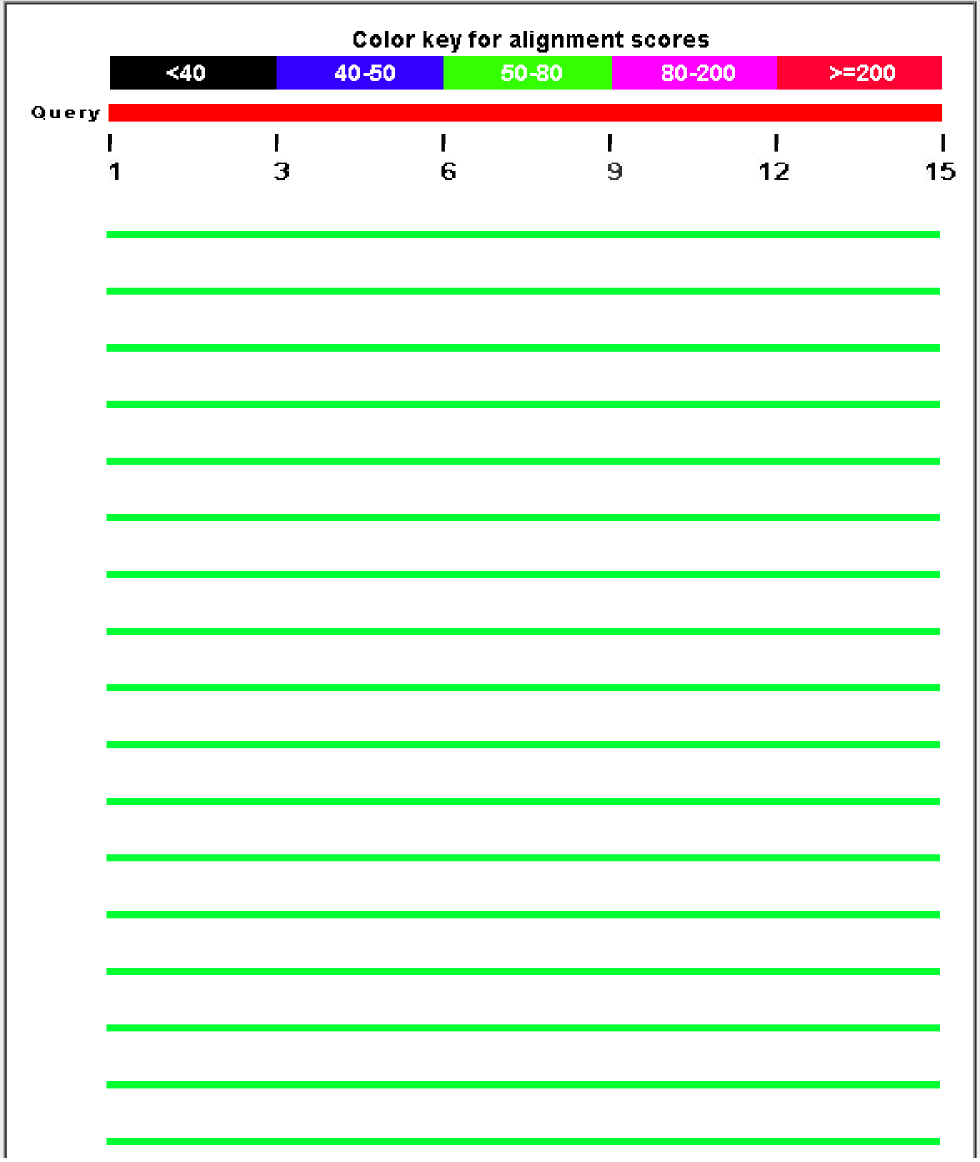
⊟ Graphic Summary

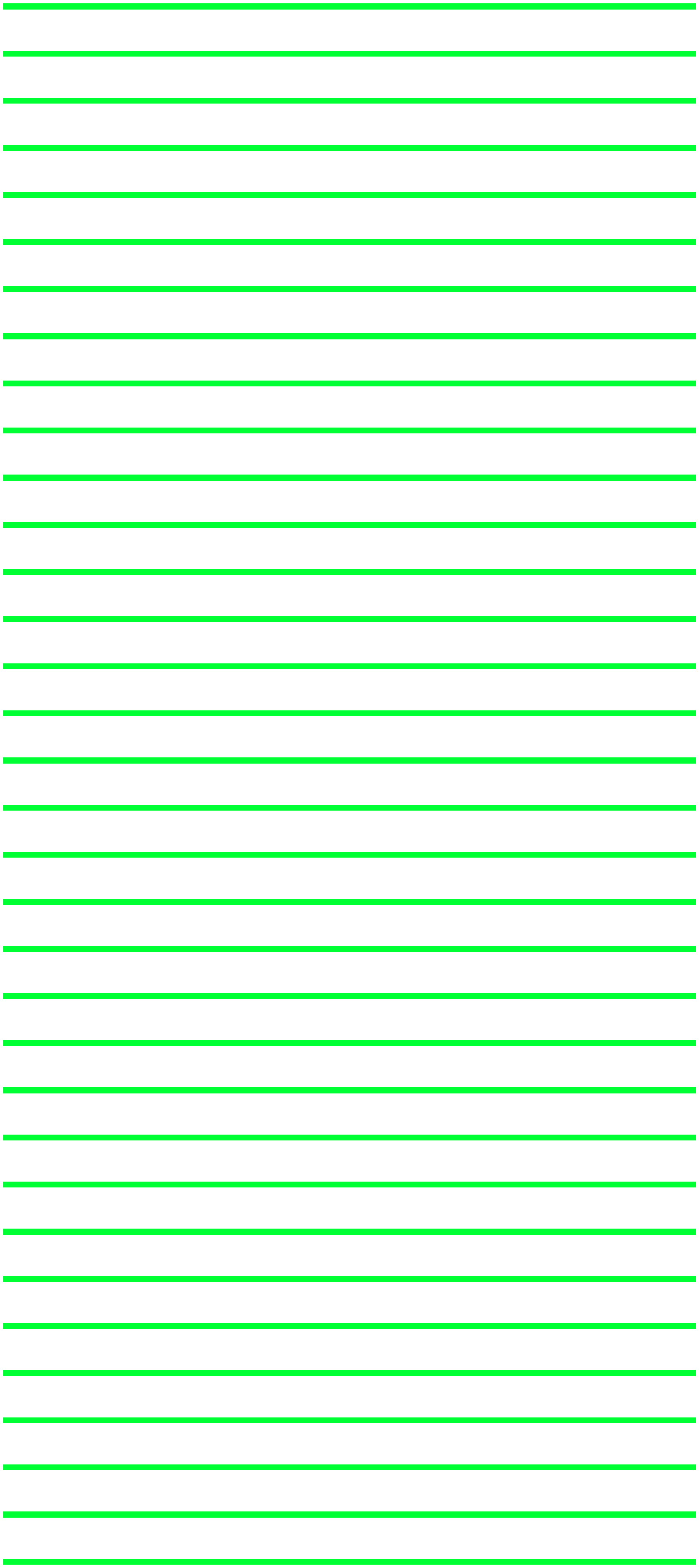
⊟ Show Conserved Domains

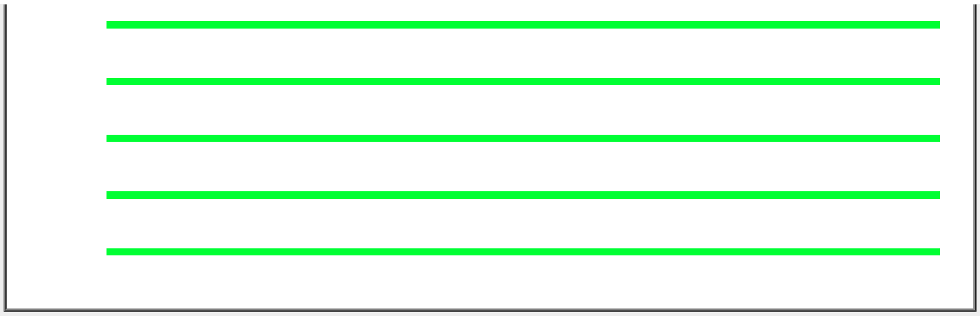
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Ra-reactive factor serine protease p100 [Rattus norvegicus]	51.5	51.5	100%	2e-06	93%	AAB65832.1
☐	Chain A, Cub1-egf-cub2 Domain Of Human Masp-1/3 [Homo sapiens]	51.5	51.5	100%	3e-06	93%	3DEM_A
☐	unnamed protein product [Homo sapiens]	51.5	51.5	100%	3e-06	93%	BAG62349.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Homo sap	51.5	51.5	100%	3e-06	93%	XP_006713764.1
☐	Chain A, Mbl-Ficolin Associated Protein-1, Map-1 Aka Map44 [Homo sapiens]	51.5	51.5	100%	3e-06	93%	4AQB_A
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Jaculus ja	51.5	51.5	100%	3e-06	93%	XP_004654346.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [Oryctolagu	51.5	51.5	100%	3e-06	93%	XP_008264861.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Bison biso	51.5	51.5	100%	3e-06	93%	XP_010852220.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X7 [Saimiri bol	51.5	51.5	100%	3e-06	93%	XP_010336013.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X7 [Callithrix ja	51.5	51.5	100%	3e-06	93%	XP_008979623.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Nannospa	51.5	51.5	100%	3e-06	93%	XP_008851360.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X5 [Eptesicus	51.5	51.5	100%	3e-06	93%	XP_008149800.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [Tarsius sy	51.5	51.5	100%	3e-06	93%	XP_008054567.1
☐	mannan-binding lectin serine protease 1 isoform 3 precursor [Homo sapiens]	51.5	51.5	100%	3e-06	93%	NP_001027019.1
☐	PREDICTED: mannan-binding lectin serine protease 1-like isoform X3 [Bubalu	51.5	51.5	100%	3e-06	93%	XP_006042840.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Peromyscu	51.5	51.5	100%	3e-06	93%	XP_006985135.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Pteropus a	51.5	51.5	100%	3e-06	93%	XP_006925890.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [Myotis dav	51.5	51.5	100%	3e-06	93%	XP_006765915.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Tupaia chi	51.5	51.5	100%	3e-06	93%	XP_006156800.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Vicugna pa	51.5	51.5	100%	3e-06	93%	XP_006201041.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Camelus fe	51.5	51.5	100%	3e-06	93%	XP_006188912.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Myotis luci	51.5	51.5	100%	3e-06	93%	XP_006084855.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Pantholops	51.5	51.5	100%	3e-06	93%	XP_005969146.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Bos mutus	51.5	51.5	100%	3e-06	93%	XP_005899711.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Myotis bra	51.5	51.5	100%	3e-06	93%	XP_005876336.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Capra hirc	51.5	51.5	100%	3e-06	93%	XP_005675200.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Sus scrofa	51.5	51.5	100%	3e-06	93%	XP_005657168.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Equus cab	51.5	51.5	100%	3e-06	93%	XP_005601937.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Macaca fa	51.5	51.5	100%	3e-06	93%	XP_005545503.1

☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Bos taurus	51.5	51.5	100%	3e-06	93%	XP_005201546.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 4 [Ceratotheriu	51.5	51.5	100%	3e-06	93%	XP_004424648.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 3 [Orcinus orca	51.5	51.5	100%	3e-06	93%	XP_004278527.1
☐	hypothetical protein [Homo sapiens]	51.5	51.5	100%	3e-06	93%	CAH18409.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [Pan troglo	51.5	51.5	100%	3e-06	93%	XP_003310212.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 2 [Nomascus l	51.5	51.5	100%	3e-06	93%	XP_003256677.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Fukomys c	51.5	51.5	100%	3e-06	93%	XP_010622449.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Cavia porc	51.5	51.5	100%	3e-06	93%	XP_005006929.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Heterocep	51.5	51.5	100%	3e-06	93%	XP_004899716.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Rhinopithe	51.5	51.5	100%	3e-06	93%	XP_010350856.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Chloroceb	51.5	51.5	100%	3e-06	93%	XP_008007690.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Macaca fa	51.5	51.5	100%	3e-06	93%	XP_005545502.1
☐	unnamed protein product [Macaca fascicularis]	51.5	51.5	100%	3e-06	93%	BAE90048.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Rattus nor	51.5	51.5	100%	3e-06	93%	XP_008767026.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Ictidomys t	51.5	51.5	100%	3e-06	93%	XP_005331047.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Mus musc	51.5	51.5	100%	3e-06	93%	XP_006521892.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [Chinchilla	51.5	51.5	100%	3e-06	93%	XP_005383312.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Pan troglo	51.5	51.5	100%	3e-06	93%	XP_009445263.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Papio anul	51.5	51.5	100%	3e-06	93%	XP_009200178.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X6 [Saimiri bol	51.5	51.5	100%	3e-06	93%	XP_010336012.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 5 [Nomascus l	51.5	51.5	100%	3e-06	93%	XP_003256680.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X6 [Callithrix ja	51.5	51.5	100%	3e-06	93%	XP_008979622.1
☐	rCG36729, isoform CRA_b [Rattus norvegicus]	51.5	51.5	100%	3e-06	93%	EDL78090.1
☐	hypothetical protein CB1_001118022 [Camelus ferus]	51.5	51.5	100%	3e-06	93%	EPY78128.1
☐	hypothetical protein [Homo sapiens]	51.5	51.5	100%	3e-06	93%	CAI46037.1
☐	MASP1 protein [Homo sapiens]	51.5	51.5	100%	3e-06	93%	AAH39724.1
☐	PREDICTED: mannan-binding lectin serine protease 1-like isoform X2 [Bubalu	51.5	51.5	100%	3e-06	93%	XP_006042839.1
☐	PREDICTED: mannan-binding lectin serine protease 1-like isoform X1 [Bubalu	51.5	51.5	100%	3e-06	93%	XP_006042838.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Bos taurus	51.5	51.5	100%	3e-06	93%	XP_005201545.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X5 [Saimiri bol	51.5	51.5	100%	3e-06	93%	XP_010336011.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Erinaceus	51.5	51.5	100%	3e-06	93%	XP_007532796.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X6 [Pongo abe	51.5	51.5	100%	3e-06	93%	XP_009237913.1
☐	PREDICTED: mannan-binding lectin serine protease 1 [Galeopterus variegatu	51.5	51.5	100%	3e-06	93%	XP_008589455.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Tarsius sy	51.5	51.5	100%	3e-06	93%	XP_008054566.1
☐	unnamed protein product [Homo sapiens]	51.5	51.5	100%	3e-06	93%	BAG65179.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Pteropus a	51.5	51.5	100%	3e-06	93%	XP_006925889.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Vicugna pa	51.5	51.5	100%	3e-06	93%	XP_006201040.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Camelus fe	51.5	51.5	100%	3e-06	93%	XP_006188911.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Bos mutus	51.5	51.5	100%	3e-06	93%	XP_005899710.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Condylura	51.5	51.5	100%	3e-06	93%	XP_004675138.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Sorex arar	51.5	51.5	100%	3e-06	93%	XP_004603078.1
☐	rCG36729, isoform CRA_a [Rattus norvegicus]	51.5	51.5	100%	3e-06	93%	EDL78089.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [Eptesicus	51.5	51.5	100%	3e-06	93%	XP_008149799.1
☐	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-	51.5	51.5	100%	3e-06	93%	EAW78150.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Jaculus jac	51.5	51.5	100%	3e-06	93%	XP_004654345.1

☐	PREDICTED: LOW QUALITY PROTEIN: mannan-binding lectin serine protea	51.5	51.5	100%	3e-06	93%	XP_002808386.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X5 [Pongo abe	51.5	51.5	100%	3e-06	93%	XP_009237912.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Pan panis	51.5	51.5	100%	3e-06	93%	XP_008954144.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Chinchilla	51.5	51.5	100%	3e-06	93%	XP_005383311.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 4 [Gorilla gorill	51.5	51.5	100%	3e-06	93%	XP_004038230.1
☐	PREDICTED: LOW QUALITY PROTEIN: mannan-binding lectin serine protea	51.5	51.5	100%	3e-06	93%	XP_003804164.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 4 [Nomascus l	51.5	51.5	100%	3e-06	93%	XP_003256679.1
☐	MASP-3 protein [Rattus norvegicus]	51.5	51.5	100%	3e-06	93%	CAD32171.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Camelus c	51.5	51.5	100%	3e-06	93%	XP_010974431.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Camelus b	51.5	51.5	100%	3e-06	93%	XP_010957528.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Bison biso	51.5	51.5	100%	3e-06	93%	XP_010852216.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Fukomys c	51.5	51.5	100%	3e-06	93%	XP_010622448.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [Rhinopithe	51.5	51.5	100%	3e-06	93%	XP_010350848.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [Nannospa	51.5	51.5	100%	3e-06	93%	XP_008851350.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Equus prz	51.5	51.5	100%	3e-06	93%	XP_008532698.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [Eptesicus	51.5	51.5	100%	3e-06	93%	XP_008149798.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Tarsius sy	51.5	51.5	100%	3e-06	93%	XP_008054564.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [Chloroceb	51.5	51.5	100%	3e-06	93%	XP_008007689.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Lipotes ve	51.5	51.5	100%	3e-06	93%	XP_007448486.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Physeter c	51.5	51.5	100%	3e-06	93%	XP_007111601.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [Peromyscu	51.5	51.5	100%	3e-06	93%	XP_006985134.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Myotis dav	51.5	51.5	100%	3e-06	93%	XP_006765916.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Tupaia chi	51.5	51.5	100%	3e-06	93%	XP_006156799.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Myotis luci	51.5	51.5	100%	3e-06	93%	XP_006084854.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Myotis bra	51.5	51.5	100%	3e-06	93%	XP_005876335.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Capra hirc	51.5	51.5	100%	3e-06	93%	XP_005675199.1

⊟ Alignments

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Ra-reactive factor serine protease p100 [Rattus norvegicus]

Sequence ID: gb|AAB65832.1| **Length:** 212 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 163 to 177 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	2e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    RFGYILHTDDRTCRV  15
            RFGYILHTD+RTCRV
Sbjct  163  RFGYILHTDNRTCRV  177
```

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Chain A, Cub1-egf-cub2 Domain Of Human Masp-1/3

Sequence ID: pdb|3DEM|A **Length:** 278 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins

Range 1: 150 to 164 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	3e-06	14/15(93%)	15/15(100%)	0/15(0%)

identical to the subject

```
Query  1    RFGYILHTDDRTCRV  15
            RFGYILHTD+RTCRV
Sbjct  150  RFGYILHTDNRTCRV  164
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG62349.1| **Length:** 354 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 143 to 157 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	3e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    RFGYILHTDDRTCRV  15
            RFGYILHTD+RTCRV
Sbjct  143  RFGYILHTDNRTCRV  157
```

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PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Homo sapiens]

Sequence ID: ref|XP_006713764.1| **Length:** 354 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 143 to 157 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	3e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    RFGYILHTDDRTCRV  15
            RFGYILHTD+RTCRV
Sbjct  143  RFGYILHTDNRTCRV  157
```

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Chain A, Mbl-Ficolin Associated Protein-1, Map-1 Aka Map44

Sequence ID: pdb|4AQB|A **Length:** 361 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 150 to 164 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.5 bits(114)	3e-06	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    RFGYILHTDDRTCRV  15
            RFGYILHTD+RTCRV
Sbjct  150  RFGYILHTDNRTCRV  164
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - B9HUH2MT01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download

How to read this page   Blast report description

MASP1_RFGYILHTDNRT_NonMod

RID B9HUH2MT01R (Expires on 01-14 14:20 pm)

Query ID	lcl|220565	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	12		
		Program	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

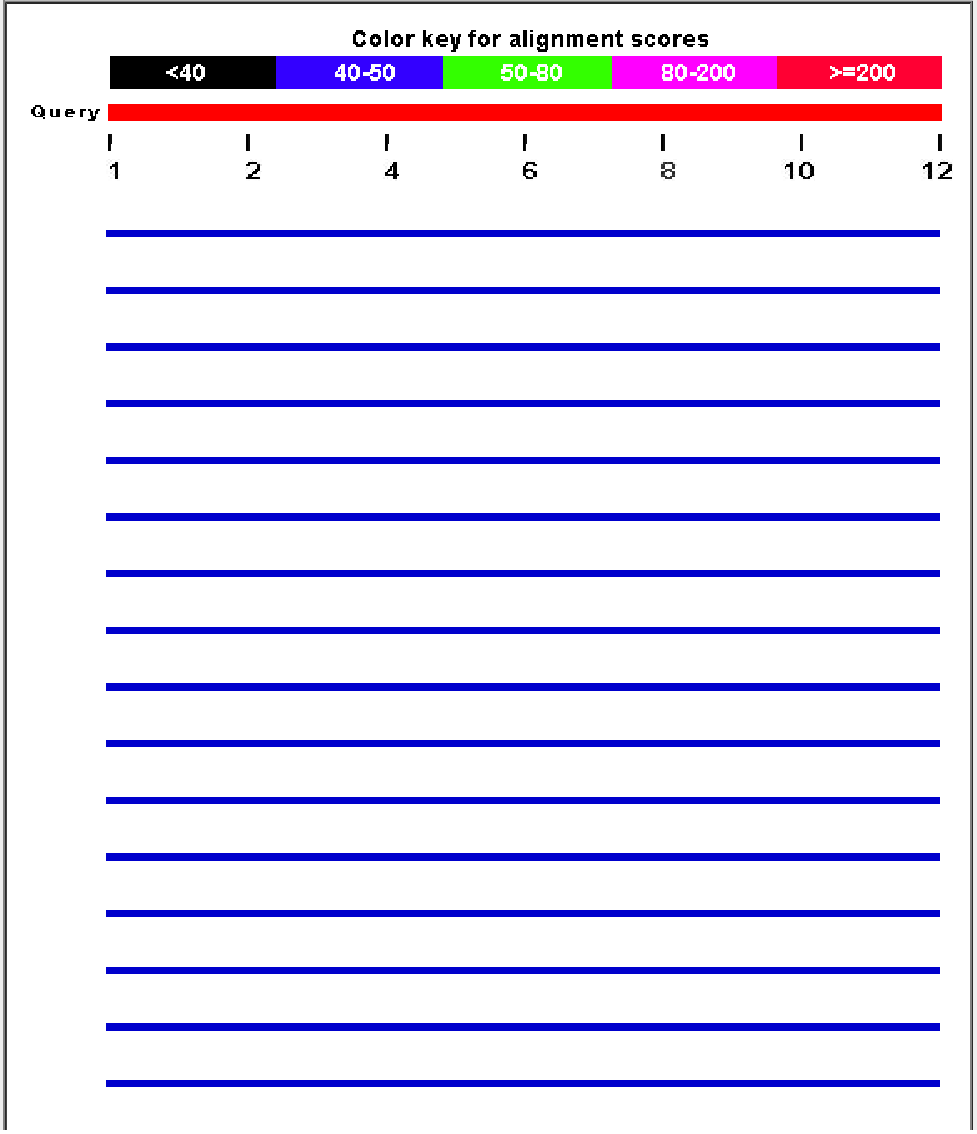
Graphic Summary

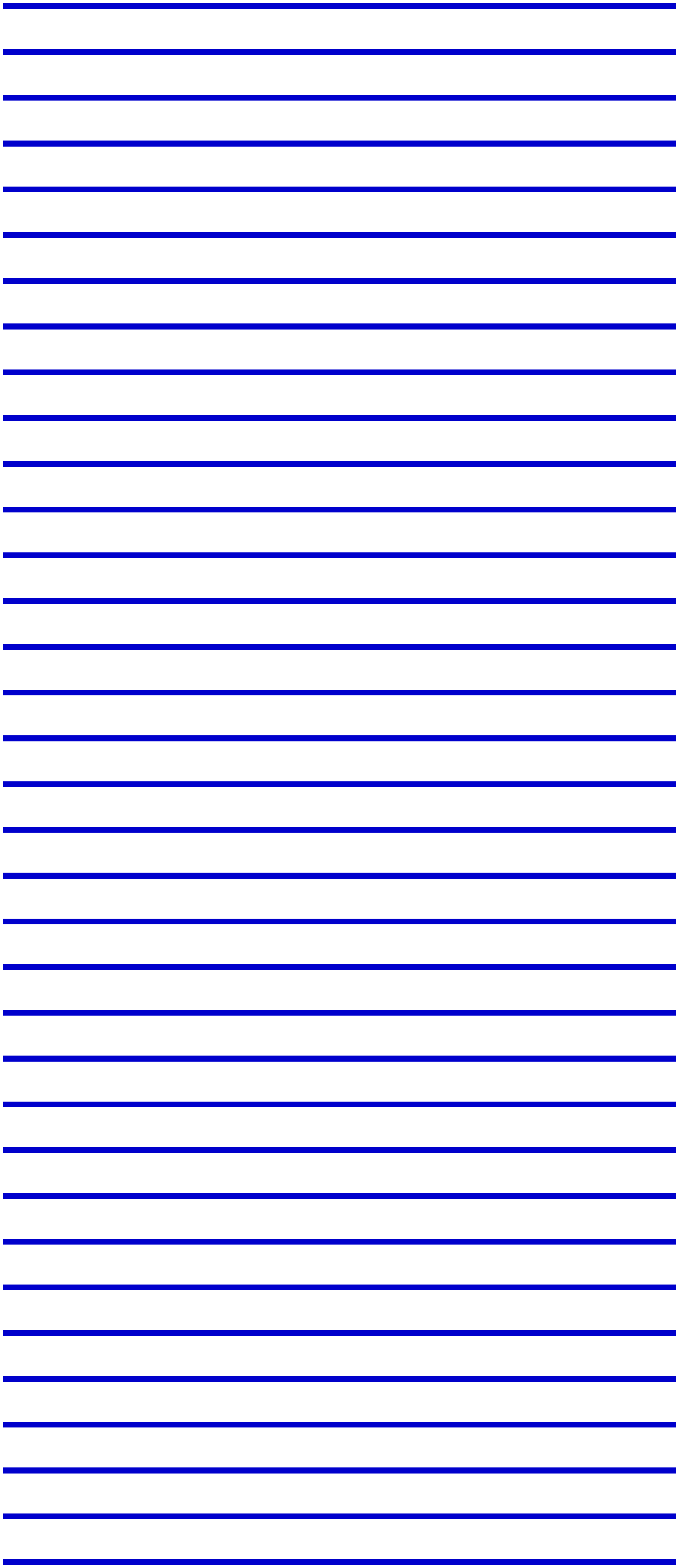
Show Conserved Domains

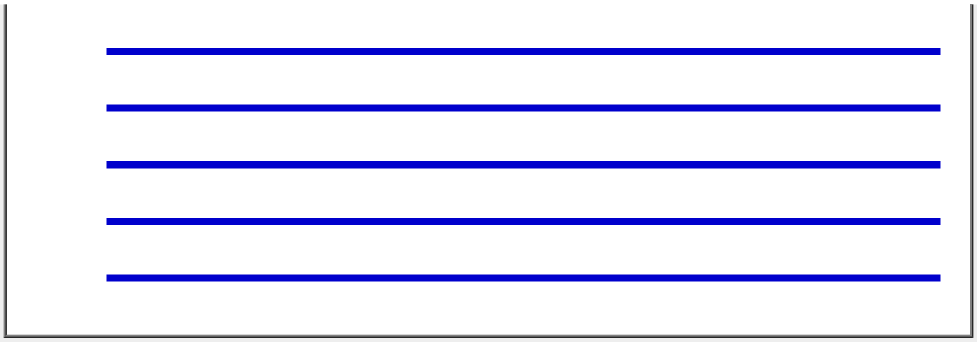
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Ra-reactive factor serine protease p100 [Rattus norvegicus]	43.5	43.5	100%	8e-04	100%	gi|2209345|AAB65832.1
☐	Chain A, Cub1-egf-cub2 Domain Of Human Masp-1/3 [Homo sapie	43.5	43.5	100%	9e-04	100%	gi|193506834|3DEM_A
☐	unnamed protein product [Homo sapiens]	43.5	43.5	100%	0.001	100%	gi|194374073|BAG62349.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|578807591|XP_006713764.1
☐	Chain A, Mbl-Ficolin Associated Protein-1, Map-1 Aka Map44 [Hom	43.5	43.5	100%	0.001	100%	gi|400260714|4AQB_A
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|507540683|XP_004654346.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [	43.5	43.5	100%	0.001	100%	gi|655853895|XP_008264861.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X7 [	43.5	43.5	100%	0.001	100%	gi|725565881|XP_010336013.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X7 [	43.5	43.5	100%	0.001	100%	gi|675726053|XP_008979623.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|674036696|XP_008851360.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X5 [	43.5	43.5	100%	0.001	100%	gi|641720317|XP_008149800.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [	43.5	43.5	100%	0.001	100%	gi|640796916|XP_008054567.1
☐	mannan-binding lectin serine protease 1 isoform 3 precursor [Homo	43.5	43.5	100%	0.001	100%	gi|73623026|NP_001027019.1
☐	PREDICTED: mannan-binding lectin serine protease 1-like isoform	43.5	43.5	100%	0.001	100%	gi|594036350|XP_006042840.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|589944897|XP_006985135.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|586554872|XP_006925890.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [	43.5	43.5	100%	0.001	100%	gi|584042008|XP_006765915.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|562856537|XP_006156800.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|560957130|XP_006201041.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|560925459|XP_006188912.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|558107313|XP_006084855.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|556747385|XP_005969146.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|555975459|XP_005899711.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|554564031|XP_005876336.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|548450456|XP_005675200.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|545865224|XP_005657168.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|545192257|XP_005601937.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|544410516|XP_005545503.1
☐							

	PREDICTED: mannan-binding lectin serine protease 1 isoform X8 [	43.5	43.5	100%	0.001	100%	gi|528936770|XP_005201546.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 4 [C	43.5	43.5	100%	0.001	100%	gi|478500665|XP_004424648.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 3 [O	43.5	43.5	100%	0.001	100%	gi|466051806|XP_004278527.1
☐	hypothetical protein [Homo sapiens]	43.5	43.5	100%	0.001	100%	gi|51476886|CAH18409.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [	43.5	43.5	100%	0.001	100%	gi|332818681|XP_003310212.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 2 [N	43.5	43.5	100%	0.001	100%	gi|332215099|XP_003256677.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|731216121|XP_010622449.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|514474780|XP_005006929.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|512902387|XP_004899716.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|724805505|XP_010350856.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|635086161|XP_008007690.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|544410514|XP_005545502.1
☐	unnamed protein product [Macaca fascicularis]	43.5	43.5	100%	0.001	100%	gi|90081136|BAE90048.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|672071419|XP_008767026.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|532090712|XP_005331047.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|568994700|XP_006521892.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [	43.5	43.5	100%	0.001	100%	gi|533136993|XP_005383312.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|694905534|XP_009445263.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|685527987|XP_009200178.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X6 [	43.5	43.5	100%	0.001	100%	gi|725565879|XP_010336012.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 5 [N	43.5	43.5	100%	0.001	100%	gi|332215105|XP_003256680.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X6 [	43.5	43.5	100%	0.001	100%	gi|675726049|XP_008979622.1
☐	rCG36729, isoform CRA_b [Rattus norvegicus]	43.5	43.5	100%	0.001	100%	gi|149019942|EDL78090.1
☐	hypothetical protein CB1_001118022 [Camelus ferus]	43.5	43.5	100%	0.001	100%	gi|528758469|EPY78128.1
☐	hypothetical protein [Homo sapiens]	43.5	43.5	100%	0.001	100%	gi|57997478|CAI46037.1
☐	MASP1 protein [Homo sapiens]	43.5	43.5	100%	0.001	100%	gi|24981014|AAH39724.1
☐	PREDICTED: mannan-binding lectin serine protease 1-like isoform	43.5	43.5	100%	0.001	100%	gi|594036348|XP_006042839.1
☐	PREDICTED: mannan-binding lectin serine protease 1-like isoform	43.5	43.5	100%	0.001	100%	gi|594036346|XP_006042838.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X7 [	43.5	43.5	100%	0.001	100%	gi|528936768|XP_005201545.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X5 [	43.5	43.5	100%	0.001	100%	gi|725565877|XP_010336011.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X6 [	43.5	43.5	100%	0.001	100%	gi|528936766|XP_005201544.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|617646016|XP_007532796.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X6 [	43.5	43.5	100%	0.001	100%	gi|686714726|XP_009237913.1
☐	PREDICTED: mannan-binding lectin serine protease 1 [Galeopterus	43.5	43.5	100%	0.001	100%	gi|667325189|XP_008589455.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|640796914|XP_008054566.1
☐	unnamed protein product [Homo sapiens]	43.5	43.5	100%	0.001	100%	gi|194385604|BAG65179.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|586554870|XP_006925889.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|560957128|XP_006201040.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|560925457|XP_006188911.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X5 [	43.5	43.5	100%	0.001	100%	gi|528936764|XP_005201543.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|507927767|XP_004675138.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|505778530|XP_004603078.1
☐	rCG36729, isoform CRA_a [Rattus norvegicus]	43.5	43.5	100%	0.001	100%	gi|149019941|EDL78089.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [	43.5	43.5	100%	0.001	100%	gi|641720315|XP_008149799.1
☐	PREDICTED: mannan-binding lectin serine protease 1-like [Python	43.5	43.5	100%	0.001	100%	gi|602673247|XP_007442121.1

☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [	43.5	43.5	100%	0.001	100%	gi|528936762|XP_005201542.1
☐	mannan-binding lectin serine peptidase 1 (C4/C2 activating compor	43.5	43.5	100%	0.001	100%	gi|119598556|EAW78150.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|507540681|XP_004654345.1
☐	PREDICTED: LOW QUALITY PROTEIN: mannan-binding lectin ser	43.5	43.5	100%	0.001	100%	gi|297287139|XP_002808386.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X5 [	43.5	43.5	100%	0.001	100%	gi|686714724|XP_009237912.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|675687274|XP_008954144.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|533136991|XP_005383311.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 4 [G	43.5	43.5	100%	0.001	100%	gi|426343256|XP_004038230.1
☐	PREDICTED: LOW QUALITY PROTEIN: mannan-binding lectin ser	43.5	43.5	100%	0.001	100%	gi|395839796|XP_003804164.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 4 [N	43.5	43.5	100%	0.001	100%	gi|332215103|XP_003256679.1
☐	MASP-3 protein [Rattus norvegicus]	43.5	43.5	100%	0.001	100%	gi|27527940|CAD32171.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|731216119|XP_010622448.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [	43.5	43.5	100%	0.001	100%	gi|724805503|XP_010350848.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [	43.5	43.5	100%	0.001	100%	gi|674036694|XP_008851350.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|664750525|XP_008532698.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	43.5	43.5	100%	0.001	100%	gi|641720313|XP_008149798.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|640796912|XP_008054564.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [	43.5	43.5	100%	0.001	100%	gi|635086159|XP_008007689.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [	43.5	43.5	100%	0.001	100%	gi|545865216|XP_005657166.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|602726051|XP_007448486.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|593732157|XP_007111601.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [	43.5	43.5	100%	0.001	100%	gi|589944895|XP_006985134.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|584042010|XP_006765916.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|554564029|XP_005876335.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	43.5	43.5	100%	0.001	100%	gi|548450449|XP_005675199.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [	43.5	43.5	100%	0.001	100%	gi|545192255|XP_001499679.3
☐	PREDICTED: mannan-binding lectin serine protease 1 [Microtus oc	43.5	43.5	100%	0.001	100%	gi|532000597|XP_005344817.1

Alignments

Download GenPept Graphics — Next Previous Descriptions

Ra-reactive factor serine protease p100 [Rattus norvegicus]

Sequence ID: gi|2209345|gb|AAB65832.1| **Length:** 212 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 163 to 174 GenPept Graphics — Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
43.5 bits(95)	8e-04	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    RFGYILHTDNRT  12
            RFGYILHTDNRT
Sbjct  163  RFGYILHTDNRT  174
```

Download GenPept Graphics — Next Previous Descriptions

Chain A, Cub1-egf-cub2 Domain Of Human Masp-1/3

Sequence ID: gi|193506834|pdb|3DEM|A **Length:** 278 **Number of Matches:** 1

See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 150 to 161 GenPept Graphics — Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
43.5 bits(95)	9e-04	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    RFGYILHTDNRT  12
            RFGYILHTDNRT
Sbjct  150  RFGYILHTDNRT  161
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: gi|194374073|dbj|BAG62349.1| **Length:** 354 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 143 to 154 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
43.5 bits(95)	0.001	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    RFGYILHTDNRT  12
            RFGYILHTDNRT
Sbjct  143  RFGYILHTDNRT  154
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Homo sapiens]

Sequence ID: gi|578807591|ref|XP_006713764.1| **Length:** 354 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 143 to 154 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
43.5 bits(95)	0.001	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    RFGYILHTDNRT  12
            RFGYILHTDNRT
Sbjct  143  RFGYILHTDNRT  154
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Mbl-Ficolin Associated Protein-1, Map-1 Aka Map44

Sequence ID: gi|400260714|pdb|4AQB|A **Length:** 361 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 150 to 161 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
43.5 bits(95)	0.001	12/12(100%)	12/12(100%)	0/12(0%)

```
Query  1    RFGYILHTDNRT  12
            RFGYILHTDNRT
Sbjct  150  RFGYILHTDNRT  161
```

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Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

MASP1_RFGYILHTDNRTCRV_NonMod

RID B9HUZBMB01R (Expires on 01-14 14:21 pm)

Query ID lcl|224324
Description None
Molecule type amino acid
Query Length 15

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

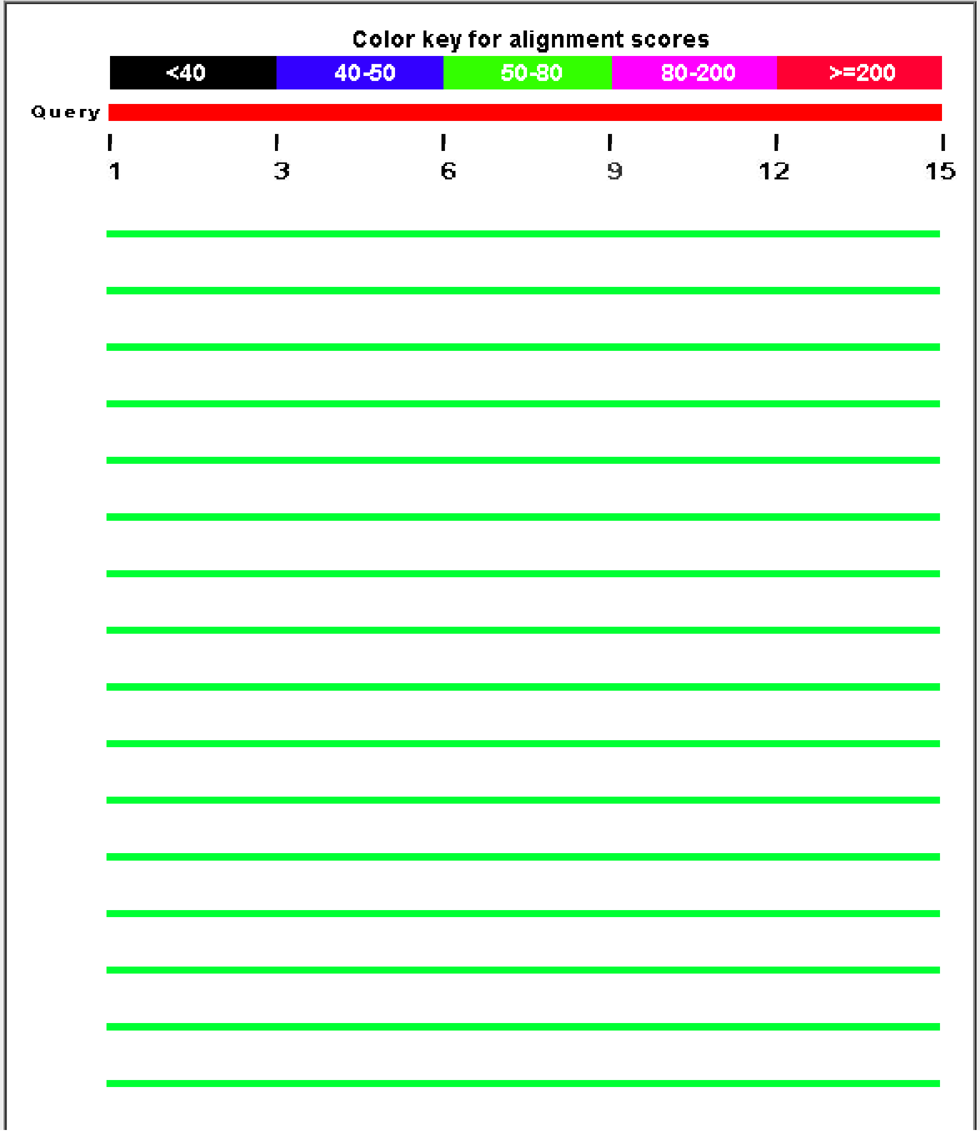
Graphic Summary

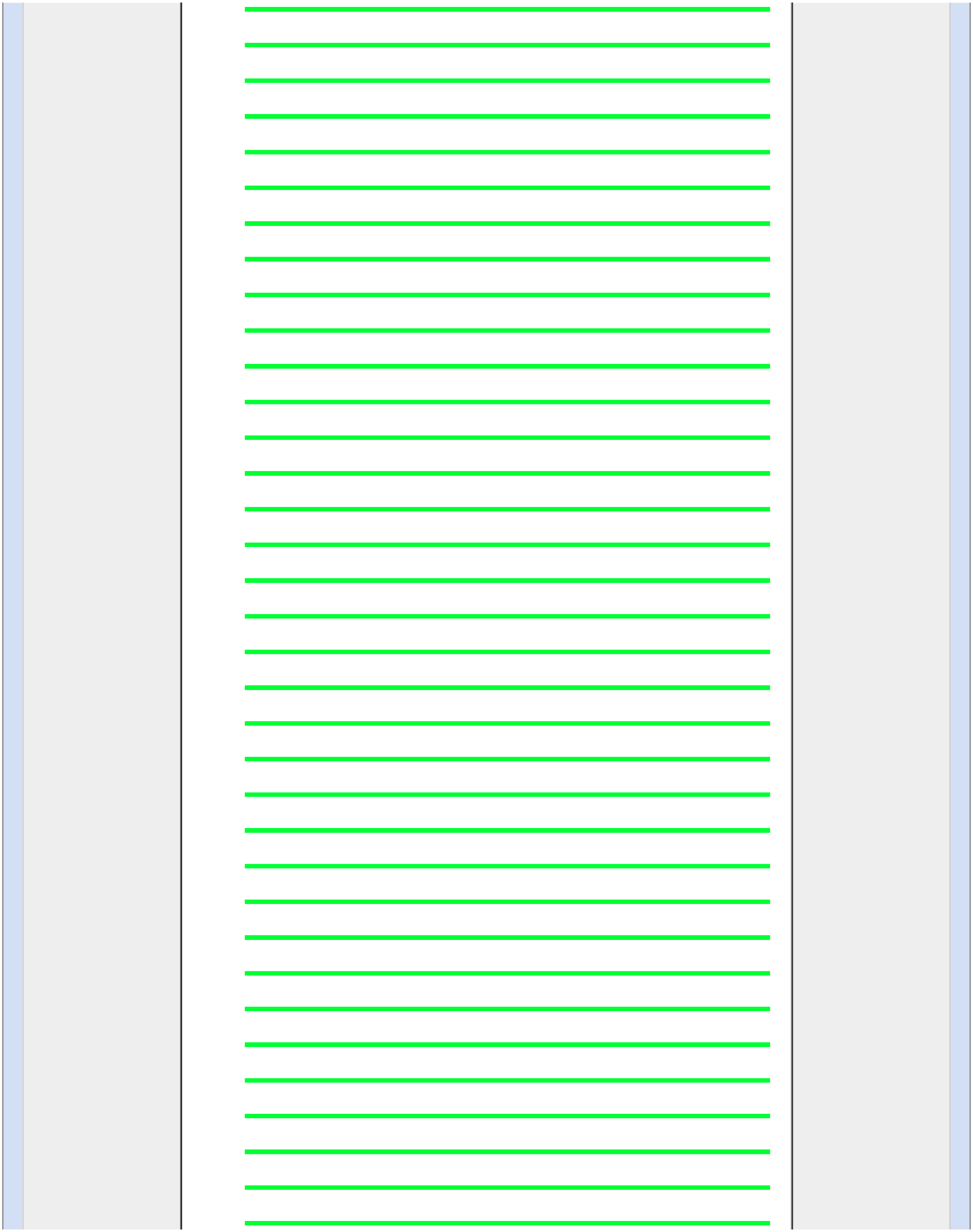
Show Conserved Domains

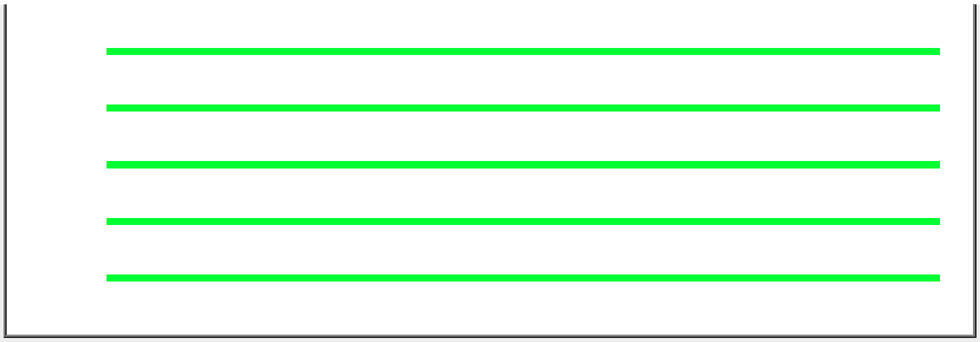
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊖Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Ra-reactive factor serine protease p100 [Rattus norvegicus]	54.1	54.1	100%	3e-07	100%	gi|2209345|AAB65832.1
☐	Chain A, Cub1-egf-cub2 Domain Of Human Masp-1/3 [Homo sapie	54.1	54.1	100%	3e-07	100%	gi|193506834|3DEM_A
☐	unnamed protein product [Homo sapiens]	54.1	54.1	100%	3e-07	100%	gi|194374073|BAG62349.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	3e-07	100%	gi|578807591|XP_006713764.1
☐	Chain A, Mbl-Ficolin Associated Protein-1, Map-1 Aka Map44 [Hom	54.1	54.1	100%	3e-07	100%	gi|400260714|4AQB_A
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	3e-07	100%	gi|507540683|XP_004654346.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [	54.1	54.1	100%	4e-07	100%	gi|655853895|XP_008264861.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X7 [	54.1	54.1	100%	4e-07	100%	gi|725565881|XP_010336013.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X7 [	54.1	54.1	100%	4e-07	100%	gi|675726053|XP_008979623.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|674036696|XP_008851360.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X5 [	54.1	54.1	100%	4e-07	100%	gi|641720317|XP_008149800.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [	54.1	54.1	100%	4e-07	100%	gi|640796916|XP_008054567.1
☐	mannan-binding lectin serine protease 1 isoform 3 precursor [Homo	54.1	54.1	100%	4e-07	100%	gi|73623026|NP_001027019.1
☐	PREDICTED: mannan-binding lectin serine protease 1-like isoform	54.1	54.1	100%	4e-07	100%	gi|594036350|XP_006042840.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|589944897|XP_006985135.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|586554872|XP_006925890.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [	54.1	54.1	100%	4e-07	100%	gi|584042008|XP_006765915.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|562856537|XP_006156800.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|560957130|XP_006201041.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|560925459|XP_006188912.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|558107313|XP_006084855.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|556747385|XP_005969146.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|555975459|XP_005899711.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|554564031|XP_005876336.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|548450456|XP_005675200.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|545865224|XP_005657168.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|545192257|XP_005601937.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|544410516|XP_005545503.1
☐							

	PREDICTED: mannan-binding lectin serine protease 1 isoform X8 [	54.1	54.1	100%	4e-07	100%	gi|528936770|XP_005201546.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 4 [C	54.1	54.1	100%	4e-07	100%	gi|478500665|XP_004424648.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 3 [O	54.1	54.1	100%	4e-07	100%	gi|466051806|XP_004278527.1
☐	hypothetical protein [Homo sapiens]	54.1	54.1	100%	4e-07	100%	gi|51476886|CAH18409.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [	54.1	54.1	100%	4e-07	100%	gi|332818681|XP_003310212.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 2 [N	54.1	54.1	100%	4e-07	100%	gi|332215099|XP_003256677.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|731216121|XP_010622449.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|514474780|XP_005006929.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|512902387|XP_004899716.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|724805505|XP_010350856.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|635086161|XP_008007690.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|544410514|XP_005545502.1
☐	unnamed protein product [Macaca fascicularis]	54.1	54.1	100%	4e-07	100%	gi|90081136|BAE90048.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|672071419|XP_008767026.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|532090712|XP_005331047.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|568994700|XP_006521892.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [	54.1	54.1	100%	4e-07	100%	gi|533136993|XP_005383312.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|694905534|XP_009445263.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|685527987|XP_009200178.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X6 [	54.1	54.1	100%	4e-07	100%	gi|725565879|XP_010336012.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 5 [N	54.1	54.1	100%	4e-07	100%	gi|332215105|XP_003256680.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X6 [	54.1	54.1	100%	4e-07	100%	gi|675726049|XP_008979622.1
☐	rCG36729, isoform CRA_b [Rattus norvegicus]	54.1	54.1	100%	4e-07	100%	gi|149019942|EDL78090.1
☐	hypothetical protein CB1_001118022 [Camelus ferus]	54.1	54.1	100%	4e-07	100%	gi|528758469|EPY78128.1
☐	hypothetical protein [Homo sapiens]	54.1	54.1	100%	4e-07	100%	gi|57997478|CAI46037.1
☐	MASP1 protein [Homo sapiens]	54.1	54.1	100%	4e-07	100%	gi|24981014|AAH39724.1
☐	PREDICTED: mannan-binding lectin serine protease 1-like isoform	54.1	54.1	100%	4e-07	100%	gi|594036348|XP_006042839.1
☐	PREDICTED: mannan-binding lectin serine protease 1-like isoform	54.1	54.1	100%	4e-07	100%	gi|594036346|XP_006042838.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X7 [	54.1	54.1	100%	4e-07	100%	gi|528936768|XP_005201545.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X5 [	54.1	54.1	100%	4e-07	100%	gi|725565877|XP_010336011.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X6 [	54.1	54.1	100%	4e-07	100%	gi|528936766|XP_005201544.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|617646016|XP_007532796.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X6 [	54.1	54.1	100%	4e-07	100%	gi|686714726|XP_009237913.1
☐	PREDICTED: mannan-binding lectin serine protease 1 [Galeopteru	54.1	54.1	100%	4e-07	100%	gi|667325189|XP_008589455.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100%	gi|640796914|XP_008054566.1
☐	unnamed protein product [Homo sapiens]	54.1	54.1	100%	4e-07	100%	gi|194385604|BAG65179.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|586554870|XP_006925889.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|560957128|XP_006201040.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|560925457|XP_006188911.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X5 [	54.1	54.1	100%	4e-07	100%	gi|528936764|XP_005201543.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|507927767|XP_004675138.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100%	gi|505778530|XP_004603078.1
☐	rCG36729, isoform CRA_a [Rattus norvegicus]	54.1	54.1	100%	4e-07	100%	gi|149019941|EDL78089.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [	54.1	54.1	100%	4e-07	100%	gi|641720315|XP_008149799.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X4 [	54.1	54.1	100%	4e-07	100%	gi|528936762|XP_005201542.1

☐	mannan-binding lectin serine peptidase 1 (C4/C2 activating compor	54.1	54.1	100%	4e-07	100% gi|119598556|EAW78150.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100% gi|507540681|XP_004654345.1
☐	PREDICTED: LOW QUALITY PROTEIN: mannan-binding lectin ser	54.1	54.1	100%	4e-07	100% gi|297287139|XP_002808386.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X5 [	54.1	54.1	100%	4e-07	100% gi|686714724|XP_009237912.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100% gi|675687274|XP_008954144.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100% gi|533136991|XP_005383311.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 4 [G	54.1	54.1	100%	4e-07	100% gi|426343256|XP_004038230.1
☐	PREDICTED: LOW QUALITY PROTEIN: mannan-binding lectin ser	54.1	54.1	100%	4e-07	100% gi|395839796|XP_003804164.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform 4 [N	54.1	54.1	100%	4e-07	100% gi|332215103|XP_003256679.1
☐	MASP-3 protein [Rattus norvegicus]	54.1	54.1	100%	4e-07	100% gi|27527940|CAD32171.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100% gi|731216119|XP_010622448.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [	54.1	54.1	100%	4e-07	100% gi|724805503|XP_010350848.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [	54.1	54.1	100%	4e-07	100% gi|674036694|XP_008851350.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100% gi|664750525|XP_008532698.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X3 [	54.1	54.1	100%	4e-07	100% gi|641720313|XP_008149798.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100% gi|640796912|XP_008054564.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [	54.1	54.1	100%	4e-07	100% gi|635086159|XP_008007689.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [	54.1	54.1	100%	4e-07	100% gi|545865216|XP_005657166.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100% gi|602726051|XP_007448486.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100% gi|593732157|XP_007111601.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [	54.1	54.1	100%	4e-07	100% gi|589944895|XP_006985134.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100% gi|584042010|XP_006765916.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100% gi|554564029|XP_005876335.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100% gi|548450449|XP_005675199.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X1 [	54.1	54.1	100%	4e-07	100% gi|545192255|XP_001499679.3
☐	PREDICTED: mannan-binding lectin serine protease 1 [Microtus oc	54.1	54.1	100%	4e-07	100% gi|532000597|XP_005344817.1
☐	PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [	54.1	54.1	100%	4e-07	100% gi|528936758|XP_005201540.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Ra-reactive factor serine protease p100 [Rattus norvegicus]

Sequence ID: gi|2209345|gb|AAB65832.1| **Length:** 212 **Number of Matches:** 1

Range 1: 163 to 177 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	3e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    RFGYILHTDNRTCRV  15
            RFGYILHTDNRTCRV
Sbjct  163  RFGYILHTDNRTCRV  177
```

Related Information

Gene - associated gene details

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Cub1-egf-cub2 Domain Of Human Masp-1/3

Sequence ID: gi|193506834|pdb|3DEM|A **Length:** 278 **Number of Matches:** 1

See 1 more title(s)

Range 1: 150 to 164 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	3e-07	15/15(100%)	15/15(100%)	0/15(0%)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

```
Query  1    RFGYILHTDNRTCRV  15
            RFGYILHTDNRTCRV
Sbjct  150  RFGYILHTDNRTCRV  164
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: gi|194374073|dbj|BAG62349.1| **Length:** 354 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 143 to 157 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	3e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    RFGYILHTDNRTCRV  15
            RFGYILHTDNRTCRV
Sbjct  143  RFGYILHTDNRTCRV  157
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: mannan-binding lectin serine protease 1 isoform X2 [Homo sapiens]

Sequence ID: gi|578807591|ref|XP_006713764.1| **Length:** 354 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 143 to 157 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	3e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    RFGYILHTDNRTCRV  15
            RFGYILHTDNRTCRV
Sbjct  143  RFGYILHTDNRTCRV  157
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Mbl-Ficolin Associated Protein-1, Map-1 Aka Map44

Sequence ID: gi|400260714|pdb|4AQB|A **Length:** 361 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 150 to 164 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.1 bits(120)	3e-07	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    RFGYILHTDNRTCRV  15
            RFGYILHTDNRTCRV
Sbjct  150  RFGYILHTDNRTCRV  164
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVJ4WU4Y01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   Formatting options   Download   How to read this page   Blast report description

MEGF8_RALLTDVSSVALGSRR_Mod

RID BVJ4WU4Y01R (Expires on 01-21 10:16 am)

Query ID lcl|348617
Description None
Molecule type amino acid
Query Length 16

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

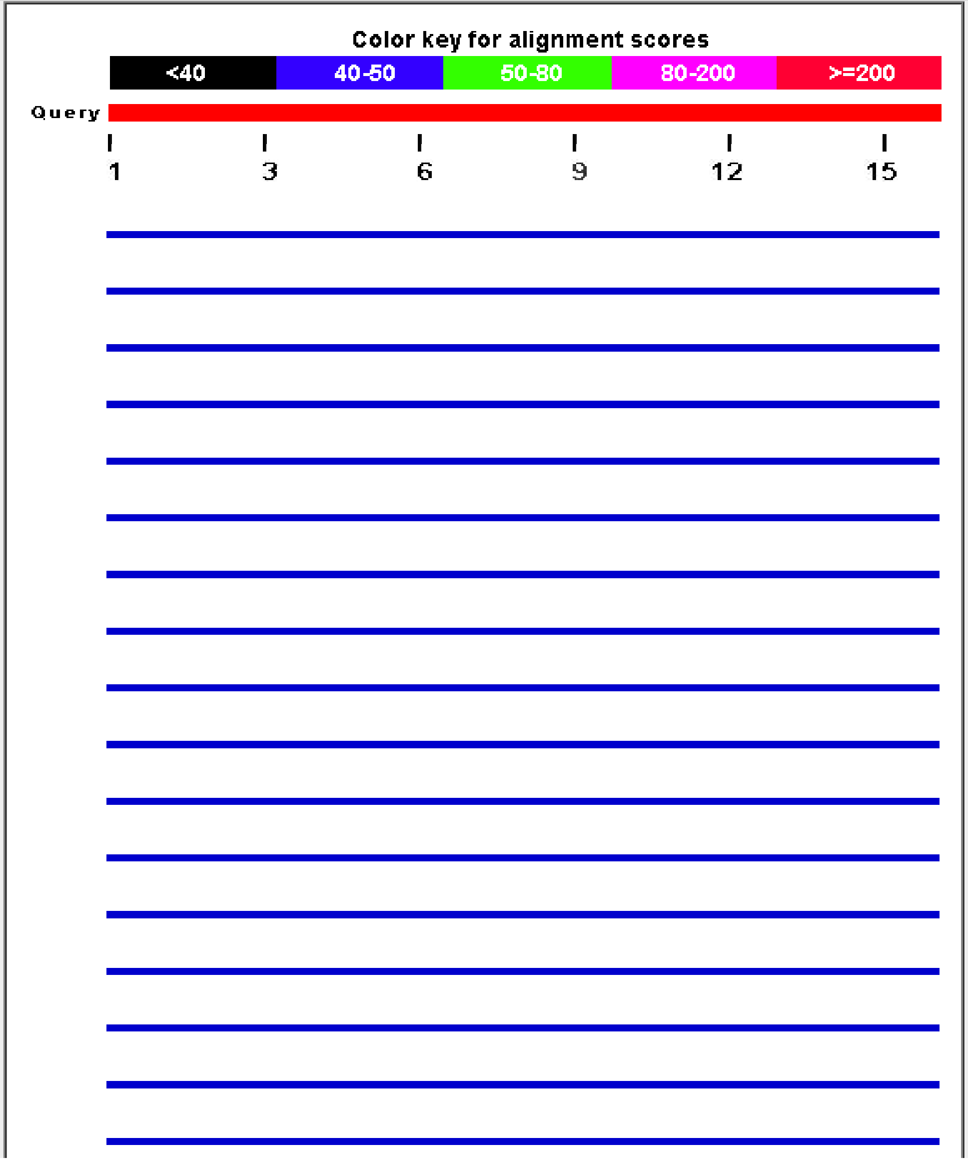
Graphic Summary

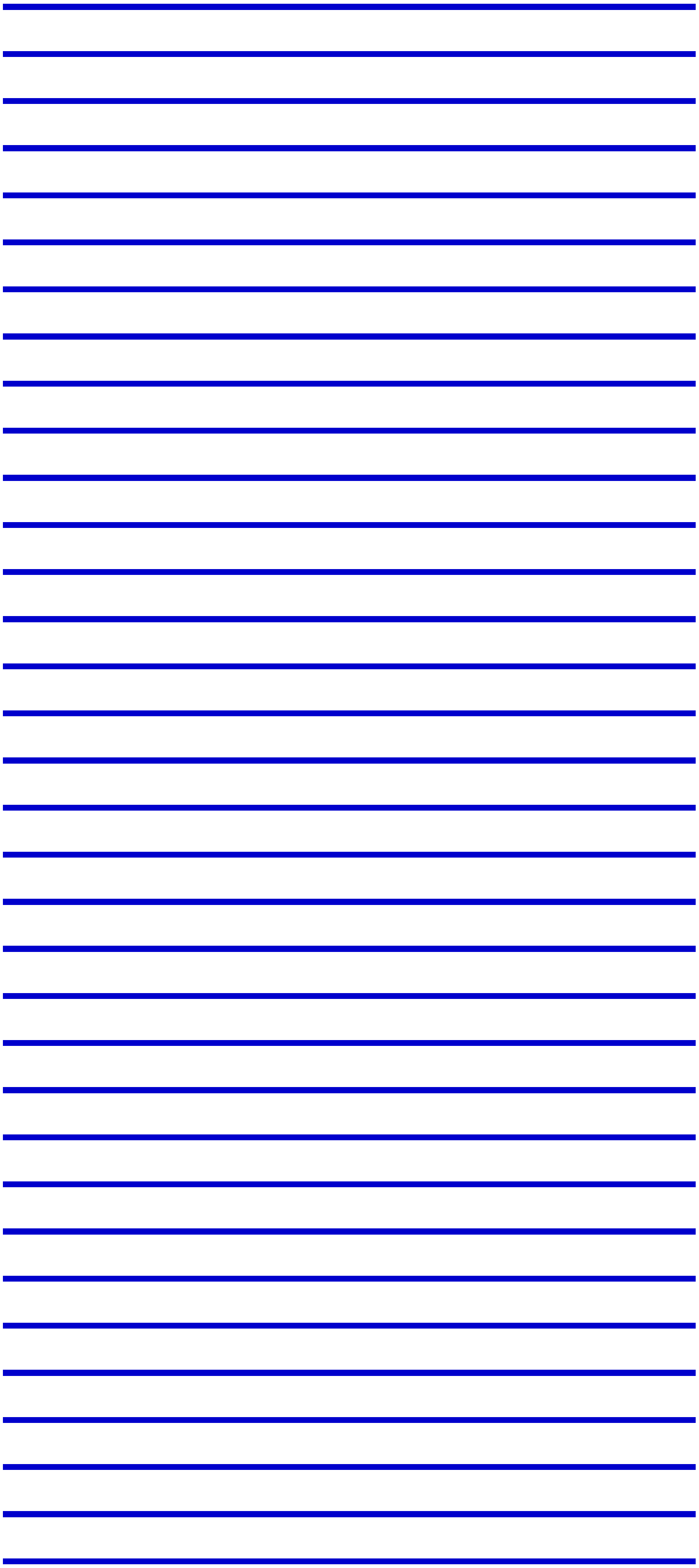
Show Conserved Domains

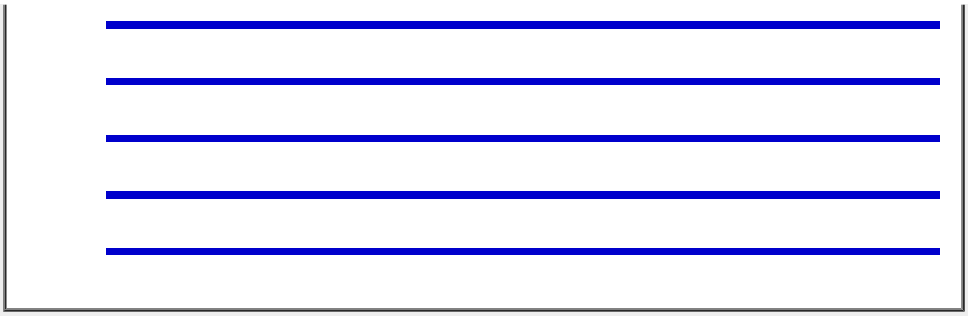
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	multiple epidermal growth factor-like domain protein 8 [Cricetulus griseus]	47.3	47.3	100%	9e-05	94%	ERE28575.1
☐	EGF-like-domain, multiple 4 [Rattus norvegicus]	47.3	47.3	100%	9e-05	94%	EDM08030.1
☐	TPA: Multiple epidermal growth factor-like domains protein 8-like [Bos taurus]	47.3	47.3	100%	9e-05	94%	DAA19729.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Sarcop	47.3	47.3	100%	9e-05	94%	XP_003766871.1
☐	EGF-like-domain, multiple 4, isoform CRA_b [Homo sapiens]	47.3	47.3	100%	9e-05	94%	EAW57133.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_007647681.1
☐	EGF-like-domain, multiple 4, isoform CRA_a [Homo sapiens]	47.3	47.3	100%	9e-05	94%	EAW57132.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_010945027.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_007102249.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_008707927.1
☐	mCG145770 [Mus musculus]	47.3	47.3	100%	9e-05	94%	EDL24275.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_010945026.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_010329368.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_009433972.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_009192884.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_008962406.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_007995187.1
☐	EGF domain-containing protein [Homo sapiens]	47.3	47.3	100%	9e-05	94%	AAP35084.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_004873071.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_004884074.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple EGF-like-domains 8 [Panthe	47.3	47.3	100%	9e-05	94%	XP_007099373.1
☐	Multiple epidermal growth factor-like domains protein 8 [Myotis davidii]	47.3	47.3	100%	9e-05	94%	ELK32302.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_003281030.2
☐	PREDICTED: LOW QUALITY PROTEIN: multiple EGF-like-domains 8 [Equus	47.3	47.3	100%	9e-05	94%	XP_005596735.1
☐	Multiple epidermal growth factor-like domains 8 [Cricetulus griseus]	47.3	47.3	100%	9e-05	94%	EGW10451.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_008844639.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Orycter	47.3	47.3	100%	9e-05	94%	XP_007941322.1
☐	Multiple epidermal growth factor-like domains protein 8 [Tupaia chinensis]	47.3	47.3	100%	9e-05	94%	ELW71057.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_007102248.1

☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_004015751.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_005971449.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Echinoj	47.3	47.3	100%	9e-05	94%	XP_004710580.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_006142201.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Sorex a	47.3	47.3	100%	9e-05	94%	XP_004620816.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Myotis	47.3	47.3	100%	9e-05	94%	XP_005883977.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Trichec	47.3	47.3	100%	9e-05	94%	XP_004388865.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Myotis	47.3	47.3	100%	9e-05	94%	XP_006761144.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_007623649.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_005001354.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_004318216.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_006103655.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_005412420.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_005338206.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_005087119.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_010585188.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_002924008.1
☐	PREDICTED: multiple EGF-like-domains 8 isoform X3 [Sus scrofa]	47.3	47.3	100%	9e-05	94%	XP_005655932.1
☐	Multiple epidermal growth factor-like domains protein 8 [Fukomys damarensis	47.3	47.3	100%	9e-05	94%	KFO33644.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_010979734.1
☐	hypothetical protein EGK_10681 [Macaca mulatta]	47.3	47.3	100%	9e-05	94%	EHH30092.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Jaculus	47.3	47.3	100%	9e-05	94%	XP_004670378.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_005692637.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Lipotes	47.3	47.3	100%	9e-05	94%	XP_007458757.1
☐	hypothetical protein EGM_09795 [Macaca fascicularis]	47.3	47.3	100%	9e-05	94%	EHH59637.1
☐	multiple epidermal growth factor-like domains protein 8 isoform 2 precursor [H	47.3	47.3	100%	9e-05	94%	NP_001401.2
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_010329367.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_010945025.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Pteropu	47.3	47.3	100%	9e-05	94%	XP_006903917.1
☐	MEGF8 [Homo sapiens]	47.3	47.3	100%	9e-05	94%	BAA32469.2
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_009433968.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Erinace	47.3	47.3	100%	9e-05	94%	XP_007532999.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_006228426.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_004873069.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_004884072.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Ochoto	47.3	47.3	100%	9e-05	94%	XP_004598048.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_003464586.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_010621622.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Galeop	47.3	47.3	100%	9e-05	94%	XP_008565470.1
☐	RecName: Full=Multiple epidermal growth factor-like domains protein 8; Short	47.3	47.3	100%	9e-05	94%	Q9QYP0.2
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_010840927.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_009192883.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_008962404.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_008844638.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Eptesic	47.3	47.3	100%	9e-05	94%	XP_008158439.1

☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_007995186.1
☐	multiple epidermal growth factor-like domains protein 8 precursor [Mus muscu	47.3	47.3	100%	9e-05	94%	NP_001153872.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Balaen	47.3	47.3	100%	9e-05	94%	XP_007168092.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_007102247.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_006988122.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple EGF-like-domains 8 [Felis c	47.3	47.3	100%	9e-05	94%	XP_006941287.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_006103654.1
☐	PREDICTED: multiple EGF-like-domains 8 isoform X1 [Sus scrofa]	47.3	47.3	100%	9e-05	94%	XP_005655930.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_005412419.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_005338205.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Microtu	47.3	47.3	100%	9e-05	94%	XP_005361208.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_005087118.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Orcinus	47.3	47.3	100%	9e-05	94%	XP_004271289.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Gorilla	47.3	47.3	100%	9e-05	94%	XP_004060891.1
☐	multiple epidermal growth factor-like domains protein 8 precursor [Rattus norv	47.3	47.3	100%	9e-05	94%	NP_446080.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_010822001.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_006988121.1
☐	Multiple epidermal growth factor-like domains 8 [Pteropus alecto]	47.3	47.3	100%	9e-05	94%	ELK19616.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_008247909.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Tarsius	47.3	47.3	100%	9e-05	94%	XP_008060623.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_004767868.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 isoform	47.3	47.3	100%	9e-05	94%	XP_010813563.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_008530249.1
☐	Multiple epidermal growth factor-like domains 8 [Heterocephalus glaber]	47.3	47.3	100%	9e-05	94%	EHB02528.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth factor-like	47.3	47.3	100%	9e-05	94%	XP_006871573.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein 8 [Condyl	47.3	47.3	100%	9e-05	94%	XP_004693985.1

Alignments

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multiple epidermal growth factor-like domain protein 8, partial [Cricetulus griseus]

Sequence ID: gb|ERE28575.1| **Length:** 639 **Number of Matches:** 1

Related Information

Range 1: 365 to 380 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.3 bits(104)	9e-05	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RALLTDVSSVALGSRR  16
            RALLT+VSSVALGSRR
Sbjct  365  RALLTNVSSVALGSRR  380
```

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EGF-like-domain, multiple 4 [Rattus norvegicus]

Sequence ID: gb|EDM08030.1| **Length:** 1221 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 807 to 822 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.3 bits(104)	9e-05	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RALLTDVSSVALGSRR  16
            RALLT+VSSVALGSRR
Sbjct  807  RALLTNVSSVALGSRR  822
```

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TPA: Multiple epidermal growth factor-like domains protein 8-like [Bos taurus]

Sequence ID: tpg|DAA19729.1| **Length:** 1397 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 235 to 250 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.3 bits(104)	9e-05	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RALLTDVSSVALGSRR  16
            RALLT+VSSVALGSRR
Sbjct  235  RALLTNVSSVALGSRR  250
```

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PREDICTED: multiple epidermal growth factor-like domains protein 8, partial [Sarcophilus harrisii]

Sequence ID: ref|XP_003766871.1| **Length:** 1566 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 230 to 245 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.3 bits(104)	9e-05	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RALLTDVSSVALGSRR  16
            RALLT+VSSVALGSRR
Sbjct  230  RALLTNVSSVALGSRR  245
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

EGF-like-domain, multiple 4, isoform CRA_b [Homo sapiens]

Sequence ID: gb|EAW57133.1| **Length:** 2091 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 512 to 527 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.3 bits(104)	9e-05	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RALLTDVSSVALGSRR  16
            RALLT+VSSVALGSRR
Sbjct  512  RALLTNVSSVALGSRR  527
```

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - B9G6T51401R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

YouTube How to read this page Blast report description

MEGF8_RALLTNVSSVALGSRR_NonMod

RID B9G6T51401R (Expires on 01-14 13:53 pm)

Query ID lcl|119030
Description None
Molecule type amino acid
Query Length 16

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

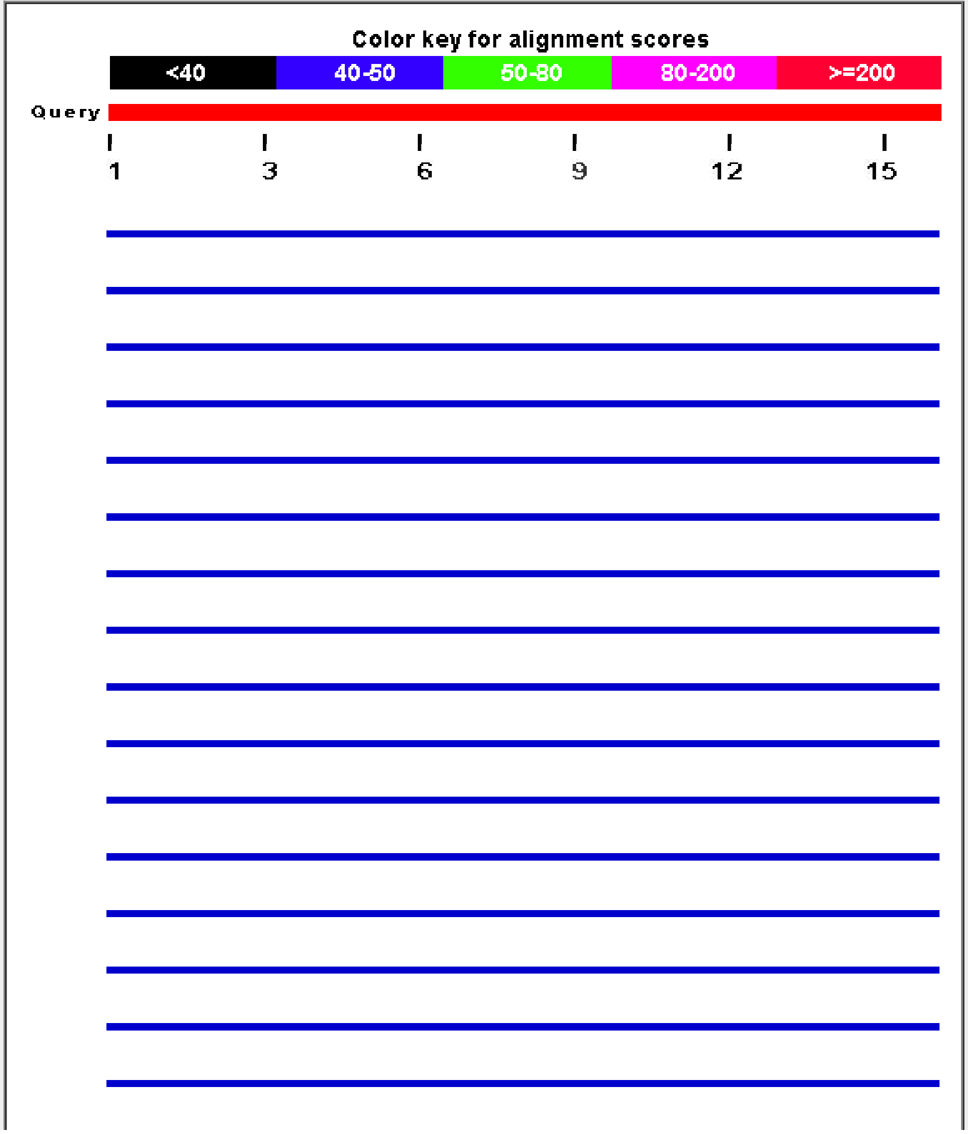
Graphic Summary

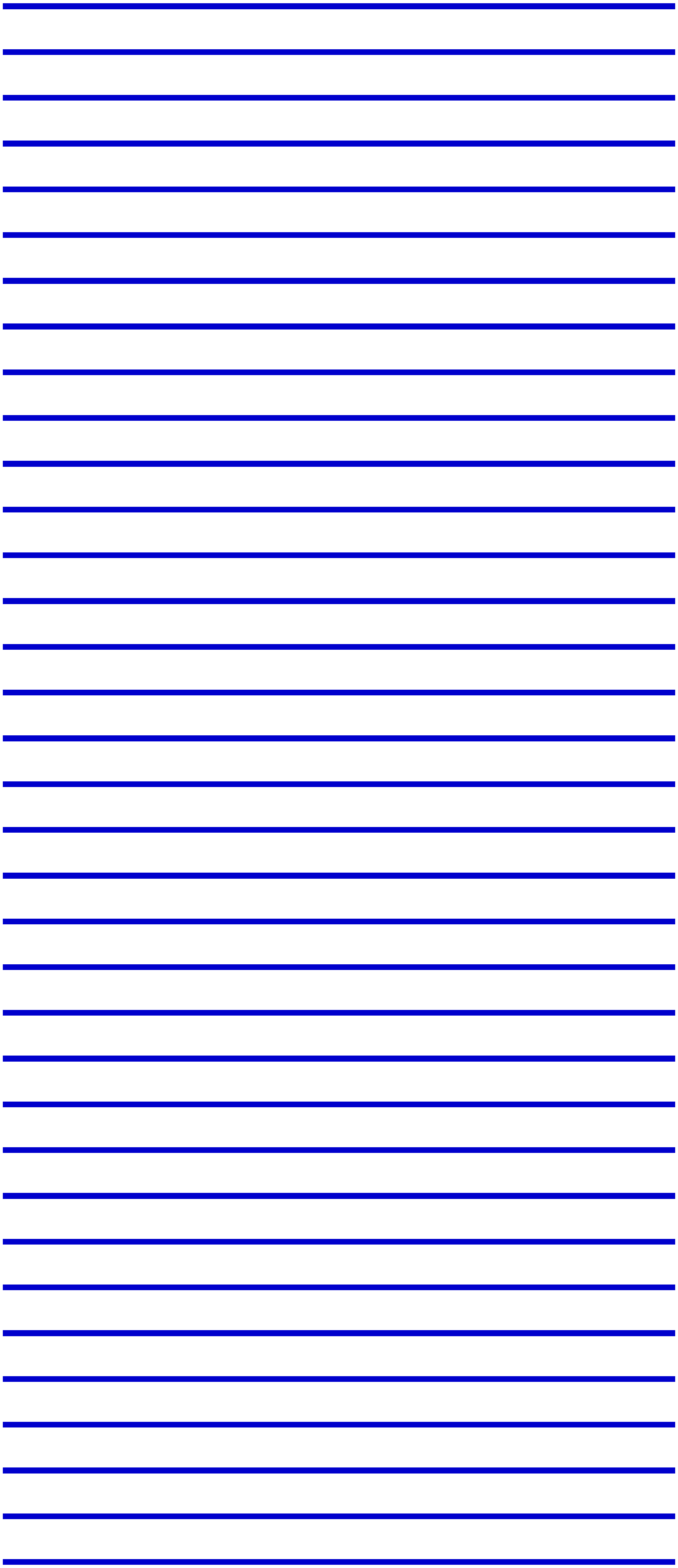
Show Conserved Domains

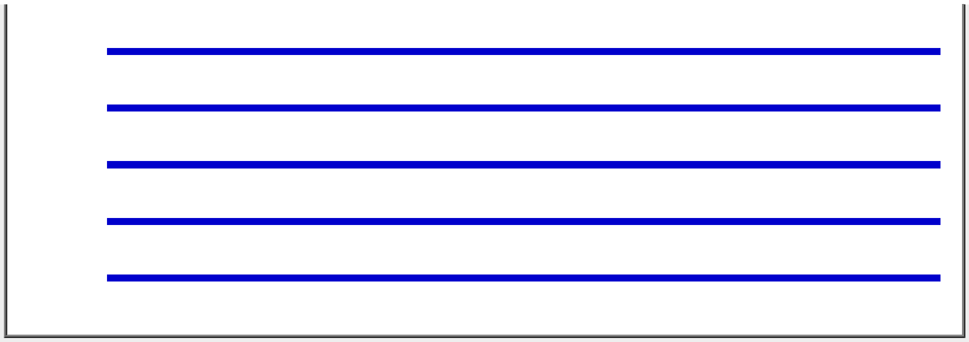
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	multiple epidermal growth factor-like domain protein 8 [Cricetulus g	49.8	49.8	100%	1e-05	100%	gi|537058530|ERE28575.1
☐	EGF-like-domain, multiple 4 [Rattus norvegicus]	49.8	49.8	100%	1e-05	100%	gi|149056599|EDM08030.1
☐	TPA: Multiple epidermal growth factor-like domains protein 8-like [	49.8	49.8	100%	1e-05	100%	gi|296477614|DAA19729.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|395529545|XP_003766871.1
☐	EGF-like-domain, multiple 4, isoform CRA_b [Homo sapiens]	49.8	49.8	100%	1e-05	100%	gi|119577537|EAW57133.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|625214225|XP_007647681.1
☐	EGF-like-domain, multiple 4, isoform CRA_a [Homo sapiens]	49.8	49.8	100%	1e-05	100%	gi|119577536|EAW57132.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|593711377|XP_007102249.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|671034203|XP_008707927.1
☐	mCG145770 [Mus musculus]	49.8	49.8	100%	1e-05	100%	gi|148692328|EDL24275.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|725605478|XP_010329368.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|694975356|XP_009433972.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|685608722|XP_009192884.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|675714718|XP_008962406.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|635039364|XP_007995187.1
☐	EGF domain-containing protein [Homo sapiens]	49.8	49.8	100%	1e-05	100%	gi|30841835|AAP35084.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|513023676|XP_004873071.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|512838904|XP_004884074.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple EGF-like-domain	49.8	49.8	100%	1e-05	100%	gi|591321080|XP_007099373.1
☐	Multiple epidermal growth factor-like domains protein 8 [Myotis dav	49.8	49.8	100%	1e-05	100%	gi|432106646|ELK32302.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|441656214|XP_003281030.2
☐	PREDICTED: LOW QUALITY PROTEIN: multiple EGF-like-domain	49.8	49.8	100%	1e-05	100%	gi|545176793|XP_005596735.1
☐	Multiple epidermal growth factor-like domains 8 [Cricetulus griseus]	49.8	49.8	100%	1e-05	100%	gi|344254347|EGW10451.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|674074682|XP_008844639.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|634854516|XP_007941322.1
☐	Multiple epidermal growth factor-like domains protein 8 [Tupaia chi	49.8	49.8	100%	1e-05	100%	gi|444730683|ELW71057.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|593711375|XP_007102248.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|426243838|XP_004015751.1
☐							

	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|556752106|XP_005971449.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|507680955|XP_004710580.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|562824919|XP_006142201.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|505854790|XP_004620816.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|554585066|XP_005883977.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|471414659|XP_004388865.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|584082657|XP_006761144.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|625264390|XP_007623649.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|514450989|XP_005001354.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|470619649|XP_004318216.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|558192196|XP_006103655.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|533199656|XP_005412420.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|532105233|XP_005338206.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|524974566|XP_005087119.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|731460637|XP_010585188.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|301777173|XP_002924008.1
☐	PREDICTED: multiple EGF-like-domains 8 isoform X3 [Sus scrofa]	49.8	49.8	100%	1e-05	100%	gi|545831091|XP_005655932.1
☐	Multiple epidermal growth factor-like domains protein 8 [Fukomys d	49.8	49.8	100%	1e-05	100%	gi|676279706|KFO33644.1
☐	hypothetical protein EGK_10681 [Macaca mulatta]	49.8	49.8	100%	1e-05	100%	gi|355703601|EHH30092.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|507573586|XP_004670378.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|548504796|XP_005692637.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|602693338|XP_007458757.1
☐	hypothetical protein EGM_09795 [Macaca fascicularis]	49.8	49.8	100%	1e-05	100%	gi|355755890|EHH59637.1
☐	multiple epidermal growth factor-like domains protein 8 isoform 2 pr	49.8	49.8	100%	1e-05	100%	gi|145701025|NP_001401.2
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|725605476|XP_010329367.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|586519074|XP_006903917.1
☐	MEGF8 [Homo sapiens]	49.8	49.8	100%	1e-05	100%	gi|58801254|BAA32469.2
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|694975350|XP_009433968.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|617646624|XP_007532999.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|564326450|XP_006228426.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|513023671|XP_004873069.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|512838897|XP_004884072.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|504177813|XP_004598048.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|348557558|XP_003464586.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|731214348|XP_010621622.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|667255277|XP_008565470.1
☐	RecName: Full=Multiple epidermal growth factor-like domains prote	49.8	49.8	100%	1e-05	100%	gi|218511692|Q9QYP0.2
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|685608720|XP_009192883.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|675714711|XP_008962404.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|674074680|XP_008844638.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|641735729|XP_008158439.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|635039362|XP_007995186.1
☐	multiple epidermal growth factor-like domains protein 8 precursor [M	49.8	49.8	100%	1e-05	100%	gi|237874245|NP_001153872.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|594629019|XP_007168092.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|593711373|XP_007102247.1

☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|589950942|XP_006988122.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple EGF-like-domain	49.8	49.8	100%	1e-05	100%	gi|587014011|XP_006941287.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|558192191|XP_006103654.1
☐	PREDICTED: multiple EGF-like-domains 8 isoform X1 [Sus scrofa]	49.8	49.8	100%	1e-05	100%	gi|545831085|XP_005655930.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|533199654|XP_005412419.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|532105231|XP_005338205.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|532036646|XP_005361208.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|524974564|XP_005087118.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|466016225|XP_004271289.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|426388952|XP_004060891.1
☐	multiple epidermal growth factor-like domains protein 8 precursor [F	49.8	49.8	100%	1e-05	100%	gi|472824971|NP_446080.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|589950940|XP_006988121.1
☐	Multiple epidermal growth factor-like domains 8 [Pteropus alecto]	49.8	49.8	100%	1e-05	100%	gi|431922711|ELK19616.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|655889437|XP_008247909.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|640808207|XP_008060623.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|511896543|XP_004767868.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|664745816|XP_008530249.1
☐	Multiple epidermal growth factor-like domains 8 [Heterocephalus gla	49.8	49.8	100%	1e-05	100%	gi|351699609|EHB02528.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|586482113|XP_006871573.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|507980664|XP_004693985.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|585714714|XP_006901022.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|478532502|XP_004440401.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|694975358|XP_003953558.2
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|555994565|XP_005909034.1
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|686759192|XP_009230946.1
☐	PREDICTED: multiple epidermal growth factor-like domains protein	49.8	49.8	100%	1e-05	100%	gi|675714722|XP_003811809.2
☐	PREDICTED: LOW QUALITY PROTEIN: multiple epidermal growth	49.8	49.8	100%	1e-05	100%	gi|544511660|XP_005589436.1

Alignments

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multiple epidermal growth factor-like domain protein 8, partial [Cricetulus griseus]

Sequence ID: gi|537058530|gb|ERE28575.1| **Length:** 639 **Number of Matches:** 1

Related Information

Range 1: 365 to 380 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	1e-05	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RALLTNVSSVALGSRR  16
            RALLTNVSSVALGSRR
Sbjct  365  RALLTNVSSVALGSRR  380
```

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EGF-like-domain, multiple 4 [Rattus norvegicus]

Sequence ID: gi|149056599|gb|EDM08030.1| **Length:** 1221 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 807 to 822 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	1e-05	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RALLTNVSSVALGSRR  16
```

```
                 RALLTNVSSVALGSRR
Sbjct  807   RALLTNVSSVALGSRR  822
```

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TPA: Multiple epidermal growth factor-like domains protein 8-like [Bos taurus]

Sequence ID: gi|296477614|tpg|DAA19729.1| **Length:** 1397 **Number of Matches:** 1

Range 1: 235 to 250 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	1e-05	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1     RALLTNVSSVALGSRR  16
             RALLTNVSSVALGSRR
Sbjct  235   RALLTNVSSVALGSRR  250
```

Related Information

Gene - associated gene details

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PREDICTED: multiple epidermal growth factor-like domains protein 8, partial [Sarcophilus harrisii]

Sequence ID: gi|395529545|ref|XP_003766871.1| **Length:** 1566 **Number of Matches:** 1

Range 1: 230 to 245 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	1e-05	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1     RALLTNVSSVALGSRR  16
             RALLTNVSSVALGSRR
Sbjct  230   RALLTNVSSVALGSRR  245
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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EGF-like-domain, multiple 4, isoform CRA_b [Homo sapiens]

Sequence ID: gi|119577537|gb|EAW57133.1| **Length:** 2091 **Number of Matches:** 1

Range 1: 512 to 527 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	1e-05	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1     RALLTNVSSVALGSRR  16
             RALLTNVSSVALGSRR
Sbjct  512   RALLTNVSSVALGSRR  527
```

Related Information

Gene - associated gene details

BLAST ®

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BVJ667M501R**

Your search parameters were adjusted to search for a short input sequence.

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MMRN1_KFNPGAESVVLSDSTLKF_Mod

RID BVJ667M501R (Expires on 01-21 10:17 am)

Query ID	lcl|359957	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	18	**Program**	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

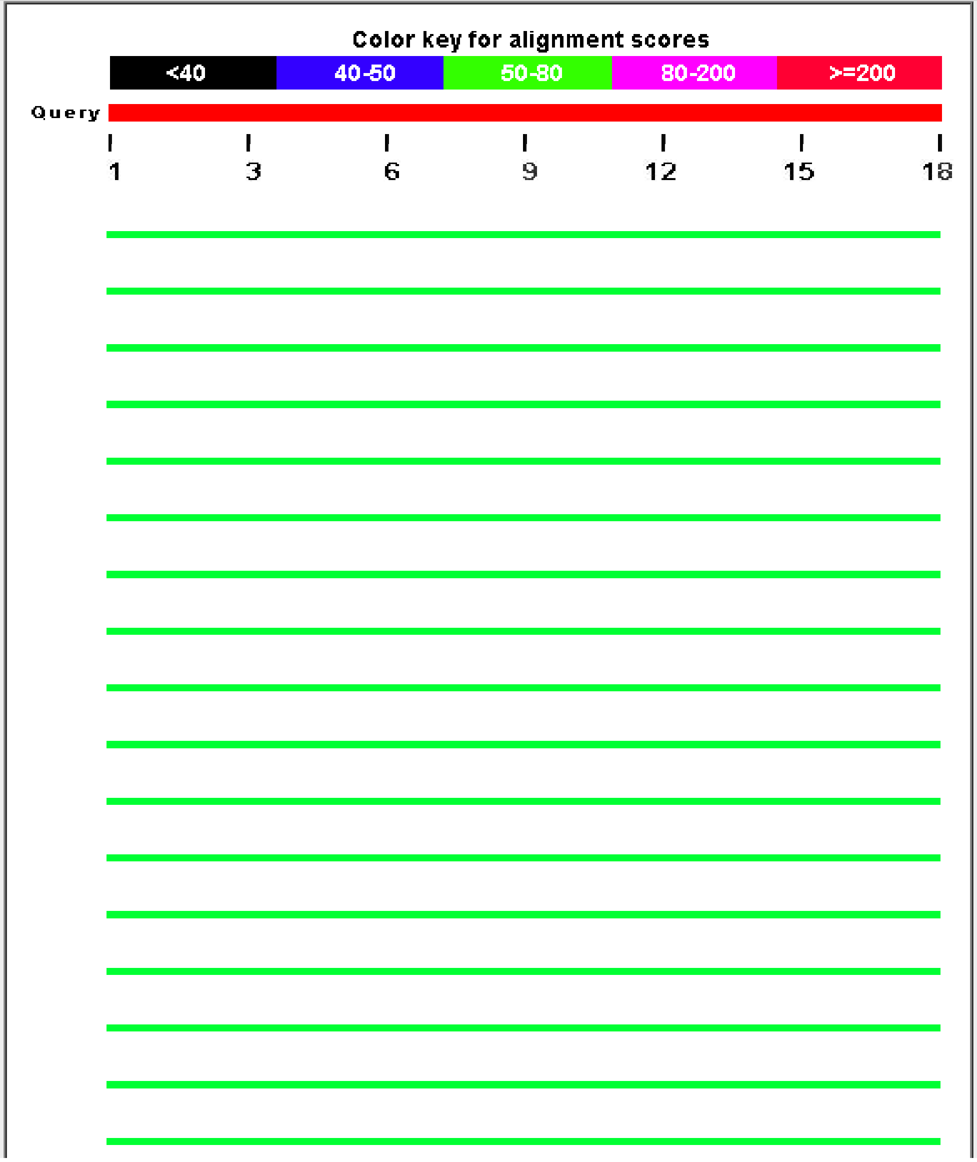
Graphic Summary

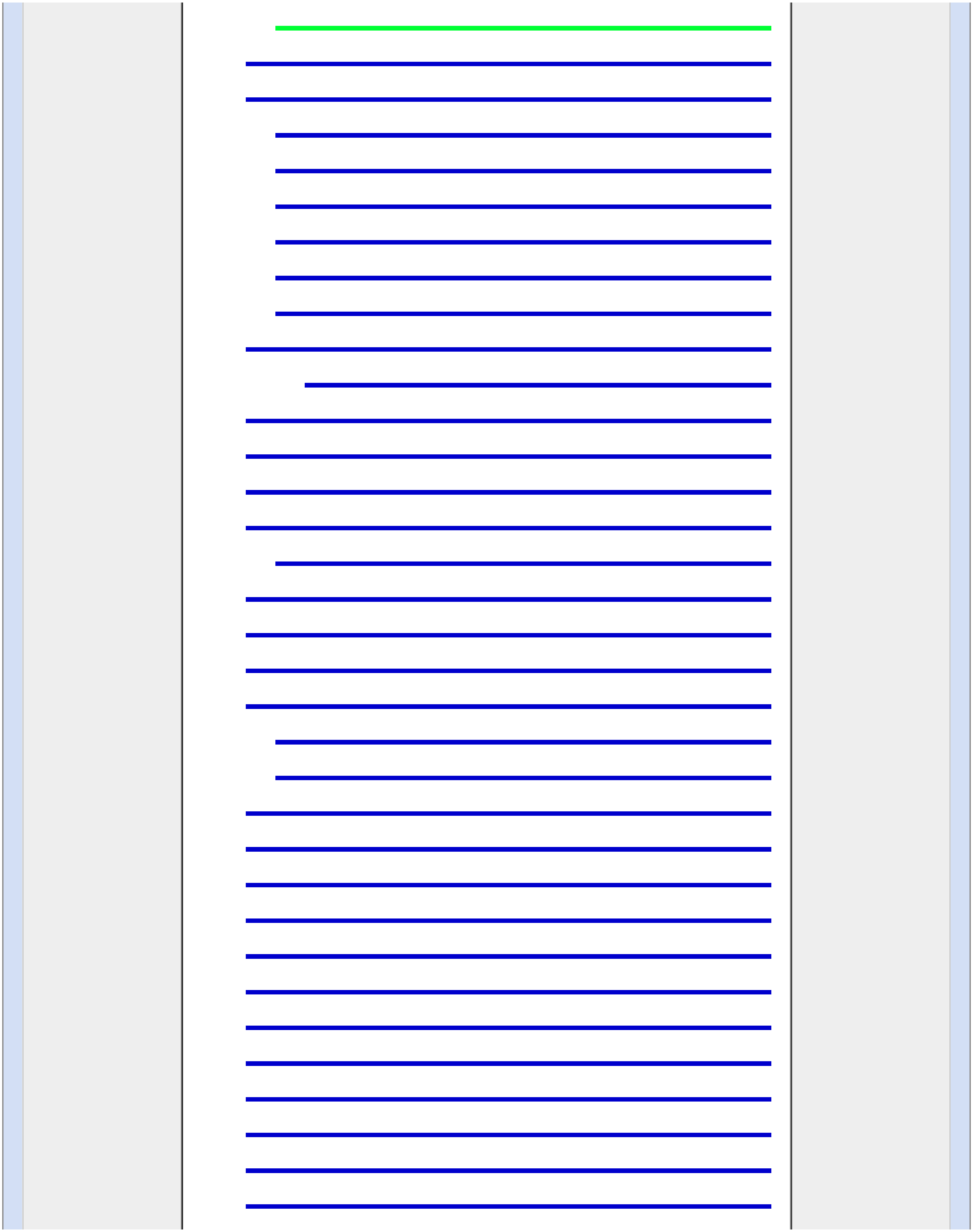
Show Conserved Domains

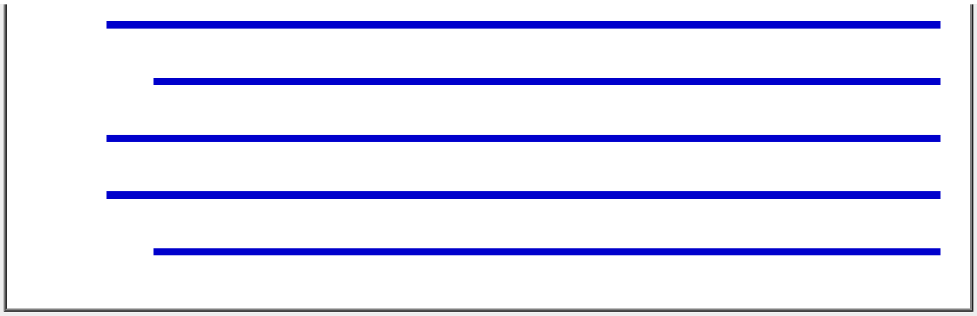
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	multimerin 1, isoform CRA_a [Homo sapiens]	55.4	55.4	100%	2e-07	94%	EAX06037.1
☐	unnamed protein product [Homo sapiens]	55.4	55.4	100%	2e-07	94%	BAC86201.1
☐	PREDICTED: multimerin-1-like [Galeopterus variegatus]	55.4	55.4	100%	2e-07	94%	XP_008591205.1
☐	PREDICTED: multimerin-1 isoform X2 [Pan troglodytes]	55.4	55.4	100%	2e-07	94%	XP_009446302.1
☐	PREDICTED: multimerin-1 isoform X1 [Homo sapiens]	55.4	55.4	100%	2e-07	94%	XP_005262913.1
☐	PREDICTED: LOW QUALITY PROTEIN: multimerin-1 [Pongo abelii]	55.4	55.4	100%	2e-07	94%	XP_002815014.1
☐	prepromultimerin [Homo sapiens]	55.4	55.4	100%	2e-07	94%	AAC52065.1
☐	multimerin-1 precursor [Homo sapiens]	55.4	55.4	100%	2e-07	94%	NP_031377.2
☐	PREDICTED: multimerin-1 [Gorilla gorilla gorilla]	55.4	55.4	100%	2e-07	94%	XP_004039176.1
☐	Multimerin 1 [Homo sapiens]	55.4	55.4	100%	2e-07	94%	AAH63848.1
☐	PREDICTED: multimerin-1 isoform 1 [Nomascus leucogenys]	55.4	55.4	100%	2e-07	94%	XP_003257586.1
☐	PREDICTED: multimerin-1 isoform X1 [Pan troglodytes]	55.4	55.4	100%	2e-07	94%	XP_517342.2
☐	Multimerin-1 [Myotis brandtii]	52.0	52.0	100%	3e-06	89%	EPQ17910.1
☐	PREDICTED: multimerin-1 [Myotis lucifugus]	52.0	52.0	100%	3e-06	89%	XP_006084681.1
☐	PREDICTED: multimerin-1 [Myotis brandtii]	52.0	52.0	100%	3e-06	89%	XP_005882685.1
☐	PREDICTED: multimerin-1 [Rhinopithecus roxellana]	52.0	52.0	100%	3e-06	89%	XP_010374576.1
☐	PREDICTED: multimerin-1 [Saimiri boliviensis boliviensis]	51.5	51.5	100%	4e-06	89%	XP_010333103.1
☐	PREDICTED: multimerin-1 [Tarsius syrichta]	50.3	50.3	94%	1e-05	88%	XP_008069714.1
☐	PREDICTED: multimerin-1 [Myotis davidii]	49.4	49.4	100%	2e-05	83%	XP_006768249.1
☐	PREDICTED: multimerin-1 [Pan paniscus]	49.4	49.4	100%	2e-05	89%	XP_003829944.1
☐	PREDICTED: multimerin-1 isoform X2 [Chlorocebus sabaeus]	49.0	49.0	94%	3e-05	88%	XP_007997465.1
☐	PREDICTED: multimerin-1 isoform X2 [Macaca fascicularis]	49.0	49.0	94%	3e-05	88%	XP_005555483.1
☐	hypothetical protein EGM_14545 [Macaca fascicularis]	49.0	49.0	94%	3e-05	88%	EHH53841.1
☐	hypothetical protein EGK_15920 [Macaca mulatta]	49.0	49.0	94%	3e-05	88%	EHH26039.1
☐	PREDICTED: multimerin-1 isoform X1 [Macaca fascicularis]	49.0	49.0	94%	3e-05	88%	XP_005555482.1
☐	PREDICTED: multimerin-1 isoform X1 [Chlorocebus sabaeus]	49.0	49.0	94%	3e-05	88%	XP_007997463.1
☐	PREDICTED: multimerin-1 [Chrysochloris asiatica]	48.6	48.6	100%	4e-05	83%	XP_006873035.1
☐	PREDICTED: multimerin-1 [Elephantulus edwardii]	48.6	48.6	88%	4e-05	94%	XP_006894545.1
☐	PREDICTED: multimerin-1 [Callithrix jacchus]	48.1	48.1	100%	6e-05	83%	XP_008991221.1

☐	PREDICTED: multimerin-1 [Echinops telfairi]	47.3	47.3	100%	1e-04	83%	XP_004703488.1
☐	PREDICTED: multimerin-1 [Oryctolagus cuniculus]	47.3	47.3	100%	1e-04	83%	XP_008265817.1
☐	PREDICTED: multimerin-1 [Otolemur garnettii]	46.0	46.0	100%	3e-04	78%	XP_003790061.1
☐	PREDICTED: multimerin-1 [Trichechus manatus latirostris]	45.6	45.6	94%	4e-04	82%	XP_004389070.1
☐	Multimerin-1 [Pteropus alecto]	45.6	45.6	100%	4e-04	83%	ELK13694.1
☐	PREDICTED: LOW QUALITY PROTEIN: multimerin-1 [Felis catus]	45.6	45.6	100%	4e-04	83%	XP_006931027.1
☐	PREDICTED: multimerin-1 [Pteropus alecto]	45.6	45.6	100%	4e-04	83%	XP_006910794.1
☐	PREDICTED: multimerin-1 [Ochotona princeps]	45.2	45.2	100%	6e-04	78%	XP_004590628.1
☐	PREDICTED: multimerin-1 [Eptesicus fuscus]	45.2	45.2	94%	6e-04	88%	XP_008141774.1
☐	PREDICTED: multimerin-1 [Papio anubis]	44.8	44.8	94%	8e-04	82%	XP_009205449.1
☐	PREDICTED: multimerin-1 isoform X2 [Bos mutus]	44.3	44.3	100%	0.001	78%	XP_005904519.1
☐	multimerin-1 precursor [Bos taurus]	44.3	44.3	100%	0.001	78%	NP_001095970.1
☐	PREDICTED: multimerin-1 isoform X3 [Bubalus bubalis]	44.3	44.3	100%	0.001	78%	XP_006066338.1
☐	PREDICTED: multimerin-1 [Pantholops hodgsonii]	44.3	44.3	100%	0.001	78%	XP_005970399.1
☐	PREDICTED: multimerin-1 isoform X2 [Capra hircus]	44.3	44.3	100%	0.001	78%	XP_005681484.1
☐	PREDICTED: multimerin-1 isoform X1 [Bos mutus]	44.3	44.3	100%	0.001	78%	XP_005904518.1
☐	PREDICTED: multimerin-1 [Ovis aries]	44.3	44.3	100%	0.001	78%	XP_004009754.1
☐	PREDICTED: multimerin-1 isoform X2 [Bison bison bison]	44.3	44.3	100%	0.001	78%	XP_010858450.1
☐	PREDICTED: multimerin-1 isoform X2 [Bubalus bubalis]	44.3	44.3	100%	0.001	78%	XP_006066337.1
☐	PREDICTED: multimerin-1 isoform X1 [Bison bison bison]	44.3	44.3	100%	0.001	78%	XP_010858449.1
☐	PREDICTED: multimerin-1 isoform X1 [Bubalus bubalis]	44.3	44.3	100%	0.001	78%	XP_006066336.1
☐	PREDICTED: multimerin-1 isoform X1 [Capra hircus]	44.3	44.3	100%	0.001	78%	XP_005681483.1
☐	PREDICTED: multimerin-1 isoform X1 [Bos taurus]	44.3	44.3	100%	0.001	78%	XP_005207828.1
☐	PREDICTED: multimerin-1 [Orycteropus afer afer]	43.9	43.9	94%	0.002	82%	XP_007952403.1
☐	PREDICTED: multimerin-1-like isoform 2 [Dasypus novemcinctus]	43.9	43.9	100%	0.002	78%	XP_004454437.1
☐	PREDICTED: multimerin-1-like isoform 1 [Dasypus novemcinctus]	43.9	43.9	100%	0.002	78%	XP_004454436.1
☐	PREDICTED: multimerin-1 isoform 2 [Macaca mulatta]	43.9	43.9	94%	0.002	82%	XP_001101702.1
☐	PREDICTED: multimerin-1 [Orcinus orca]	43.5	43.5	94%	0.002	82%	XP_004277020.1
☐	PREDICTED: multimerin-1 [Lipotes vexillifer]	43.5	43.5	94%	0.002	82%	XP_007450078.1
☐	PREDICTED: multimerin-1 [Balaenoptera acutorostrata scammoni]	43.5	43.5	94%	0.002	82%	XP_007184155.1
☐	PREDICTED: multimerin-1 [Ceratotherium simum simum]	43.5	43.5	100%	0.002	83%	XP_004431014.1
☐	PREDICTED: multimerin-1 isoform X1 [Sus scrofa]	43.5	43.5	94%	0.002	82%	XP_003129371.2
☐	PREDICTED: multimerin-1 isoform X2 [Sus scrofa]	43.5	43.5	94%	0.002	82%	XP_005667049.1
☐	multimerin-1 isoform 2 [Camelus ferus]	43.1	43.1	100%	0.003	78%	EPY80404.1
☐	PREDICTED: multimerin-1 isoform X3 [Mustela putorius furo]	43.1	43.1	100%	0.003	78%	XP_004756128.1
☐	PREDICTED: multimerin-1 isoform X1 [Mustela putorius furo]	43.1	43.1	100%	0.003	78%	XP_004756126.1
☐	PREDICTED: multimerin-1 [Leptonychotes weddellii]	43.1	43.1	100%	0.003	78%	XP_006727121.1
☐	PREDICTED: multimerin-1 [Odobenus rosmarus divergens]	43.1	43.1	100%	0.003	78%	XP_004391570.1
☐	PREDICTED: multimerin-1 [Camelus ferus]	43.1	43.1	100%	0.003	78%	XP_006185760.1
☐	PREDICTED: multimerin-1 [Camelus dromedarius]	43.1	43.1	100%	0.003	78%	XP_010998048.1
☐	PREDICTED: multimerin-1 [Camelus bactrianus]	43.1	43.1	100%	0.003	78%	XP_010968268.1
☐	hypothetical protein PANDA_006107 [Ailuropoda melanoleuca]	43.1	43.1	100%	0.003	78%	EFB19438.1
☐	PREDICTED: multimerin-1-like [Ailuropoda melanoleuca]	43.1	43.1	100%	0.003	78%	XP_002917756.1
☐	PREDICTED: multimerin-1 [Ursus maritimus]	43.1	43.1	100%	0.003	78%	XP_008705370.1
☐	PREDICTED: multimerin-1 [Heterocephalus glaber]	42.6	42.6	83%	0.004	87%	XP_004903189.1

☐	PREDICTED: multimerin-1 [Panthera tigris altaica]	42.2	42.2	100%	0.005	78%	XP_007074744.1
☐	PREDICTED: multimerin-1 [Physeter catodon]	40.9	40.9	94%	0.014	76%	XP_007105448.1
☐	PREDICTED: multimerin-1 [Ictidomys tridecemlineatus]	40.5	40.5	83%	0.019	87%	XP_005337593.1
☐	PREDICTED: multimerin-1 [Vicugna pacos]	40.1	40.1	94%	0.026	76%	XP_006210017.1
☐	PREDICTED: multimerin-1 isoformX2 [Canis lupus familiaris]	39.7	39.7	88%	0.036	81%	XP_544980.2
☐	PREDICTED: multimerin-1 isoform X3 [Canis lupus familiaris]	39.7	39.7	88%	0.036	81%	XP_005639245.1
☐	Multimerin-1 [Tupaia chinensis]	39.2	39.2	100%	0.049	72%	ELW70184.1
☐	PREDICTED: multimerin-1 [Tupaia chinensis]	39.2	39.2	100%	0.049	72%	XP_006143301.1
☐	PREDICTED: multimerin-1 [Condylura cristata]	38.0	38.0	100%	0.13	72%	XP_004681178.1
☐	PREDICTED: multimerin-1 [Loxodonta africana]	36.7	36.7	83%	0.32	80%	XP_003414128.1
☐	PREDICTED: multimerin-1 isoform X1 [Cavia porcellus]	36.3	36.3	94%	0.44	71%	XP_003467522.1
☐	PREDICTED: multimerin-1 isoform X2 [Cavia porcellus]	36.3	36.3	94%	0.44	71%	XP_005002721.1
☐	PREDICTED: multimerin-1 isoform X2 [Chinchilla lanigera]	36.3	36.3	94%	0.44	59%	XP_005374311.1
☐	PREDICTED: multimerin-1 isoform X1 [Chinchilla lanigera]	36.3	36.3	94%	0.44	59%	XP_005374310.1
☐	PREDICTED: multimerin-1-like [Peromyscus maniculatus bairdii]	35.8	35.8	83%	0.60	73%	XP_006992024.1
☐	PREDICTED: multimerin-1-like [Octodon degus]	35.4	35.4	77%	0.81	79%	XP_004648455.1
☐	PREDICTED: multimerin-1 [Nannospalax galili]	33.7	33.7	83%	2.8	73%	XP_008842849.1
☐	PREDICTED: multimerin-1 [Jaculus jaculus]	33.7	33.7	77%	2.8	71%	XP_004665470.1
☐	PREDICTED: multimerin-1 [Equus caballus]	33.7	33.7	94%	2.8	71%	XP_001497011.1
☐	PREDICTED: multimerin-1 [Equus przewalskii]	33.7	33.7	94%	2.8	71%	XP_008512609.1
☐	hypothetical protein [Phaeobacter daeponensis]	32.5	32.5	72%	6.6	72%	WP_027246211.1
☐	hypothetical protein [Phaeobacter daeponensis]	32.5	32.5	72%	6.6	72%	WP_027246178.1
☐	hypothetical protein GLOTRDRAFT_139696 [Gloeophyllum trabeum ATCC 11	32.0	32.0	88%	9.5	69%	XP_007867799.1
☐	unnamed protein product [Oncorhynchus mykiss]	31.6	31.6	61%	12	91%	CDQ60969.1
☐	PREDICTED: protein phosphatase PTC7 homolog [Esox lucius]	31.6	31.6	61%	12	91%	XP_010875817.1
☐	PREDICTED: protein phosphatase PTC7 homolog [Notothenia coriiceps]	31.6	31.6	61%	12	91%	XP_010778629.1

⊟ Alignments

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multimerin 1, isoform CRA_a [Homo sapiens]

Sequence ID: gb|EAX06037.1| **Length:** 531 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 90 to 107 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.4 bits(123)	2e-07	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KFNPGAESVVLSDSTLKF  18
            KFNPGAESVVLS+STLKF
Sbjct  90   KFNPGAESVVLSNSTLKF  107
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAC86201.1| **Length:** 531 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 90 to 107 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.4 bits(123)	2e-07	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KFNPGAESVVLSDSTLKF  18
            KFNPGAESVVLS+STLKF
Sbjct  90   KFNPGAESVVLSNSTLKF  107
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: multimerin-1-like [Galeopterus variegatus]

Sequence ID: ref|XP_008591205.1| **Length:** 988 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 125 to 142 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.4 bits(123)	2e-07	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KFNPGAESVVLSDSTLKF  18
            KFNPGAESVVLS+STLKF
Sbjct  125  KFNPGAESVVLSNSTLKF  142
```

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PREDICTED: multimerin-1 isoform X2 [Pan troglodytes]

Sequence ID: ref|XP_009446302.1| **Length:** 1193 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 124 to 141 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.4 bits(123)	2e-07	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KFNPGAESVVLSDSTLKF  18
            KFNPGAESVVLS+STLKF
Sbjct  124  KFNPGAESVVLSNSTLKF  141
```

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PREDICTED: multimerin-1 isoform X1 [Homo sapiens]

Sequence ID: ref|XP_005262913.1| **Length:** 1193 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 124 to 141 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
55.4 bits(123)	2e-07	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KFNPGAESVVLSDSTLKF  18
            KFNPGAESVVLS+STLKF
Sbjct  124  KFNPGAESVVLSNSTLKF  141
```

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BVJ8BSK101R**

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MMRN1_KLQDLTLPTDASIKF_Mod

RID BVJ8BSK101R (Expires on 01-21 10:18 am)

Query ID lcl|20561
Description None
Molecule type amino acid
Query Length 15

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

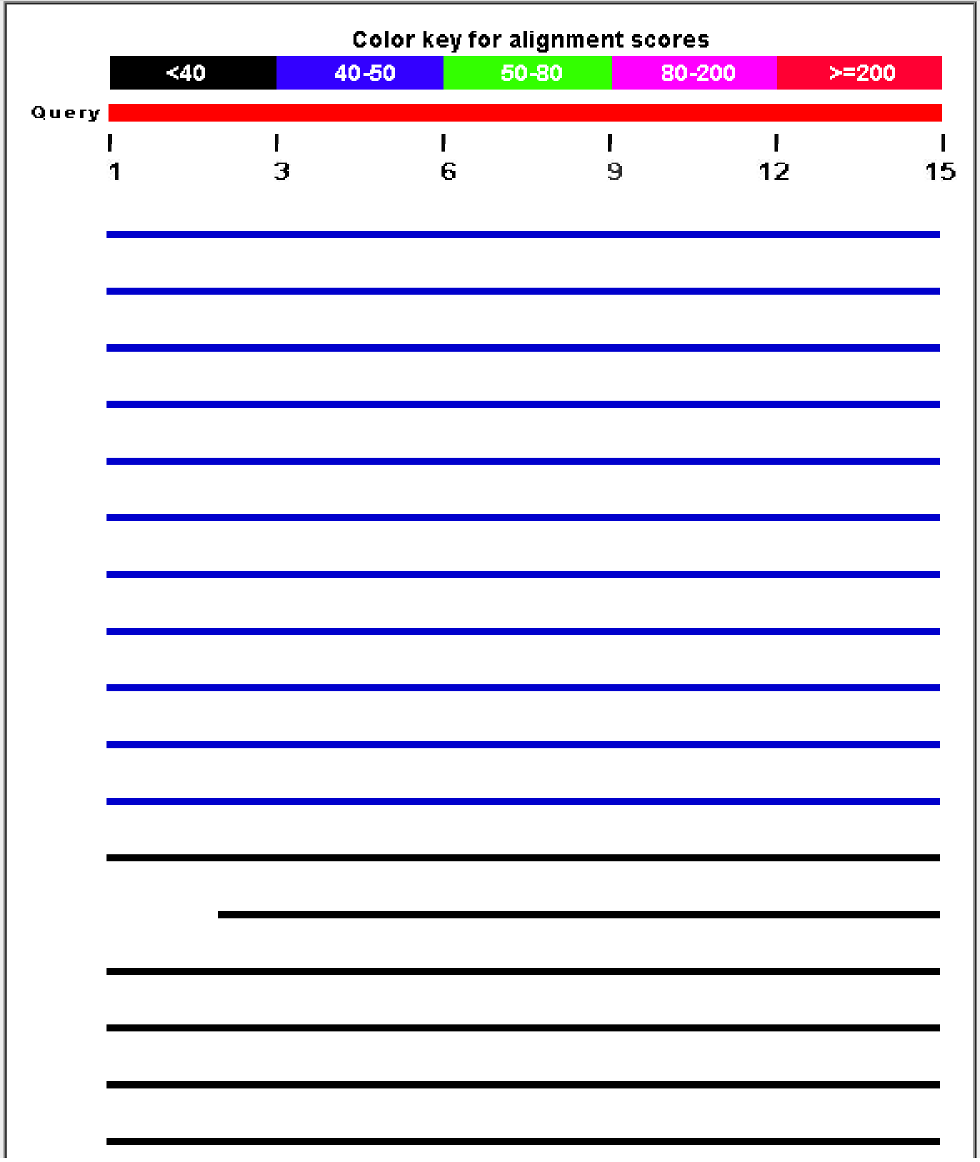
Graphic Summary

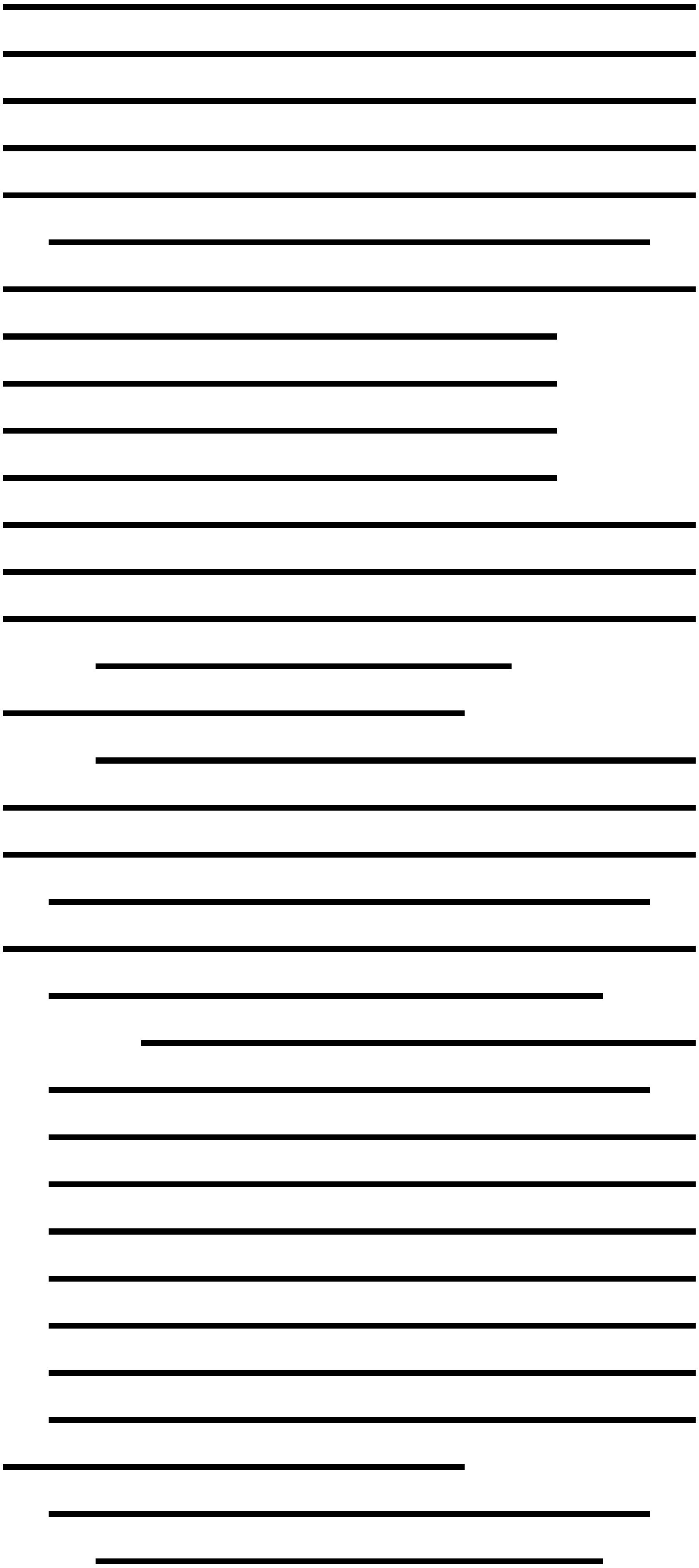
Show Conserved Domains

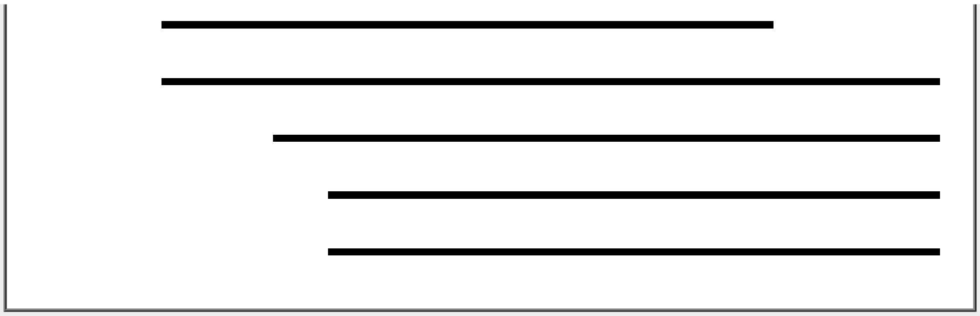
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	multimerin 1, isoform CRA_a [Homo sapiens]	44.8	44.8	100%	5e-04	87%	EAX06037.1
☐	unnamed protein product [Homo sapiens]	44.8	44.8	100%	5e-04	87%	BAC86201.1
☐	PREDICTED: multimerin-1 isoform X2 [Pan troglodytes]	44.8	44.8	100%	6e-04	87%	XP_009446302.1
☐	PREDICTED: multimerin-1 isoform X1 [Homo sapiens]	44.8	44.8	100%	6e-04	87%	XP_005262913.1
☐	PREDICTED: LOW QUALITY PROTEIN: multimerin-1 [Pongo abelii]	44.8	44.8	100%	6e-04	87%	XP_002815014.1
☐	PREDICTED: multimerin-1 [Pan paniscus]	44.8	44.8	100%	6e-04	87%	XP_003829944.1
☐	prepromultimerin [Homo sapiens]	44.8	44.8	100%	6e-04	87%	AAC52065.1
☐	multimerin-1 precursor [Homo sapiens]	44.8	44.8	100%	6e-04	87%	NP_031377.2
☐	PREDICTED: multimerin-1 [Gorilla gorilla gorilla]	44.8	44.8	100%	6e-04	87%	XP_004039176.1
☐	Multimerin 1 [Homo sapiens]	44.8	44.8	100%	6e-04	87%	AAH63848.1
☐	PREDICTED: multimerin-1 isoform X1 [Pan troglodytes]	44.8	44.8	100%	6e-04	87%	XP_517342.2
☐	PREDICTED: multimerin-1 [Rhinopithecus roxellana]	39.7	39.7	100%	0.028	80%	XP_010374576.1
☐	PREDICTED: multimerin-1 isoform 1 [Nomascus leucogenys]	38.8	38.8	86%	0.052	85%	XP_003257586.1
☐	phosphoenolpyruvate carboxylase [Psychromonas hadalis]	35.0	35.0	100%	0.89	68%	WP_022942648.1
☐	PREDICTED: multimerin-1 isoform X2 [Chlorocebus sabaeus]	35.0	35.0	100%	0.90	73%	XP_007997465.1
☐	PREDICTED: multimerin-1 isoform X2 [Macaca fascicularis]	35.0	35.0	100%	0.90	73%	XP_005555483.1
☐	hypothetical protein EGM_14545 [Macaca fascicularis]	35.0	35.0	100%	0.90	73%	EHH53841.1
☐	PREDICTED: multimerin-1 isoform 2 [Macaca mulatta]	35.0	35.0	100%	0.90	73%	XP_001101702.1
☐	PREDICTED: multimerin-1 [Papio anubis]	35.0	35.0	100%	0.90	73%	XP_009205449.1
☐	PREDICTED: multimerin-1 isoform X1 [Macaca fascicularis]	35.0	35.0	100%	0.90	73%	XP_005555482.1
☐	PREDICTED: multimerin-1 isoform X1 [Chlorocebus sabaeus]	35.0	35.0	100%	0.90	73%	XP_007997463.1
☐	PREDICTED: multimerin-1 [Saimiri boliviensis boliviensis]	34.6	34.6	100%	1.2	73%	XP_010333103.1
☐	PREDICTED: multimerin-1 [Ictidomys tridecemlineatus]	34.6	34.6	86%	1.2	77%	XP_005337593.1
☐	PREDICTED: multimerin-1 [Orycteropus afer afer]	33.3	33.3	100%	3.1	67%	XP_007952403.1
☐	hypothetical protein [Porphyromonas sp. COT-108_OH2963]	31.6	31.6	80%	10	73%	WP_036864374.1
☐	hypothetical protein [Porphyromonas canoris]	31.6	31.6	80%	10	73%	WP_036791018.1
☐	hypothetical protein [Porphyromonas sp. COT-108_OH1349]	31.6	31.6	80%	10	73%	WP_036848306.1
☐	hypothetical protein [Porphyromonas canoris]	31.6	31.6	80%	10	73%	WP_036867510.1
☐	phosphoenolpyruvate carboxylase [Psychromonas ossibalaenae]	31.6	31.6	100%	11	68%	WP_019615923.1

☐	Multimerin-1 [Pteropus alecto]	31.6	31.6	100%	11	67%	ELK13694.1
☐	PREDICTED: multimerin-1 [Pteropus alecto]	31.6	31.6	100%	11	67%	XP_006910794.1
☐	hypothetical protein [Halomonas zhanjiangensis]	31.2	31.2	60%	14	100%	WP_018916207.1
☐	hypothetical protein FOWG_16134 [Fusarium oxysporum f. sp. lycopersici MN	31.2	31.2	66%	14	90%	EWZ79806.1
☐	PREDICTED: multimerin-1 [Chrysochloris asiatica]	31.2	31.2	86%	15	69%	XP_006873035.1
☐	PREDICTED: multimerin-1 [Callithrix jacchus]	31.2	31.2	100%	15	67%	XP_008991221.1
☐	hypothetical protein V499_07655 [Pseudogymnoascus pannorum VKM F-103	30.8	30.8	100%	19	67%	KFY72188.1
☐	hypothetical protein [Gardnerella vaginalis]	30.8	30.8	86%	20	77%	WP_004128804.1
☐	hypothetical protein EGK_15920 [Macaca mulatta]	30.8	30.8	100%	20	67%	EHH26039.1
☐	hypothetical protein [Flexibacter litoralis]	30.3	30.3	80%	25	75%	WP_014799626.1
☐	hypothetical protein [Cytophaga fermentans]	30.3	30.3	80%	27	52%	WP_027470994.1
☐	hypothetical protein ACD_46C00522G0006 [uncultured bacterium]	30.3	30.3	86%	27	73%	EKD70491.1
☐	hypothetical protein [Vibrio parahaemolyticus]	29.9	29.9	93%	31	71%	WP_031849783.1
☐	hypothetical protein EM49_19725 [Vibrio parahaemolyticus]	29.9	29.9	93%	33	71%	KEE73909.1
☐	hypothetical protein [Vibrio jasicida]	29.9	29.9	93%	33	71%	WP_038872131.1
☐	hypothetical protein [Vibrio parahaemolyticus]	29.9	29.9	93%	33	71%	WP_025639665.1
☐	hypothetical protein [Vibrio parahaemolyticus]	29.9	29.9	93%	33	71%	WP_020838860.1
☐	hypothetical protein [Vibrio harveyi]	29.9	29.9	93%	33	71%	WP_017190352.1
☐	hypothetical protein EM78_09700 [Vibrio parahaemolyticus]	29.9	29.9	93%	34	71%	KEE82834.1
☐	MULTISPECIES: hypothetical protein [Parabacteroides]	29.9	29.9	66%	37	90%	WP_010802263.1
☐	PREDICTED: protein CASC5 [Phalacrocorax carbo]	29.9	29.9	86%	37	73%	XP_009510534.1
☐	glycoside hydrolase family 47 protein [Jaapia argillacea MUCL 33604]	29.5	29.5	73%	49	82%	KDQ58337.1
☐	possible exported protein [Grimontia hollisae]	29.5	29.5	73%	50	82%	WP_005502223.1
☐	hypothetical protein [Chryseobacterium jeonii]	29.5	29.5	93%	50	63%	WP_039351852.1
☐	Phenylalanyl-tRNA synthetase beta subunit [uncultured bacterium]	29.1	29.1	80%	58	67%	EKE11218.1
☐	hypothetical protein [Shewanella marina]	29.1	29.1	73%	63	82%	WP_025820399.1
☐	Secretory pathway protein Sec39 [Blumeria graminis f. sp. tritici 96224]	29.1	29.1	73%	68	73%	EPQ66354.1
☐	hypothetical protein FOWG_04277 [Fusarium oxysporum f. sp. lycopersici MN	29.1	29.1	80%	68	83%	EWZ97076.1
☐	unnamed protein product [Penicillium roqueforti FM164]	28.6	28.6	93%	87	71%	CDM36912.1
☐	hypothetical protein PRUPE_ppa020384mg [Prunus persica]	28.6	28.6	80%	87	71%	XP_007203351.1
☐	PREDICTED: PRA1 family protein F2-like [Prunus mume]	28.6	28.6	80%	88	71%	XP_008242408.1
☐	hypothetical protein DI43_15215 [Geobacillus sp. CAMR12739]	28.6	28.6	66%	89	71%	KDE46291.1
☐	GTP cyclohydrolase [Platynereis dumerilii]	28.6	28.6	60%	89	89%	AIT11920.1
☐	peptidase M20 [Pandoraea sp. RB-44]	28.6	28.6	73%	90	82%	WP_023871670.1
☐	MULTISPECIES: peptidase M20 [Pandoraea]	28.6	28.6	73%	90	82%	WP_024788613.1
☐	peptidase M20 [Pandoraea pnomenusa]	28.6	28.6	73%	90	82%	WP_023595404.1
☐	unnamed protein product [Penicillium roqueforti FM164]	28.6	28.6	93%	91	71%	CDM30137.1
☐	hypothetical protein HELRODRAFT_110051 [Helobdella robusta]	28.6	28.6	93%	91	64%	XP_009013176.1
☐	hypothetical protein BRAFLDRAFT_217213 [Branchiostoma floridae]	28.6	28.6	73%	91	73%	XP_002604890.1
☐	TonB-dependent receptor [Chryseobacterium soli]	28.6	28.6	80%	92	59%	WP_034710303.1
☐	MATE efflux family protein subfamily [Trichosporon asahii var. asahii CBS 89	28.6	28.6	66%	92	90%	EKC97848.1
☐	MATE efflux family protein subfamily [Trichosporon asahii var. asahii CBS 247	28.6	28.6	66%	92	90%	EJT49131.1
☐	hypothetical protein IW15_06475 [Chryseobacterium soli]	28.6	28.6	80%	92	59%	KFF13437.1
☐	hypothetical protein [Chryseobacterium luteum]	28.6	28.6	80%	92	59%	WP_034705311.1
☐	hypothetical protein [Chryseobacterium caeni]	28.6	28.6	80%	92	59%	WP_027383905.1

☐	phosphoenolpyruvate carboxylase [Psychromonas aquimarina]	28.6	28.6	93%	92	67%	WP_028862380.1
☐	PREDICTED: multimerin-1-like [Galeopterus variegatus]	28.6	28.6	100%	92	63%	XP_008591205.1
☐	PREDICTED: multimerin-1 [Panthera tigris altaica]	28.6	28.6	100%	93	67%	XP_007074744.1
☐	PREDICTED: LOW QUALITY PROTEIN: multimerin-1 [Felis catus]	28.6	28.6	100%	93	67%	XP_006931027.1
☐	PREDICTED: protein CASC5 [Caprimulgus carolinensis]	28.6	28.6	73%	93	73%	XP_010164966.1
☐	spoU family RNA methylase [Prevotella sp. CAG:1092]	28.2	28.2	53%	111	100%	WP_021991197.1
☐	iron ABC transporter [Photobacterium leiognathi]	28.2	28.2	53%	121	100%	WP_008989570.1
☐	histidinol phosphatase [Leuconostoc lactis]	28.2	28.2	60%	121	89%	WP_029510314.1
☐	histidinol phosphatase [Leuconostoc lactis]	28.2	28.2	60%	121	89%	WP_010000985.1
☐	hypothetical protein [Caulobacter sp. UNC358MFTsu5.1]	28.2	28.2	53%	122	100%	WP_029911009.1
☐	hypothetical protein [Caulobacter henricii]	28.2	28.2	53%	122	100%	WP_035073808.1
☐	eukaryotic aspartyl protease [Rhizoctonia solani AG-3 Rhs1AP]	28.2	28.2	80%	122	67%	EUC53735.1
☐	permease [Hafnia alvei FB1]	28.2	28.2	86%	123	64%	AIU73358.1
☐	hypothetical protein PTSG_10810 [Salpingoeca rosetta]	28.2	28.2	100%	123	57%	XP_004988775.1
☐	Hypothetical protein SS50377_17976 [Spironucleus salmonicida]	28.2	28.2	86%	124	61%	EST42420.1
☐	hypothetical protein F443_04437 [Phytophthora parasitica P1569]	28.2	28.2	53%	126	100%	ETI52400.1
☐	hypothetical protein L969DRAFT_49956 [Mixia osmundae IAM 14324]	28.2	28.2	53%	126	100%	KEI38670.1
☐	hypothetical protein E5Q_03545 [Mixia osmundae IAM 14324]	28.2	28.2	53%	126	100%	GAA96872.1
☐	MULTISPECIES: phosphinothricin acetyltransferase [Vibrio]	27.8	27.8	66%	160	80%	WP_006074211.1
☐	type VI secretion protein [Variovorax paradoxus]	27.8	27.8	86%	161	79%	WP_013539055.1
☐	hypothetical protein JAAARDRAFT_47044 [Jaapia argillacea MUCL 33604]	27.8	27.8	100%	164	67%	KDQ58670.1
☐	hypothetical protein IL54_3232 [Sphingobium sp. ba1]	27.8	27.8	86%	164	69%	KFL47805.1
☐	membrane protein [Sphingobium sp. ba1]	27.8	27.8	86%	165	69%	WP_037476657.1
☐	membrane protein [Sphingobium sp. Ant17]	27.8	27.8	86%	165	69%	EXS69799.1
☐	hemolysin [Methylopila sp. M107]	27.8	27.8	60%	165	89%	WP_026362771.1
☐	transcriptional activator, putative, Baf family [Synechococcus sp. PCC 7335]	27.8	27.8	60%	166	89%	WP_006454569.1

⊟ Alignments

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multimerin 1, isoform CRA_a [Homo sapiens]

Sequence ID: gb|EAX06037.1| **Length:** 531 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 77 to 91 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.8 bits(98)	5e-04	13/15(87%)	15/15(100%)	0/15(0%)

```
Query  1   KLQDLTLPTDASIKF  15
           KLQ+LTLPT+ASIKF
Sbjct  77  KLQNLTLPTNASIKF  91
```

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unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAC86201.1| **Length:** 531 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 77 to 91 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.8 bits(98)	5e-04	13/15(87%)	15/15(100%)	0/15(0%)

```
Query  1   KLQDLTLPTDASIKF  15
           KLQ+LTLPT+ASIKF
Sbjct  77  KLQNLTLPTNASIKF  91
```

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PREDICTED: multimerin-1 isoform X2 [Pan troglodytes]

Sequence ID: ref|XP_009446302.1| **Length:** 1193 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 111 to 125 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.8 bits(98)	6e-04	13/15(87%)	15/15(100%)	0/15(0%)

```
Query  1    KLQDLTLPTDASIKF  15
            KLQ+LTLPT+ASIKF
Sbjct  111  KLQNLTLPTNASIKF  125
```

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PREDICTED: multimerin-1 isoform X1 [Homo sapiens]

Sequence ID: ref|XP_005262913.1| **Length:** 1193 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 111 to 125 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.8 bits(98)	6e-04	13/15(87%)	15/15(100%)	0/15(0%)

```
Query  1    KLQDLTLPTDASIKF  15
            KLQ+LTLPT+ASIKF
Sbjct  111  KLQNLTLPTNASIKF  125
```

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PREDICTED: LOW QUALITY PROTEIN: multimerin-1 [Pongo abelii]

Sequence ID: ref|XP_002815014.1| **Length:** 1222 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 111 to 125 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.8 bits(98)	6e-04	13/15(87%)	15/15(100%)	0/15(0%)

```
Query  1    KLQDLTLPTDASIKF  15
            KLQ+LTLPT+ASIKF
Sbjct  111  KLQNLTLPTNASIKF  125
```

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MMRN1_KLQNLTLPTNASIKF_NonMod

RID B9P97ME701R (Expires on 01-14 15:36 pm)

Query ID	lcl|127451	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	15		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

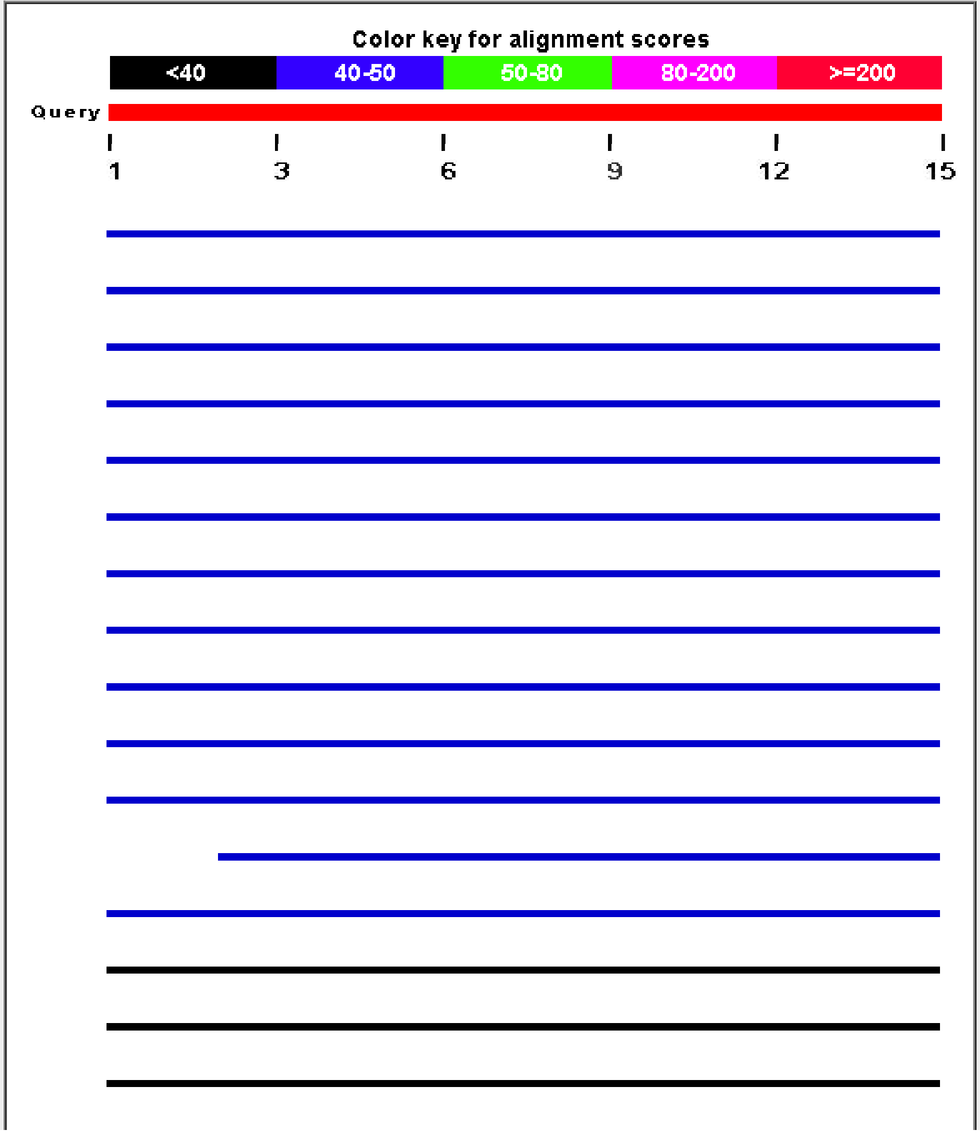
Graphic Summary

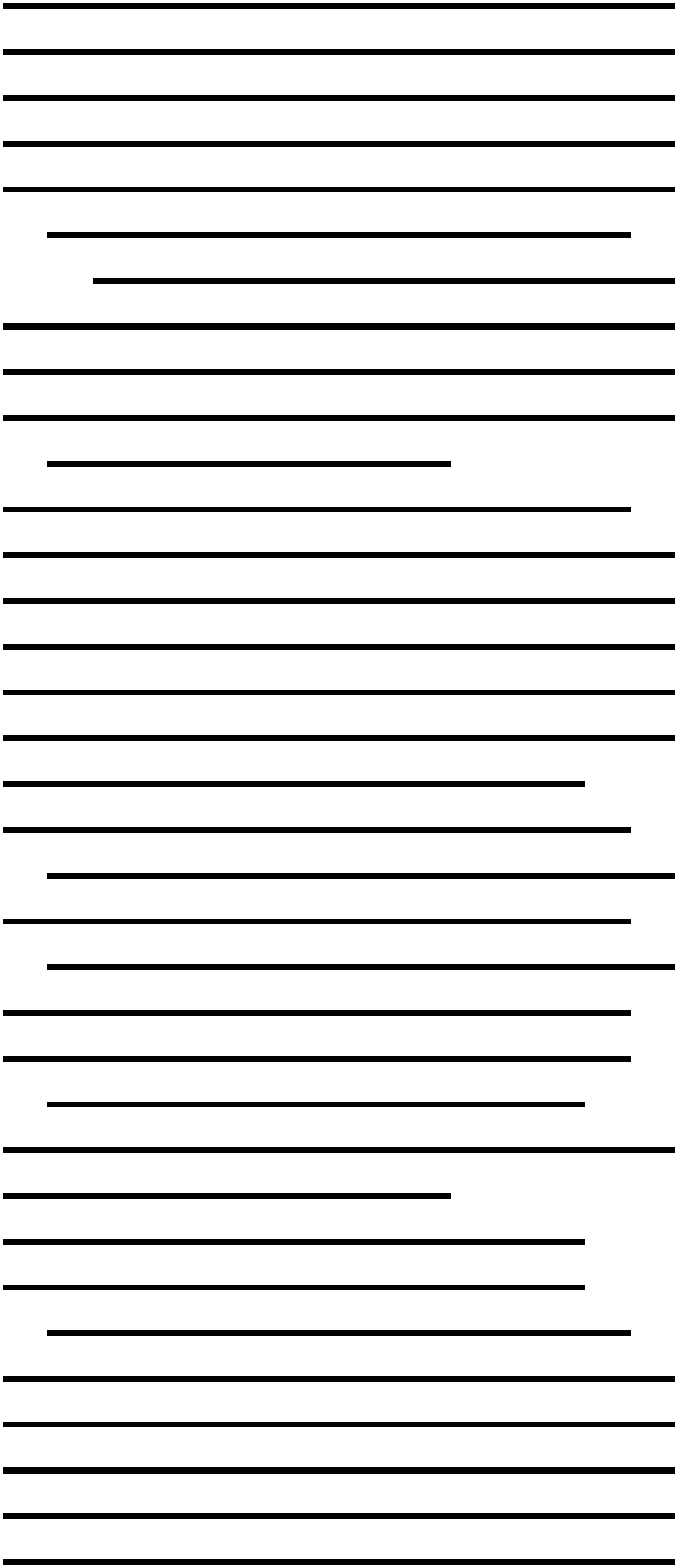
Show Conserved Domains

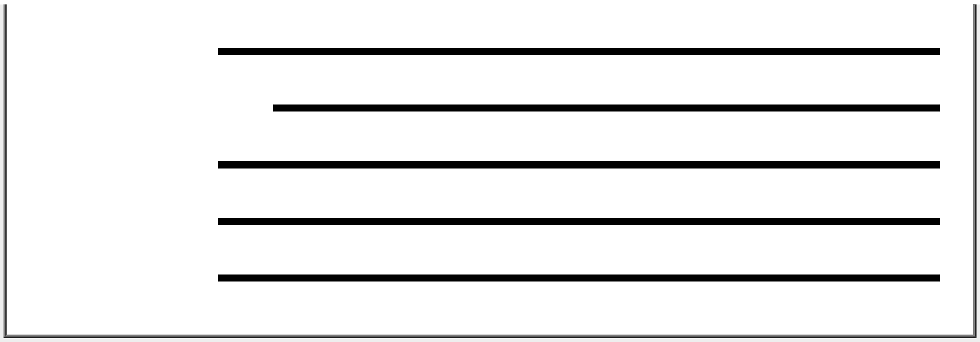
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊖ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	multimerin 1, isoform CRA_a [Homo sapiens]	49.8	49.8	100%	1e-05	100%	gi|119626442|EAX06037.1
☐	unnamed protein product [Homo sapiens]	49.8	49.8	100%	1e-05	100%	gi|34531690|BAC86201.1
☐	PREDICTED: multimerin-1 isoform X2 [Pan troglodytes]	49.8	49.8	100%	1e-05	100%	gi|694908198|XP_009446302.1
☐	PREDICTED: multimerin-1 isoform X1 [Homo sapiens]	49.8	49.8	100%	1e-05	100%	gi|530377406|XP_005262913.1
☐	PREDICTED: LOW QUALITY PROTEIN: multimerin-1 [Pongo abeli	49.8	49.8	100%	1e-05	100%	gi|297673972|XP_002815014.1
☐	PREDICTED: multimerin-1 [Pan paniscus]	49.8	49.8	100%	1e-05	100%	gi|397519601|XP_003829944.1
☐	prepromultimerin [Homo sapiens]	49.8	49.8	100%	1e-05	100%	gi|927596|AAC52065.1
☐	multimerin-1 precursor [Homo sapiens]	49.8	49.8	100%	1e-05	100%	gi|45269141|NP_031377.2
☐	PREDICTED: multimerin-1 [Gorilla gorilla gorilla]	49.8	49.8	100%	1e-05	100%	gi|426344970|XP_004039176.1
☐	Multimerin 1 [Homo sapiens]	49.8	49.8	100%	1e-05	100%	gi|39645323|AAH63848.1
☐	PREDICTED: multimerin-1 isoform X1 [Pan troglodytes]	49.8	49.8	100%	1e-05	100%	gi|114595173|XP_517342.2
☐	PREDICTED: multimerin-1 isoform 1 [Nomascus leucogenys]	43.9	43.9	86%	0.001	100%	gi|332216893|XP_003257586.1
☐	PREDICTED: multimerin-1 [Rhinopithecus roxellana]	43.5	43.5	100%	0.001	87%	gi|724888364|XP_010374576.1
☐	PREDICTED: multimerin-1 isoform X2 [Chlorocebus sabaeus]	38.8	38.8	100%	0.049	80%	gi|635043771|XP_007997465.1
☐	PREDICTED: multimerin-1 isoform X2 [Macaca fascicularis]	38.8	38.8	100%	0.049	80%	gi|544433553|XP_005555483.1
☐	hypothetical protein EGM_14545 [Macaca fascicularis]	38.8	38.8	100%	0.049	80%	gi|355749442|EHH53841.1
☐	PREDICTED: multimerin-1 isoform 2 [Macaca mulatta]	38.8	38.8	100%	0.049	80%	gi|109074983|XP_001101702.1
☐	PREDICTED: multimerin-1 [Papio anubis]	38.8	38.8	100%	0.049	80%	gi|685542090|XP_009205449.1
☐	PREDICTED: multimerin-1 isoform X1 [Macaca fascicularis]	38.8	38.8	100%	0.049	80%	gi|544433551|XP_005555482.1
☐	PREDICTED: multimerin-1 isoform X1 [Chlorocebus sabaeus]	38.8	38.8	100%	0.049	80%	gi|635043767|XP_007997463.1
☐	PREDICTED: multimerin-1 [Saimiri boliviensis boliviensis]	38.4	38.4	100%	0.068	80%	gi|725558699|XP_010333103.1
☐	PREDICTED: multimerin-1 [Ictidomys tridecemlineatus]	35.4	35.4	86%	0.62	85%	gi|532103995|XP_005337593.1
☐	PREDICTED: multimerin-1 [Chrysochloris asiatica]	35.0	35.0	86%	0.85	77%	gi|586485083|XP_006873035.1
☐	PREDICTED: multimerin-1 [Callithrix jacchus]	35.0	35.0	100%	0.85	73%	gi|675648553|XP_008991221.1
☐	hypothetical protein EGK_15920 [Macaca mulatta]	34.6	34.6	100%	1.2	73%	gi|355687455|EHH26039.1
☐	PREDICTED: multimerin-1 [Orycteropus afer afer]	33.3	33.3	100%	2.9	67%	gi|634885587|XP_007952403.1
☐	hypothetical protein [Dictyoglomus thermophilum]	31.6	31.6	60%	9.6	100%	gi|501543543|WP_012548656.1
☐	MULTISPECIES: hemolysin D [Clostridium]	31.2	31.2	93%	13	80%	gi|503003899|WP_013238875.1
☐							

	Multimerin-1 [Pteropus alecto]	31.2	31.2	100%	14	67%	gi|431911488|ELK13694.1
☐	PREDICTED: multimerin-1 [Panthera tigris altaica]	31.2	31.2	100%	14	67%	gi|591295050|XP_007074744.1
☐	PREDICTED: LOW QUALITY PROTEIN: multimerin-1 [Felis catus]	31.2	31.2	100%	14	67%	gi|586984339|XP_006931027.1
☐	PREDICTED: multimerin-1 [Pteropus alecto]	31.2	31.2	100%	14	67%	gi|586551480|XP_006910794.1
☐	PREDICTED: multimerin-1 [Otolemur garnettii]	31.2	31.2	100%	14	60%	gi|395834121|XP_003790061.1
☐	predicted protein [Naegleria gruberi strain NEG-M]	31.2	31.2	86%	14	65%	gi|290976432|XP_002670944.1
☐	PREDICTED: toll-like receptor 1 [Zonotrichia albicollis]	30.8	30.8	93%	19	79%	gi|542163848|XP_005490559.1
☐	PREDICTED: multimerin-1 [Tarsius syrichta]	30.8	30.8	93%	19	64%	gi|640825228|XP_008069714.1
☐	PREDICTED: uncharacterized protein LOC101774446 [Setaria italic	30.3	30.3	93%	25	67%	gi|514813686|XP_004981625.1
☐	hypothetical protein An02g10500 [Aspergillus niger]	29.9	29.9	93%	32	71%	gi|134057111|CAK44399.1
☐	sodium:proton antiporter [Clostridium botulinum]	29.9	29.9	93%	34	69%	gi|501425231|WP_012449901.1
☐	hypothetical protein SORBIDRAFT_01g006920 [Sorghum bicolor]	29.9	29.9	93%	34	67%	gi|242032863|XP_002463826.1
☐	family 3 glycoside hydrolase [Phytophthora sojae]	29.9	29.9	80%	34	69%	gi|695391545|XP_009520058.1
☐	PREDICTED: multimerin-1-like [Galeopterus variegatus]	29.9	29.9	100%	35	69%	gi|667330346|XP_008591205.1
☐	putative ESAT-secreted protein, BA2188 homolog [Paenibacillus sp	29.5	29.5	66%	45	90%	gi|565876420|WP_023957733.1
☐	PREDICTED: toll-like receptor 1 isoform X1 [Ficedula albicollis]	29.5	29.5	86%	47	77%	gi|524995230|XP_005045420.1
☐	PREDICTED: toll-like receptor 1 [Geospiza fortis]	29.5	29.5	86%	47	77%	gi|543244114|XP_005415510.1
☐	hypothetical protein [Dyadobacter beijingensis]	29.5	29.5	86%	47	79%	gi|518784338|WP_019941627.1
☐	PREDICTED: multimerin-1 isoform X3 [Mustela putorius furo]	29.5	29.5	100%	47	67%	gi|511870693|XP_004756128.1
☐	PREDICTED: multimerin-1 isoform X1 [Mustela putorius furo]	29.5	29.5	100%	47	67%	gi|511870687|XP_004756126.1
☐	PREDICTED: multimerin-1 [Leptonychotes weddellii]	29.5	29.5	100%	47	67%	gi|585149232|XP_006727121.1
☐	PREDICTED: multimerin-1 [Balaenoptera acutorostrata scammoni]	29.5	29.5	100%	47	60%	gi|594672475|XP_007184155.1
☐	PREDICTED: multimerin-1 [Ursus maritimus]	29.5	29.5	100%	47	67%	gi|671029176|XP_008705370.1
☐	hypothetical protein Phum_PHUM221870 [Pediculus humanus corp	29.5	29.5	86%	47	71%	gi|242010134|XP_002425831.1
☐	Phenylalanyl-tRNA synthetase beta subunit [uncultured bacterium]	29.1	29.1	80%	55	67%	gi|406991759|EKE11218.1
☐	hypothetical protein CISIN_1g0392312mg [Citrus sinensis]	29.1	29.1	86%	61	69%	gi|641817332|KDO38777.1
☐	hypothetical protein CISIN_1g036471mg [Citrus sinensis]	29.1	29.1	86%	63	69%	gi|641858195|KDO76917.1
☐	hypothetical protein CICLE_v10014868mg [Citrus clementina]	29.1	29.1	86%	63	69%	gi|567912219|XP_006448423.1
☐	hypothetical protein PSAKL28_00270 [Pseudomonas alkylphenolia]	29.1	29.1	93%	63	61%	gi|675318936|AIL59265.1
☐	PREDICTED: probable receptor-like protein kinase At1g67000-like	29.1	29.1	86%	63	69%	gi|568828835|XP_006468743.1
☐	hypothetical protein CICLE_v10014492mg [Citrus clementina]	29.1	29.1	86%	63	69%	gi|567912201|XP_006448414.1
☐	recombinase RecJ [Psychrilyobacter atlanticus]	29.1	29.1	66%	64	90%	gi|655473680|WP_028856519.1
☐	hypothetical protein CICLE_v10014231mg [Citrus clementina]	29.1	29.1	86%	64	69%	gi|567912207|XP_006448417.1
☐	hypothetical protein SEPMUDRAFT_149012 [Sphaerulina musiva S	29.1	29.1	93%	64	69%	gi|453085824|EMF13867.1
☐	GGDEF domain protein [Cyclobacteriaceae bacterium AK24]	29.1	29.1	80%	64	71%	gi|499124481|WP_010853371.1
☐	unnamed protein product [Albugo candida]	29.1	29.1	73%	64	82%	gi|635360053|CCI11005.1
☐	PREDICTED: multimerin-1 [Physeter catodon]	29.1	29.1	100%	64	60%	gi|593718138|XP_007105448.1
☐	general secretion pathway protein G [Sphingomonas parapaucimob	28.6	28.6	73%	80	82%	gi|723385750|GAM00671.1
☐	unnamed protein product [Penicillium roqueforti FM164]	28.6	28.6	93%	82	71%	gi|584408082|CDM36912.1
☐	hypothetical protein PRUPE_ppa020384mg [Prunus persica]	28.6	28.6	80%	82	71%	gi|595812142|XP_007203351.1
☐	PREDICTED: PRA1 family protein F2-like [Prunus mume]	28.6	28.6	80%	82	71%	gi|645274586|XP_008242408.1
☐	PREDICTED: toll-like receptor 1 [Mesitornis unicolor]	28.6	28.6	80%	83	83%	gi|704573972|XP_010186347.1
☐	formyltetrahydrofolate deformylase [Francisella tularensis]	28.6	28.6	86%	84	77%	gi|504360783|WP_014547885.1
☐	hypothetical protein CISIN_1g045366mg [Citrus sinensis]	28.6	28.6	100%	84	45%	gi|641823498|KDO42902.1
☐	hypothetical protein CICLE_v10003553mg [Citrus clementina]	28.6	28.6	100%	84	45%	gi|567879199|XP_006432158.1

☐ replication associated protein [Tomato leaf curl Antsiranana virus]	28.6	28.6	60%	85	89%	gi|154090423|CAM91945.1
☐ replication associated protein [Tobacco leaf curl Comoros virus]	28.6	28.6	60%	85	89%	gi|154090379|CAM91908.1
☐ replication associated protein [Tobacco leaf curl Comoros virus]	28.6	28.6	60%	85	89%	gi|154090390|CAM91917.1
☐ hypothetical protein [Algoriphagus marincola]	28.6	28.6	80%	85	77%	gi|652553724|WP_026947324.1
☐ Hydroxymethylglutaryl-CoA synthase [Mycobacterium marinum]	28.6	28.6	60%	85	89%	gi|522805207|WP_020729397.1
☐ Hydroxymethylglutaryl-CoA synthase [Mycobacterium marinum]	28.6	28.6	60%	85	89%	gi|522731922|WP_020725611.1
☐ Hydroxymethylglutaryl-CoA synthase [Mycobacterium sp. 012931]	28.6	28.6	60%	85	89%	gi|523653246|WP_020787124.1
☐ hydroxymethylglutaryl-coenzyme A synthase, PksG [Mycobacteriun	28.6	28.6	60%	85	89%	gi|505169048|WP_015356150.1
☐ 3-hydroxy-3-methylglutaryl-CoA synthase [Mycobacterium marinum	28.6	28.6	60%	85	89%	gi|501363310|WP_012394876.1
☐ unnamed protein product [Penicillium roqueforti FM164]	28.6	28.6	93%	86	71%	gi|584411374|CDM30137.1
☐ hypothetical protein HETIRDRAFT_474453 [Heterobasidion irregula	28.6	28.6	80%	86	52%	gi|695550226|XP_009545576.1
☐ Alpha-glucosidase [Cerapachys biroi]	28.6	28.6	80%	87	75%	gi|607365917|EZA60093.1
☐ PREDICTED: multimerin-1 [Orcinus orca]	28.6	28.6	100%	87	60%	gi|466044414|XP_004277020.1
☐ hypothetical protein [Catenovulum agarivorans]	28.6	28.6	100%	87	61%	gi|515521939|WP_016955193.1
☐ TetR family transcriptional regulator [Acinetobacter baumannii]	28.2	28.2	80%	104	56%	gi|645914882|WP_025468867.1
☐ TetR family transcriptional regulator [Acinetobacter baumannii]	28.2	28.2	80%	105	56%	gi|691164973|WP_032071071.1
☐ TetR family transcriptional regulator [Acinetobacter baumannii ABNI	28.2	28.2	80%	108	56%	gi|475944208|EMU11513.1
☐ Putative membrane protein [Staphylococcus xylosus]	28.2	28.2	100%	110	61%	gi|683403486|CEF18275.1
☐ hypothetical protein, ydb-like protein [Staphylococcus xylosus]	28.2	28.2	100%	110	61%	gi|657168032|AID42270.1
☐ hypothetical protein [Staphylococcus xylosus]	28.2	28.2	100%	110	61%	gi|657290509|WP_029377959.1
☐ hypothetical protein [Staphylococcus xylosus]	28.2	28.2	100%	110	61%	gi|516331459|WP_017722118.1
☐ TetR family transcriptional regulator [Acinetobacter baumannii]	28.2	28.2	80%	111	56%	gi|487944513|WP_002017979.1
☐ TetR family transcriptional regulator [Acinetobacter baumannii]	28.2	28.2	80%	111	56%	gi|691082399|WP_032018237.1
☐ TetR family transcriptional regulator [Acinetobacter baumannii]	28.2	28.2	80%	111	56%	gi|516427340|WP_017816702.1
☐ TetR family transcriptional regulator [Acinetobacter baumannii]	28.2	28.2	80%	111	56%	gi|488001344|WP_002073183.1
☐ Zinc carboxypeptidase A 1 [Acromyrmex echinatior]	28.2	28.2	86%	112	63%	gi|332032038|EGI71157.1
☐ PREDICTED: PRA1 family protein F2-like [Malus domestica]	28.2	28.2	80%	112	71%	gi|658005128|XP_008337698.1

⊟ Alignments

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multimerin 1, isoform CRA_a [Homo sapiens]

Sequence ID: gi|119626442|gb|EAX06037.1| **Length:** 531 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 77 to 91 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KLQNLTLPTNASIKF  15
            KLQNLTLPTNASIKF
Sbjct  77   KLQNLTLPTNASIKF  91
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|34531690|dbj|BAC86201.1| **Length:** 531 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 77 to 91 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KLQNLTLPTNASIKF  15
```

```
               KLQNLTLPTNASIKF
Sbjct  77  KLQNLTLPTNASIKF  91
```

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PREDICTED: multimerin-1 isoform X2 [Pan troglodytes]

Sequence ID: gi|694908198|ref|XP_009446302.1| **Length:** 1193 **Number of Matches:** 1

Range 1: 111 to 125 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KLQNLTLPTNASIKF  15
            KLQNLTLPTNASIKF
Sbjct  111  KLQNLTLPTNASIKF  125
```

Related Information

Gene - associated gene details

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PREDICTED: multimerin-1 isoform X1 [Homo sapiens]

Sequence ID: gi|530377406|ref|XP_005262913.1| **Length:** 1193 **Number of Matches:** 1

Range 1: 111 to 125 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KLQNLTLPTNASIKF  15
            KLQNLTLPTNASIKF
Sbjct  111  KLQNLTLPTNASIKF  125
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: multimerin-1 [Pongo abelii]

Sequence ID: gi|297673972|ref|XP_002815014.1| **Length:** 1222 **Number of Matches:** 1

Range 1: 111 to 125 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.8 bits(110)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KLQNLTLPTNASIKF  15
            KLQNLTLPTNASIKF
Sbjct  111  KLQNLTLPTNASIKF  125
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

MMRN1_KTQAALSDLTCCIDRS_Mod

RID BVJAT7FR01R (Expires on 01-21 10:19 am)

Query ID	lcl|6104	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	16		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

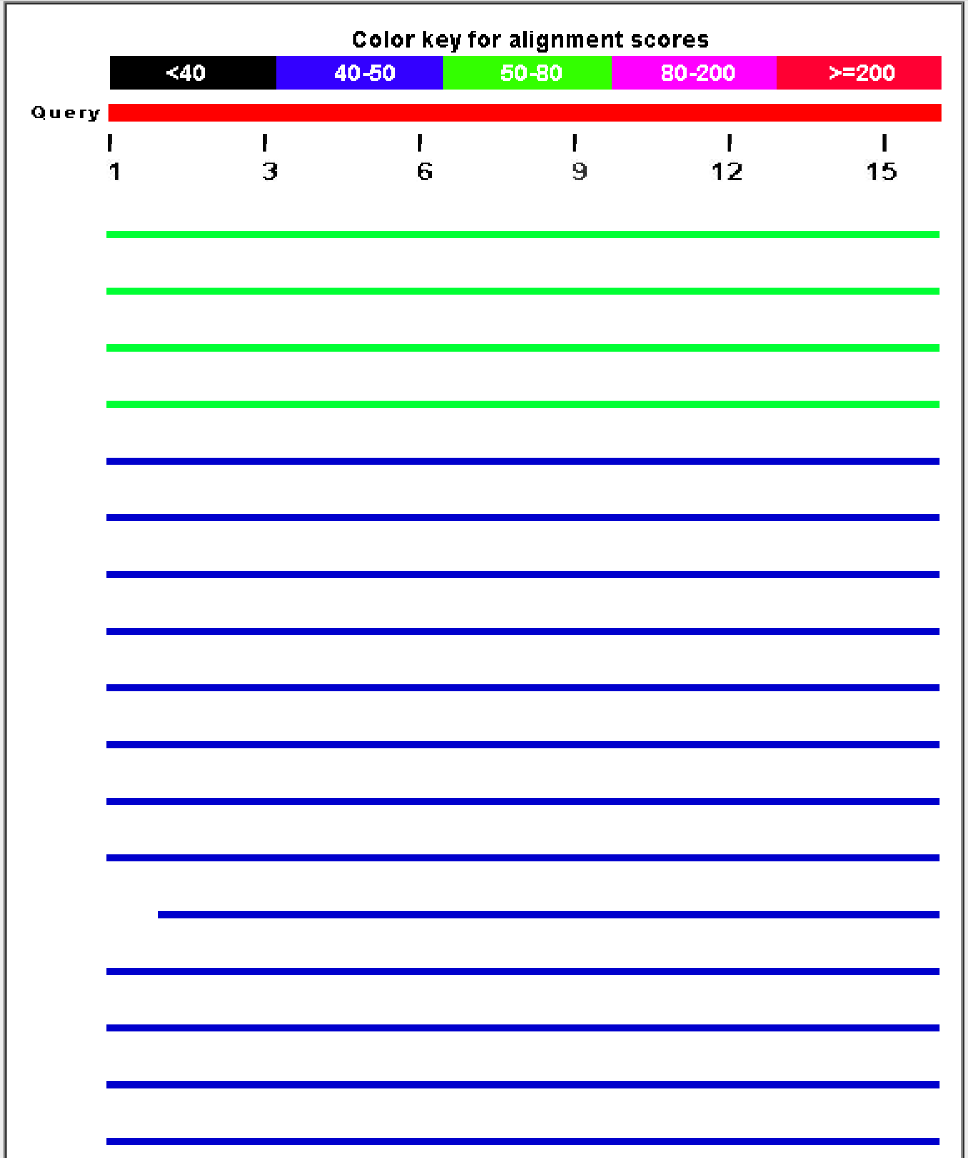
Graphic Summary

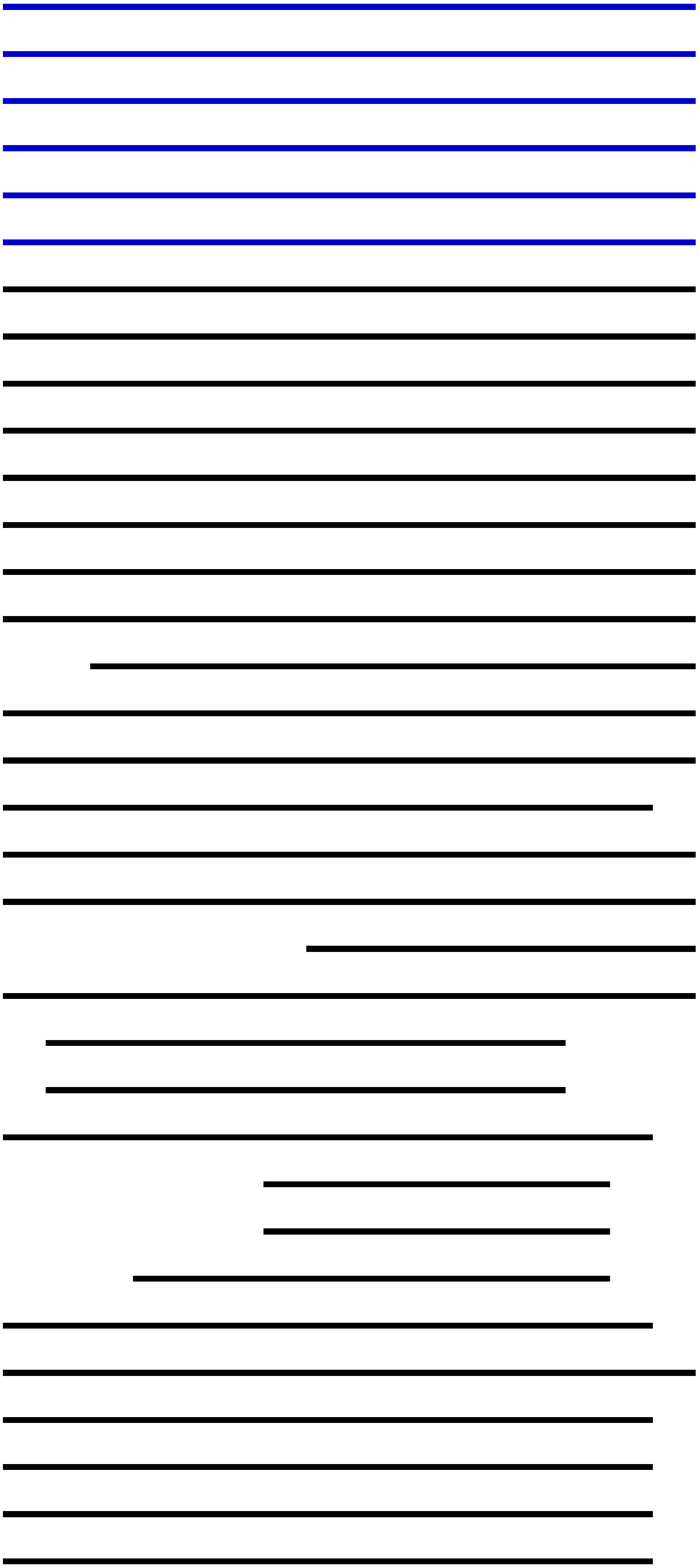
Show Conserved Domains

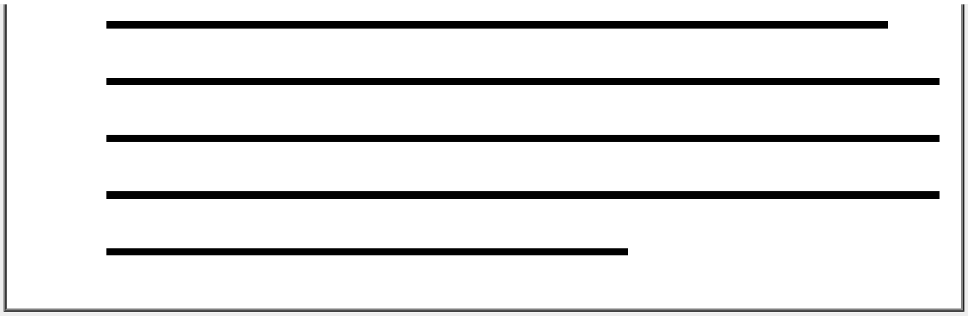
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	51.1	51.1	100%	5e-06	94%	BAH13704.1
☐	PREDICTED: multimerin-1 isoform X1 [Homo sapiens]	51.1	51.1	100%	5e-06	94%	XP_005262913.1
☐	multimerin-1 precursor [Homo sapiens]	51.1	51.1	100%	5e-06	94%	NP_031377.2
☐	Multimerin 1 [Homo sapiens]	51.1	51.1	100%	5e-06	94%	AAH63848.1
☐	PREDICTED: multimerin-1 isoform X2 [Pan troglodytes]	47.7	47.7	100%	7e-05	88%	XP_009446302.1
☐	PREDICTED: LOW QUALITY PROTEIN: multimerin-1 [Pongo abelii]	47.7	47.7	100%	7e-05	88%	XP_002815014.1
☐	PREDICTED: multimerin-1 [Gorilla gorilla gorilla]	47.7	47.7	100%	7e-05	88%	XP_004039176.1
☐	PREDICTED: multimerin-1 isoform X1 [Pan troglodytes]	47.7	47.7	100%	7e-05	88%	XP_517342.2
☐	PREDICTED: multimerin-1 isoform 2 [Nomascus leucogenys]	46.4	46.4	100%	2e-04	88%	XP_004089067.1
☐	PREDICTED: multimerin-1 isoform 1 [Nomascus leucogenys]	46.4	46.4	100%	2e-04	88%	XP_003257586.1
☐	PREDICTED: multimerin-1 [Pan paniscus]	45.2	45.2	100%	5e-04	81%	XP_003829944.1
☐	prepromultimerin [Homo sapiens]	44.8	44.8	100%	6e-04	88%	AAC52065.1
☐	PREDICTED: multimerin-1 [Rhinopithecus roxellana]	44.8	44.8	93%	6e-04	87%	XP_010374576.1
☐	PREDICTED: multimerin-1 [Macaca mulatta]	43.5	43.5	100%	0.002	81%	XP_002804181.1
☐	PREDICTED: multimerin-1 isoform X2 [Macaca fascicularis]	43.5	43.5	100%	0.002	81%	XP_005555483.1
☐	hypothetical protein EGM_14545 [Macaca fascicularis]	43.5	43.5	100%	0.002	81%	EHH53841.1
☐	hypothetical protein EGK_15920 [Macaca mulatta]	43.5	43.5	100%	0.002	81%	EHH26039.1
☐	PREDICTED: multimerin-1 isoform 2 [Macaca mulatta]	43.5	43.5	100%	0.002	81%	XP_001101702.1
☐	PREDICTED: multimerin-1 [Papio anubis]	43.5	43.5	100%	0.002	81%	XP_009205449.1
☐	PREDICTED: multimerin-1 isoform X1 [Macaca fascicularis]	43.5	43.5	100%	0.002	81%	XP_005555482.1
☐	PREDICTED: multimerin-1 [Saimiri boliviensis boliviensis]	43.5	43.5	100%	0.002	81%	XP_010333103.1
☐	PREDICTED: multimerin-1 isoform X2 [Chlorocebus sabaeus]	40.9	40.9	100%	0.012	75%	XP_007997465.1
☐	PREDICTED: multimerin-1 isoform X1 [Chlorocebus sabaeus]	40.9	40.9	100%	0.012	75%	XP_007997463.1
☐	PREDICTED: multimerin-1 [Callithrix jacchus]	39.7	39.7	100%	0.030	75%	XP_008991221.1
☐	PREDICTED: multimerin-1 [Trichechus manatus latirostris]	34.6	34.6	100%	1.3	81%	XP_004389070.1
☐	Multimerin-1 [Tupaia chinensis]	34.6	34.6	100%	1.3	81%	ELW70184.1
☐	PREDICTED: multimerin-1 [Chrysochloris asiatica]	34.6	34.6	100%	1.3	81%	XP_006873035.1
☐	PREDICTED: multimerin-1 [Oryctolagus cuniculus]	34.6	34.6	100%	1.3	81%	XP_008265817.1
☐	PREDICTED: multimerin-1 [Loxodonta africana]	34.6	34.6	100%	1.3	81%	XP_003414128.1

☐	PREDICTED: multimerin-1 [Tupaia chinensis]	34.6	34.6	100%	1.3	81%	XP_006143301.1
☐	PREDICTED: multimerin-1 [Tarsius syrichta]	33.3	33.3	100%	3.4	75%	XP_008069714.1
☐	hypothetical protein COCVIDRAFT_82402 [Bipolaris victoriae FI3]	32.5	32.5	87%	5.8	60%	EUN22480.1
☐	PREDICTED: multimerin-1-like isoform 2 [Dasypus novemcinctus]	32.0	32.0	100%	8.4	75%	XP_004454437.1
☐	PREDICTED: multimerin-1-like isoform 1 [Dasypus novemcinctus]	32.0	32.0	100%	8.5	75%	XP_004454436.1
☐	PREDICTED: multimerin-1 [Ictidomys tridecemlineatus]	32.0	32.0	93%	8.5	80%	XP_005337593.1
☐	PREDICTED: multimerin-1 [Ochotona princeps]	31.6	31.6	100%	11	75%	XP_004590628.1
☐	PREDICTED: multimerin-1 [Elephantulus edwardii]	31.6	31.6	100%	11	75%	XP_006894545.1
☐	Gamma-tubulin complex component 2 [Triticum urartu]	31.2	31.2	56%	15	89%	EMS52405.1
☐	PREDICTED: multimerin-1 [Otolemur garnettii]	31.2	31.2	100%	16	75%	XP_003790061.1
☐	membrane lipoprotein tmpC precursor [Halorubrum californiense]	30.8	30.8	75%	20	58%	WP_008441495.1
☐	membrane lipoprotein tmpC precursor [Halorubrum coriense]	30.8	30.8	75%	20	58%	WP_006112854.1
☐	PREDICTED: multimerin-1 [Mesocricetus auratus]	30.8	30.8	93%	21	80%	XP_005076113.1
☐	hypothetical protein [Trypanosoma brucei TREU927]	30.3	30.3	50%	28	100%	XP_828719.1
☐	unnamed protein product [Trypanosoma congolense IL3000]	30.3	30.3	50%	28	100%	CCC95274.1
☐	VP1 protein homologue [Craterostigma plantagineum]	30.3	30.3	68%	29	82%	CAA04184.1
☐	Multimerin-1 [Cricetulus griseus]	30.3	30.3	93%	29	73%	EGV92276.1
☐	PREDICTED: multimerin-1 [Orycteropus afer afer]	30.3	30.3	100%	29	75%	XP_007952403.1
☐	multimerin-1 [Cricetulus griseus]	30.3	30.3	93%	29	73%	ERE67090.1
☐	PREDICTED: multimerin-1 isoform X2 [Cricetulus griseus]	30.3	30.3	93%	29	73%	XP_007635662.1
☐	PREDICTED: multimerin-1 isoform X2 [Cricetulus griseus]	30.3	30.3	93%	29	73%	XP_007642492.1
☐	PREDICTED: multimerin-1 isoform X1 [Cricetulus griseus]	30.3	30.3	93%	29	73%	XP_007635661.1
☐	PREDICTED: multimerin-1 isoform X1 [Cricetulus griseus]	30.3	30.3	93%	29	73%	XP_003503775.1
☐	PREDICTED: multimerin-1 [Ceratotherium simum simum]	30.3	30.3	100%	29	69%	XP_004431014.1
☐	PREDICTED: multimerin-1 [Equus caballus]	30.3	30.3	100%	29	69%	XP_001497011.1
☐	PREDICTED: multimerin-1 [Equus przewalskii]	30.3	30.3	100%	29	69%	XP_008512609.1
☐	multimerin-1 [Mus musculus]	29.9	29.9	62%	38	90%	CAE52464.1
☐	acyl-CoA dehydrogenase [Bordetella avium]	29.9	29.9	93%	38	67%	WP_012418659.1
☐	Mmrn1 protein [Mus musculus]	29.9	29.9	62%	38	90%	AAH46425.1
☐	PREDICTED: multimerin-1 isoform X2 [Microtus ochrogaster]	29.9	29.9	62%	39	90%	XP_005360610.1
☐	PREDICTED: multimerin-1 isoform X1 [Microtus ochrogaster]	29.9	29.9	62%	39	90%	XP_005360609.1
☐	Mmrn1 protein [Mus musculus]	29.9	29.9	62%	39	90%	AAI44790.1
☐	multimerin-1 isoform b precursor [Mus musculus]	29.9	29.9	62%	39	90%	NP_001156979.1
☐	multimerin-1 isoform a precursor [Mus musculus]	29.9	29.9	62%	39	90%	NP_081889.1
☐	RecName: Full=Multimerin-1; Flags: Precursor [Mus musculus]	29.9	29.9	62%	39	90%	B2RPV6.2
☐	Multimerin 1 [Mus musculus]	29.9	29.9	62%	39	90%	AAI37624.1
☐	PREDICTED: multimerin-1-like [Peromyscus maniculatus bairdii]	29.9	29.9	62%	39	90%	XP_006992024.1
☐	XRE family transcriptional regulator [Acinetobacter junii]	29.5	29.5	93%	43	67%	WP_005403322.1
☐	hypothetical protein COCSADRAFT_70880 [Bipolaris sorokiniana ND90Pr]	29.5	29.5	87%	51	55%	XP_007704439.1
☐	hypothetical protein DAPPUDRAFT_263068 [Daphnia pulex]	29.5	29.5	56%	52	100%	EFX66515.1
☐	PREDICTED: multimerin-1 [Condylura cristata]	29.5	29.5	100%	53	63%	XP_004681178.1
☐	conserved hypothetical protein [Albugo laibachii Nc14]	29.5	29.5	68%	53	82%	CCA14698.1
☐	methenyltetrahydrofolate cyclohydrolase [Pseudomonas syringae pv. syringae	29.1	29.1	87%	68	71%	KEZ65083.1
☐	methenyltetrahydrofolate cyclohydrolase [Pseudomonas syringae]	29.1	29.1	87%	70	71%	WP_029571777.1
☐	methenyltetrahydrofolate cyclohydrolase [Pseudomonas syringae]	29.1	29.1	87%	70	71%	WP_024647974.1

☐	methenyltetrahydrofolate cyclohydrolase [Pseudomonas syringae]	29.1	29.1	87%	70	71%	WP_003404473.1
☐	methenyltetrahydrofolate cyclohydrolase [Pseudomonas sp. 45MFCol3.1]	29.1	29.1	87%	70	71%	WP_019648405.1
☐	MULTISPECIES: methenyltetrahydrofolate cyclohydrolase [Pseudomonas]	29.1	29.1	87%	70	71%	WP_018925421.1
☐	methenyltetrahydrofolate cyclohydrolase [Pseudomonas syringae]	29.1	29.1	87%	70	71%	WP_017278097.1
☐	Bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene	29.1	29.1	87%	70	71%	WP_016567611.1
☐	Bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene	29.1	29.1	87%	70	71%	WP_004418524.1
☐	methenyltetrahydrofolate cyclohydrolase [Pseudomonas syringae]	29.1	29.1	87%	70	71%	WP_003415751.1
☐	methenyltetrahydrofolate cyclohydrolase [Pseudomonas sp. GM18]	29.1	29.1	87%	70	71%	WP_007940405.1
☐	methenyltetrahydrofolate cyclohydrolase [Pseudomonas syringae]	29.1	29.1	87%	70	71%	WP_003304374.1
☐	methenyltetrahydrofolate cyclohydrolase [Pseudomonas syringae]	29.1	29.1	87%	70	71%	WP_010437123.1
☐	serine/threonine protein kinase [Streptomyces griseus]	29.1	29.1	87%	72	71%	WP_037709105.1
☐	serine/threonine protein kinase [Streptomyces sp. NRRL F-5727]	29.1	29.1	87%	72	71%	WP_031012850.1
☐	serine/threonine protein kinase [Microtetraspora glauca]	29.1	29.1	87%	72	71%	WP_030495013.1
☐	hypothetical protein [Sulfitobacter mediterraneus]	28.6	28.6	56%	90	89%	WP_025050044.1
☐	putative acyl-CoA dehydrogenase [Bordetella hinzii 8-296-03]	28.6	28.6	81%	97	69%	KCB36636.1
☐	acyl-CoA dehydrogenase [Bordetella hinzii]	28.6	28.6	81%	97	69%	WP_029580134.1
☐	hypothetical protein O988_05182 [Pseudogymnoascus pannorum VKM F-380	28.6	28.6	50%	97	88%	KFX96755.1
☐	hypothetical protein LPMP_281060 [Leishmania panamensis]	28.6	28.6	56%	97	75%	XP_010700446.1
☐	hypothetical protein, conserved [Leishmania donovani]	28.6	28.6	62%	97	90%	XP_003862207.1
☐	conserved hypothetical protein [Leishmania mexicana MHOM/GT/2001/U110	28.6	28.6	62%	97	90%	XP_003876937.1
☐	conserved hypothetical protein [Leishmania infantum JPCM5]	28.6	28.6	62%	97	90%	XP_001470138.1
☐	conserved hypothetical protein [Leishmania braziliensis MHOM/BR/75/M2904	28.6	28.6	56%	97	75%	XP_001566137.1
☐	conserved hypothetical protein [Leishmania major strain Friedlin]	28.6	28.6	62%	97	90%	XP_001684380.1
☐	BnaC09g40530D [Brassica napus]	28.6	28.6	50%	98	88%	CDY16926.1
☐	putative het domain-containing protein [Eutypa lata UCREL1]	28.6	28.6	75%	98	58%	XP_007791007.1
☐	PREDICTED: gamma-tubulin complex component 2-like isoform X3 [Camelina	28.6	28.6	50%	98	88%	XP_010420460.1

Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAH13704.1| **Length:** 970 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 716 to 731 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.1 bits(113)	5e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    KTQAALSDLTCCIDRS  16
            KTQAALS+LTCCIDRS
Sbjct  716  KTQAALSNLTCCIDRS  731
```

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PREDICTED: multimerin-1 isoform X1 [Homo sapiens]

Sequence ID: ref|XP_005262913.1| **Length:** 1193 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 939 to 954 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.1 bits(113)	5e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    KTQAALSDLTCCIDRS  16
            KTQAALS+LTCCIDRS
Sbjct  939  KTQAALSNLTCCIDRS  954
```

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multimerin-1 precursor [Homo sapiens]

Sequence ID: ref|NP_031377.2| **Length:** 1228 **Number of Matches:** 1

See 5 more title(s)

Range 1: 974 to 989 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.1 bits(113)	5e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    KTQAALSDLTCCIDRS  16
            KTQAALS+LTCCIDRS
Sbjct  974  KTQAALSNLTCCIDRS  989
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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Multimerin 1 [Homo sapiens]

Sequence ID: gb|AAH63848.1| **Length:** 1228 **Number of Matches:** 1

See 2 more title(s)

Range 1: 974 to 989 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
51.1 bits(113)	5e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    KTQAALSDLTCCIDRS  16
            KTQAALS+LTCCIDRS
Sbjct  974  KTQAALSNLTCCIDRS  989
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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PREDICTED: multimerin-1 isoform X2 [Pan troglodytes]

Sequence ID: ref|XP_009446302.1| **Length:** 1193 **Number of Matches:** 1

Range 1: 939 to 954 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
47.7 bits(105)	7e-05	14/16(88%)	15/16(93%)	0/16(0%)

```
Query  1    KTQAALSDLTCCIDRS  16
            KTQA LS+LTCCIDRS
Sbjct  939  KTQAVLSNLTCCIDRS  954
```

Related Information

Gene - associated gene details

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ **Formatting Results - B9G8D3VU01R**

Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

MMRN1_KTQAALSNLTCCIDRS_NonMod

RID	B9G8D3VU01R (Expires on 01-14 13:54 pm)		
Query ID	lcl|59156	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	16		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

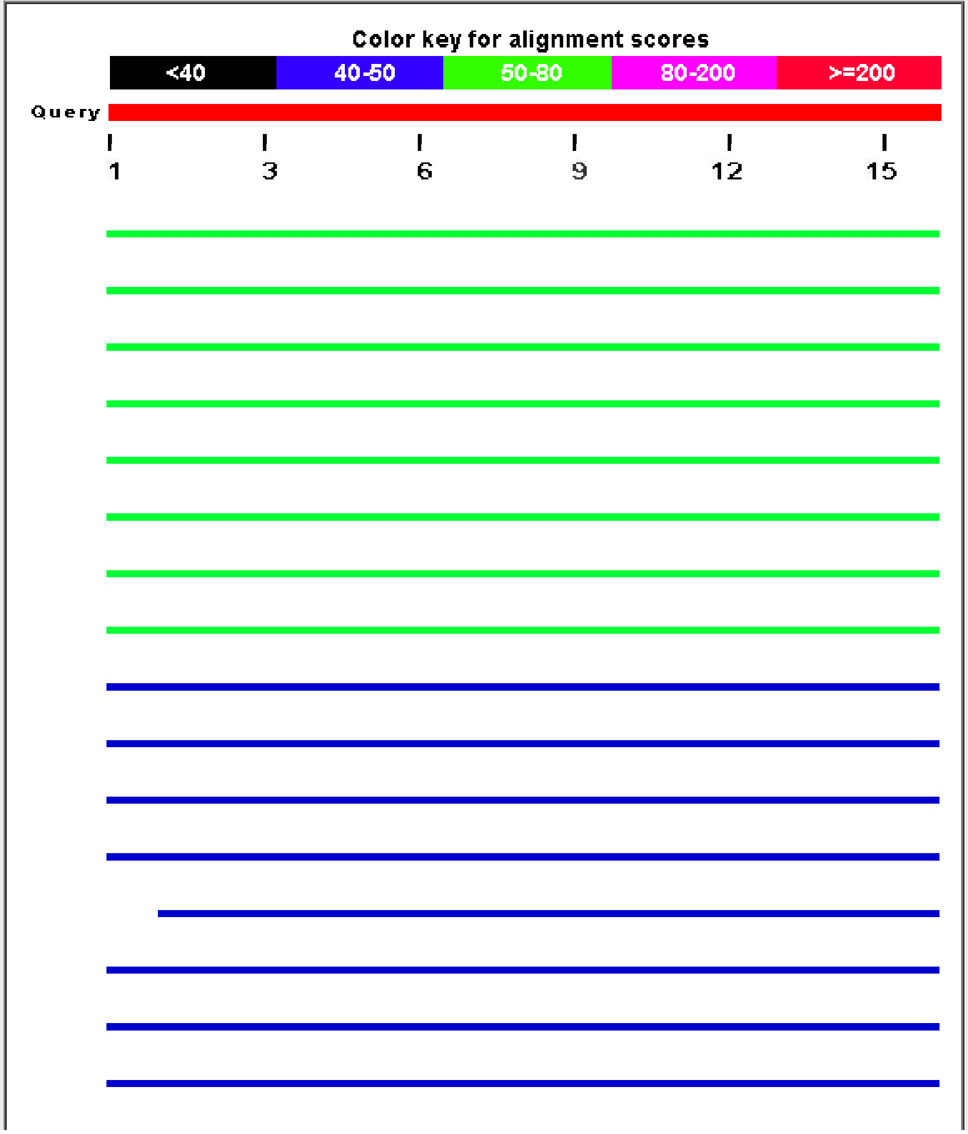
Graphic Summary

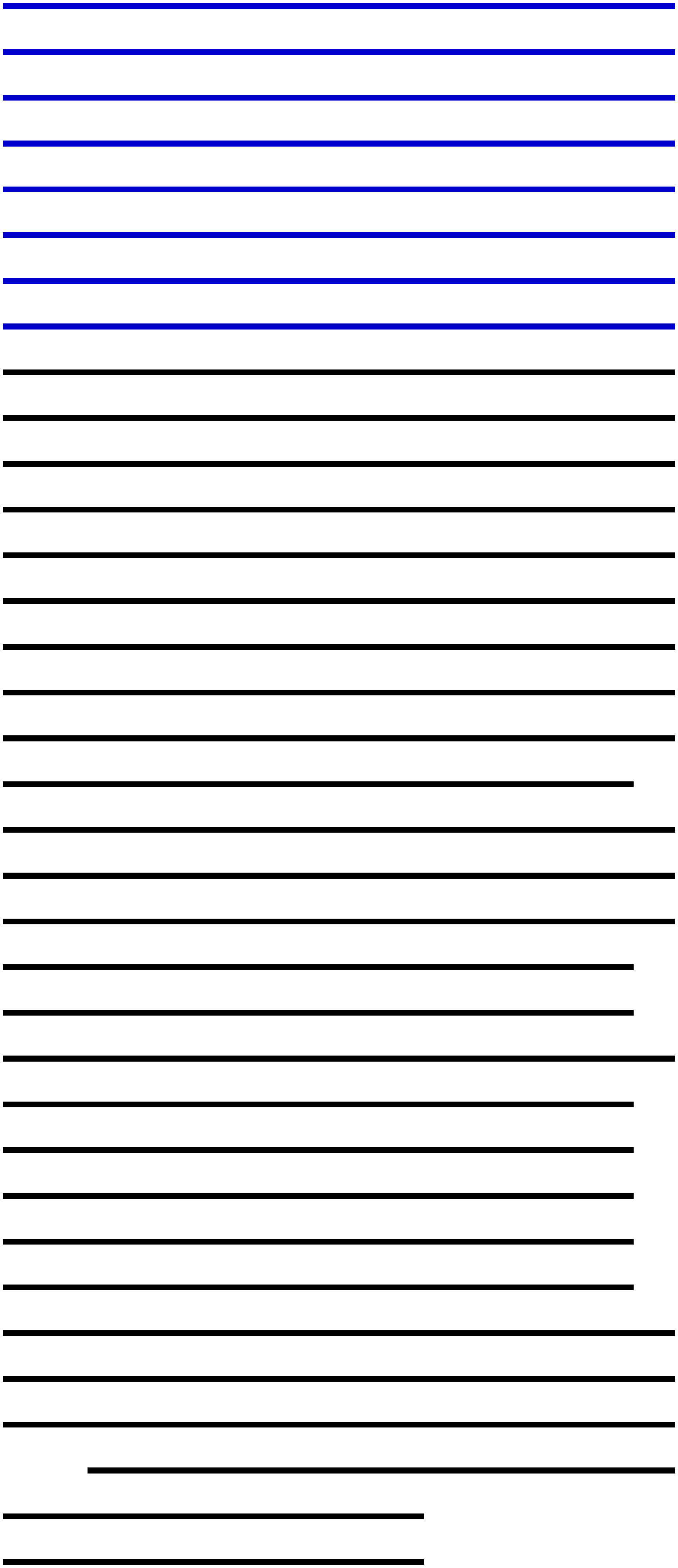
Show Conserved Domains

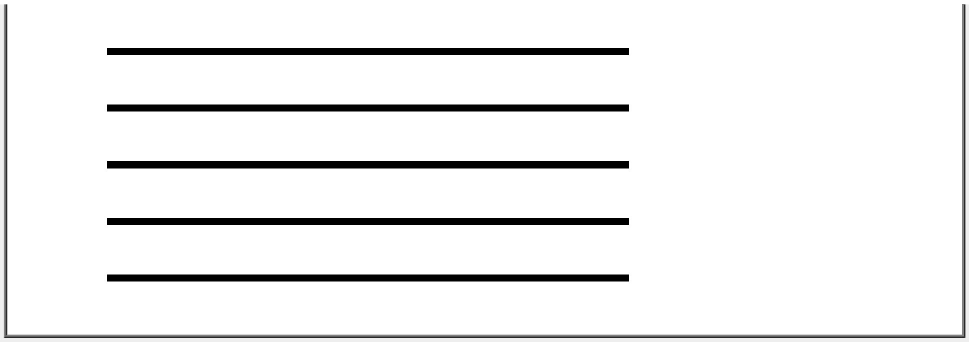
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	53.7	53.7	100%	6e-07	100%	gi|221044054|BAH13704.1
☐	PREDICTED: multimerin-1 isoform X1 [Homo sapiens]	53.7	53.7	100%	6e-07	100%	gi|530377406|XP_005262913.1
☐	multimerin-1 precursor [Homo sapiens]	53.7	53.7	100%	6e-07	100%	gi|45269141|NP_031377.2
☐	Multimerin 1 [Homo sapiens]	53.7	53.7	100%	6e-07	100%	gi|39645323|AAH63848.1
☐	PREDICTED: multimerin-1 isoform X2 [Pan troglodytes]	50.3	50.3	100%	9e-06	94%	gi|694908198|XP_009446302.1
☐	PREDICTED: LOW QUALITY PROTEIN: multimerin-1 [Pongo abeli	50.3	50.3	100%	9e-06	94%	gi|297673972|XP_002815014.1
☐	PREDICTED: multimerin-1 [Gorilla gorilla gorilla]	50.3	50.3	100%	9e-06	94%	gi|426344970|XP_004039176.1
☐	PREDICTED: multimerin-1 isoform X1 [Pan troglodytes]	50.3	50.3	100%	9e-06	94%	gi|114595173|XP_517342.2
☐	PREDICTED: multimerin-1 isoform 2 [Nomascus leucogenys]	49.0	49.0	100%	2e-05	94%	gi|441625381|XP_004089067.1
☐	PREDICTED: multimerin-1 isoform 1 [Nomascus leucogenys]	49.0	49.0	100%	2e-05	94%	gi|332216893|XP_003257586.1
☐	PREDICTED: multimerin-1 [Pan paniscus]	47.7	47.7	100%	6e-05	88%	gi|397519601|XP_003829944.1
☐	prepromultimerin [Homo sapiens]	47.3	47.3	100%	9e-05	94%	gi|927596|AAC52065.1
☐	PREDICTED: multimerin-1 [Rhinopithecus roxellana]	47.3	47.3	93%	9e-05	93%	gi|724888364|XP_010374576.1
☐	PREDICTED: multimerin-1 [Macaca mulatta]	46.0	46.0	100%	2e-04	88%	gi|297293024|XP_002804181.1
☐	PREDICTED: multimerin-1 isoform X2 [Macaca fascicularis]	46.0	46.0	100%	2e-04	88%	gi|544433553|XP_005555483.1
☐	hypothetical protein EGM_14545 [Macaca fascicularis]	46.0	46.0	100%	2e-04	88%	gi|355749442|EHH53841.1
☐	hypothetical protein EGK_15920 [Macaca mulatta]	46.0	46.0	100%	2e-04	88%	gi|355687455|EHH26039.1
☐	PREDICTED: multimerin-1 isoform 2 [Macaca mulatta]	46.0	46.0	100%	2e-04	88%	gi|109074983|XP_001101702.1
☐	PREDICTED: multimerin-1 [Papio anubis]	46.0	46.0	100%	2e-04	88%	gi|685542090|XP_009205449.1
☐	PREDICTED: multimerin-1 isoform X1 [Macaca fascicularis]	46.0	46.0	100%	2e-04	88%	gi|544433551|XP_005555482.1
☐	PREDICTED: multimerin-1 [Saimiri boliviensis boliviensis]	46.0	46.0	100%	2e-04	88%	gi|725558699|XP_010333103.1
☐	PREDICTED: multimerin-1 isoform X2 [Chlorocebus sabaeus]	43.5	43.5	100%	0.002	81%	gi|635043771|XP_007997465.1
☐	PREDICTED: multimerin-1 isoform X1 [Chlorocebus sabaeus]	43.5	43.5	100%	0.002	81%	gi|635043767|XP_007997463.1
☐	PREDICTED: multimerin-1 [Callithrix jacchus]	42.2	42.2	100%	0.004	81%	gi|675648553|XP_008991221.1
☐	PREDICTED: multimerin-1 [Trichechus manatus latirostris]	37.1	37.1	100%	0.19	88%	gi|471415079|XP_004389070.1
☐	Multimerin-1 [Tupaia chinensis]	37.1	37.1	100%	0.19	88%	gi|444729780|ELW70184.1
☐	PREDICTED: multimerin-1 [Chrysochloris asiatica]	37.1	37.1	100%	0.19	88%	gi|586485083|XP_006873035.1
☐	PREDICTED: multimerin-1 [Oryctolagus cuniculus]	37.1	37.1	100%	0.19	88%	gi|655857200|XP_008265817.1
☐							

	PREDICTED: multimerin-1 [Loxodonta africana]	37.1	37.1	100%	0.19	88%	gi|344284751|XP_003414128.1
☐	PREDICTED: multimerin-1 [Tupaia chinensis]	37.1	37.1	100%	0.19	88%	gi|562827341|XP_006143301.1
☐	PREDICTED: multimerin-1 [Tarsius syrichta]	35.8	35.8	100%	0.49	81%	gi|640825228|XP_008069714.1
☐	PREDICTED: multimerin-1-like isoform 2 [Dasypus novemcinctus]	34.6	34.6	100%	1.2	81%	gi|488525158|XP_004454437.1
☐	PREDICTED: multimerin-1-like isoform 1 [Dasypus novemcinctus]	34.6	34.6	100%	1.2	81%	gi|488525156|XP_004454436.1
☐	PREDICTED: multimerin-1 [Ictidomys tridecemlineatus]	34.6	34.6	93%	1.2	87%	gi|532103995|XP_005337593.1
☐	PREDICTED: multimerin-1 [Ochotona princeps]	34.1	34.1	100%	1.7	81%	gi|504158342|XP_004590628.1
☐	PREDICTED: multimerin-1 [Elephantulus edwardii]	34.1	34.1	100%	1.7	81%	gi|585690668|XP_006894545.1
☐	PREDICTED: multimerin-1 [Otolemur garnettii]	33.7	33.7	100%	2.3	81%	gi|395834121|XP_003790061.1
☐	PREDICTED: multimerin-1 [Mesocricetus auratus]	33.3	33.3	93%	3.2	87%	gi|524952230|XP_005076113.1
☐	Multimerin-1 [Cricetulus griseus]	32.9	32.9	93%	4.3	80%	gi|344236173|EGV92276.1
☐	PREDICTED: multimerin-1 [Orycteropus afer afer]	32.9	32.9	100%	4.3	81%	gi|634885587|XP_007952403.1
☐	multimerin-1 [Cricetulus griseus]	32.9	32.9	93%	4.3	80%	gi|537138121|ERE67090.1
☐	PREDICTED: multimerin-1 isoform X2 [Cricetulus griseus]	32.9	32.9	93%	4.3	80%	gi|625287884|XP_007635662.1
☐	PREDICTED: multimerin-1 isoform X2 [Cricetulus griseus]	32.9	32.9	93%	4.3	80%	gi|625201541|XP_007642492.1
☐	PREDICTED: multimerin-1 isoform X1 [Cricetulus griseus]	32.9	32.9	93%	4.3	80%	gi|625287882|XP_007635661.1
☐	PREDICTED: multimerin-1 isoform X1 [Cricetulus griseus]	32.9	32.9	93%	4.3	80%	gi|354483185|XP_003503775.1
☐	PREDICTED: multimerin-1 [Ceratotherium simum simum]	32.9	32.9	100%	4.3	75%	gi|478513518|XP_004431014.1
☐	PREDICTED: multimerin-1 [Equus caballus]	32.9	32.9	100%	4.3	75%	gi|149701546|XP_001497011.1
☐	PREDICTED: multimerin-1 [Equus przewalskii]	32.9	32.9	100%	4.3	75%	gi|664711276|XP_008512609.1
☐	hypothetical protein COCVIDRAFT_82402 [Bipolaris victoriae FI3]	32.5	32.5	87%	5.4	60%	gi|578484972|EUN22480.1
☐	multimerin-1 [Mus musculus]	32.5	32.5	62%	5.5	100%	gi|48290287|CAE52464.1
☐	Mmrn1 protein [Mus musculus]	32.5	32.5	62%	5.6	100%	gi|28386085|AAH46425.1
☐	PREDICTED: multimerin-1 isoform X2 [Microtus ochrogaster]	32.5	32.5	62%	5.8	100%	gi|532035424|XP_005360610.1
☐	PREDICTED: multimerin-1 isoform X1 [Microtus ochrogaster]	32.5	32.5	62%	5.8	100%	gi|532035422|XP_005360609.1
☐	Mmrn1 protein [Mus musculus]	32.5	32.5	62%	5.8	100%	gi|219519560|AAI44790.1
☐	multimerin-1 isoform b precursor [Mus musculus]	32.5	32.5	62%	5.8	100%	gi|254588077|NP_001156979.1
☐	multimerin-1 isoform a precursor [Mus musculus]	32.5	32.5	62%	5.8	100%	gi|254588075|NP_081889.1
☐	RecName: Full=Multimerin-1; Flags: Precursor [Mus musculus]	32.5	32.5	62%	5.8	100%	gi|229486321|B2RPV6.2
☐	Multimerin 1 [Mus musculus]	32.5	32.5	62%	5.8	100%	gi|187950723|AAI37624.1
☐	PREDICTED: multimerin-1-like [Peromyscus maniculatus bairdii]	32.5	32.5	62%	5.8	100%	gi|589958869|XP_006992024.1
☐	PREDICTED: multimerin-1 [Condylura cristata]	32.0	32.0	100%	8.0	69%	gi|507942523|XP_004681178.1
☐	PREDICTED: multimerin-1 [Fukomys damarensis]	30.8	30.8	93%	20	80%	gi|731190588|XP_010624565.1
☐	PREDICTED: multimerin-1 [Jaculus jaculus]	30.8	30.8	81%	20	77%	gi|507563580|XP_004665470.1
☐	PREDICTED: multimerin-1-like [Galeopterus variegatus]	30.3	30.3	100%	27	75%	gi|667259514|XP_008566937.1
☐	PREDICTED: multimerin-1-like [Galeopterus variegatus]	30.3	30.3	100%	27	75%	gi|667330346|XP_008591205.1
☐	PREDICTED: multimerin-1 isoform X1 [Sus scrofa]	30.3	30.3	100%	27	69%	gi|335294081|XP_003129371.2
☐	PREDICTED: multimerin-1 isoform X2 [Sus scrofa]	30.3	30.3	100%	27	69%	gi|545846726|XP_005667049.1
☐	WSSV511 [Shrimp white spot syndrome virus]	29.9	29.9	50%	31	100%	gi|19482103|AAL89379.1
☐	wsv451 [Shrimp white spot syndrome virus]	29.9	29.9	50%	31	100%	gi|17158552|NP_477973.1
☐	wsv451 [White spot syndrome virus]	29.9	29.9	50%	31	100%	gi|417072679|AFX59828.1
☐	unnamed protein product [Oikopleura dioica]	29.9	29.9	56%	36	89%	gi|313225274|CBY06748.1
☐	PREDICTED: multimerin-1 [Heterocephalus glaber]	29.9	29.9	87%	37	79%	gi|512916002|XP_004903189.1
☐	XRE family transcriptional regulator [Acinetobacter junii]	29.5	29.5	93%	40	67%	gi|491545706|WP_005403322.1
☐	hypothetical protein COCSADRAFT_70880 [Bipolaris sorokiniana N	29.5	29.5	87%	48	55%	gi|628085178|XP_007704439.1

☐	Protein Bm2028, isoform g [Brugia malayi]	29.5	29.5	68%	50	69%	gi|671415026|CDP92562.1
☐	calpain family protein 1, isoform d [Brugia malayi]	29.5	29.5	68%	50	69%	gi|170581386|XP_001895660.1
☐	kinesin light chain 3 [Pyrenophora tritici-repentis Pt-1C-BFP]	29.5	29.5	81%	50	58%	gi|189210760|XP_001941711.1
☐	hypothetical protein [Advenella kashmirensis]	29.1	29.1	87%	66	69%	gi|665874760|WP_031241966.1
☐	glycosyl transferase [Advenella kashmirensis W13003]	29.1	29.1	87%	67	69%	gi|565409456|ETF03785.1
☐	inositolphosphorylceramide synthase, putative; phosphatidylinositol	29.1	29.1	62%	67	90%	gi|241955385|XP_002420413.1
☐	PREDICTED: multimerin-1 isoform X3 [Rattus norvegicus]	29.1	29.1	62%	69	90%	gi|564303841|XP_006225012.1
☐	PREDICTED: multimerin-1 isoform X2 [Rattus norvegicus]	29.1	29.1	62%	69	90%	gi|564303839|XP_006225011.1
☐	PREDICTED: multimerin-1 isoform X1 [Rattus norvegicus]	29.1	29.1	62%	69	90%	gi|293346833|XP_001065496.2
☐	isochorismate synthase [Enterovibrio calviensis]	28.6	28.6	62%	92	90%	gi|654557540|WP_028024913.1
☐	Gamma-tubulin complex component 2 [Triticum urartu]	28.6	28.6	56%	93	78%	gi|474005391|EMS52405.1
☐	PREDICTED: multimerin-1-like [Tursiops truncatus]	28.6	28.6	100%	93	69%	gi|470612518|XP_004316075.1
☐	PREDICTED: multimerin-1 [Echinops telfairi]	28.6	28.6	100%	93	75%	gi|507648892|XP_004703488.1
☐	PREDICTED: multimerin-1 [Orcinus orca]	28.6	28.6	100%	93	69%	gi|466044414|XP_004277020.1
☐	PREDICTED: multimerin-1 [Lipotes vexillifer]	28.6	28.6	100%	93	69%	gi|602729302|XP_007450078.1
☐	PREDICTED: multimerin-1 [Physeter catodon]	28.6	28.6	100%	93	69%	gi|593718138|XP_007105448.1
☐	PREDICTED: multimerin-1 [Balaenoptera acutorostrata scammoni]	28.6	28.6	100%	93	69%	gi|594672475|XP_007184155.1
☐	PREDICTED: multimerin-1 isoform X2 [Chinchilla lanigera]	28.6	28.6	100%	93	67%	gi|533117571|XP_005374311.1
☐	PREDICTED: multimerin-1 isoform X1 [Chinchilla lanigera]	28.6	28.6	100%	93	67%	gi|533117569|XP_005374310.1
☐	tail protein [Eggerthella lenta]	28.2	28.2	62%	122	71%	gi|506241535|WP_015761310.1
☐	membrane lipoprotein tmpC precursor [Halorubrum californiense]	28.2	28.2	75%	124	53%	gi|495716916|WP_008441495.1
☐	membrane lipoprotein tmpC precursor [Halorubrum coriense]	28.2	28.2	75%	124	53%	gi|493053490|WP_006112854.1
☐	glycoside hydrolase family 30 protein [Thielavia terrestris NRRL 81	28.2	28.2	75%	125	80%	gi|367054370|XP_003657563.1
☐	PREDICTED: NADPH oxidase 3 [Pan troglodytes]	28.2	28.2	87%	126	63%	gi|114609915|XP_527546.2
☐	PREDICTED: multimerin-1 isoform X1 [Cavia porcellus]	28.2	28.2	62%	127	90%	gi|348563454|XP_003467522.1
☐	PREDICTED: multimerin-1 isoform X2 [Cavia porcellus]	28.2	28.2	62%	127	90%	gi|514456652|XP_005002721.1
☐	PREDICTED: multimerin-1-like [Octodon degus]	28.2	28.2	62%	127	90%	gi|507714859|XP_004648455.1

⊟ Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221044054|dbj|BAH13704.1| **Length:** 970 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 716 to 731 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
53.7 bits(119)	6e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    KTQAALSNLTCCIDRS  16
            KTQAALSNLTCCIDRS
Sbjct  716  KTQAALSNLTCCIDRS  731
```

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PREDICTED: multimerin-1 isoform X1 [Homo sapiens]

Sequence ID: gi|530377406|ref|XP_005262913.1| **Length:** 1193 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 939 to 954 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
53.7 bits(119)	6e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    KTQAALSNLTCCIDRS  16
```

```
            KTQAALSNLTCCIDRS
Sbjct  939  KTQAALSNLTCCIDRS  954
```

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multimerin-1 precursor [Homo sapiens]

Sequence ID: gi|45269141|ref|NP_031377.2| **Length:** 1228 **Number of Matches:** 1

See 5 more title(s)

Range 1: 974 to 989 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
53.7 bits(119)	6e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    KTQAALSNLTCCIDRS  16
            KTQAALSNLTCCIDRS
Sbjct  974  KTQAALSNLTCCIDRS  989
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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Multimerin 1 [Homo sapiens]

Sequence ID: gi|39645323|gb|AAH63848.1| **Length:** 1228 **Number of Matches:** 1

See 2 more title(s)

Range 1: 974 to 989 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
53.7 bits(119)	6e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    KTQAALSNLTCCIDRS  16
            KTQAALSNLTCCIDRS
Sbjct  974  KTQAALSNLTCCIDRS  989
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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PREDICTED: multimerin-1 isoform X2 [Pan troglodytes]

Sequence ID: gi|694908198|ref|XP_009446302.1| **Length:** 1193 **Number of Matches:** 1

Range 1: 939 to 954 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
50.3 bits(111)	9e-06	15/16(94%)	15/16(93%)	0/16(0%)

```
Query  1    KTQAALSNLTCCIDRS  16
            KTQA LSNLTCCIDRS
Sbjct  939  KTQAVLSNLTCCIDRS  954
```

Related Information

Gene - associated gene details

BLAST ®

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVJBTM5501R

Your search parameters were adjusted to search for a short input sequence.

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MST1_KGEGYRGTADTTTAGVPCQRW_Mod

RID BVJBTM5501R (Expires on 01-21 10:20 am)

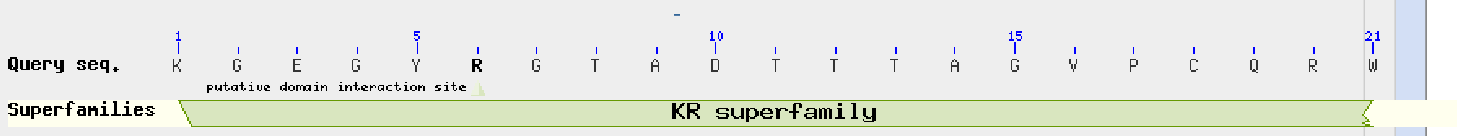
Query ID	lcl|55271	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ ▷ Citation
Query Length	21		

Other reports: ▷ Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

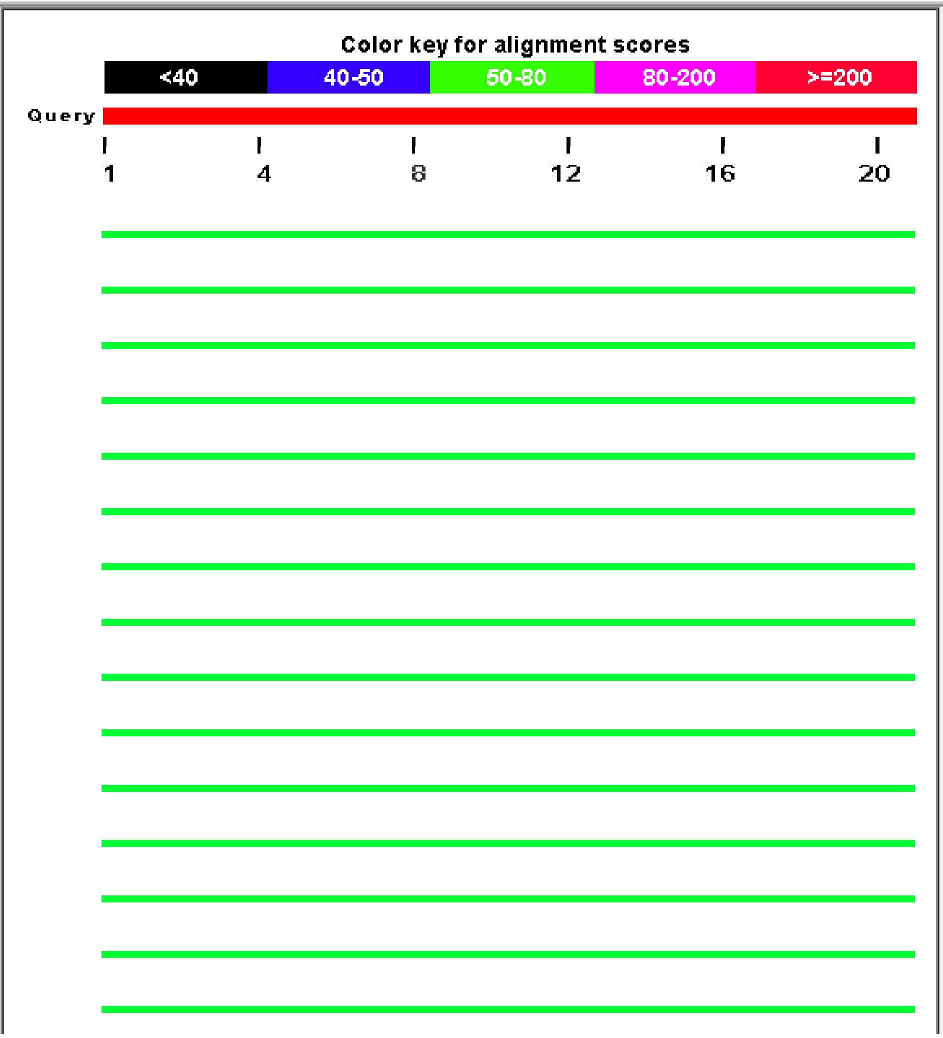
Show Conserved Domains

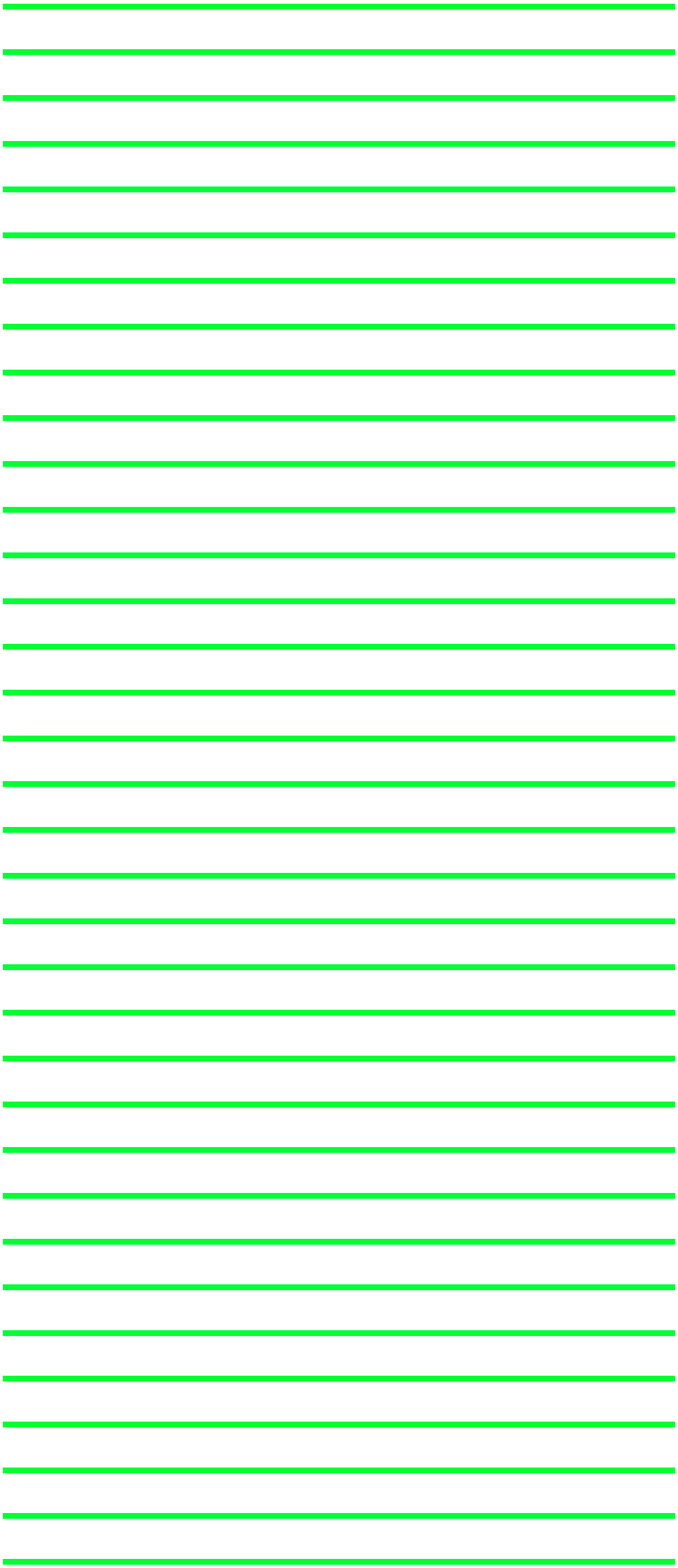
Putative conserved domains have been detected, click on the image below for detailed results.

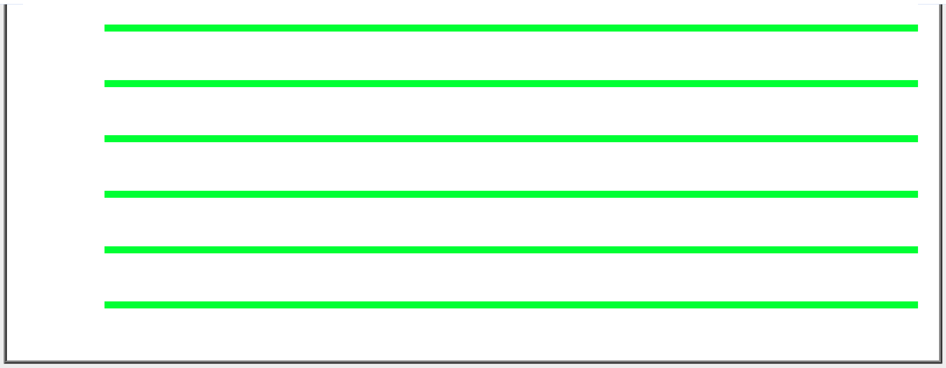


Distribution of 367 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	MST1 protein [Homo sapiens]	68.1	99.3	100%	1e-11	95%	AAH44862.1
☐	unnamed protein product [Homo sapiens]	68.1	133	100%	1e-11	95%	BAH12793.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like), isoform CRA_d [Ho	68.1	99.3	100%	1e-11	95%	EAW65002.1
☐	unnamed protein product [Homo sapiens]	68.1	133	100%	1e-11	95%	BAH11736.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Homo sapiens	68.1	167	100%	2e-11	95%	XP_006713232.1
☐	hepatocyte growth factor-like protein homolog [Homo sapiens]	68.1	159	100%	2e-11	95%	AAC63092.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Macaca fascic	68.1	168	100%	2e-11	95%	XP_005547205.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like), isoform CRA_e [Ho	68.1	132	100%	2e-11	95%	EAW65003.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Homo sapiens	68.1	167	100%	2e-11	95%	XP_006713230.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X5 [Chlorocebus s	68.1	135	100%	2e-11	95%	XP_007982450.1
☐	PREDICTED: hepatocyte growth factor-like protein [Echinops telfairi]	68.1	136	100%	2e-11	95%	XP_004715222.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Papio anubis]	68.1	168	100%	2e-11	95%	XP_009199018.1
☐	macrophage-stimulating protein [Homo sapiens]	68.1	167	100%	2e-11	95%	AAA59872.1
☐	RecName: Full=Hepatocyte growth factor-like protein; AltName: Full=Macroph	68.1	167	100%	2e-11	95%	P26927.2
☐	hepatocyte growth factor-like protein [Homo sapiens]	68.1	167	100%	2e-11	95%	AAA50165.1
☐	hypothetical protein EGM_20500 [Macaca fascicularis]	68.1	168	100%	2e-11	95%	EHH62249.1
☐	hypothetical protein EGK_11631 [Macaca mulatta]	68.1	168	100%	2e-11	95%	EHH16360.1
☐	hypothetical protein [Macaca fascicularis]	68.1	168	100%	2e-11	95%	BAF47378.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like) variant [Homo sapie	68.1	170	100%	2e-11	95%	BAD96613.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Chlorocebus s	68.1	135	100%	2e-11	95%	XP_007982449.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Cavia porcellu	68.1	153	100%	2e-11	95%	XP_003476721.1
☐	PREDICTED: hepatocyte growth factor-like protein [Pteropus alecto]	68.1	171	100%	2e-11	95%	XP_006909162.1
☐	PREDICTED: hepatocyte growth factor-like protein [Pongo abelii]	68.1	169	100%	2e-11	95%	XP_002813790.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Chlorocebus s	68.1	168	100%	2e-11	95%	XP_007982448.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Macaca fascic	68.1	168	100%	2e-11	95%	XP_005547204.1
☐	PREDICTED: hepatocyte growth factor-like protein [Gorilla gorilla gorilla]	68.1	167	100%	2e-11	95%	XP_004034204.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Papio anubis]	68.1	168	100%	2e-11	95%	XP_003894463.1
☐	PREDICTED: hepatocyte growth factor-like protein [Nomascus leucogenys]	68.1	163	100%	2e-11	95%	XP_003257123.1
☐	hepatocyte growth factor-like protein precursor [Homo sapiens]	68.1	167	100%	2e-11	95%	NP_066278.3

☐	PREDICTED: hepatocyte growth factor-like protein [Macaca mulatta]	68.1	168	100%	2e-11	95%	XP_001107946.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Chlorocebus s	68.1	135	100%	2e-11	95%	XP_007982445.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Cavia porcellu	68.1	153	100%	2e-11	95%	XP_005006713.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Chlorocebus s	68.1	135	100%	2e-11	95%	XP_007982444.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein	68.1	165	100%	2e-11	95%	XP_516465.4
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein	65.1	163	100%	2e-10	90%	XP_005326984.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Equus przewa	64.7	167	100%	2e-10	90%	XP_008522208.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Saimiri bolivie	64.7	161	100%	2e-10	90%	XP_010345462.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Equus caballu	64.7	139	100%	2e-10	90%	XP_005600717.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Equus przewa	64.7	167	100%	2e-10	90%	XP_008522206.1
☐	hypothetical protein PANDA_009343 [Ailuropoda melanoleuca]	64.7	156	100%	2e-10	90%	EFB13926.1
☐	PREDICTED: hepatocyte growth factor-like protein [Erinaceus europaeus]	64.7	148	100%	2e-10	90%	XP_007527316.1
☐	PREDICTED: hepatocyte growth factor-like protein [Galeopterus variegatus]	64.7	162	100%	2e-10	90%	XP_008569781.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tarsius syrichta]	64.7	168	100%	2e-10	90%	XP_008061363.1
☐	PREDICTED: hepatocyte growth factor-like protein [Orycteropus afer afer]	64.7	166	100%	2e-10	90%	XP_007953538.1
☐	PREDICTED: hepatocyte growth factor-like protein [Leptonychotes weddellii]	64.7	161	100%	2e-10	90%	XP_006744596.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tupaia chinensis]	64.7	161	100%	2e-10	90%	XP_006171012.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Mustela putori	64.7	156	100%	2e-10	90%	XP_004820133.1
☐	PREDICTED: hepatocyte growth factor-like protein [Mustela putorius furo]	64.7	156	100%	2e-10	90%	XP_004760697.1
☐	PREDICTED: hepatocyte growth factor-like protein [Odobenus rosmarus dive	64.7	158	100%	2e-10	90%	XP_004399304.1
☐	PREDICTED: hepatocyte growth factor-like protein [Ceratotherium simum sim	64.7	160	100%	2e-10	90%	XP_004419765.1
☐	PREDICTED: hepatocyte growth factor-like protein [Sorex araneus]	64.7	158	100%	2e-10	90%	XP_004615300.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein	64.7	170	100%	2e-10	90%	XP_003409924.1
☐	PREDICTED: hepatocyte growth factor-like protein [Eptesicus fuscus]	64.7	153	100%	2e-10	90%	XP_008153797.1
☐	PREDICTED: hepatocyte growth factor-like protein [Pantholops hodgsonii]	64.7	130	100%	2e-10	90%	XP_005969335.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Equus caballu	64.7	167	100%	2e-10	90%	XP_005600716.1
☐	PREDICTED: hepatocyte growth factor-like protein [Felis catus]	64.7	165	100%	2e-10	90%	XP_003982280.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Saimiri bolivie	64.7	161	100%	2e-10	90%	XP_003936704.1
☐	PREDICTED: hepatocyte growth factor-like protein [Canis lupus familiaris]	64.7	161	100%	2e-10	90%	XP_541884.3
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein	64.7	125	100%	2e-10	90%	XP_004018505.1
☐	Hepatocyte growth factor-like protein [Tupaia chinensis]	64.7	161	100%	2e-10	90%	ELV09642.1
☐	PREDICTED: hepatocyte growth factor-like protein-like [Ailuropoda melanoleu	64.7	156	100%	2e-10	90%	XP_002920612.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Chinchilla lani	64.3	122	100%	3e-10	90%	XP_005410271.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Chinchilla lani	64.3	122	100%	3e-10	90%	XP_005410270.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Chinchilla lani	64.3	122	100%	3e-10	90%	XP_005410269.1
☐	PREDICTED: hepatocyte growth factor-like protein [Rhinopithecus roxellana]	63.8	165	100%	4e-10	90%	XP_010367959.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Callithrix jacch	62.6	122	100%	1e-09	86%	XP_008979888.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Callithrix jacch	62.6	156	100%	1e-09	86%	XP_002758398.1
☐	PREDICTED: hepatocyte growth factor-like protein [Otolemur garnettii]	62.1	164	100%	2e-09	86%	XP_003800642.1
☐	PREDICTED: hepatocyte growth factor-like protein [Elephantulus edwardii]	61.7	166	100%	2e-09	86%	XP_006892963.1
☐	PREDICTED: hepatocyte growth factor-like protein [Dasypus novemcinctus]	61.7	164	100%	2e-09	86%	XP_004451933.1
☐	PREDICTED: hepatocyte growth factor-like protein [Bubalus bubalis]	61.3	131	100%	3e-09	86%	XP_006053335.1
☐	PREDICTED: hepatocyte growth factor-like protein [Bos mutus]	61.3	131	100%	3e-09	86%	XP_005892185.1
☐	TPA: hepatocyte growth factor-like protein [Bos taurus]	61.3	131	100%	3e-09	86%	DAA16921.1
☐	hepatocyte growth factor-like protein precursor [Bos taurus]	61.3	131	100%	3e-09	86%	NP_001069145.1
☐	PREDICTED: hepatocyte growth factor-like protein [Camelus bactrianus]	61.3	158	100%	3e-09	86%	XP_010967473.1

☐	Hepatocyte growth factor-like protein [Bos mutus]	61.3	131	100%	3e-09	86%	ELR58967.1
☐	PREDICTED: hepatocyte growth factor-like protein [Jaculus jaculus]	61.3	151	100%	3e-09	86%	XP_004664298.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Bison bison bi	61.3	131	100%	3e-09	86%	XP_010850156.1
☐	PREDICTED: hepatocyte growth factor-like protein [Balaenoptera acutorostrat	61.3	157	100%	3e-09	86%	XP_007168789.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Bison bison bi	61.3	131	100%	3e-09	86%	XP_010850155.1
☐	PREDICTED: hepatocyte growth factor-like protein [Lipotes vexillifer]	61.3	157	100%	3e-09	86%	XP_007446274.1
☐	PREDICTED: hepatocyte growth factor-like protein [Physeter catodon]	61.3	153	100%	3e-09	86%	XP_007129906.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like proteir	61.3	158	100%	3e-09	86%	XP_006196588.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Bos taurus]	61.3	131	100%	3e-09	86%	XP_005222861.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tursiops truncatus]	61.3	157	100%	3e-09	86%	XP_004314855.1
☐	PREDICTED: hepatocyte growth factor-like protein [Orcinus orca]	61.3	157	100%	3e-09	86%	XP_004284002.1
☐	PREDICTED: hepatocyte growth factor-like protein [Camelus dromedarius]	61.3	158	100%	3e-09	86%	XP_010976658.1
☐	PREDICTED: hepatocyte growth factor-like protein [Octodon degus]	60.9	155	100%	4e-09	86%	XP_004625159.1
☐	PREDICTED: hepatocyte growth factor-like protein [Ochotona princeps]	60.9	147	100%	4e-09	86%	XP_004581815.1
☐	PREDICTED: hepatocyte growth factor-like protein [Trichechus manatus latiro	60.4	171	100%	6e-09	86%	XP_004368594.1
☐	PREDICTED: hepatocyte growth factor-like protein [Chrysochloris asiatica]	59.6	160	100%	1e-08	81%	XP_006873659.1
☐	Hepatocyte growth factor-like protein [Cricetulus griseus]	58.3	58.3	100%	1e-08	81%	EGW08932.1
☐	hepatocyte growth factor-like protein [Cricetulus griseus]	58.3	81.9	100%	3e-08	81%	ERE75628.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Mus musculus	58.3	144	100%	3e-08	81%	XP_006511702.1
☐	PREDICTED: hepatocyte growth factor-like protein [Nannospalax galili]	58.3	108	100%	3e-08	81%	XP_008851489.1
☐	Macrophage stimulating 1 (hepatocyte growth factor-like) [Mus musculus]	58.3	144	100%	3e-08	81%	AAH10551.1
☐	hepatocyte growth factor-like protein precursor [Mus musculus]	58.3	144	100%	3e-08	81%	NP_032269.3
☐	PREDICTED: hepatocyte growth factor-like protein [Mesocricetus auratus]	58.3	134	100%	3e-08	81%	XP_005074975.1
☐	unnamed protein product [Mus musculus]	58.3	144	100%	3e-08	81%	BAE22056.1
☐	hepatocyte growth factor-like protein [Mus musculus]	58.3	144	100%	3e-08	81%	AAA50167.1

⊟ Alignments

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MST1 protein [Homo sapiens]

Sequence ID: gb|AAH44862.1| **Length:** 188 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 150 to 170 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	1e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KGEGYRGTADTTTAGVPCQRW  21
            KGEGYRGTA+TTTAGVPCQRW
Sbjct  150  KGEGYRGTANTTTAGVPCQRW  170
```

Range 2: 59 to 78 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
31.2 bits(66)	21	12/20(60%)	12/20(60%)	0/20(0%)

```
Query  2   GEGYRGTADTTTAGVPCQRW  21
           GE YRG  D T  G   CQRW
Sbjct  59  GEEYRGAVDRTESGRECQRW  78
```

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unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAH12793.1| **Length:** 264 **Number of Matches:** 3

Related Information

Range 1: 226 to 246 GenPept Graphics ▼ Next Match ▲ Previous Match

Gene - associated gene details

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	1e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KGEGYRGTADTTTAGVPCQRW  21
            KGEGYRGTA+TTTAGVPCQRW
Sbjct  226  KGEGYRGTANTTTAGVPCQRW  246
```

Range 2: 56 to 73 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
34.6 bits(74)	1.7	12/18(67%)	12/18(66%)	0/18(0%)

```
Query  4   GYRGTADTTTAGVPCQRW  21
           GYRGT  TT  G PCQ W
Sbjct  56  GYRGTMATTVGGLPCQAW  73
```

Range 3: 135 to 154 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
31.2 bits(66)	21	12/20(60%)	12/20(60%)	0/20(0%)

```
Query  2    GEGYRGTADTTTAGVPCQRW  21
            GE YRG  D T  G  CQRW
Sbjct  135  GEEYRGAVDRTESGRECQRW  154
```

Download ⌄ GenPept Graphics **Sort by:** 0 ▼ Next ▲ Previous ▲ Descriptions

macrophage stimulating 1 (hepatocyte growth factor-like), isoform CRA_d [Homo sapiens]

Sequence ID: gb|EAW65002.1| **Length:** 331 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 225 to 245 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	1e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KGEGYRGTADTTTAGVPCQRW  21
            KGEGYRGTA+TTTAGVPCQRW
Sbjct  225  KGEGYRGTANTTTAGVPCQRW  245
```

Range 2: 134 to 153 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
31.2 bits(66)	21	12/20(60%)	12/20(60%)	0/20(0%)

```
Query  2    GEGYRGTADTTTAGVPCQRW  21
            GE YRG  D T  G  CQRW
Sbjct  134  GEEYRGAVDRTESGRECQRW  153
```

Download ⌄ GenPept Graphics **Sort by:** 0 ▼ Next ▲ Previous ▲ Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAH11736.1| **Length:** 339 **Number of Matches:** 3

Related Information

Gene - associated gene details

Range 1: 301 to 321 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	1e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KGEGYRGTADTTTAGVPCQRW  21
            KGEGYRGTA+TTTAGVPCQRW
Sbjct  301  KGEGYRGTANTTTAGVPCQRW  321
```

Range 2: 131 to 148 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
34.6 bits(74)	1.7	12/18(67%)	12/18(66%)	0/18(0%)

```
Query  4    GYRGTADTTTAGVPCQRW  21
            GYRGT  TT  G PCQ W
Sbjct  131  GYRGTMATTVGGLPCQAW  148
```

Range 3: 210 to 229 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Identities	Positives	Gaps
31.2 bits(66)	21	12/20(60%)	12/20(60%)	0/20(0%)

```
Query  2    GEGYRGTADTTTAGVPCQRW  21
            GE YRG  D T  G  CQRW
Sbjct  210  GEEYRGAVDRTESGRECQRW  229
```

Download ⌄ GenPept Graphics **Sort by:** 0 ▼ Next ▲ Previous ▲ Descriptions

PREDICTED: hepatocyte growth factor-like protein isoform X4 [Homo sapiens]

Sequence ID: ref|XP_006713232.1| **Length:** 519 **Number of Matches:** 4

Range 1: 301 to 321 GenPept Graphics

Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
68.1 bits(153)	2e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1    KGEGYRGTADTTTAGVPCQRW  21
            KGEGYRGTA+TTTAGVPCQRW
Sbjct  301  KGEGYRGTANTTTAGVPCQRW  321
```

Range 2: 131 to 148 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Identities	Positives	Gaps
34.6 bits(74)	1.8	12/18(67%)	12/18(66%)	0/18(0%)

```
Query  4    GYRGTADTTTAGVPCQRW  21
            GYRGT  TT  G PCQ W
Sbjct  131  GYRGTMATTVGGLPCQAW  148
```

Range 3: 389 to 408 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Identities	Positives	Gaps
33.7 bits(72)	3.3	13/20(65%)	13/20(65%)	0/20(0%)

```
Query  2    GEGYRGTADTTTAGVPCQRW  21
            GE YRGT   T  GV CQRW
Sbjct  389  GEQYRGTVSKTRKGVQCQRW  408
```

Range 4: 210 to 229 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Identities	Positives	Gaps
31.2 bits(66)	22	12/20(60%)	12/20(60%)	0/20(0%)

```
Query  2    GEGYRGTADTTTAGVPCQRW  21
            GE YRG  D T  G  CQRW
Sbjct  210  GEEYRGAVDRTESGRECQRW  229
```

Related Information

Gene - associated gene details

BLAST ®

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How to read this page Blast report description

MST1_KGEGYRGTANTTTAGVPCQRW_NonMod

RID B9P2EFER01R (Expires on 01-14 15:33 pm)

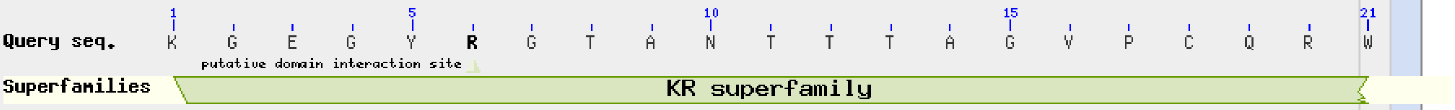
Query ID	lcl|23225	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	21		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

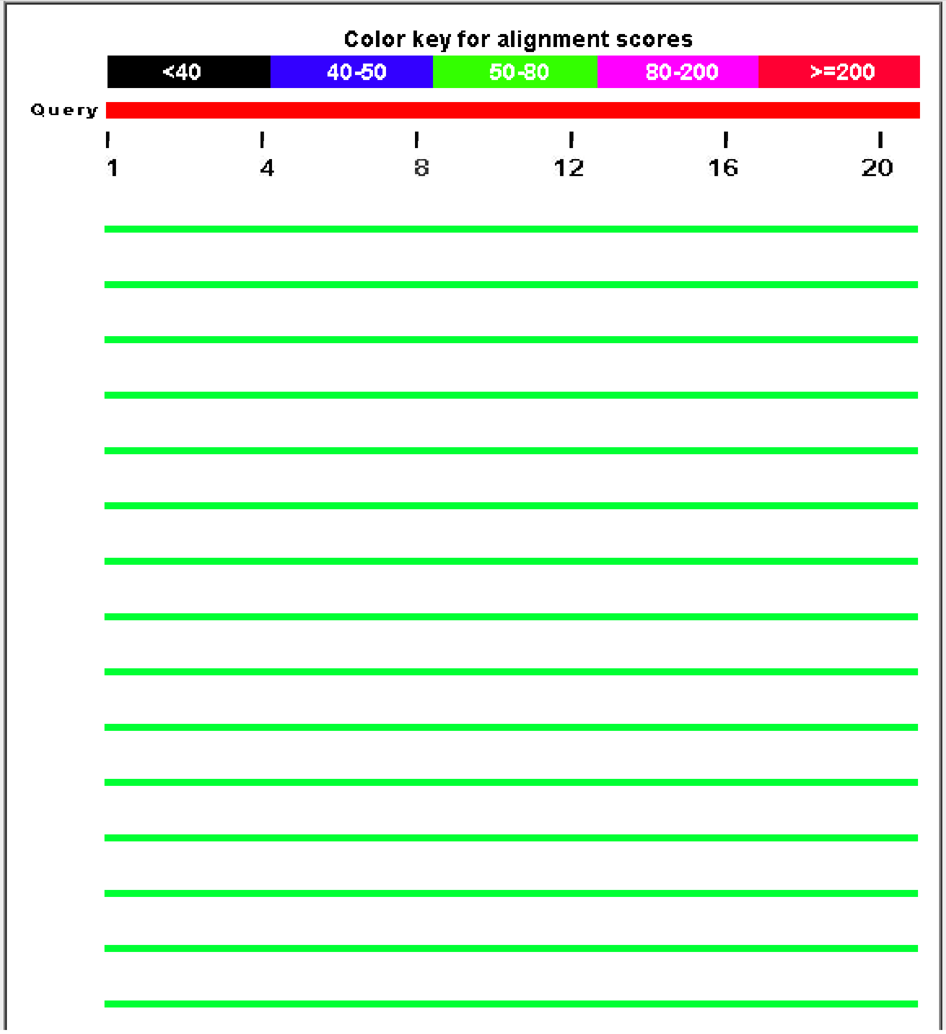
Show Conserved Domains

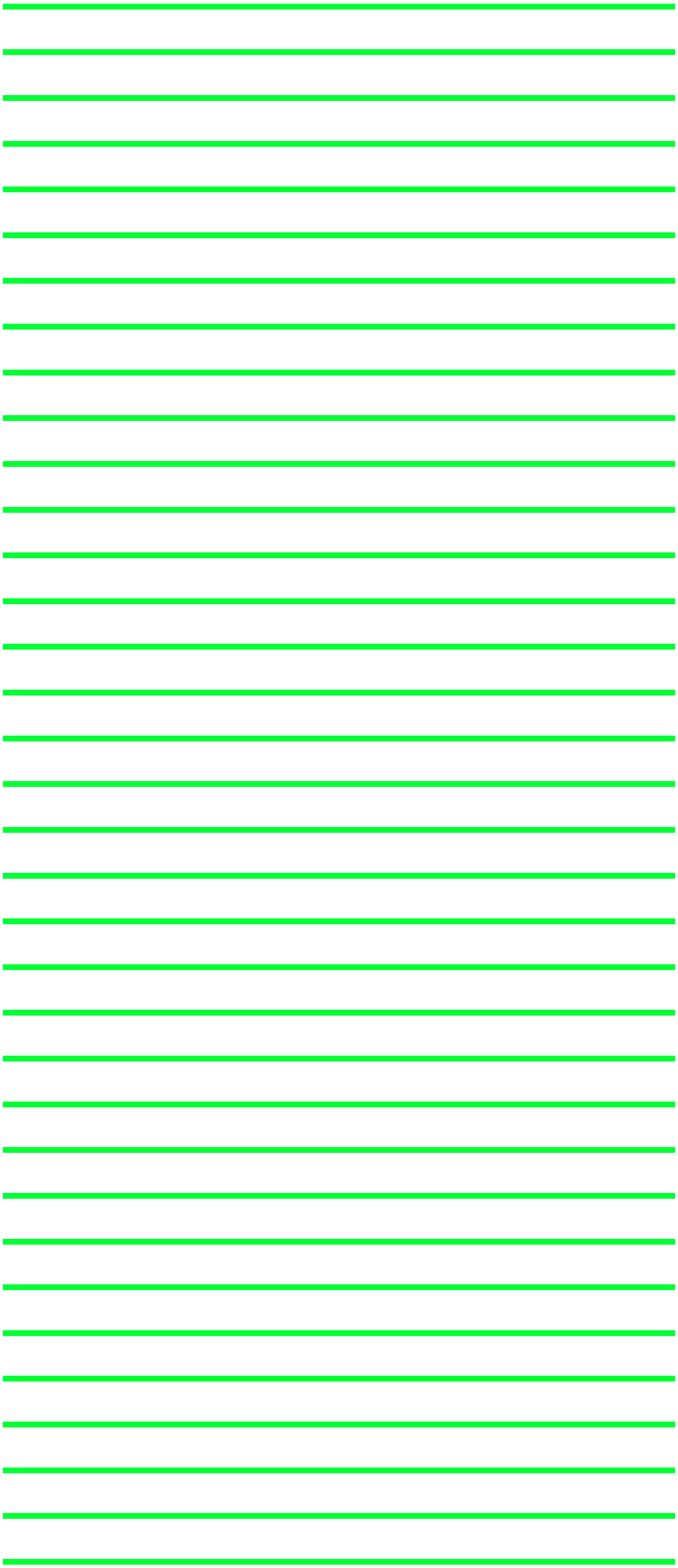
Putative conserved domains have been detected, click on the image below for detailed results.

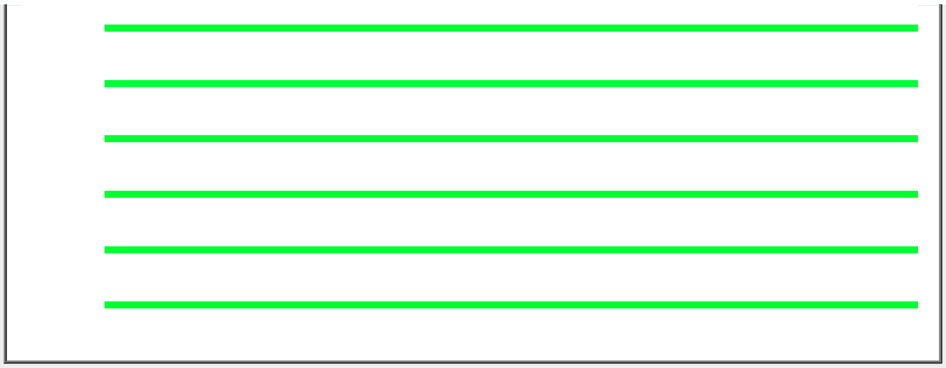


Distribution of 379 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	MST1 protein [Homo sapiens]	70.6	99.3	100%	1e-12	100%	gi|71297286|AAH44862.1
☐	unnamed protein product [Homo sapiens]	70.6	133	100%	2e-12	100%	gi|221042232|BAH12793.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like), isoform C	70.6	99.3	100%	2e-12	100%	gi|119585406|EAW65002.1
☐	unnamed protein product [Homo sapiens]	70.6	133	100%	2e-12	100%	gi|221039946|BAH11736.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Hor	70.6	168	100%	2e-12	100%	gi|578806141|XP_006713232.1
☐	hepatocyte growth factor-like protein homolog [Homo sapiens]	70.6	160	100%	2e-12	100%	gi|1141775|AAC63092.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Mac	70.6	170	100%	2e-12	100%	gi|544414366|XP_005547205.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like), isoform C	70.6	134	100%	2e-12	100%	gi|119585407|EAW65003.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Hor	70.6	168	100%	2e-12	100%	gi|578806131|XP_006713230.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X5 [Chl	70.6	134	100%	2e-12	100%	gi|635118817|XP_007982450.1
☐	PREDICTED: hepatocyte growth factor-like protein [Echinops telfair	70.6	161	100%	2e-12	100%	gi|507700568|XP_004715222.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Pap	70.6	170	100%	2e-12	100%	gi|685524931|XP_009199018.1
☐	macrophage-stimulating protein [Homo sapiens]	70.6	168	100%	2e-12	100%	gi|398038|AAA59872.1
☐	RecName: Full=Hepatocyte growth factor-like protein; AltName: Fu	70.6	168	100%	2e-12	100%	gi|147744563|P26927.2
☐	hepatocyte growth factor-like protein [Homo sapiens]	70.6	168	100%	2e-12	100%	gi|183977|AAA50165.1
☐	hypothetical protein EGM_20500 [Macaca fascicularis]	70.6	170	100%	2e-12	100%	gi|355764094|EHH62249.1
☐	hypothetical protein EGK_11631 [Macaca mulatta]	70.6	170	100%	2e-12	100%	gi|355559632|EHH16360.1
☐	hypothetical protein [Macaca fascicularis]	70.6	170	100%	2e-12	100%	gi|126143528|BAF47378.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like) variant [H	70.6	172	100%	2e-12	100%	gi|62897345|BAD96613.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Chl	70.6	134	100%	2e-12	100%	gi|635118815|XP_007982449.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Cav	70.6	135	100%	2e-12	100%	gi|348581912|XP_003476721.1
☐	PREDICTED: hepatocyte growth factor-like protein [Pteropus alecto	70.6	173	100%	2e-12	100%	gi|586548158|XP_006909162.1
☐	PREDICTED: hepatocyte growth factor-like protein [Pongo abelii]	70.6	170	100%	2e-12	100%	gi|297671325|XP_002813790.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Chl	70.6	170	100%	2e-12	100%	gi|635118813|XP_007982448.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Mac	70.6	170	100%	2e-12	100%	gi|544414364|XP_005547204.1
☐	PREDICTED: hepatocyte growth factor-like protein [Gorilla gorilla g	70.6	169	100%	2e-12	100%	gi|426340575|XP_004034204.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Pap	70.6	170	100%	2e-12	100%	gi|402860079|XP_003894463.1
☐	PREDICTED: hepatocyte growth factor-like protein [Nomascus leuc	70.6	165	100%	2e-12	100%	gi|332215988|XP_003257123.1
☐	hepatocyte growth factor-like protein precursor [Homo sapiens]	70.6	168	100%	2e-12	100%	gi|205277383|NP_066278.3

☐	PREDICTED: hepatocyte growth factor-like protein [Macaca mulatt	70.6	170	100%	2e-12	100%	gi|109039656|XP_001107946.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Chl	70.6	134	100%	2e-12	100%	gi|635118807|XP_007982445.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Cav	70.6	135	100%	2e-12	100%	gi|514473830|XP_005006713.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Chl	70.6	134	100%	2e-12	100%	gi|635118805|XP_007982444.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	70.6	166	100%	2e-12	100%	gi|410036983|XP_516465.4
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	67.7	165	100%	2e-11	95%	gi|532082473|XP_005326984.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Equ	67.2	168	100%	3e-11	95%	gi|664730013|XP_008522208.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Sai	67.2	162	100%	3e-11	95%	gi|725588970|XP_010345462.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Equ	67.2	139	100%	3e-11	95%	gi|545188630|XP_005600717.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Equ	67.2	168	100%	3e-11	95%	gi|664730009|XP_008522206.1
☐	hypothetical protein PANDA_009343 [Ailuropoda melanoleuca]	67.2	157	100%	3e-11	95%	gi|281338342|EFB13926.1
☐	PREDICTED: hepatocyte growth factor-like protein [Erinaceus euro	67.2	151	100%	3e-11	95%	gi|617622190|XP_007527316.1
☐	PREDICTED: hepatocyte growth factor-like protein [Galeopterus va	67.2	164	100%	3e-11	95%	gi|667267781|XP_008569781.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tarsius syricht	67.2	169	100%	3e-11	95%	gi|640809594|XP_008061363.1
☐	PREDICTED: hepatocyte growth factor-like protein [Orycteropus af	67.2	167	100%	3e-11	95%	gi|634888659|XP_007953538.1
☐	PREDICTED: hepatocyte growth factor-like protein [Leptonychotes	67.2	162	100%	3e-11	95%	gi|585186199|XP_006744596.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tupaia chinens	67.2	162	100%	3e-11	95%	gi|562887217|XP_006171012.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Mus	67.2	158	100%	3e-11	95%	gi|512005359|XP_004820133.1
☐	PREDICTED: hepatocyte growth factor-like protein [Mustela putori	67.2	158	100%	3e-11	95%	gi|511881610|XP_004760697.1
☐	PREDICTED: hepatocyte growth factor-like protein [Odobenus ros	67.2	159	100%	3e-11	95%	gi|472359375|XP_004399304.1
☐	PREDICTED: hepatocyte growth factor-like protein [Ceratotherium	67.2	162	100%	3e-11	95%	gi|478490786|XP_004419765.1
☐	PREDICTED: hepatocyte growth factor-like protein [Sorex araneus]	67.2	159	100%	3e-11	95%	gi|505843606|XP_004615300.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	67.2	172	100%	3e-11	95%	gi|344276255|XP_003409924.1
☐	PREDICTED: hepatocyte growth factor-like protein [Eptesicus fusc	67.2	154	100%	3e-11	95%	gi|641693981|XP_008153797.1
☐	PREDICTED: hepatocyte growth factor-like protein [Pantholops ho	67.2	153	100%	3e-11	95%	gi|556747770|XP_005969335.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Equ	67.2	168	100%	3e-11	95%	gi|545188628|XP_005600716.1
☐	PREDICTED: hepatocyte growth factor-like protein [Felis catus]	67.2	167	100%	3e-11	95%	gi|410951187|XP_003982280.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Sai	67.2	162	100%	3e-11	95%	gi|403291235|XP_003936704.1
☐	PREDICTED: hepatocyte growth factor-like protein [Canis lupus far	67.2	162	100%	3e-11	95%	gi|345787353|XP_541884.3
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	67.2	147	100%	3e-11	95%	gi|426249535|XP_004018505.1
☐	Hepatocyte growth factor-like protein [Tupaia chinensis]	67.2	162	100%	3e-11	95%	gi|444510620|ELV09642.1
☐	PREDICTED: hepatocyte growth factor-like protein-like [Ailuropoda	67.2	157	100%	3e-11	95%	gi|301770361|XP_002920612.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Chi	66.8	148	100%	4e-11	95%	gi|533195097|XP_005410271.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Chi	66.8	148	100%	4e-11	95%	gi|533195095|XP_005410270.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Chi	66.8	148	100%	4e-11	95%	gi|533195093|XP_005410269.1
☐	PREDICTED: hepatocyte growth factor-like protein [Rhinopithecus	66.4	166	100%	6e-11	95%	gi|724799330|XP_010367959.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Call	65.1	124	100%	2e-10	90%	gi|675727602|XP_008979888.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Call	65.1	157	100%	2e-10	90%	gi|296225219|XP_002758398.1
☐	PREDICTED: hepatocyte growth factor-like protein [Otolemur garn	64.7	165	100%	2e-10	90%	gi|395856451|XP_003800642.1
☐	PREDICTED: hepatocyte growth factor-like protein [Elephantulus e	64.3	168	100%	3e-10	90%	gi|585684863|XP_006892963.1
☐	PREDICTED: hepatocyte growth factor-like protein [Dasypus nover	64.3	165	100%	3e-10	90%	gi|488519988|XP_004451933.1
☐	PREDICTED: hepatocyte growth factor-like protein [Bubalus bubali	63.8	155	100%	4e-10	90%	gi|594058341|XP_006053335.1
☐	PREDICTED: hepatocyte growth factor-like protein [Bos mutus]	63.8	153	100%	4e-10	90%	gi|555960159|XP_005892185.1
☐	TPA: hepatocyte growth factor-like protein [Bos taurus]	63.8	153	100%	4e-10	90%	gi|296474806|DAA16921.1
☐	hepatocyte growth factor-like protein precursor [Bos taurus]	63.8	153	100%	4e-10	90%	gi|115496876|NP_001069145.1
☐	Hepatocyte growth factor-like protein [Bos mutus]	63.8	153	100%	4e-10	90%	gi|440909008|ELR58967.1

☐	PREDICTED: hepatocyte growth factor-like protein [Jaculus jaculus	63.8	153	100%	4e-10	90%	gi|507561196|XP_004664298.1
☐	PREDICTED: hepatocyte growth factor-like protein [Balaenoptera a	63.8	159	100%	4e-10	90%	gi|594630485|XP_007168789.1
☐	PREDICTED: hepatocyte growth factor-like protein [Lipotes vexillife	63.8	159	100%	4e-10	90%	gi|602681551|XP_007446274.1
☐	PREDICTED: hepatocyte growth factor-like protein [Physeter catod	63.8	154	100%	4e-10	90%	gi|593749341|XP_007129906.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	63.8	159	100%	4e-10	90%	gi|560948035|XP_006196588.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Bos	63.8	153	100%	4e-10	90%	gi|529001498|XP_005222861.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tursiops trunca	63.8	159	100%	4e-10	90%	gi|470608261|XP_004314855.1
☐	PREDICTED: hepatocyte growth factor-like protein [Orcinus orca]	63.8	159	100%	4e-10	90%	gi|466078823|XP_004284002.1
☐	PREDICTED: hepatocyte growth factor-like protein [Octodon degus	63.4	157	100%	6e-10	90%	gi|507620447|XP_004625159.1
☐	PREDICTED: hepatocyte growth factor-like protein [Ochotona princ	63.4	148	100%	6e-10	90%	gi|504138720|XP_004581815.1
☐	PREDICTED: hepatocyte growth factor-like protein [Trichechus ma	63.0	173	100%	8e-10	90%	gi|471355983|XP_004368594.1
☐	PREDICTED: hepatocyte growth factor-like protein [Chrysochloris a	62.1	161	100%	2e-09	86%	gi|586486348|XP_006873659.1
☐	Hepatocyte growth factor-like protein [Cricetulus griseus]	60.9	60.9	100%	2e-09	86%	gi|344252828|EGW08932.1
☐	hepatocyte growth factor-like protein [Cricetulus griseus]	60.9	86.1	100%	4e-09	86%	gi|537178774|ERE75628.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Mus	60.9	145	100%	4e-09	86%	gi|568962765|XP_006511702.1
☐	PREDICTED: hepatocyte growth factor-like protein [Nannospalax g	60.9	110	100%	4e-09	86%	gi|674087268|XP_008851489.1
☐	Macrophage stimulating 1 (hepatocyte growth factor-like) [Mus mus	60.9	145	100%	4e-09	86%	gi|14714805|AAH10551.1
☐	hepatocyte growth factor-like protein precursor [Mus musculus]	60.9	145	100%	4e-09	86%	gi|254675205|NP_032269.3
☐	PREDICTED: hepatocyte growth factor-like protein [Mesocricetus a	60.9	135	100%	4e-09	86%	gi|524949917|XP_005074975.1
☐	unnamed protein product [Mus musculus]	60.9	145	100%	4e-09	86%	gi|74140912|BAE22056.1
☐	hepatocyte growth factor-like protein [Mus musculus]	60.9	145	100%	4e-09	86%	gi|193834|AAA50167.1
☐	hepatocyte growth factor-like protein precursor [Rattus norvegicus]	60.9	145	100%	4e-09	86%	gi|13242239|NP_077328.1
☐	PREDICTED: hepatocyte growth factor-like protein [Peromyscus ma	60.9	141	100%	4e-09	86%	gi|589931181|XP_006978395.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Mic	60.9	145	100%	4e-09	86%	gi|532008239|XP_005347942.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Mic	60.9	145	100%	4e-09	86%	gi|532008241|XP_005347943.1

Alignments

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MST1 protein [Homo sapiens]

Sequence ID: gi|71297286|gb|AAH44862.1| **Length:** 188 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 150 to 170 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.6 bits(159)	1e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1     KGEGYRGTANTTTAGVPCQRW  21
             KGEGYRGTANTTTAGVPCQRW
Sbjct  150   KGEGYRGTANTTTAGVPCQRW  170
```

Range 2: 59 to 78 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
28.6 bits(60)	142	11/20(55%)	12/20(60%)	0/20(0%)

```
Query  2    GEGYRGTANTTTAGVPCQRW  21
            GE YRG  + T  G  CQRW
Sbjct  59   GEEYRGAVDRTESGRECQRW  78
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221042232|dbj|BAH12793.1| **Length:** 264 **Number of Matches:** 3

Related Information

Gene - associated gene details

Range 1: 226 to 246 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps

70.6 bits(159)	2e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KGEGYRGTANTTTAGVPCQRW  21
            KGEGYRGTANTTTAGVPCQRW
Sbjct  226  KGEGYRGTANTTTAGVPCQRW  246
```

Range 2: 56 to 73 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
34.1 bits(73)	2.2	12/18(67%)	12/18(66%)	0/18(0%)

```
Query  4    GYRGTANTTTAGVPCQRW  21
            GYRGT  TT  G PCQ W
Sbjct  56   GYRGTMATTVGGLPCQAW  73
```

Range 3: 135 to 154 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
28.6 bits(60)	143	11/20(55%)	12/20(60%)	0/20(0%)

```
Query  2    GEGYRGTANTTTAGVPCQRW  21
            GE YRG  + T  G  CQRW
Sbjct  135  GEEYRGAVDRTESGRECQRW  154
```

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macrophage stimulating 1 (hepatocyte growth factor-like), isoform CRA_d [Homo sapiens]

Sequence ID: gi|119585406|gb|EAW65002.1| **Length:** 331 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 225 to 245 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.6 bits(159)	2e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KGEGYRGTANTTTAGVPCQRW  21
            KGEGYRGTANTTTAGVPCQRW
Sbjct  225  KGEGYRGTANTTTAGVPCQRW  245
```

Range 2: 134 to 153 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
28.6 bits(60)	144	11/20(55%)	12/20(60%)	0/20(0%)

```
Query  2    GEGYRGTANTTTAGVPCQRW  21
            GE YRG  + T  G  CQRW
Sbjct  134  GEEYRGAVDRTESGRECQRW  153
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221039946|dbj|BAH11736.1| **Length:** 339 **Number of Matches:** 3

Related Information

Gene - associated gene details

Range 1: 301 to 321 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.6 bits(159)	2e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KGEGYRGTANTTTAGVPCQRW  21
            KGEGYRGTANTTTAGVPCQRW
Sbjct  301  KGEGYRGTANTTTAGVPCQRW  321
```

Range 2: 131 to 148 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
34.1 bits(73)	2.2	12/18(67%)	12/18(66%)	0/18(0%)

```
Query  4    GYRGTANTTTAGVPCQRW  21
            GYRGT  TT  G PCQ W
Sbjct  131  GYRGTMATTVGGLPCQAW  148
```

Range 3: 210 to 229 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
28.6 bits(60)	144	11/20(55%)	12/20(60%)	0/20(0%)

```
Query  2    GEGYRGTANTTTAGVPCQRW  21
            GE YRG  + T  G  CQRW
Sbjct  210  GEEYRGAVDRTESGRECQRW  229
```

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PREDICTED: hepatocyte growth factor-like protein isoform X4 [Homo sapiens]

Sequence ID: gi|578806141|ref|XP_006713232.1| **Length:** 519 **Number of Matches:** 4

Related Information

Gene - associated gene details

Range 1: 301 to 321 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
70.6 bits(159)	2e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KGEGYRGTANTTTAGVPCQRW  21
            KGEGYRGTANTTTAGVPCQRW
Sbjct  301  KGEGYRGTANTTTAGVPCQRW  321
```

Range 2: 389 to 408 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
35.4 bits(76)	0.89	13/20(65%)	13/20(65%)	0/20(0%)

```
Query  2    GEGYRGTANTTTAGVPCQRW  21
            GE YRGT   T  GV CQRW
Sbjct  389  GEQYRGTVSKTRKGVQCQRW  408
```

Range 3: 131 to 148 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
34.1 bits(73)	2.3	12/18(67%)	12/18(66%)	0/18(0%)

```
Query  4    GYRGTANTTTAGVPCQRW  21
            GYRGT  TT  G PCQ W
Sbjct  131  GYRGTMATTVGGLPCQAW  148
```

Range 4: 210 to 229 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
28.6 bits(60)	145	11/20(55%)	12/20(60%)	0/20(0%)

```
Query  2    GEGYRGTANTTTAGVPCQRW  21
            GE YRG  + T  G  CQRW
Sbjct  210  GEEYRGAVDRTESGRECQRW  229
```

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MST1_KGTGDDTVLNVALLNVISNQECNIKH_Mod

RID BVJMG49T01R (Expires on 01-21 10:25 am)

Query ID	lcl|155489	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	26		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

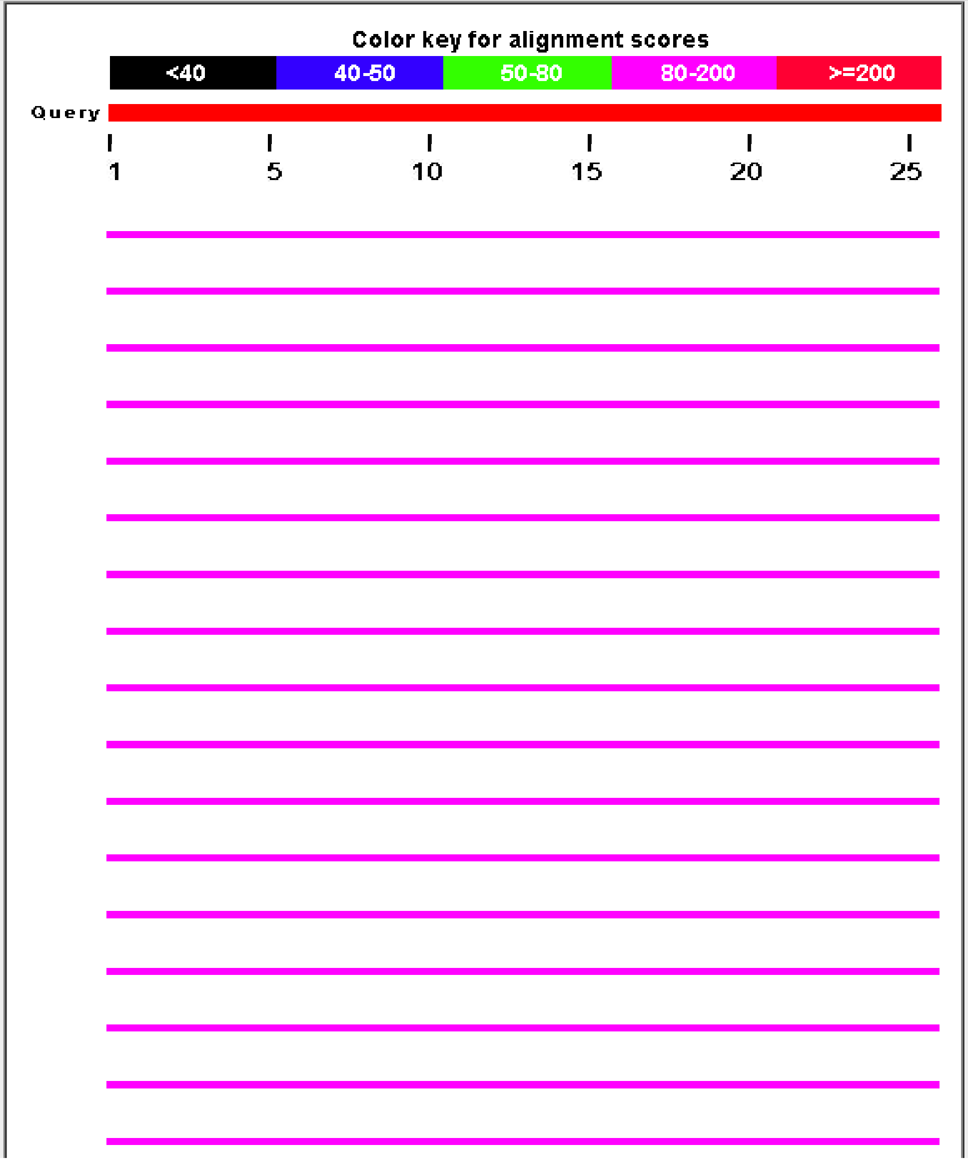
Graphic Summary

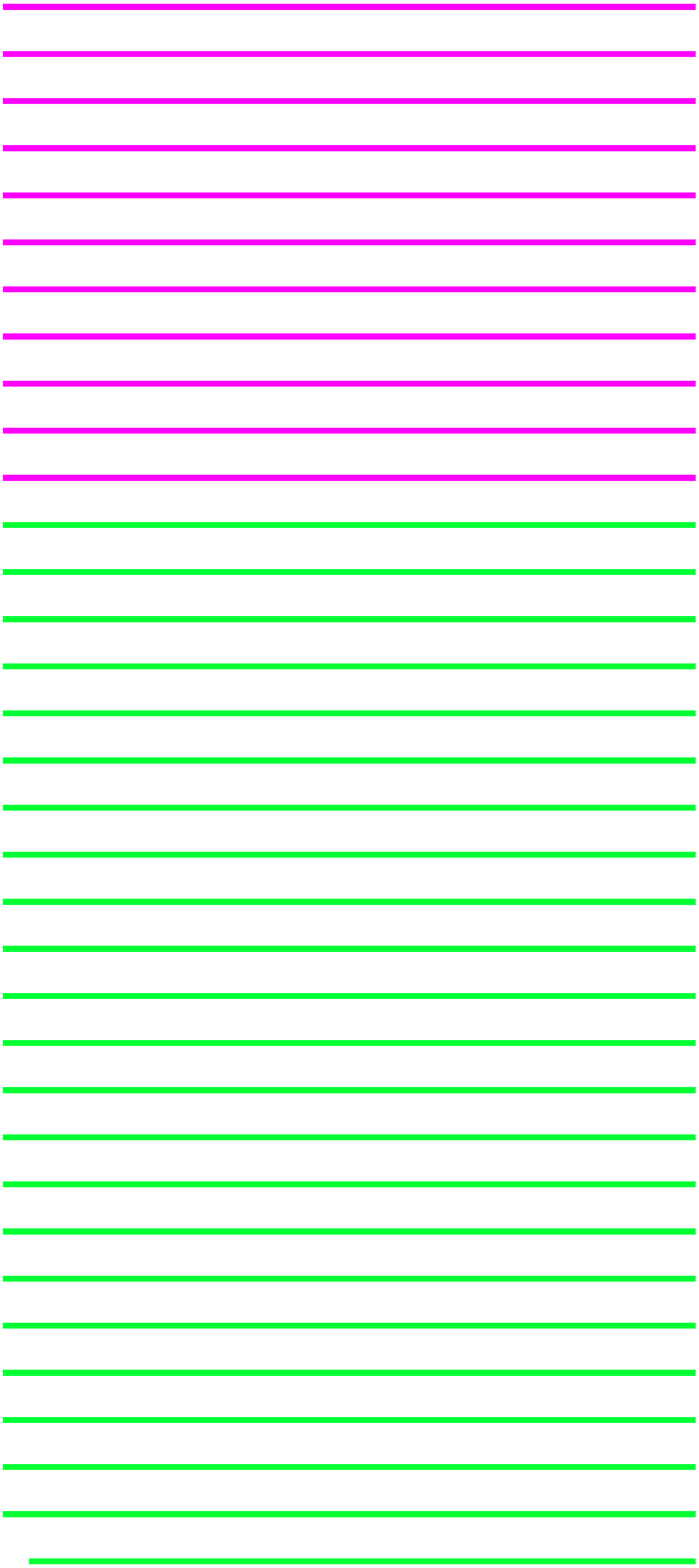
Show Conserved Domains

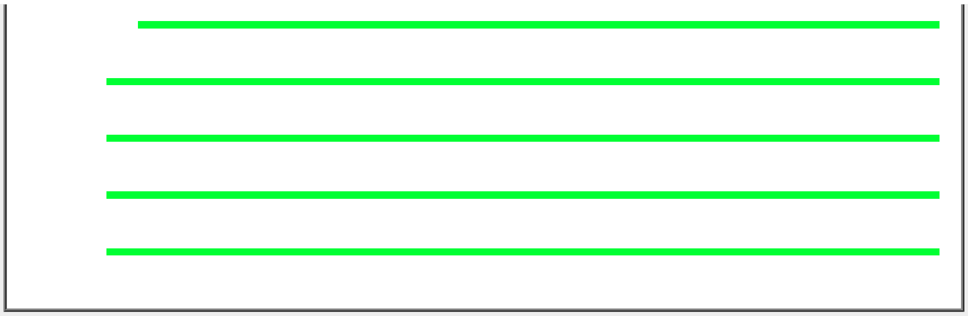
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	macrophage stimulating 1 (hepatocyte growth factor-like), isoform CRA_c [Ho	82.5	82.5	100%	2e-16	96%	EAW65001.1
☐	Chain B, Crystal Structure Of The Beta-Chain Of HgflMSP [Homo sapiens]	82.5	82.5	100%	3e-16	96%	2ASU_B
☐	Chain C, Crystal Structure Of Ron Sema-psi-ipt1 Extracellular Domains In Coi	82.5	82.5	100%	3e-16	96%	4QT8_C
☐	hepatocyte growth factor-like protein homolog [Homo sapiens]	82.5	82.5	100%	3e-16	96%	AAC35412.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Macaca fascic	82.5	82.5	100%	4e-16	96%	XP_005547205.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Homo sapiens	82.5	82.5	100%	4e-16	96%	XP_006713231.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like), isoform CRA_e [Ho	82.5	82.5	100%	4e-16	96%	EAW65003.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Homo sapiens	82.5	82.5	100%	4e-16	96%	XP_006713229.1
☐	brain-rescue-factor-1 [Homo sapiens]	82.5	82.5	100%	4e-16	96%	AAP20103.1
☐	putative macrophage stimulating 1-like protein [Homo sapiens]	82.5	82.5	100%	4e-16	96%	NP_001258662.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Papio anubis]	82.5	82.5	100%	4e-16	96%	XP_009199018.1
☐	RecName: Full=Hepatocyte growth factor-like protein; AltName: Full=Macroph	82.5	82.5	100%	4e-16	96%	P26927.2
☐	hepatocyte growth factor-like protein [Homo sapiens]	82.5	82.5	100%	4e-16	96%	AAA50165.1
☐	hypothetical protein EGM_20500 [Macaca fascicularis]	82.5	82.5	100%	4e-16	96%	EHH62249.1
☐	hypothetical protein EGK_11631 [Macaca mulatta]	82.5	82.5	100%	4e-16	96%	EHH16360.1
☐	hypothetical protein [Macaca fascicularis]	82.5	82.5	100%	4e-16	96%	BAF47378.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like) variant [Homo sapie	82.5	82.5	100%	4e-16	96%	BAD96613.1
☐	RecName: Full=Putative macrophage stimulating 1-like protein; AltName: Full	82.5	82.5	100%	4e-16	96%	Q2TV78.2
☐	PREDICTED: hepatocyte growth factor-like protein [Pongo abelii]	82.5	82.5	100%	4e-16	96%	XP_002813790.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Macaca fascic	82.5	82.5	100%	4e-16	96%	XP_005547204.1
☐	PREDICTED: hepatocyte growth factor-like protein [Gorilla gorilla gorilla]	82.5	82.5	100%	4e-16	96%	XP_004034204.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Papio anubis]	82.5	82.5	100%	4e-16	96%	XP_003894463.1
☐	hepatocyte growth factor-like protein precursor [Homo sapiens]	82.5	82.5	100%	4e-16	96%	NP_066278.3
☐	PREDICTED: hepatocyte growth factor-like protein [Macaca mulatta]	82.5	82.5	100%	4e-16	96%	XP_001107946.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like proteir	82.5	82.5	100%	4e-16	96%	XP_516465.4
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like proteir	80.4	80.4	100%	2e-15	92%	XP_005696011.1
☐	PREDICTED: hepatocyte growth factor-like protein [Pantholops hodgsonii]	80.4	80.4	100%	2e-15	92%	XP_005969335.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like proteir	80.4	80.4	100%	2e-15	92%	XP_004018505.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Saimiri bolivier	78.7	78.7	100%	7e-15	92%	XP_003936704.1

☐	macrophage-stimulating protein [Homo sapiens]	78.3	78.3	100%	1e-14	92%	AAA59872.1
☐	PREDICTED: hepatocyte growth factor-like protein [Rhinopithecus roxellana]	77.8	77.8	100%	1e-14	92%	XP_010367959.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Callithrix jacch	77.0	77.0	100%	3e-14	92%	XP_008979888.1
☐	PREDICTED: hepatocyte growth factor-like protein [Bubalus bubalis]	77.0	77.0	100%	3e-14	88%	XP_006053335.1
☐	PREDICTED: hepatocyte growth factor-like protein [Bos mutus]	77.0	77.0	100%	3e-14	88%	XP_005892185.1
☐	TPA: hepatocyte growth factor-like protein [Bos taurus]	77.0	77.0	100%	3e-14	88%	DAA16921.1
☐	hepatocyte growth factor-like protein precursor [Bos taurus]	77.0	77.0	100%	3e-14	88%	NP_001069145.1
☐	Hepatocyte growth factor-like protein [Bos mutus]	77.0	77.0	100%	3e-14	88%	ELR58967.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Bison bison bi	77.0	77.0	100%	3e-14	88%	XP_010850156.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Bison bison bi	77.0	77.0	100%	3e-14	88%	XP_010850155.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Callithrix jacch	77.0	77.0	100%	3e-14	92%	XP_002758398.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Bos taurus]	77.0	77.0	100%	3e-14	88%	XP_005222861.1
☐	PREDICTED: hepatocyte growth factor-like protein [Nomascus leucogenys]	77.0	77.0	100%	3e-14	92%	XP_003257123.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Bos taurus]	77.0	77.0	100%	3e-14	88%	XP_005222860.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X6 [Chlorocebus s	76.1	76.1	100%	5e-14	92%	XP_007982452.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X5 [Chlorocebus s	76.1	76.1	100%	5e-14	92%	XP_007982450.1
☐	PREDICTED: hepatocyte growth factor-like protein [Galeopterus variegatus]	76.1	76.1	100%	6e-14	92%	XP_008569781.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Chlorocebus s	76.1	76.1	100%	6e-14	92%	XP_007982449.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Chlorocebus s	76.1	76.1	100%	6e-14	92%	XP_007982448.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Chlorocebus s	76.1	76.1	100%	6e-14	92%	XP_007982445.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Chlorocebus s	76.1	76.1	100%	6e-14	92%	XP_007982444.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Oryctolagus cu	73.2	73.2	96%	6e-13	92%	XP_008258875.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Oryctolagus cu	73.2	73.2	96%	6e-13	92%	XP_008258874.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Sus scrofa]	72.7	72.7	100%	8e-13	88%	XP_005669634.1
☐	PREDICTED: hepatocyte growth factor-like protein-like [Sus scrofa]	72.7	72.7	100%	8e-13	88%	XP_005674335.1
☐	PREDICTED: hepatocyte growth factor-like protein [Otolemur garnettii]	72.7	72.7	100%	8e-13	88%	XP_003800642.1
☐	PREDICTED: hepatocyte growth factor-like protein [Ochotona princeps]	72.7	72.7	100%	8e-13	88%	XP_004581815.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Sus scrofa]	72.7	72.7	100%	8e-13	88%	XP_003132263.1
☐	Hepatocyte growth factor-like protein [Heterocephalus glaber]	71.0	71.0	100%	3e-12	88%	EHB14811.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Fukomys dam	71.0	71.0	100%	3e-12	88%	XP_010613848.1
☐	Hepatocyte growth factor-like protein [Fukomys damarensis]	71.0	71.0	100%	3e-12	88%	KFO18588.1
☐	PREDICTED: hepatocyte growth factor-like protein [Camelus bactrianus]	71.0	71.0	100%	3e-12	88%	XP_010967473.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein	71.0	71.0	100%	3e-12	88%	XP_006174176.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Fukomys dam	71.0	71.0	100%	3e-12	88%	XP_010613847.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein	71.0	71.0	100%	3e-12	88%	XP_004903551.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Heterocephalu	71.0	71.0	100%	3e-12	88%	XP_004834104.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Fukomys dam	71.0	71.0	100%	3e-12	88%	XP_010613846.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Heterocephalu	71.0	71.0	100%	3e-12	88%	XP_004834103.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein	71.0	71.0	100%	3e-12	88%	XP_006196588.1
☐	macrophage stimulating 1-like protein [Camelus ferus]	71.0	71.0	100%	3e-12	88%	EQB77066.1
☐	PREDICTED: hepatocyte growth factor-like protein [Camelus dromedarius]	71.0	71.0	100%	3e-12	88%	XP_010976658.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Equus caballu	70.2	70.2	100%	6e-12	85%	XP_005600717.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Equus przewa	70.2	70.2	100%	6e-12	85%	XP_008522206.1
☐	PREDICTED: hepatocyte growth factor-like protein [Dasypus novemcinctus]	70.2	70.2	100%	6e-12	88%	XP_004451933.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Equus caballu	70.2	70.2	100%	6e-12	85%	XP_005600716.1

☐	PREDICTED: hepatocyte growth factor-like protein [Lipotes vexillifer]	69.8	69.8	100%	8e-12	85%	XP_007446274.1
☐	PREDICTED: hepatocyte growth factor-like protein [Physeter catodon]	69.8	69.8	100%	8e-12	85%	XP_007129906.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tursiops truncatus]	69.8	69.8	100%	8e-12	85%	XP_004314855.1
☐	PREDICTED: hepatocyte growth factor-like protein [Orcinus orca]	69.8	69.8	100%	8e-12	85%	XP_004284002.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protei	69.4	69.4	100%	1e-11	85%	XP_007088585.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tupaia chinensis]	69.4	69.4	96%	1e-11	88%	XP_006171012.1
☐	PREDICTED: hepatocyte growth factor-like protein [Ceratotherium simum sim	69.4	69.4	100%	1e-11	85%	XP_004419765.1
☐	PREDICTED: hepatocyte growth factor-like protein [Felis catus]	69.4	69.4	100%	1e-11	85%	XP_003982280.1
☐	PREDICTED: hepatocyte growth factor-like protein [Canis lupus familiaris]	69.4	69.4	100%	1e-11	85%	XP_541884.3
☐	Hepatocyte growth factor-like protein [Tupaia chinensis]	69.4	69.4	96%	1e-11	88%	ELV09642.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tarsius syrichta]	68.5	68.5	100%	2e-11	85%	XP_008061363.1
☐	PREDICTED: hepatocyte growth factor-like protein [Odobenus rosmarus dive	68.1	68.1	100%	3e-11	81%	XP_004399304.1
☐	Hepatocyte growth factor-like protein [Myotis brandtii]	67.7	67.7	92%	4e-11	83%	EPQ07261.1
☐	PREDICTED: hepatocyte growth factor-like protein [Myotis brandtii]	67.7	67.7	92%	4e-11	83%	XP_005865438.1
☐	PREDICTED: hepatocyte growth factor-like protein [Eptesicus fuscus]	67.7	67.7	92%	4e-11	83%	XP_008153797.1
☐	PREDICTED: hepatocyte growth factor-like protein [Leptonychotes weddellii]	66.8	66.8	100%	8e-11	81%	XP_006744596.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protei	66.0	66.0	100%	2e-10	81%	XP_005326984.1
☐	PREDICTED: hepatocyte growth factor-like protein [Ursus maritimus]	65.5	65.5	100%	2e-10	81%	XP_008702001.1
☐	hypothetical protein PANDA_009343 [Ailuropoda melanoleuca]	65.5	65.5	100%	2e-10	81%	EFB13926.1
☐	PREDICTED: hepatocyte growth factor-like protein [Elephantulus edwardii]	65.5	65.5	100%	2e-10	81%	XP_006892963.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Mustela putori	65.5	65.5	100%	2e-10	81%	XP_004820133.1
☐	PREDICTED: hepatocyte growth factor-like protein [Mustela putorius furo]	65.5	65.5	100%	2e-10	81%	XP_004760697.1
☐	PREDICTED: hepatocyte growth factor-like protein [Sorex araneus]	65.5	65.5	100%	2e-10	81%	XP_004615300.1
☐	PREDICTED: hepatocyte growth factor-like protein-like [Ailuropoda melanoleu	65.5	65.5	100%	2e-10	81%	XP_002920612.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Mustela putori	65.5	65.5	100%	2e-10	81%	XP_004820132.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Mustela putori	65.5	65.5	100%	2e-10	81%	XP_004820131.1

⊟ Alignments

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macrophage stimulating 1 (hepatocyte growth factor-like), isoform CRA_c [Homo sapiens]

Sequence ID: gb|EAW65001.1| **Length:** 183 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 83 to 108 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.5 bits(187)	2e-16	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1     KGTGDDTVLNVALLNVISNQECNIKH  26
             KGTG+DTVLNVALLNVISNQECNIKH
Sbjct  83    KGTGNDTVLNVALLNVISNQECNIKH  108
```

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Chain B, Crystal Structure Of The Beta-Chain Of HgflMSP

Sequence ID: pdb|2ASU|B **Length:** 234 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 128 to 153 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.5 bits(187)	3e-16	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    KGTGDDTVLNVALLNVISNQECNIKH  26
            KGTG+DTVLNVALLNVISNQECNIKH
Sbjct  128  KGTGNDTVLNVALLNVISNQECNIKH  153
```

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Chain C, Crystal Structure Of Ron Sema-psi-ipt1 Extracellular Domains In Complex With Msp Beta-chain

Sequence ID: pdb|4QT8|C **Length:** 253 **Number of Matches:** 1

See 1 more title(s)

Range 1: 147 to 172 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.5 bits(187)	3e-16	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    KGTGDDTVLNVALLNVISNQECNIKH  26
            KGTG+DTVLNVALLNVISNQECNIKH
Sbjct  147  KGTGNDTVLNVALLNVISNQECNIKH  172
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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hepatocyte growth factor-like protein homolog [Homo sapiens]

Sequence ID: gb|AAC35412.1| **Length:** 286 **Number of Matches:** 1

Range 1: 186 to 211 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.5 bits(187)	3e-16	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    KGTGDDTVLNVALLNVISNQECNIKH  26
            KGTG+DTVLNVALLNVISNQECNIKH
Sbjct  186  KGTGNDTVLNVALLNVISNQECNIKH  211
```

Related Information

Gene - associated gene details

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PREDICTED: hepatocyte growth factor-like protein isoform X2 [Macaca fascicularis]

Sequence ID: ref|XP_005547205.1| **Length:** 600 **Number of Matches:** 1

Range 1: 500 to 525 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.5 bits(187)	4e-16	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    KGTGDDTVLNVALLNVISNQECNIKH  26
            KGTG+DTVLNVALLNVISNQECNIKH
Sbjct  500  KGTGNDTVLNVALLNVISNQECNIKH  525
```

Related Information

Gene - associated gene details

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

MST1_KGTGNDTVLNVALLNVISNQECNIKH_NonMod

RID B9P624AG01R (Expires on 01-14 15:35 pm)

Query ID	lcl|66740	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	26		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

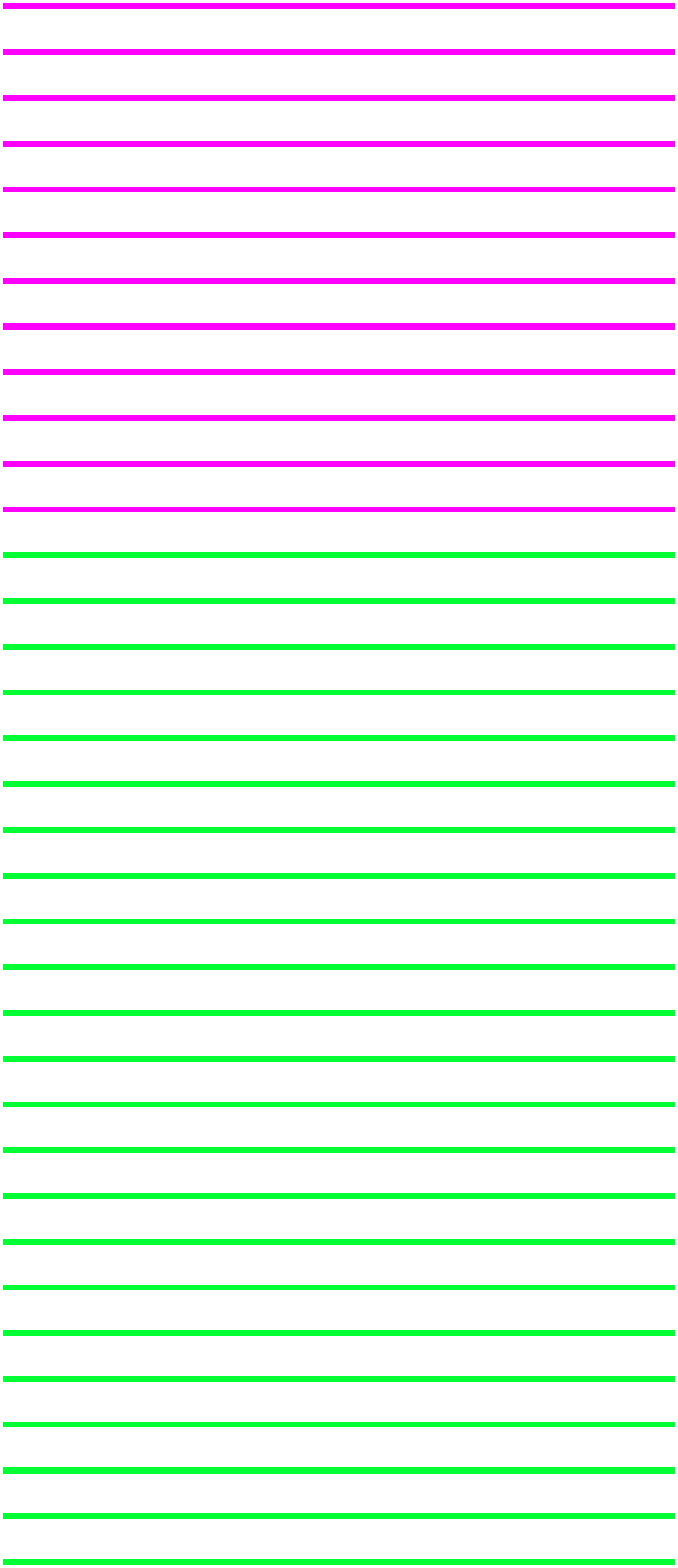
Graphic Summary

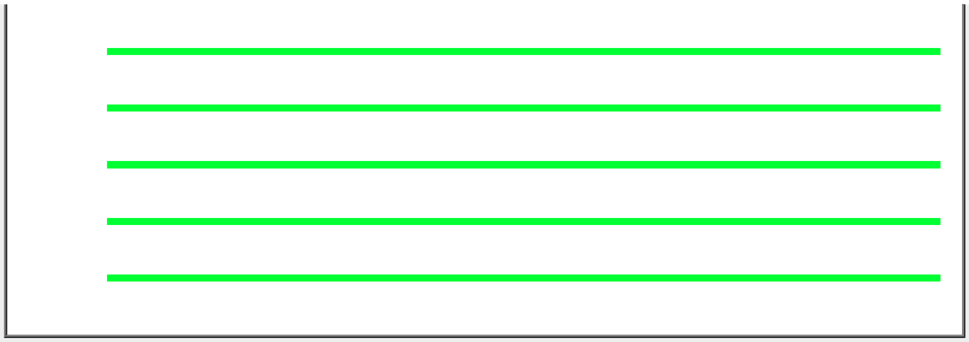
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	macrophage stimulating 1 (hepatocyte growth factor-like), isoform C	85.0	85.0	100%	3e-17	100%	gi|119585405|EAW65001.1
☐	Chain B, Crystal Structure Of The Beta-Chain Of HgflMSP [Homo s	85.0	85.0	100%	3e-17	100%	gi|83754035|2ASU_B
☐	Chain C, Crystal Structure Of Ron Sema-psi-ipt1 Extracellular Dom	85.0	85.0	100%	4e-17	100%	gi|685425760|4QT8_C
☐	hepatocyte growth factor-like protein homolog [Homo sapiens]	85.0	85.0	100%	4e-17	100%	gi|1141777|AAC35412.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Mac	85.0	85.0	100%	5e-17	100%	gi|544414366|XP_005547205.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Hor	85.0	85.0	100%	5e-17	100%	gi|578806133|XP_006713231.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like), isoform C	85.0	85.0	100%	5e-17	100%	gi|119585407|EAW65003.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Hor	85.0	85.0	100%	5e-17	100%	gi|578806129|XP_006713229.1
☐	brain-rescue-factor-1 [Homo sapiens]	85.0	85.0	100%	5e-17	100%	gi|37780053|AAP20103.1
☐	putative macrophage stimulating 1-like protein [Homo sapiens]	85.0	85.0	100%	5e-17	100%	gi|413081806|NP_001258662.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Pap	85.0	85.0	100%	5e-17	100%	gi|685524931|XP_009199018.1
☐	RecName: Full=Hepatocyte growth factor-like protein; AltName: Fu	85.0	85.0	100%	5e-17	100%	gi|147744563|P26927.2
☐	hepatocyte growth factor-like protein [Homo sapiens]	85.0	85.0	100%	5e-17	100%	gi|183977|AAA50165.1
☐	hypothetical protein EGM_20500 [Macaca fascicularis]	85.0	85.0	100%	5e-17	100%	gi|355764094|EHH62249.1
☐	hypothetical protein EGK_11631 [Macaca mulatta]	85.0	85.0	100%	5e-17	100%	gi|355559632|EHH16360.1
☐	hypothetical protein [Macaca fascicularis]	85.0	85.0	100%	5e-17	100%	gi|126143528|BAF47378.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like) variant [H	85.0	85.0	100%	5e-17	100%	gi|62897345|BAD96613.1
☐	RecName: Full=Putative macrophage stimulating 1-like protein; AltN	85.0	85.0	100%	5e-17	100%	gi|205829211|Q2TV78.2
☐	PREDICTED: hepatocyte growth factor-like protein [Pongo abelii]	85.0	85.0	100%	5e-17	100%	gi|297671325|XP_002813790.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Mac	85.0	85.0	100%	5e-17	100%	gi|544414364|XP_005547204.1
☐	PREDICTED: hepatocyte growth factor-like protein [Gorilla gorilla g	85.0	85.0	100%	5e-17	100%	gi|426340575|XP_004034204.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Pap	85.0	85.0	100%	5e-17	100%	gi|402860079|XP_003894463.1
☐	hepatocyte growth factor-like protein precursor [Homo sapiens]	85.0	85.0	100%	5e-17	100%	gi|205277383|NP_066278.3
☐	PREDICTED: hepatocyte growth factor-like protein [Macaca mulatta	85.0	85.0	100%	5e-17	100%	gi|109039656|XP_001107946.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	85.0	85.0	100%	5e-17	100%	gi|410036983|XP_516465.4
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Sai	81.2	81.2	100%	1e-15	96%	gi|403291235|XP_003936704.1
☐	macrophage-stimulating protein [Homo sapiens]	80.8	80.8	100%	1e-15	96%	gi|398038|AAA59872.1
☐	PREDICTED: hepatocyte growth factor-like protein [Rhinopithecus	80.4	80.4	100%	2e-15	96%	gi|724799330|XP_010367959.1
☐							

	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Call	79.5	79.5	100%	4e-15	96%	gi|675727602|XP_008979888.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Call	79.5	79.5	100%	4e-15	96%	gi|296225219|XP_002758398.1
☐	PREDICTED: hepatocyte growth factor-like protein [Nomascus leuc	79.5	79.5	100%	4e-15	96%	gi|332215988|XP_003257123.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X6 [Chl	78.7	78.7	100%	7e-15	96%	gi|635118819|XP_007982452.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X5 [Chl	78.7	78.7	100%	7e-15	96%	gi|635118817|XP_007982450.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Chl	78.7	78.7	100%	7e-15	96%	gi|635118815|XP_007982449.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Chl	78.7	78.7	100%	7e-15	96%	gi|635118813|XP_007982448.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Chl	78.7	78.7	100%	7e-15	96%	gi|635118807|XP_007982445.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Chl	78.7	78.7	100%	7e-15	96%	gi|635118805|XP_007982444.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	77.8	77.8	100%	1e-14	88%	gi|548515581|XP_005696011.1
☐	PREDICTED: hepatocyte growth factor-like protein [Pantholops hoc	77.8	77.8	100%	1e-14	88%	gi|556747770|XP_005969335.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	77.8	77.8	100%	1e-14	88%	gi|426249535|XP_004018505.1
☐	PREDICTED: hepatocyte growth factor-like protein [Bubalus bubalis	74.4	74.4	100%	2e-13	85%	gi|594058341|XP_006053335.1
☐	PREDICTED: hepatocyte growth factor-like protein [Bos mutus]	74.4	74.4	100%	2e-13	85%	gi|555960159|XP_005892185.1
☐	TPA: hepatocyte growth factor-like protein [Bos taurus]	74.4	74.4	100%	2e-13	85%	gi|296474806|DAA16921.1
☐	hepatocyte growth factor-like protein precursor [Bos taurus]	74.4	74.4	100%	2e-13	85%	gi|115496876|NP_001069145.1
☐	Hepatocyte growth factor-like protein [Bos mutus]	74.4	74.4	100%	2e-13	85%	gi|440909008|ELR58967.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Bos	74.4	74.4	100%	2e-13	85%	gi|529001498|XP_005222861.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Bos	74.4	74.4	100%	2e-13	85%	gi|529001496|XP_005222860.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Bos	74.4	74.4	100%	2e-13	85%	gi|529001494|XP_005222859.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Bos	74.4	74.4	100%	2e-13	85%	gi|529001492|XP_005222858.1
☐	PREDICTED: hepatocyte growth factor-like protein [Galeopterus va	73.6	73.6	100%	4e-13	88%	gi|667267781|XP_008569781.1
☐	Hepatocyte growth factor-like protein [Heterocephalus glaber]	72.7	72.7	100%	7e-13	88%	gi|351711892|EHB14811.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Fuk	72.7	72.7	100%	7e-13	88%	gi|731291722|XP_010613848.1
☐	Hepatocyte growth factor-like protein [Fukomys damarensis]	72.7	72.7	100%	7e-13	88%	gi|676261358|KFO18588.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Fuk	72.7	72.7	100%	7e-13	88%	gi|731291719|XP_010613847.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	72.7	72.7	100%	7e-13	88%	gi|512917516|XP_004903551.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Het	72.7	72.7	100%	7e-13	88%	gi|512943136|XP_004834104.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Fuk	72.7	72.7	100%	7e-13	88%	gi|731291717|XP_010613846.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Het	72.7	72.7	100%	7e-13	88%	gi|512943134|XP_004834103.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	71.9	71.9	100%	1e-12	88%	gi|591325127|XP_007088585.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tupaia chinens	71.9	71.9	96%	1e-12	92%	gi|562887217|XP_006171012.1
☐	PREDICTED: hepatocyte growth factor-like protein [Felis catus]	71.9	71.9	100%	1e-12	88%	gi|410951187|XP_003982280.1
☐	PREDICTED: hepatocyte growth factor-like protein [Canis lupus far	71.9	71.9	100%	1e-12	88%	gi|345787353|XP_541884.3
☐	Hepatocyte growth factor-like protein [Tupaia chinensis]	71.9	71.9	96%	1e-12	92%	gi|444510620|ELV09642.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tarsius syrichta	71.0	71.0	100%	3e-12	88%	gi|640809594|XP_008061363.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Ory	70.6	70.6	96%	4e-12	88%	gi|655834514|XP_008258875.1
☐	PREDICTED: hepatocyte growth factor-like protein [Odobenus rosm	70.6	70.6	100%	4e-12	85%	gi|472359375|XP_004399304.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Ory	70.6	70.6	96%	4e-12	88%	gi|655834511|XP_008258874.1
☐	Hepatocyte growth factor-like protein [Myotis brandtii]	70.2	70.2	92%	5e-12	88%	gi|521025473|EPQ07261.1
☐	PREDICTED: hepatocyte growth factor-like protein [Myotis brandtii]	70.2	70.2	92%	5e-12	88%	gi|554541621|XP_005865438.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Sus	70.2	70.2	100%	5e-12	85%	gi|545862433|XP_005669634.1
☐	PREDICTED: hepatocyte growth factor-like protein-like [Sus scrofa	70.2	70.2	100%	5e-12	85%	gi|545890597|XP_005674335.1
☐	PREDICTED: hepatocyte growth factor-like protein [Otolemur garne	70.2	70.2	100%	5e-12	85%	gi|395856451|XP_003800642.1
☐	PREDICTED: hepatocyte growth factor-like protein [Eptesicus fuscu	70.2	70.2	92%	5e-12	88%	gi|641693981|XP_008153797.1

☐	PREDICTED: hepatocyte growth factor-like protein [Ochotona princ	70.2	70.2	100%	5e-12	85%	gi|504138720|XP_004581815.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Sus	70.2	70.2	100%	5e-12	85%	gi|311268909|XP_003132263.1
☐	PREDICTED: hepatocyte growth factor-like protein [Leptonychotes	69.4	69.4	100%	1e-11	85%	gi|585186199|XP_006744596.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	68.5	68.5	100%	2e-11	85%	gi|560895401|XP_006174176.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	68.5	68.5	100%	2e-11	85%	gi|560948035|XP_006196588.1
☐	macrophage stimulating 1-like protein [Camelus ferus]	68.5	68.5	100%	2e-11	85%	gi|530666765|EQB77066.1
☐	PREDICTED: hepatocyte growth factor-like protein [Ursus maritimu	68.1	68.1	100%	3e-11	85%	gi|671022372|XP_008702001.1
☐	hypothetical protein PANDA_009343 [Ailuropoda melanoleuca]	68.1	68.1	100%	3e-11	85%	gi|281338342|EFB13926.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Mus	68.1	68.1	100%	3e-11	85%	gi|512005359|XP_004820133.1
☐	PREDICTED: hepatocyte growth factor-like protein [Mustela putoriu	68.1	68.1	100%	3e-11	85%	gi|511881610|XP_004760697.1
☐	PREDICTED: hepatocyte growth factor-like protein-like [Ailuropoda	68.1	68.1	100%	3e-11	85%	gi|301770361|XP_002920612.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Mus	68.1	68.1	100%	3e-11	85%	gi|512005357|XP_004820132.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Mus	68.1	68.1	100%	3e-11	85%	gi|512005355|XP_004820131.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Equ	67.7	67.7	100%	4e-11	81%	gi|545188630|XP_005600717.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Equ	67.7	67.7	100%	4e-11	81%	gi|664730009|XP_008522206.1
☐	PREDICTED: hepatocyte growth factor-like protein [Dasypus nover	67.7	67.7	100%	4e-11	85%	gi|488519988|XP_004451933.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Equ	67.7	67.7	100%	4e-11	81%	gi|545188628|XP_005600716.1
☐	PREDICTED: hepatocyte growth factor-like protein [Lipotes vexillife	67.2	67.2	100%	5e-11	81%	gi|602681551|XP_007446274.1
☐	PREDICTED: hepatocyte growth factor-like protein [Physeter catod	67.2	67.2	100%	5e-11	81%	gi|593749341|XP_007129906.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tursiops trunca	67.2	67.2	100%	5e-11	81%	gi|470608261|XP_004314855.1
☐	PREDICTED: hepatocyte growth factor-like protein [Orcinus orca]	67.2	67.2	100%	5e-11	81%	gi|466078823|XP_004284002.1
☐	PREDICTED: hepatocyte growth factor-like protein [Ceratotherium s	66.8	66.8	100%	8e-11	81%	gi|478490786|XP_004419765.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Chi	66.4	66.4	96%	1e-10	84%	gi|533195097|XP_005410271.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Chi	66.4	66.4	96%	1e-10	84%	gi|533195095|XP_005410270.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Chi	66.4	66.4	96%	1e-10	84%	gi|533195093|XP_005410269.1
☐	PREDICTED: hepatocyte growth factor-like protein [Orycteropus afe	65.5	65.5	100%	2e-10	85%	gi|634888659|XP_007953538.1
☐	PREDICTED: hepatocyte growth factor-like protein [Trichechus mai	65.5	65.5	100%	2e-10	85%	gi|471355983|XP_004368594.1

⊟ Alignments

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macrophage stimulating 1 (hepatocyte growth factor-like), isoform CRA_c [Homo sapiens]

Sequence ID: gi|119585405|gb|EAW65001.1| **Length:** 183 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 83 to 108 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
85.0 bits(193)	3e-17	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KGTGNDTVLNVALLNVISNQECNIKH  26
            KGTGNDTVLNVALLNVISNQECNIKH
Sbjct  83   KGTGNDTVLNVALLNVISNQECNIKH  108
```

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Chain B, Crystal Structure Of The Beta-Chain Of HgflMSP

Sequence ID: gi|83754035|pdb|2ASU|B **Length:** 234 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 128 to 153 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
85.0 bits(193)	3e-17	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KGTGNDTVLNVALLNVISNQECNIKH  26
```

```
                KGTGNDTVLNVALLNVISNQECNIKH
Sbjct  128  KGTGNDTVLNVALLNVISNQECNIKH  153
```

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Chain C, Crystal Structure Of Ron Sema-psi-ipt1 Extracellular Domains In Complex With Msp Beta-chain

Sequence ID: gi|685425760|pdb|4QT8|C **Length:** 253 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 147 to 172 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
85.0 bits(193)	4e-17	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KGTGNDTVLNVALLNVISNQECNIKH  26
            KGTGNDTVLNVALLNVISNQECNIKH
Sbjct  147  KGTGNDTVLNVALLNVISNQECNIKH  172
```

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hepatocyte growth factor-like protein homolog [Homo sapiens]

Sequence ID: gi|1141777|gb|AAC35412.1| **Length:** 286 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 186 to 211 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
85.0 bits(193)	4e-17	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KGTGNDTVLNVALLNVISNQECNIKH  26
            KGTGNDTVLNVALLNVISNQECNIKH
Sbjct  186  KGTGNDTVLNVALLNVISNQECNIKH  211
```

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PREDICTED: hepatocyte growth factor-like protein isoform X2 [Macaca fascicularis]

Sequence ID: gi|544414366|ref|XP_005547205.1| **Length:** 600 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 500 to 525 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
85.0 bits(193)	5e-17	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    KGTGNDTVLNVALLNVISNQECNIKH  26
            KGTGNDTVLNVALLNVISNQECNIKH
Sbjct  500  KGTGNDTVLNVALLNVISNQECNIKH  525
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   Formatting options   Download   How to read this page   Blast report description

MST1_RGKGEGYRGTADTTTAGVPCQRW_Mod

RID BVJKKGCZ01R (Expires on 01-21 10:24 am)

Query ID lcl|141497
Description None
Molecule type amino acid
Query Length 23

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

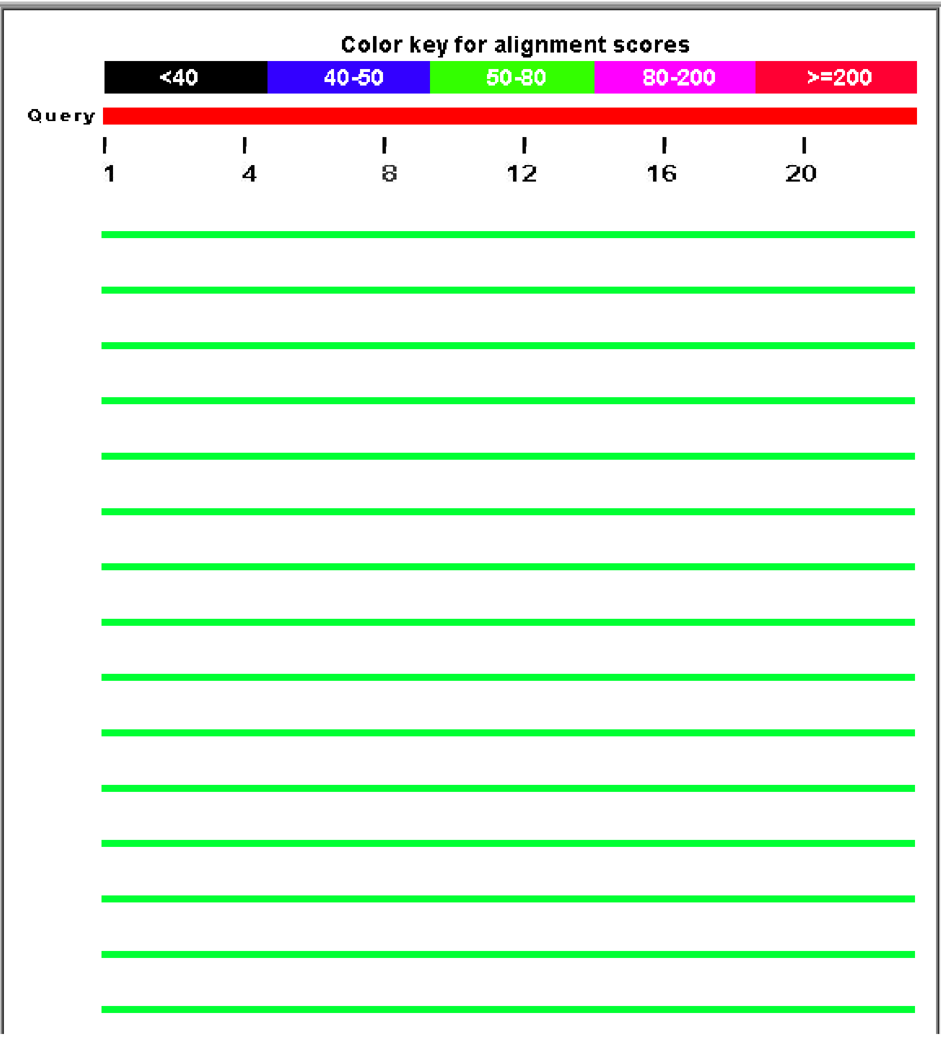
Graphic Summary

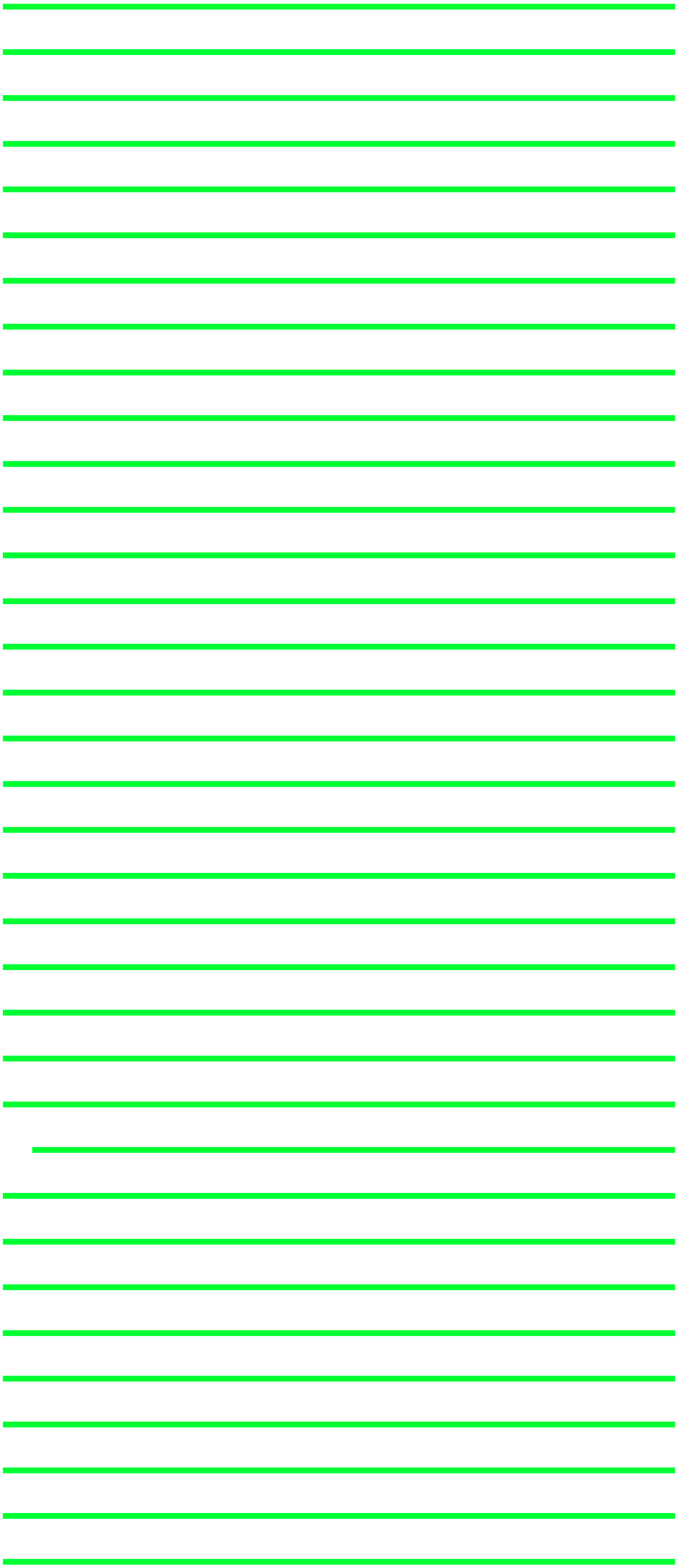
Show Conserved Domains

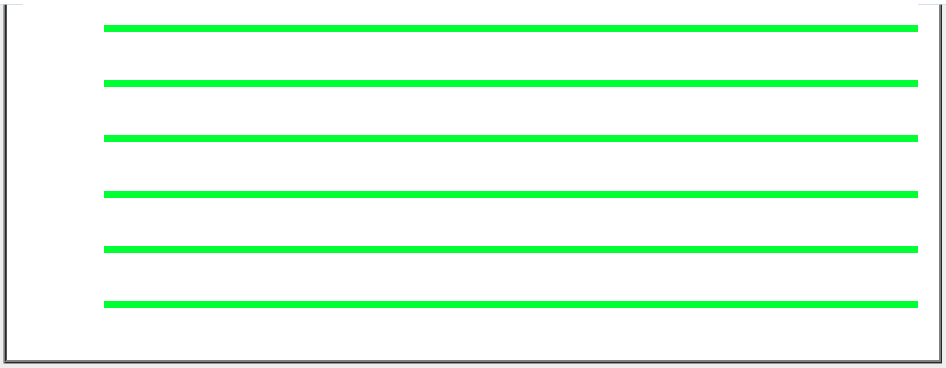
Putative conserved domains have been detected, click on the image below for detailed results.

Distribution of 372 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	MST1 protein [Homo sapiens]	74.0	105	100%	1e-13	96%	AAH44862.1
☐	unnamed protein product [Homo sapiens]	74.0	139	100%	2e-13	96%	BAH12793.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like), isoform CRA_d [Ho	74.0	105	100%	2e-13	96%	EAW65002.1
☐	unnamed protein product [Homo sapiens]	74.0	139	100%	2e-13	96%	BAH11736.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Homo sapiens	74.0	173	100%	2e-13	96%	XP_006713232.1
☐	hepatocyte growth factor-like protein homolog [Homo sapiens]	74.0	165	100%	2e-13	96%	AAC63092.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Macaca fascic	74.0	176	100%	2e-13	96%	XP_005547205.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like), isoform CRA_e [Ho	74.0	138	100%	2e-13	96%	EAW65003.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Homo sapiens	74.0	173	100%	2e-13	96%	XP_006713230.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X5 [Chlorocebus s	74.0	141	100%	2e-13	96%	XP_007982450.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Papio anubis]	74.0	176	100%	2e-13	96%	XP_009199018.1
☐	macrophage-stimulating protein [Homo sapiens]	74.0	173	100%	2e-13	96%	AAA59872.1
☐	RecName: Full=Hepatocyte growth factor-like protein; AltName: Full=Macroph	74.0	173	100%	2e-13	96%	P26927.2
☐	hepatocyte growth factor-like protein [Homo sapiens]	74.0	173	100%	2e-13	96%	AAA50165.1
☐	hypothetical protein EGM_20500 [Macaca fascicularis]	74.0	176	100%	2e-13	96%	EHH62249.1
☐	hypothetical protein EGK_11631 [Macaca mulatta]	74.0	176	100%	2e-13	96%	EHH16360.1
☐	hypothetical protein [Macaca fascicularis]	74.0	176	100%	2e-13	96%	BAF47378.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like) variant [Homo sapie	74.0	176	100%	2e-13	96%	BAD96613.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Chlorocebus s	74.0	141	100%	2e-13	96%	XP_007982449.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Cavia porcellu	74.0	160	100%	2e-13	96%	XP_003476721.1
☐	PREDICTED: hepatocyte growth factor-like protein [Pteropus alecto]	74.0	177	100%	2e-13	96%	XP_006909162.1
☐	PREDICTED: hepatocyte growth factor-like protein [Pongo abelii]	74.0	175	100%	2e-13	96%	XP_002813790.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Chlorocebus s	74.0	176	100%	2e-13	96%	XP_007982448.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Macaca fascic	74.0	176	100%	2e-13	96%	XP_005547204.1
☐	PREDICTED: hepatocyte growth factor-like protein [Gorilla gorilla gorilla]	74.0	173	100%	2e-13	96%	XP_004034204.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Papio anubis]	74.0	176	100%	2e-13	96%	XP_003894463.1
☐	PREDICTED: hepatocyte growth factor-like protein [Nomascus leucogenys]	74.0	169	100%	2e-13	96%	XP_003257123.1
☐	hepatocyte growth factor-like protein precursor [Homo sapiens]	74.0	173	100%	2e-13	96%	NP_066278.3
☐	PREDICTED: hepatocyte growth factor-like protein [Macaca mulatta]	74.0	176	100%	2e-13	96%	XP_001107946.1

☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Chlorocebus s	74.0	141	100%	2e-13	96%	XP_007982445.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Cavia porcellu	74.0	160	100%	2e-13	96%	XP_005006713.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Chlorocebus s	74.0	141	100%	2e-13	96%	XP_007982444.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein	74.0	170	100%	2e-13	96%	XP_516465.4
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein	71.0	170	100%	2e-12	91%	XP_005326984.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Equus przewa	70.6	175	100%	3e-12	91%	XP_008522208.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Saimiri bolivier	70.6	168	100%	3e-12	91%	XP_010345462.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Equus caballu	70.6	145	100%	3e-12	91%	XP_005600717.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Equus przewa	70.6	175	100%	3e-12	91%	XP_008522206.1
☐	hypothetical protein PANDA_009343 [Ailuropoda melanoleuca]	70.6	162	100%	3e-12	91%	EFB13926.1
☐	PREDICTED: hepatocyte growth factor-like protein [Erinaceus europaeus]	70.6	158	100%	3e-12	91%	XP_007527316.1
☐	PREDICTED: hepatocyte growth factor-like protein [Echinops telfairi]	70.6	138	95%	3e-12	95%	XP_004715222.1
☐	PREDICTED: hepatocyte growth factor-like protein [Galeopterus variegatus]	70.6	168	100%	3e-12	91%	XP_008569781.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tarsius syrichta]	70.6	175	100%	3e-12	91%	XP_008061363.1
☐	PREDICTED: hepatocyte growth factor-like protein [Orycteropus afer afer]	70.6	172	100%	3e-12	91%	XP_007953538.1
☐	PREDICTED: hepatocyte growth factor-like protein [Leptonychotes weddellii]	70.6	167	100%	3e-12	91%	XP_006744596.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tupaia chinensis]	70.6	167	100%	3e-12	91%	XP_006171012.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Mustela putori	70.6	162	100%	3e-12	91%	XP_004820133.1
☐	PREDICTED: hepatocyte growth factor-like protein [Mustela putorius furo]	70.6	162	100%	3e-12	91%	XP_004760697.1
☐	PREDICTED: hepatocyte growth factor-like protein [Odobenus rosmarus diver	70.6	164	100%	3e-12	91%	XP_004399304.1
☐	PREDICTED: hepatocyte growth factor-like protein [Ceratotherium simum sim	70.6	166	100%	3e-12	91%	XP_004419765.1
☐	PREDICTED: hepatocyte growth factor-like protein [Sorex araneus]	70.6	164	100%	3e-12	91%	XP_004615300.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein	70.6	178	100%	3e-12	91%	XP_003409924.1
☐	PREDICTED: hepatocyte growth factor-like protein [Eptesicus fuscus]	70.6	160	100%	3e-12	91%	XP_008153797.1
☐	PREDICTED: hepatocyte growth factor-like protein [Pantholops hodgsonii]	70.6	136	100%	3e-12	91%	XP_005969335.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Equus caballu	70.6	175	100%	3e-12	91%	XP_005600716.1
☐	PREDICTED: hepatocyte growth factor-like protein [Felis catus]	70.6	171	100%	3e-12	91%	XP_003982280.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Saimiri bolivier	70.6	168	100%	3e-12	91%	XP_003936704.1
☐	PREDICTED: hepatocyte growth factor-like protein [Canis lupus familiaris]	70.6	167	100%	3e-12	91%	XP_541884.3
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein	70.6	131	100%	3e-12	91%	XP_004018505.1
☐	Hepatocyte growth factor-like protein [Tupaia chinensis]	70.6	167	100%	3e-12	91%	ELV09642.1
☐	PREDICTED: hepatocyte growth factor-like protein-like [Ailuropoda melanoleu	70.6	162	100%	3e-12	91%	XP_002920612.1
☐	PREDICTED: hepatocyte growth factor-like protein [Rhinopithecus roxellana]	69.8	172	100%	5e-12	91%	XP_010367959.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Callithrix jacch	68.5	129	100%	1e-11	87%	XP_008979888.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Callithrix jacch	68.5	163	100%	1e-11	87%	XP_002758398.1
☐	PREDICTED: hepatocyte growth factor-like protein [Otolemur garnettii]	68.1	171	100%	2e-11	87%	XP_003800642.1
☐	PREDICTED: hepatocyte growth factor-like protein [Elephantulus edwardii]	67.7	175	100%	3e-11	87%	XP_006892963.1
☐	PREDICTED: hepatocyte growth factor-like protein [Dasypus novemcinctus]	67.7	170	100%	3e-11	87%	XP_004451933.1
☐	PREDICTED: hepatocyte growth factor-like protein [Bubalus bubalis]	67.2	137	100%	4e-11	87%	XP_006053335.1
☐	PREDICTED: hepatocyte growth factor-like protein [Bos mutus]	67.2	137	100%	4e-11	87%	XP_005892185.1
☐	TPA: hepatocyte growth factor-like protein [Bos taurus]	67.2	137	100%	4e-11	87%	DAA16921.1
☐	hepatocyte growth factor-like protein precursor [Bos taurus]	67.2	137	100%	4e-11	87%	NP_001069145.1
☐	PREDICTED: hepatocyte growth factor-like protein [Camelus bactrianus]	67.2	164	100%	4e-11	87%	XP_010967473.1
☐	Hepatocyte growth factor-like protein [Bos mutus]	67.2	137	100%	4e-11	87%	ELR58967.1
☐	PREDICTED: hepatocyte growth factor-like protein [Jaculus jaculus]	67.2	158	100%	4e-11	87%	XP_004664298.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Bison bison bi	67.2	137	100%	4e-11	87%	XP_010850156.1

☐	PREDICTED: hepatocyte growth factor-like protein [Balaenoptera acutorostrat	67.2	163	100%	4e-11	87%	XP_007168789.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Bison bison bi	67.2	137	100%	4e-11	87%	XP_010850155.1
☐	PREDICTED: hepatocyte growth factor-like protein [Lipotes vexillifer]	67.2	163	100%	4e-11	87%	XP_007446274.1
☐	PREDICTED: hepatocyte growth factor-like protein [Physeter catodon]	67.2	159	100%	4e-11	87%	XP_007129906.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-like protein	67.2	164	100%	4e-11	87%	XP_006196588.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Bos taurus]	67.2	137	100%	4e-11	87%	XP_005222861.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tursiops truncatus]	67.2	163	100%	4e-11	87%	XP_004314855.1
☐	PREDICTED: hepatocyte growth factor-like protein [Orcinus orca]	67.2	163	100%	4e-11	87%	XP_004284002.1
☐	PREDICTED: hepatocyte growth factor-like protein [Camelus dromedarius]	67.2	164	100%	4e-11	87%	XP_010976658.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Chinchilla lani	66.8	125	95%	6e-11	91%	XP_005410271.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Chinchilla lani	66.8	125	95%	6e-11	91%	XP_005410270.1
☐	PREDICTED: hepatocyte growth factor-like protein [Octodon degus]	66.8	162	100%	6e-11	87%	XP_004625159.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Chinchilla lani	66.8	125	95%	6e-11	91%	XP_005410269.1
☐	PREDICTED: hepatocyte growth factor-like protein [Ochotona princeps]	66.8	154	100%	6e-11	87%	XP_004581815.1
☐	PREDICTED: hepatocyte growth factor-like protein [Trichechus manatus latiro	66.4	179	100%	8e-11	87%	XP_004368594.1
☐	PREDICTED: hepatocyte growth factor-like protein [Chrysochloris asiatica]	65.5	166	100%	2e-10	83%	XP_006873659.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Mus musculus	64.3	151	100%	4e-10	83%	XP_006511702.1
☐	PREDICTED: hepatocyte growth factor-like protein [Nannospalax galili]	64.3	115	100%	4e-10	83%	XP_008851489.1
☐	Macrophage stimulating 1 (hepatocyte growth factor-like) [Mus musculus]	64.3	151	100%	4e-10	83%	AAH10551.1
☐	hepatocyte growth factor-like protein precursor [Mus musculus]	64.3	151	100%	4e-10	83%	NP_032269.3
☐	PREDICTED: hepatocyte growth factor-like protein [Mesocricetus auratus]	64.3	141	100%	4e-10	83%	XP_005074975.1
☐	unnamed protein product [Mus musculus]	64.3	151	100%	4e-10	83%	BAE22056.1
☐	hepatocyte growth factor-like protein [Mus musculus]	64.3	151	100%	4e-10	83%	AAA50167.1
☐	hepatocyte growth factor-like protein precursor [Rattus norvegicus]	64.3	151	100%	4e-10	83%	NP_077328.1
☐	PREDICTED: hepatocyte growth factor-like protein [Peromyscus maniculatus	64.3	148	100%	4e-10	83%	XP_006978395.1

⊟ Alignments

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MST1 protein [Homo sapiens]

Sequence ID: gb|AAH44862.1| **Length:** 188 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 148 to 170 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
74.0 bits(167)	1e-13	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    RGKGEGYRGTADTTTAGVPCQRW  23
            RGKGEGYRGTA+TTTAGVPCQRW
Sbjct  148  RGKGEGYRGTANTTTAGVPCQRW  170
```

Range 2: 59 to 78 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
31.2 bits(66)	25	12/20(60%)	12/20(60%)	0/20(0%)

```
Query  4   GEGYRGTADTTTAGVPCQRW  23
           GE YRG  D T  G   CQRW
Sbjct  59  GEEYRGAVDRTESGRECQRW  78
```

Download ⌄ GenPept Graphics **Sort by:** 0 ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAH12793.1| **Length:** 264 **Number of Matches:** 3

Related Information

Range 1: 224 to 246 GenPept Graphics ▼ Next Match ▲ Previous Match

Gene - associated gene details

Score	Expect	Identities	Positives	Gaps
74.0 bits(167)	2e-13	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    RGKGEGYRGTADTTTAGVPCQRW  23
            RGKGEGYRGTA+TTTAGVPCQRW
Sbjct  224  RGKGEGYRGTANTTTAGVPCQRW  246
```

Range 2: 56 to 73 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
34.6 bits(74)	1.9	12/18(67%)	12/18(66%)	0/18(0%)

```
Query  6   GYRGTADTTTAGVPCQRW  23
           GYRGT  TT  G PCQ W
Sbjct  56  GYRGTMATTVGGLPCQAW  73
```

Range 3: 135 to 154 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
31.2 bits(66)	26	12/20(60%)	12/20(60%)	0/20(0%)

```
Query  4    GEGYRGTADTTTAGVPCQRW  23
            GE YRG  D T  G  CQRW
Sbjct  135  GEEYRGAVDRTESGRECQRW  154
```

Download ⌄ GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

macrophage stimulating 1 (hepatocyte growth factor-like), isoform CRA_d [Homo sapiens]

Sequence ID: gb|EAW65002.1| **Length:** 331 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 223 to 245 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
74.0 bits(167)	2e-13	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    RGKGEGYRGTADTTTAGVPCQRW  23
            RGKGEGYRGTA+TTTAGVPCQRW
Sbjct  223  RGKGEGYRGTANTTTAGVPCQRW  245
```

Range 2: 134 to 153 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
31.2 bits(66)	26	12/20(60%)	12/20(60%)	0/20(0%)

```
Query  4    GEGYRGTADTTTAGVPCQRW  23
            GE YRG  D T  G  CQRW
Sbjct  134  GEEYRGAVDRTESGRECQRW  153
```

Download ⌄ GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAH11736.1| **Length:** 339 **Number of Matches:** 3

Related Information

Gene - associated gene details

Range 1: 299 to 321 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
74.0 bits(167)	2e-13	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    RGKGEGYRGTADTTTAGVPCQRW  23
            RGKGEGYRGTA+TTTAGVPCQRW
Sbjct  299  RGKGEGYRGTANTTTAGVPCQRW  321
```

Range 2: 131 to 148 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
34.6 bits(74)	2.0	12/18(67%)	12/18(66%)	0/18(0%)

```
Query  6    GYRGTADTTTAGVPCQRW  23
            GYRGT  TT  G PCQ W
Sbjct  131  GYRGTMATTVGGLPCQAW  148
```

Range 3: 210 to 229 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
31.2 bits(66)	26	12/20(60%)	12/20(60%)	0/20(0%)

```
Query  4    GEGYRGTADTTTAGVPCQRW  23
            GE YRG  D T  G  CQRW
Sbjct  210  GEEYRGAVDRTESGRECQRW  229
```

Download ⌄ GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

PREDICTED: hepatocyte growth factor-like protein isoform X4 [Homo sapiens]

Sequence ID: ref|XP_006713232.1| **Length:** 519 **Number of Matches:** 4

Range 1: 299 to 321 GenPept Graphics

Next Match Previous Match

Score	Expect	Identities	Positives	Gaps
74.0 bits(167)	2e-13	22/23(96%)	23/23(100%)	0/23(0%)

```
Query  1    RGKGEGYRGTADTTTAGVPCQRW  23
            RGKGEGYRGTA+TTTAGVPCQRW
Sbjct  299  RGKGEGYRGTANTTTAGVPCQRW  321
```

Range 2: 131 to 148 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Identities	Positives	Gaps
34.6 bits(74)	2.0	12/18(67%)	12/18(66%)	0/18(0%)

```
Query  6    GYRGTADTTTAGVPCQRW  23
            GYRGT  TT  G PCQ W
Sbjct  131  GYRGTMATTVGGLPCQAW  148
```

Range 3: 389 to 408 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Identities	Positives	Gaps
33.7 bits(72)	3.8	13/20(65%)	13/20(65%)	0/20(0%)

```
Query  4    GEGYRGTADTTTAGVPCQRW  23
            GE YRGT   T  GV CQRW
Sbjct  389  GEQYRGTVSKTRKGVQCQRW  408
```

Range 4: 210 to 229 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Identities	Positives	Gaps
31.2 bits(66)	26	12/20(60%)	12/20(60%)	0/20(0%)

```
Query  4    GEGYRGTADTTTAGVPCQRW  23
            GE YRG  D T  G  CQRW
Sbjct  210  GEEYRGAVDRTESGRECQRW  229
```

Related Information

Gene - associated gene details

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

MST1_RGKGEGYRGTANTTTAGVPCQRW_NonMod

RID B9P4AWX201R (Expires on 01-14 15:34 pm)

Query ID lcl|41900
Description None
Molecule type amino acid
Query Length 23

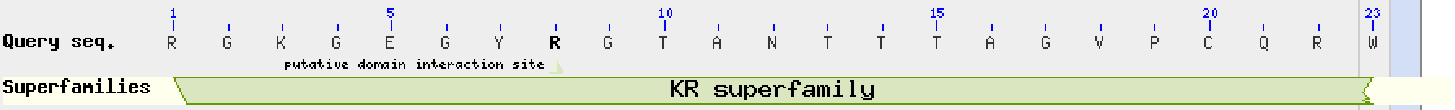
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

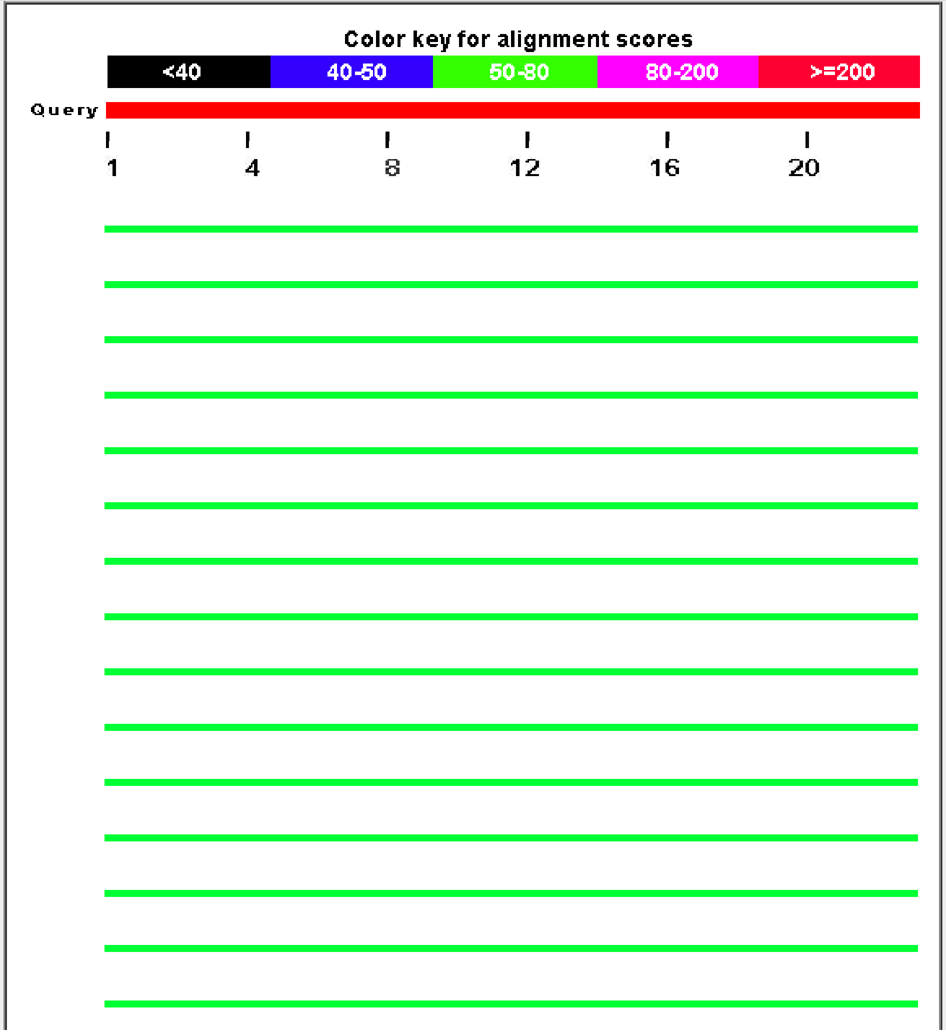
Show Conserved Domains

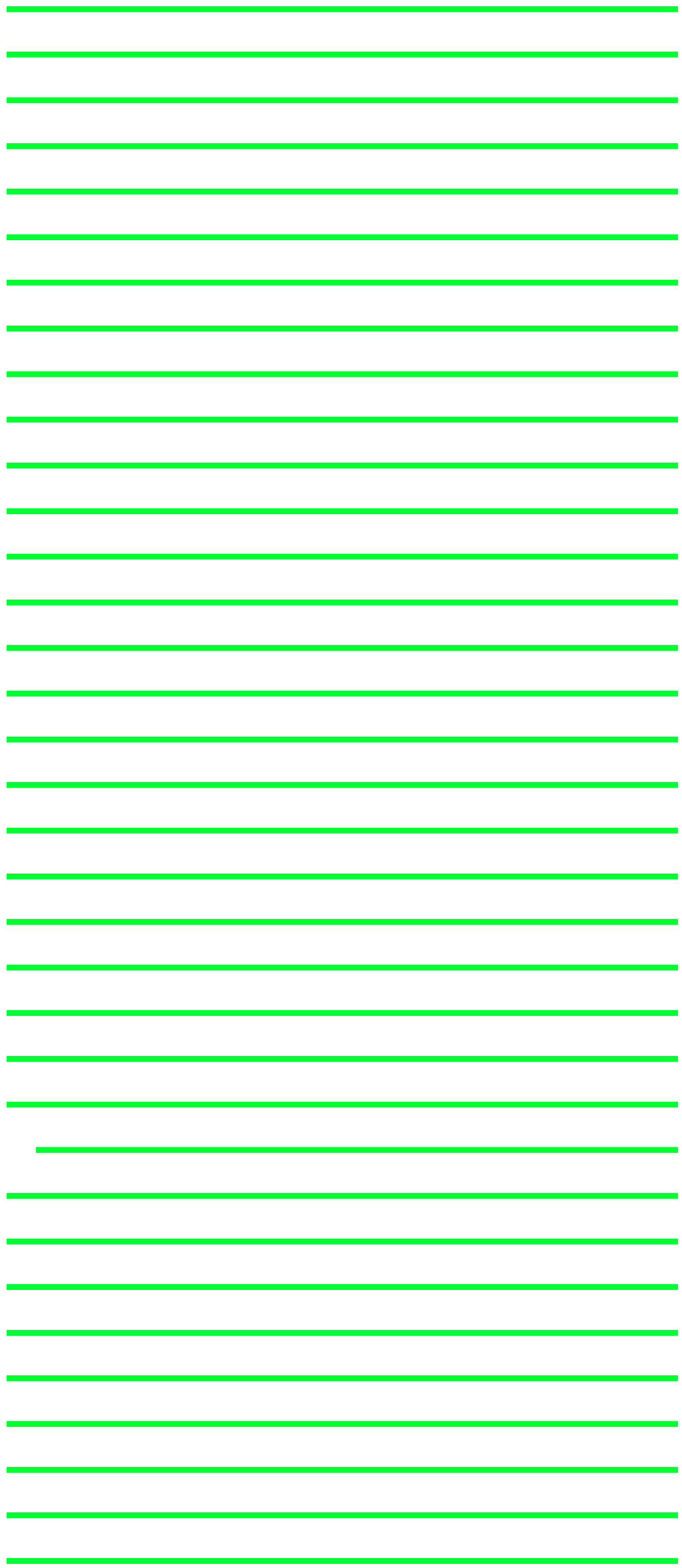
Putative conserved domains have been detected, click on the image below for detailed results.

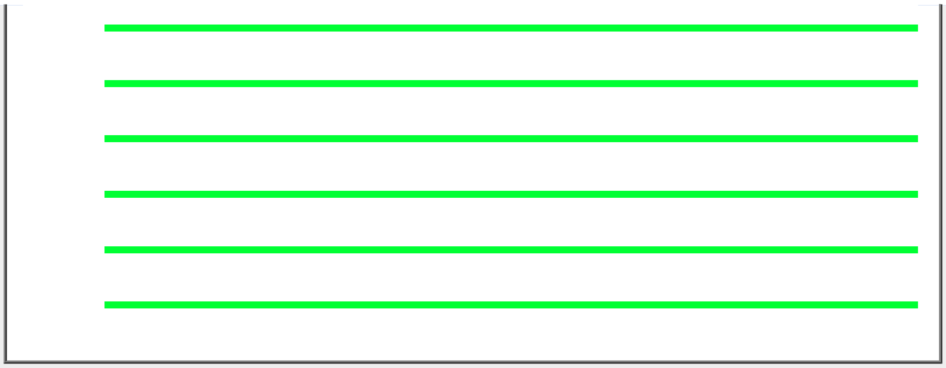


Distribution of 384 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	MST1 protein [Homo sapiens]	76.6	105	100%	2e-14	100%	gi|71297286|AAH44862.1
☐	unnamed protein product [Homo sapiens]	76.6	139	100%	2e-14	100%	gi|221042232|BAH12793.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like), isoform C	76.6	105	100%	2e-14	100%	gi|119585406|EAW65002.1
☐	unnamed protein product [Homo sapiens]	76.6	139	100%	2e-14	100%	gi|221039946|BAH11736.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Hor	76.6	174	100%	2e-14	100%	gi|578806141|XP_006713232.1
☐	hepatocyte growth factor-like protein homolog [Homo sapiens]	76.6	166	100%	2e-14	100%	gi|1141775|AAC63092.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Mac	76.6	177	100%	2e-14	100%	gi|544414366|XP_005547205.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like), isoform C	76.6	140	100%	2e-14	100%	gi|119585407|EAW65003.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Hor	76.6	174	100%	2e-14	100%	gi|578806131|XP_006713230.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X5 [Chl	76.6	140	100%	2e-14	100%	gi|635118817|XP_007982450.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Pap	76.6	177	100%	2e-14	100%	gi|685524931|XP_009199018.1
☐	macrophage-stimulating protein [Homo sapiens]	76.6	174	100%	2e-14	100%	gi|398038|AAA59872.1
☐	RecName: Full=Hepatocyte growth factor-like protein; AltName: Fu	76.6	174	100%	2e-14	100%	gi|147744563|P26927.2
☐	hepatocyte growth factor-like protein [Homo sapiens]	76.6	174	100%	2e-14	100%	gi|183977|AAA50165.1
☐	hypothetical protein EGM_20500 [Macaca fascicularis]	76.6	177	100%	2e-14	100%	gi|355764094|EHH62249.1
☐	hypothetical protein EGK_11631 [Macaca mulatta]	76.6	177	100%	2e-14	100%	gi|355559632|EHH16360.1
☐	hypothetical protein [Macaca fascicularis]	76.6	177	100%	2e-14	100%	gi|126143528|BAF47378.1
☐	macrophage stimulating 1 (hepatocyte growth factor-like) variant [H	76.6	178	100%	2e-14	100%	gi|62897345|BAD96613.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Chl	76.6	140	100%	2e-14	100%	gi|635118815|XP_007982449.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Cav	76.6	142	100%	2e-14	100%	gi|348581912|XP_003476721.1
☐	PREDICTED: hepatocyte growth factor-like protein [Pteropus alectc	76.6	179	100%	2e-14	100%	gi|586548158|XP_006909162.1
☐	PREDICTED: hepatocyte growth factor-like protein [Pongo abelii]	76.6	176	100%	2e-14	100%	gi|297671325|XP_002813790.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Chl	76.6	177	100%	2e-14	100%	gi|635118813|XP_007982448.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Mac	76.6	177	100%	2e-14	100%	gi|544414364|XP_005547204.1
☐	PREDICTED: hepatocyte growth factor-like protein [Gorilla gorilla g	76.6	175	100%	2e-14	100%	gi|426340575|XP_004034204.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Pap	76.6	177	100%	2e-14	100%	gi|402860079|XP_003894463.1
☐	PREDICTED: hepatocyte growth factor-like protein [Nomascus leuc	76.6	170	100%	2e-14	100%	gi|332215988|XP_003257123.1
☐	hepatocyte growth factor-like protein precursor [Homo sapiens]	76.6	174	100%	2e-14	100%	gi|205277383|NP_066278.3
☐	PREDICTED: hepatocyte growth factor-like protein [Macaca mulatta	76.6	177	100%	2e-14	100%	gi|109039656|XP_001107946.1

☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Chl	76.6	140	100%	2e-14	100%	gi|635118807|XP_007982445.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Cav	76.6	142	100%	2e-14	100%	gi|514473830|XP_005006713.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Chl	76.6	140	100%	2e-14	100%	gi|635118805|XP_007982444.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	76.6	172	100%	2e-14	100%	gi|410036983|XP_516465.4
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	73.6	171	100%	3e-13	96%	gi|532082473|XP_005326984.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Equ	73.2	176	100%	3e-13	96%	gi|664730013|XP_008522208.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Sai	73.2	170	100%	3e-13	96%	gi|725588970|XP_010345462.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Equ	73.2	145	100%	4e-13	96%	gi|545188630|XP_005600717.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Equ	73.2	176	100%	4e-13	96%	gi|664730009|XP_008522206.1
☐	hypothetical protein PANDA_009343 [Ailuropoda melanoleuca]	73.2	163	100%	4e-13	96%	gi|281338342|EFB13926.1
☐	PREDICTED: hepatocyte growth factor-like protein [Erinaceus euro	73.2	162	100%	4e-13	96%	gi|617622190|XP_007527316.1
☐	PREDICTED: hepatocyte growth factor-like protein [Echinops telfai	73.2	164	95%	4e-13	100%	gi|507700568|XP_004715222.1
☐	PREDICTED: hepatocyte growth factor-like protein [Galeopterus va	73.2	170	100%	4e-13	96%	gi|667267781|XP_008569781.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tarsius syrichta	73.2	176	100%	4e-13	96%	gi|640809594|XP_008061363.1
☐	PREDICTED: hepatocyte growth factor-like protein [Orycteropus af	73.2	173	100%	4e-13	96%	gi|634888659|XP_007953538.1
☐	PREDICTED: hepatocyte growth factor-like protein [Leptonychotes	73.2	168	100%	4e-13	96%	gi|585186199|XP_006744596.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tupaia chinens	73.2	168	100%	4e-13	96%	gi|562887217|XP_006171012.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Mus	73.2	164	100%	4e-13	96%	gi|512005359|XP_004820133.1
☐	PREDICTED: hepatocyte growth factor-like protein [Mustela putoriu	73.2	164	100%	4e-13	96%	gi|511881610|XP_004760697.1
☐	PREDICTED: hepatocyte growth factor-like protein [Odobenus rosm	73.2	165	100%	4e-13	96%	gi|472359375|XP_004399304.1
☐	PREDICTED: hepatocyte growth factor-like protein [Ceratotherium	73.2	167	100%	4e-13	96%	gi|478490786|XP_004419765.1
☐	PREDICTED: hepatocyte growth factor-like protein [Sorex araneus]	73.2	165	100%	4e-13	96%	gi|505843606|XP_004615300.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	73.2	180	100%	4e-13	96%	gi|344276255|XP_003409924.1
☐	PREDICTED: hepatocyte growth factor-like protein [Eptesicus fuscu	73.2	161	100%	4e-13	96%	gi|641693981|XP_008153797.1
☐	PREDICTED: hepatocyte growth factor-like protein [Pantholops hoc	73.2	159	100%	4e-13	96%	gi|556747770|XP_005969335.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Equ	73.2	176	100%	4e-13	96%	gi|545188628|XP_005600716.1
☐	PREDICTED: hepatocyte growth factor-like protein [Felis catus]	73.2	173	100%	4e-13	96%	gi|410951187|XP_003982280.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Sai	73.2	170	100%	4e-13	96%	gi|403291235|XP_003936704.1
☐	PREDICTED: hepatocyte growth factor-like protein [Canis lupus far	73.2	168	100%	4e-13	96%	gi|345787353|XP_541884.3
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	73.2	153	100%	4e-13	96%	gi|426249535|XP_004018505.1
☐	Hepatocyte growth factor-like protein [Tupaia chinensis]	73.2	168	100%	4e-13	96%	gi|444510620|ELV09642.1
☐	PREDICTED: hepatocyte growth factor-like protein-like [Ailuropoda	73.2	163	100%	4e-13	96%	gi|301770361|XP_002920612.1
☐	PREDICTED: hepatocyte growth factor-like protein [Rhinopithecus	72.3	173	100%	7e-13	96%	gi|724799330|XP_010367959.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Call	71.0	131	100%	2e-12	91%	gi|675727602|XP_008979888.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Call	71.0	164	100%	2e-12	91%	gi|296225219|XP_002758398.1
☐	PREDICTED: hepatocyte growth factor-like protein [Otolemur garne	70.6	172	100%	3e-12	91%	gi|395856451|XP_003800642.1
☐	PREDICTED: hepatocyte growth factor-like protein [Elephantulus e	70.2	177	100%	4e-12	91%	gi|585684863|XP_006892963.1
☐	PREDICTED: hepatocyte growth factor-like protein [Dasypus nover	70.2	171	100%	4e-12	91%	gi|488519988|XP_004451933.1
☐	PREDICTED: hepatocyte growth factor-like protein [Bubalus bubali	69.8	161	100%	5e-12	91%	gi|594058341|XP_006053335.1
☐	PREDICTED: hepatocyte growth factor-like protein [Bos mutus]	69.8	159	100%	5e-12	91%	gi|555960159|XP_005892185.1
☐	TPA: hepatocyte growth factor-like protein [Bos taurus]	69.8	159	100%	5e-12	91%	gi|296474806|DAA16921.1
☐	hepatocyte growth factor-like protein precursor [Bos taurus]	69.8	159	100%	5e-12	91%	gi|115496876|NP_001069145.1
☐	Hepatocyte growth factor-like protein [Bos mutus]	69.8	159	100%	5e-12	91%	gi|440909008|ELR58967.1
☐	PREDICTED: hepatocyte growth factor-like protein [Jaculus jaculus	69.8	160	100%	5e-12	91%	gi|507561196|XP_004664298.1
☐	PREDICTED: hepatocyte growth factor-like protein [Balaenoptera a	69.8	165	100%	5e-12	91%	gi|594630485|XP_007168789.1
☐	PREDICTED: hepatocyte growth factor-like protein [Lipotes vexillife	69.8	165	100%	5e-12	91%	gi|602681551|XP_007446274.1

☐	PREDICTED: hepatocyte growth factor-like protein [Physeter catod	69.8	160	100%	5e-12	91%	gi|593749341|XP_007129906.1
☐	PREDICTED: LOW QUALITY PROTEIN: hepatocyte growth factor-	69.8	165	100%	5e-12	91%	gi|560948035|XP_006196588.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X4 [Bos	69.8	159	100%	5e-12	91%	gi|529001498|XP_005222861.1
☐	PREDICTED: hepatocyte growth factor-like protein [Tursiops trunca	69.8	165	100%	5e-12	91%	gi|470608261|XP_004314855.1
☐	PREDICTED: hepatocyte growth factor-like protein [Orcinus orca]	69.8	165	100%	5e-12	91%	gi|466078823|XP_004284002.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X3 [Chi	69.4	151	95%	7e-12	95%	gi|533195097|XP_005410271.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Chi	69.4	151	95%	7e-12	95%	gi|533195095|XP_005410270.1
☐	PREDICTED: hepatocyte growth factor-like protein [Octodon degus	69.4	164	100%	7e-12	91%	gi|507620447|XP_004625159.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Chi	69.4	151	95%	7e-12	95%	gi|533195093|XP_005410269.1
☐	PREDICTED: hepatocyte growth factor-like protein [Ochotona princ	69.4	156	100%	7e-12	91%	gi|504138720|XP_004581815.1
☐	PREDICTED: hepatocyte growth factor-like protein [Trichechus ma	68.9	181	100%	1e-11	91%	gi|471355983|XP_004368594.1
☐	PREDICTED: hepatocyte growth factor-like protein [Chrysochloris a	68.1	167	100%	2e-11	87%	gi|586486348|XP_006873659.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Mus	66.8	152	100%	5e-11	87%	gi|568962765|XP_006511702.1
☐	PREDICTED: hepatocyte growth factor-like protein [Nannospalax g	66.8	116	100%	5e-11	87%	gi|674087268|XP_008851489.1
☐	Macrophage stimulating 1 (hepatocyte growth factor-like) [Mus mus	66.8	152	100%	5e-11	87%	gi|14714805|AAH10551.1
☐	hepatocyte growth factor-like protein precursor [Mus musculus]	66.8	152	100%	5e-11	87%	gi|254675205|NP_032269.3
☐	PREDICTED: hepatocyte growth factor-like protein [Mesocricetus a	66.8	142	100%	5e-11	87%	gi|524949917|XP_005074975.1
☐	unnamed protein product [Mus musculus]	66.8	152	100%	5e-11	87%	gi|74140912|BAE22056.1
☐	hepatocyte growth factor-like protein [Mus musculus]	66.8	152	100%	5e-11	87%	gi|193834|AAA50167.1
☐	hepatocyte growth factor-like protein precursor [Rattus norvegicus]	66.8	152	100%	5e-11	87%	gi|13242239|NP_077328.1
☐	PREDICTED: hepatocyte growth factor-like protein [Peromyscus ma	66.8	149	100%	5e-11	87%	gi|589931181|XP_006978395.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Mic	66.8	151	100%	5e-11	87%	gi|532008239|XP_005347942.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X2 [Mic	66.8	151	100%	5e-11	87%	gi|532008241|XP_005347943.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Rat	66.8	152	100%	5e-11	87%	gi|564365338|XP_006243768.1
☐	PREDICTED: hepatocyte growth factor-like protein isoform X1 [Mus	66.8	152	100%	5e-11	87%	gi|568962763|XP_006511701.1

Alignments

Download GenPept Graphics **Sort by:** 0 ▼ Next ▲ Previous Descriptions

MST1 protein [Homo sapiens]

Sequence ID: gi|71297286|gb|AAH44862.1| **Length:** 188 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 148 to 170 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(173)	2e-14	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    RGKGEGYRGTANTTTAGVPCQRW  23
            RGKGEGYRGTANTTTAGVPCQRW
Sbjct  148  RGKGEGYRGTANTTTAGVPCQRW  170
```

Range 2: 59 to 78 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
28.6 bits(60)	180	11/20(55%)	12/20(60%)	0/20(0%)

```
Query  4    GEGYRGTANTTTAGVPCQRW  23
            GE YRG  + T  G  CQRW
Sbjct  59   GEEYRGAVDRTESGRECQRW  78
```

Download GenPept Graphics **Sort by:** 0 ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: gi|221042232|dbj|BAH12793.1| **Length:** 264 **Number of Matches:** 3

Related Information

Gene - associated gene details

Range 1: 224 to 246 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps

76.6 bits(173)	2e-14	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    RGKGEGYRGTANTTTAGVPCQRW  23
            RGKGEGYRGTANTTTAGVPCQRW
Sbjct  224  RGKGEGYRGTANTTTAGVPCQRW  246
```

Range 2: 56 to 73 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
34.1 bits(73)	2.5	12/18(67%)	12/18(66%)	0/18(0%)

```
Query  6   GYRGTANTTTAGVPCQRW  23
           GYRGT  TT  G PCQ W
Sbjct  56  GYRGTMATTVGGLPCQAW  73
```

Range 3: 135 to 154 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
28.6 bits(60)	182	11/20(55%)	12/20(60%)	0/20(0%)

```
Query  4    GEGYRGTANTTTAGVPCQRW  23
            GE YRG  + T  G  CQRW
Sbjct  135  GEEYRGAVDRTESGRECQRW  154
```

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macrophage stimulating 1 (hepatocyte growth factor-like), isoform CRA_d [Homo sapiens]

Sequence ID: gi|119585406|gb|EAW65002.1| **Length:** 331 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 223 to 245 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(173)	2e-14	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    RGKGEGYRGTANTTTAGVPCQRW  23
            RGKGEGYRGTANTTTAGVPCQRW
Sbjct  223  RGKGEGYRGTANTTTAGVPCQRW  245
```

Range 2: 134 to 153 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
28.6 bits(60)	183	11/20(55%)	12/20(60%)	0/20(0%)

```
Query  4    GEGYRGTANTTTAGVPCQRW  23
            GE YRG  + T  G  CQRW
Sbjct  134  GEEYRGAVDRTESGRECQRW  153
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|221039946|dbj|BAH11736.1| **Length:** 339 **Number of Matches:** 3

Related Information

Gene - associated gene details

Range 1: 299 to 321 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(173)	2e-14	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    RGKGEGYRGTANTTTAGVPCQRW  23
            RGKGEGYRGTANTTTAGVPCQRW
Sbjct  299  RGKGEGYRGTANTTTAGVPCQRW  321
```

Range 2: 131 to 148 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
34.1 bits(73)	2.5	12/18(67%)	12/18(66%)	0/18(0%)

```
Query  6    GYRGTANTTTAGVPCQRW  23
            GYRGT  TT  G PCQ W
Sbjct  131  GYRGTMATTVGGLPCQAW  148
```

Range 3: 210 to 229 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
28.6 bits(60)	183	11/20(55%)	12/20(60%)	0/20(0%)

```
Query  4    GEGYRGTANTTTAGVPCQRW  23
            GE YRG  + T  G  CQRW
Sbjct  210  GEEYRGAVDRTESGRECQRW  229
```

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PREDICTED: hepatocyte growth factor-like protein isoform X4 [Homo sapiens]

Sequence ID: gi|578806141|ref|XP_006713232.1| **Length:** 519 **Number of Matches:** 4

Related Information

Gene - associated gene details

Range 1: 299 to 321 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(173)	2e-14	23/23(100%)	23/23(100%)	0/23(0%)

```
Query  1    RGKGEGYRGTANTTTAGVPCQRW  23
            RGKGEGYRGTANTTTAGVPCQRW
Sbjct  299  RGKGEGYRGTANTTTAGVPCQRW  321
```

Range 2: 389 to 408 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Identities	Positives	Gaps
35.4 bits(76)	1.0	13/20(65%)	13/20(65%)	0/20(0%)

```
Query  4    GEGYRGTANTTTAGVPCQRW  23
            GE YRGT   T  GV CQRW
Sbjct  389  GEQYRGTVSKTRKGVQCQRW  408
```

Range 3: 131 to 148 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Identities	Positives	Gaps
34.1 bits(73)	2.6	12/18(67%)	12/18(66%)	0/18(0%)

```
Query  6    GYRGTANTTTAGVPCQRW  23
            GYRGT  TT  G PCQ W
Sbjct  131  GYRGTMATTVGGLPCQAW  148
```

Range 4: 210 to 229 GenPept Graphics

Next Match Previous Match First Match

Score	Expect	Identities	Positives	Gaps
28.6 bits(60)	185	11/20(55%)	12/20(60%)	0/20(0%)

```
Query  4    GEGYRGTANTTTAGVPCQRW  23
            GE YRG   + T  G  CQRW
Sbjct  210  GEEYRGAVDRTESGRECQRW  229
```

BLAST ®

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVJR5A1G01R

Your search parameters were adjusted to search for a short input sequence.

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ORM1_REYQTRQDQCIYDTTYLNVQRE_Mod

RID BVJR5A1G01R (Expires on 01-21 10:26 am)

Query ID	lcl|189329	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ ▷Citation
Query Length	22		

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

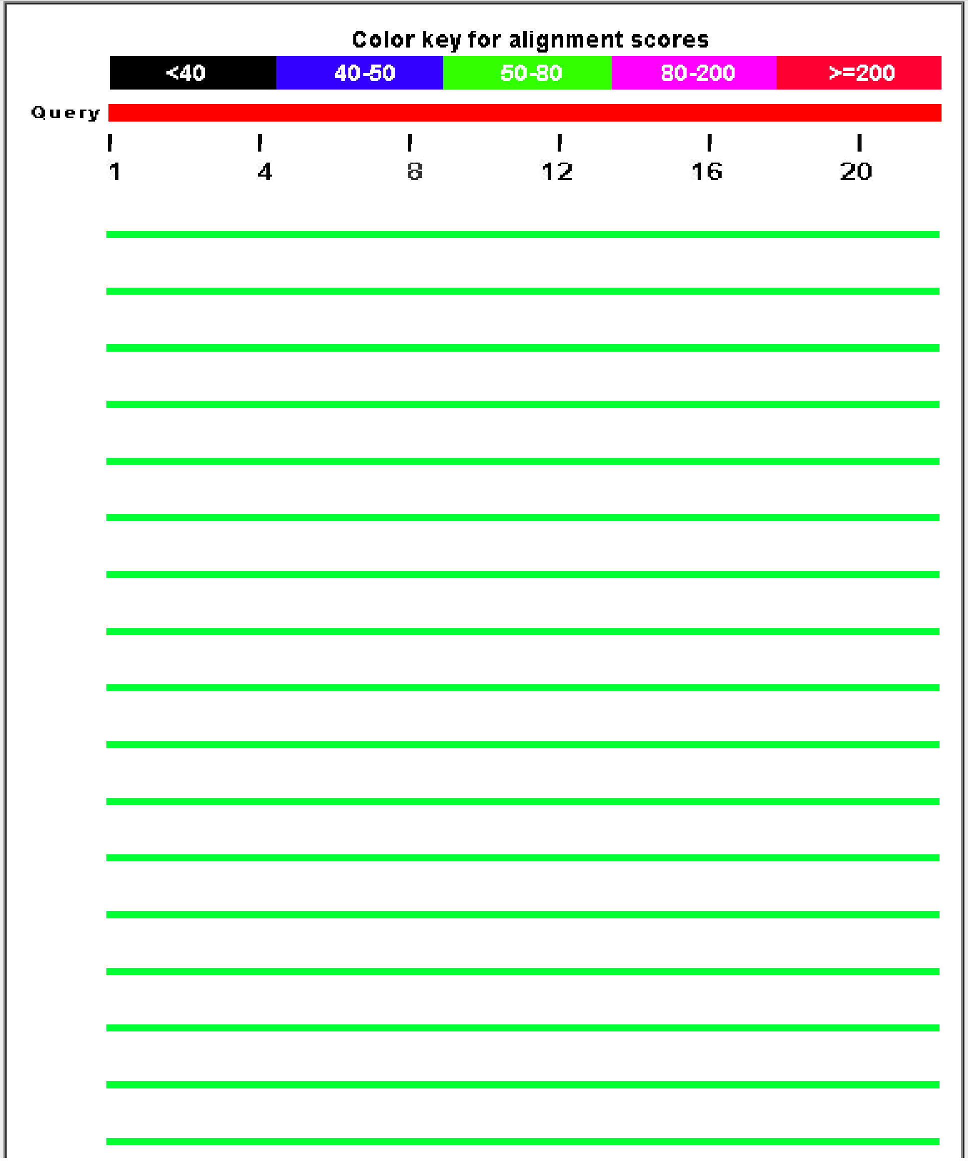
Graphic Summary

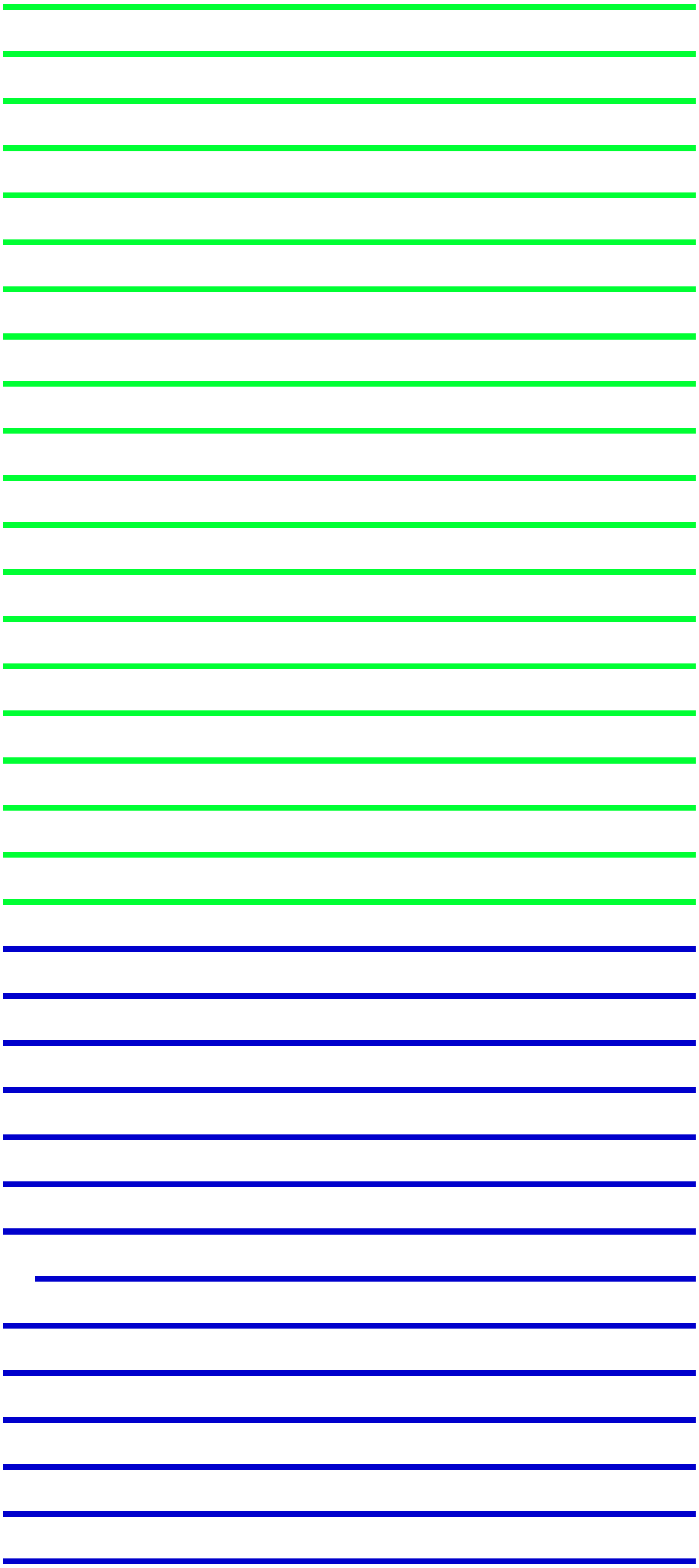
Show Conserved Domains

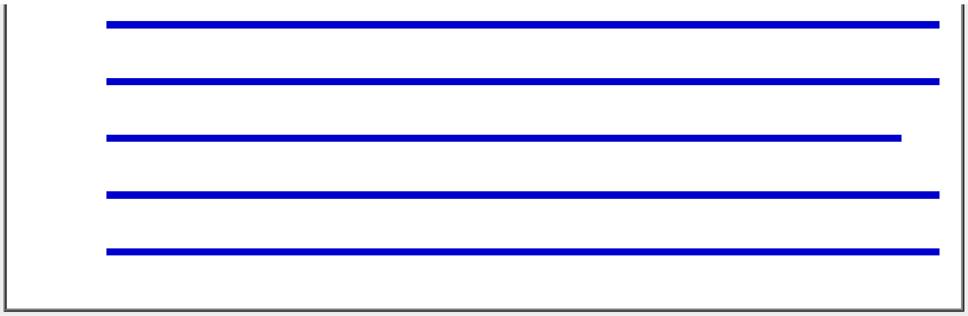
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	protein,alpha1 acid glyco [Homo sapiens]	76.6	76.6	100%	1e-14	95%	720005A
☐	Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein [Homo sapien	76.6	76.6	100%	2e-14	95%	3KQ0_A
☐	Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein [Homo sapier	76.6	76.6	100%	2e-14	95%	3BX6_A
☐	ORM1 [synthetic construct]	76.6	76.6	100%	2e-14	95%	AIC54852.1
☐	Orosomucoid 1 [Homo sapiens]	76.6	76.6	100%	2e-14	95%	AAI43315.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	76.6	76.6	100%	2e-14	95%	CAA29229.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltName: Full=Orc	76.6	76.6	100%	2e-14	95%	P02763.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	76.6	76.6	100%	2e-14	95%	NP_000598.2
☐	orosomucoid 1 [synthetic construct]	76.6	76.6	100%	2e-14	95%	AAV38575.1
☐	orosomucoid 1 [synthetic construct]	76.6	76.6	100%	2e-14	95%	AAV38574.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	72.3	72.3	100%	5e-13	91%	XP_004048543.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 1 [Pan tro	72.3	72.3	100%	5e-13	91%	XP_009455427.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform 1 [Nomascus leucogenys]	72.3	72.3	100%	5e-13	91%	XP_003264088.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Pongo abelii]	72.3	72.3	100%	5e-13	91%	XP_002820180.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like isoform 2 [Macaca mulatta]	71.0	71.0	100%	1e-12	86%	XP_001100289.1
☐	Alpha-1-acid glycoprotein 1 [Macaca mulatta]	71.0	71.0	100%	1e-12	86%	EHH23840.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Chlorocebus sabaeus]	71.0	71.0	100%	1e-12	86%	XP_007966502.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X3 [Macaca fascicularis]	68.1	68.1	100%	1e-11	82%	XP_005581033.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Macaca fascicularis]	68.1	68.1	100%	1e-11	82%	XP_005581032.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Macaca fascicularis]	68.1	68.1	100%	1e-11	82%	XP_005581031.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Papio anubis]	67.2	67.2	100%	3e-11	82%	XP_009186482.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Rhinopithecus roxellana]	65.1	65.1	100%	1e-10	77%	XP_010368793.1
☐	Chain A, Crystal Structure Of The A Variant Of Human Alpha1-Acid Glycoprot	63.8	63.8	100%	4e-10	77%	3APU_A
☐	ORM2 [synthetic construct]	63.8	63.8	100%	4e-10	77%	AIC54853.1
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	63.8	63.8	100%	4e-10	77%	CAA29873.2
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	63.8	63.8	100%	4e-10	77%	NP_000599.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	63.8	63.8	100%	4e-10	77%	XP_004048546.1
☐	ORM2 [Homo sapiens]	63.8	63.8	100%	4e-10	77%	CAG33211.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Pan troglodytes]	63.8	63.8	100%	4e-10	77%	XP_520209.3

☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 2 [Pan pa	63.8	63.8	100%	4e-10	77%	XP_008957108.1
☐	unnamed protein product [Homo sapiens]	61.3	61.3	100%	3e-09	73%	BAG35159.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Callithrix jacchus]	55.8	55.8	100%	2e-07	73%	XP_002760492.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variegatus]	52.4	52.4	100%	3e-06	68%	XP_008588097.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Galeopterus variegatus]	52.4	52.4	100%	3e-06	68%	XP_008588094.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Elephantulus edwardii]	52.0	52.0	100%	4e-06	68%	XP_006890779.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Saimiri boliviensis boliviensis]	51.5	51.5	100%	6e-06	64%	XP_003925252.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	51.1	51.1	100%	8e-06	68%	XP_003407553.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Otolemur garnettii]	49.4	49.4	100%	3e-05	68%	XP_003785445.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Orycteropus afer afer]	48.6	48.6	100%	5e-05	68%	XP_007934876.1
☐	PREDICTED: alpha-1-acid glycoprotein [Felis catus]	48.1	48.1	100%	7e-05	64%	XP_003995824.1
☐	hypothetical protein PANDA_003840 [Ailuropoda melanoleuca]	47.7	47.7	100%	8e-05	64%	EFB15505.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ailuropoda melanoleuca]	47.7	47.7	100%	1e-04	64%	XP_002915823.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Nannospalax galili]	46.4	46.4	100%	3e-04	64%	XP_008831764.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Trichechus manatus latirostris]	46.4	46.4	100%	3e-04	64%	XP_004372401.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Chrysochloris asiatica]	46.0	46.0	95%	4e-04	62%	XP_006865789.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Panthera tigris altaica]	45.6	45.6	100%	5e-04	59%	XP_007094388.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Canis lupus familiaris]	44.8	44.8	100%	0.001	59%	XP_005627010.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Canis lupus familiaris]	44.8	44.8	100%	0.001	59%	XP_003431634.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variegatus]	44.3	44.3	100%	0.001	64%	XP_008588096.1
☐	Alpha-1-acid glycoprotein [Myotis davidii]	43.9	43.9	100%	0.001	64%	ELK26646.1
☐	alpha-1-acid glycoprotein precursor [Rattus norvegicus]	43.5	43.5	100%	0.002	64%	NP_445740.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Trichechus manatus latirostris]	43.5	43.5	100%	0.002	59%	XP_004391192.1
☐	alpha-1-acid glycoprotein [Mus musculus]	43.1	43.1	100%	0.003	55%	AAA91744.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Erinaceus europaeus]	43.1	43.1	95%	0.003	62%	XP_007526815.1
☐	alpha-1-acid glycoprotein (AGP) precursor [Mus caroli]	43.1	43.1	100%	0.003	55%	AAA37197.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltName: Full=Or	43.1	43.1	100%	0.003	55%	P21350.1
☐	alpha-1-acid glycoprotein 2 precursor [Mus musculus]	43.1	43.1	100%	0.003	55%	NP_035146.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Mustela putorius furo]	42.2	42.2	100%	0.006	59%	XP_004828368.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Echinops telfairi]	42.2	42.2	100%	0.006	64%	XP_004718018.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	42.2	42.2	100%	0.006	59%	XP_008707882.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	42.2	42.2	100%	0.006	59%	XP_008707881.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Echinops telfairi]	42.2	42.2	100%	0.006	64%	XP_004712638.1
☐	Alpha-1-acid glycoprotein 1 [Cricetulus griseus]	41.4	41.4	95%	0.012	57%	EGW06649.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Cricetulus griseus]	41.4	41.4	95%	0.012	57%	XP_003503497.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Equus caballus]	41.4	41.4	100%	0.012	64%	XP_001488199.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	41.4	41.4	100%	0.012	55%	XP_003407554.1
☐	alpha-1-acid glycoprotein 1 [Cricetulus griseus]	41.4	41.4	95%	0.012	57%	ERE86355.1
☐	alpha-1-acid glycoprotein 1 [Cricetulus griseus]	41.4	41.4	95%	0.012	57%	ERE86354.1
☐	PREDICTED: LOW QUALITY PROTEIN: orosomucoid 1 [Myotis lucifugus]	40.9	40.9	100%	0.017	59%	XP_006109685.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	40.9	40.9	100%	0.017	55%	XP_010586317.1
☐	alpha-1 acid glycoprotein [Sus scrofa]	40.1	40.1	100%	0.030	59%	AAA30983.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Sus scrofa]	40.1	40.1	100%	0.030	59%	XP_005660423.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	40.1	40.1	100%	0.031	64%	XP_003407551.1
☐	PREDICTED: alpha-1-acid glycoprotein isoform X1 [Sus scrofa]	40.1	40.1	100%	0.031	59%	XP_005660428.1

☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	39.2	39.2	100%	0.057	59%	XP_006108237.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X2 [Tupaia chinensis]	38.8	38.8	100%	0.078	59%	XP_006142836.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Peromyscus maniculatus bairdii]	38.4	38.4	95%	0.11	57%	XP_006979617.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Microtus ochrogaster]	38.4	38.4	95%	0.11	57%	XP_005352666.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Myotis brandtii]	38.0	38.0	100%	0.13	59%	XP_005880983.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	38.0	38.0	100%	0.15	64%	XP_006099427.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Trichechus manatus latirostris]	38.0	38.0	100%	0.15	55%	XP_004391229.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Myotis lucifugus]	38.0	38.0	100%	0.15	59%	XP_006099428.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Pteropus alecto]	37.5	37.5	100%	0.20	55%	XP_006917195.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Jaculus jaculus]	37.1	37.1	95%	0.27	57%	XP_004662736.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	37.1	37.1	100%	0.27	59%	XP_006099415.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Tarsius syrichta]	36.7	36.7	100%	0.37	59%	XP_008055404.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X4 [Equus przewalskii]	36.3	36.3	100%	0.48	59%	XP_008509904.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X2 [Equus przewalskii]	36.3	36.3	100%	0.49	59%	XP_008509901.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X2 [Equus caballus]	36.3	36.3	100%	0.51	59%	XP_005605797.1
☐	alpha-1 acid glycoprotein [Capra hircus]	35.8	35.8	86%	0.67	58%	CAL48252.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ovis aries]	35.8	35.8	86%	0.69	58%	XP_004004031.1
☐	alpha 1 acid glycoprotein precursor [Capra hircus]	35.8	35.8	86%	0.69	58%	NP_001272559.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 1-like [My	35.8	35.8	100%	0.69	64%	XP_005880984.1
☐	mCG7142, isoform CRA_b [Mus musculus]	35.4	35.4	100%	0.93	59%	EDL31111.1
☐	RecName: Full=Alpha-1-acid glycoprotein 3; Short=AGP 3; AltName: Full=Or	35.4	35.4	100%	0.95	50%	Q63805.1
☐	alpha-1-acid glycoprotein 3 precursor [Mus musculus]	35.4	35.4	100%	0.95	50%	NP_038651.2
☐	alpha-1-acid glycoprotein precursor [Mus caroli]	35.4	35.4	100%	0.95	59%	AAB67844.1
☐	alpha-1-acid glycoprotein 1 precursor [Mus musculus]	35.4	35.4	100%	0.95	59%	NP_032794.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Condylura cristata]	35.4	35.4	90%	0.95	55%	XP_004677999.1
☐	Orosomucoid 1 [Mus musculus]	35.4	35.4	100%	0.95	59%	AAH12725.1

⊟ Alignments

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protein,alpha1 acid glyco

Sequence ID: prf||720005A **Length:** 182 **Number of Matches:** 1

Related Information

Range 1: 64 to 85 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(173)	1e-14	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1   REYQTRQDQCIYDTTYLNVQRE  22
           REYQTRQDQCIY+TTYLNVQRE
Sbjct  64  REYQTRQDQCIYNTTYLNVQRE  85
```

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Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein

Sequence ID: pdb|3KQ0|A **Length:** 192 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 63 to 84 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(173)	2e-14	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1   REYQTRQDQCIYDTTYLNVQRE  22
           REYQTRQDQCIY+TTYLNVQRE
Sbjct  63  REYQTRQDQCIYNTTYLNVQRE  84
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein

Sequence ID: pdb|3BX6|A **Length:** 192 **Number of Matches:** 1

Related Information

Range 1: 63 to 84 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(173)	2e-14	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1   REYQTRQDQCIYDTTYLNVQRE  22
           REYQTRQDQCIY+TTYLNVQRE
Sbjct  63  REYQTRQDQCIYNTTYLNVQRE  84
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

ORM1, partial [synthetic construct]

Sequence ID: gb|AIC54852.1| **Length:** 201 **Number of Matches:** 1

Related Information

Range 1: 81 to 102 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(173)	2e-14	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1    REYQTRQDQCIYDTTYLNVQRE  22
            REYQTRQDQCIY+TTYLNVQRE
Sbjct  81   REYQTRQDQCIYNTTYLNVQRE  102
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Orosomucoid 1 [Homo sapiens]

Sequence ID: gb|AAI43315.1| **Length:** 201 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 81 to 102 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(173)	2e-14	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1    REYQTRQDQCIYDTTYLNVQRE  22
            REYQTRQDQCIY+TTYLNVQRE
Sbjct  81   REYQTRQDQCIYNTTYLNVQRE  102
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVJS1C0B01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

ORM1_REYQTRQDQCIYDTTYLNVQRENGTISRY_Mod

RID BVJS1C0B01R (Expires on 01-21 10:26 am)

Query ID	lcl|199553	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	29		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

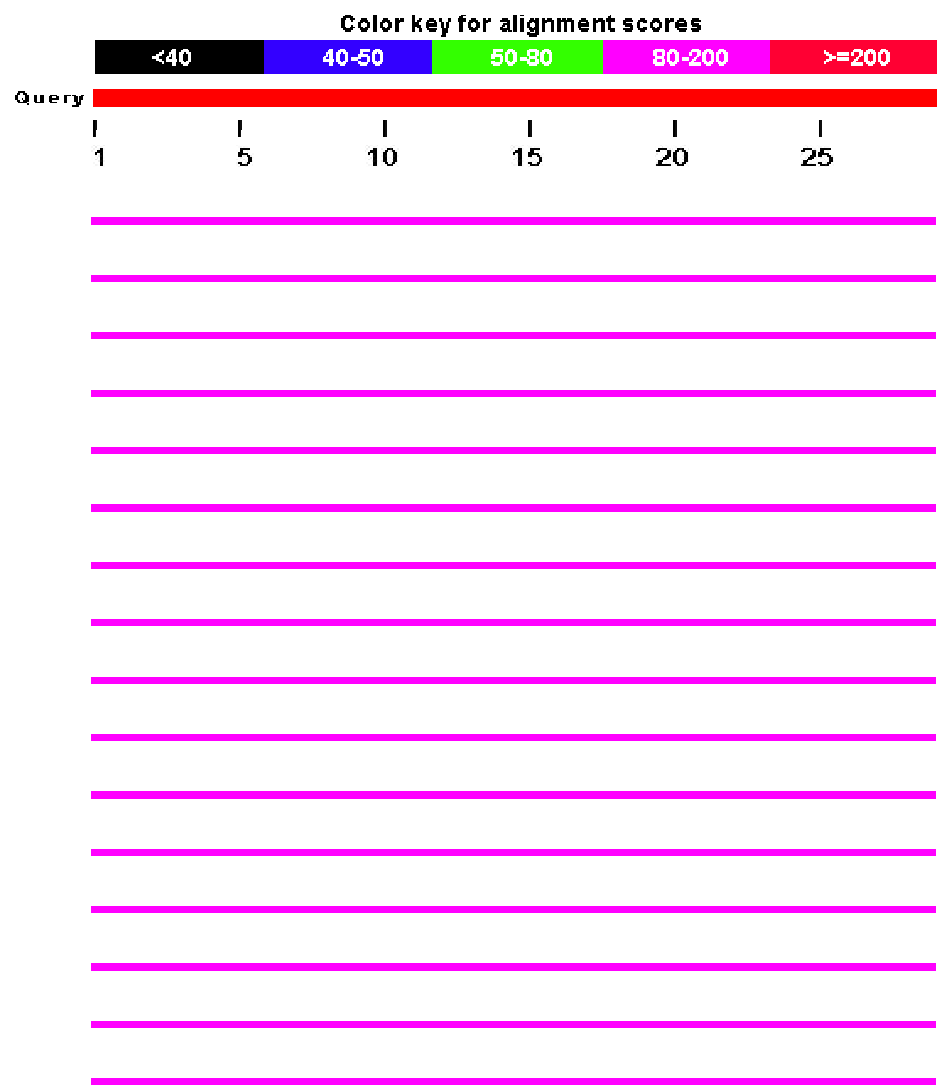
Graphic Summary

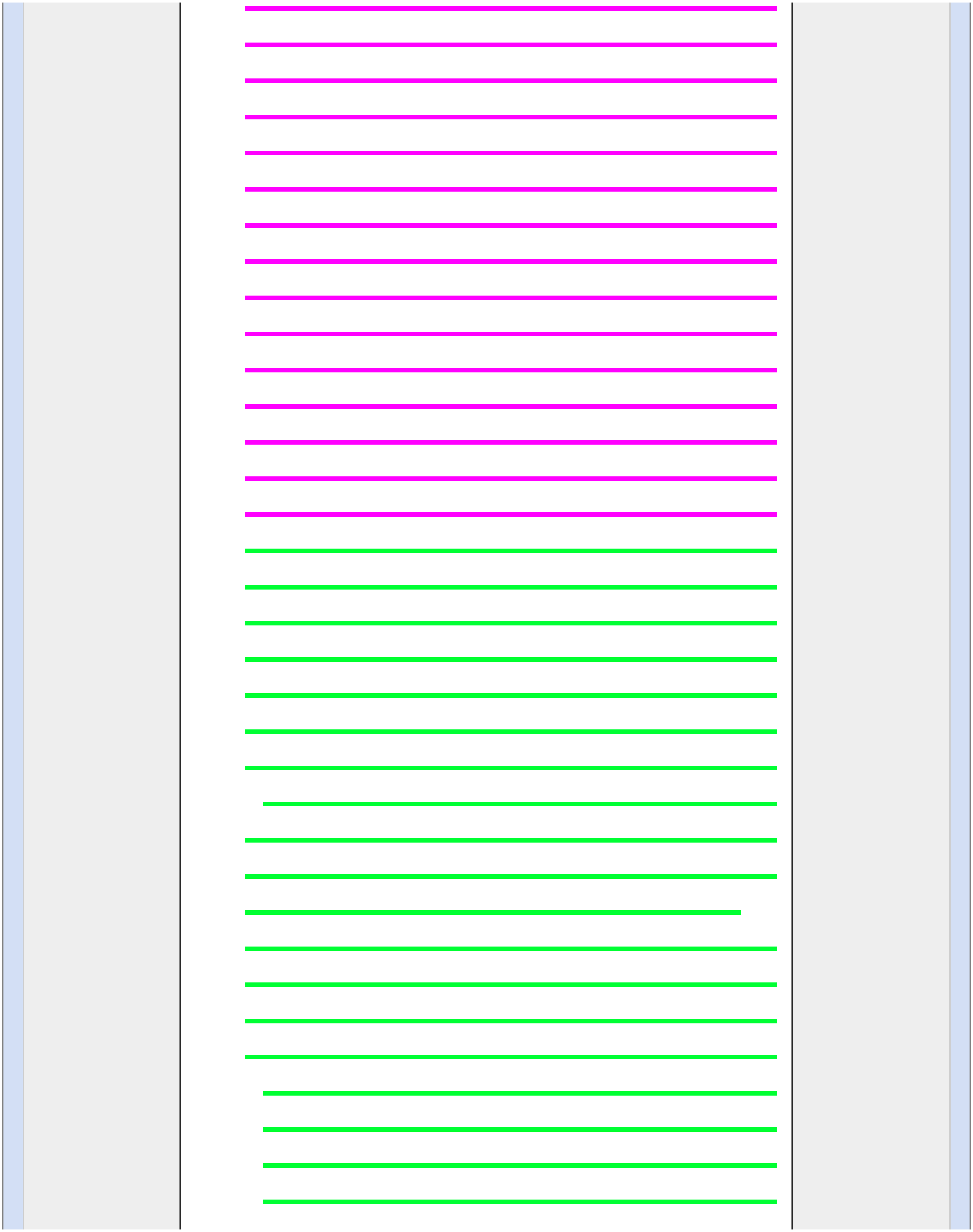
Show Conserved Domains

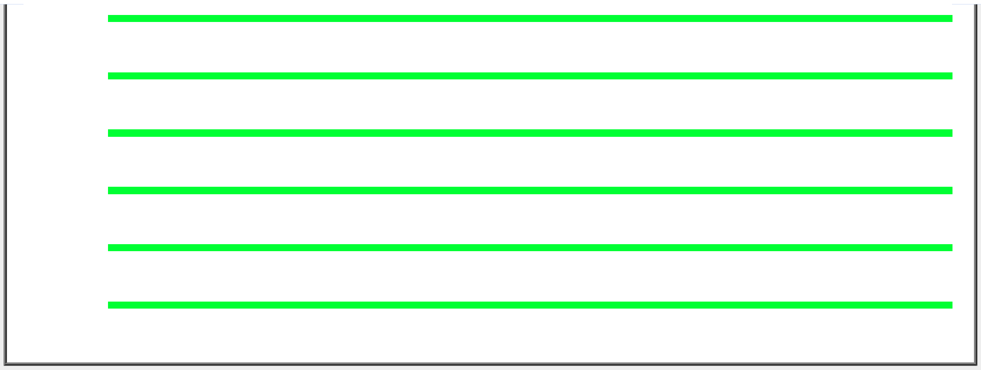
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	protein.alpha1 acid glyco [Homo s	99.0	99.0	100%	6e-22	97%	720005A
☐	Chain A, Crystal Structure Of Hum	99.0	99.0	100%	6e-22	97%	3KQ0_A
☐	Chain A, Crystal Structure Of Hum	99.0	99.0	100%	6e-22	97%	3BX6_A
☐	ORM1 [synthetic construct]	99.0	99.0	100%	7e-22	97%	AIC54852.1
☐	Orosomucoid 1 [Homo sapiens]	99.0	99.0	100%	7e-22	97%	AAI43315.1
☐	alpha-1-acid glycoprotein 1 precur	99.0	99.0	100%	7e-22	97%	CAA29229.1
☐	RecName: Full=Alpha-1-acid glyc	99.0	99.0	100%	7e-22	97%	P02763.1
☐	alpha-1-acid glycoprotein 1 precur	99.0	99.0	100%	7e-22	97%	NP_000598.2
☐	orosomucoid 1 [synthetic construc	99.0	99.0	100%	7e-22	97%	AAV38575.1
☐	orosomucoid 1 [synthetic construc	99.0	99.0	100%	7e-22	97%	AAV38574.1
☐	PREDICTED: alpha-1-acid glycopı	94.8	94.8	100%	2e-20	93%	XP_004048543.1
☐	PREDICTED: alpha-1-acid glycopı	94.8	94.8	100%	2e-20	93%	XP_002820180.1
☐	PREDICTED: alpha-1-acid glycopı	93.5	93.5	100%	6e-20	90%	XP_007966502.1
☐	PREDICTED: LOW QUALITY PRC	92.3	92.3	100%	2e-19	90%	XP_009455427.1
☐	PREDICTED: alpha-1-acid glycopı	92.3	92.3	100%	2e-19	90%	XP_003264088.1
☐	PREDICTED: alpha-1-acid glycopı	90.1	90.1	100%	8e-19	86%	XP_001100289.1
☐	Alpha-1-acid glycoprotein 1 [Maca	90.1	90.1	100%	8e-19	86%	EHH23840.1
☐	PREDICTED: alpha-1-acid glycopı	87.2	87.2	100%	9e-18	83%	XP_005581033.1
☐	PREDICTED: alpha-1-acid glycopı	87.2	87.2	100%	9e-18	83%	XP_005581032.1
☐	PREDICTED: alpha-1-acid glycopı	87.2	87.2	100%	1e-17	83%	XP_005581031.1
☐	PREDICTED: alpha-1-acid glycopı	86.3	86.3	100%	2e-17	83%	XP_009186482.1
☐	PREDICTED: alpha-1-acid glycopı	84.2	84.2	100%	1e-16	79%	XP_010368793.1
☐	Chain A, Crystal Structure Of The	83.8	83.8	100%	1e-16	79%	3APU_A
☐	ORM2 [synthetic construct]	83.8	83.8	100%	1e-16	79%	AIC54853.1
☐	alpha-1-acid glycoprotein 2 precur	83.8	83.8	100%	1e-16	79%	CAA29873.2

☐	alpha-1-acid glycoprotein 2 precur	83.8	83.8	100%	1e-16	79%	NP_000599.1
☐	PREDICTED: alpha-1-acid glycopr	83.8	83.8	100%	1e-16	79%	XP_004048546.1
☐	ORM2 [Homo sapiens]	83.8	83.8	100%	1e-16	79%	CAG33211.1
☐	PREDICTED: alpha-1-acid glycopr	83.8	83.8	100%	1e-16	79%	XP_520209.3
☐	PREDICTED: LOW QUALITY PR	83.8	83.8	100%	2e-16	79%	XP_008957108.1
☐	unnamed protein product [Homo s	81.2	81.2	100%	1e-15	76%	BAG35159.1
☐	PREDICTED: alpha-1-acid glycopr	71.5	71.5	100%	2e-12	72%	XP_002760492.1
☐	PREDICTED: alpha-1-acid glycopr	68.5	68.5	100%	2e-11	72%	XP_003785445.1
☐	PREDICTED: alpha-1-acid glycopr	67.2	67.2	100%	6e-11	66%	XP_003925252.1
☐	PREDICTED: alpha-1-acid glycopr	66.4	66.4	100%	1e-10	69%	XP_003407553.1
☐	PREDICTED: alpha-1-acid glycopr	65.1	65.1	100%	3e-10	69%	XP_004372401.1
☐	PREDICTED: alpha-1-acid glycopr	64.7	64.7	100%	4e-10	66%	XP_008588097.1
☐	PREDICTED: alpha-1-acid glycopr	64.7	64.7	100%	4e-10	66%	XP_008588094.1
☐	PREDICTED: alpha-1-acid glycopr	64.7	64.7	96%	4e-10	68%	XP_006865789.1
☐	hypothetical protein PANDA_0038	63.0	63.0	100%	1e-09	66%	EFB15505.1
☐	PREDICTED: alpha-1-acid glycopr	63.4	63.4	100%	1e-09	69%	XP_007934876.1
☐	PREDICTED: alpha-1-acid glycopr	63.0	63.0	93%	2e-09	70%	XP_006890779.1
☐	PREDICTED: alpha-1-acid glycopr	63.0	63.0	100%	2e-09	66%	XP_002915823.1
☐	PREDICTED: alpha-1-acid glycopr	62.1	62.1	100%	3e-09	66%	XP_004391192.1
☐	PREDICTED: alpha-1-acid glycopr	61.3	61.3	100%	6e-09	62%	XP_005627010.1
☐	PREDICTED: alpha-1-acid glycopr	61.3	61.3	100%	6e-09	62%	XP_003431634.1
☐	Alpha-1-acid glycoprotein 1 [Cricet	60.4	60.4	96%	1e-08	64%	EGW06649.1
☐	PREDICTED: alpha-1-acid glycopr	60.4	60.4	96%	1e-08	64%	XP_003503497.1
☐	alpha-1-acid glycoprotein 1 [Cricet	60.4	60.4	96%	1e-08	64%	ERE86355.1
☐	alpha-1-acid glycoprotein 1 [Cricet	60.4	60.4	96%	1e-08	64%	ERE86354.1
☐	PREDICTED: alpha-1-acid glycopr	58.7	58.7	100%	4e-08	62%	XP_008707881.1
☐	alpha-1-acid glycoprotein [Mus mu	58.3	58.3	100%	5e-08	59%	AAA91744.1
☐	PREDICTED: alpha-1-acid glycopr	58.3	58.3	100%	6e-08	62%	XP_008831764.1
☐	alpha-1-acid glycoprotein (AGP) p	58.3	58.3	100%	6e-08	59%	AAA37197.1
☐	RecName: Full=Alpha-1-acid glyc	58.3	58.3	100%	6e-08	59%	P21350.1
☐	alpha-1-acid glycoprotein 2 precur	58.3	58.3	100%	6e-08	59%	NP_035146.1
☐	PREDICTED: alpha-1-acid glycopr	57.9	57.9	100%	8e-08	66%	XP_006142836.1
☐	PREDICTED: alpha-1-acid glycopr	57.5	57.5	100%	9e-08	62%	XP_004828368.1
☐	PREDICTED: alpha-1-acid glycopr	57.5	57.5	100%	1e-07	62%	XP_008707882.1
☐	PREDICTED: alpha-1-acid glycopr	56.6	56.6	100%	2e-07	62%	XP_004391229.1
☐	PREDICTED: alpha-1-acid glycopr	56.6	56.6	100%	2e-07	59%	XP_003407554.1
☐	PREDICTED: alpha-1-acid glycopr	56.2	56.2	93%	3e-07	63%	XP_003995824.1
☐	Alpha-1-acid glycoprotein [Myotis	55.8	55.8	100%	3e-07	62%	ELK26646.1
☐	PREDICTED: alpha-1-acid glycopr	55.4	55.4	100%	6e-07	66%	XP_008055404.1
☐	alpha-1-acid glycoprotein precurs	54.5	54.5	93%	1e-06	67%	NP_445740.1
☐	PREDICTED: alpha-1-acid glycopr	53.7	53.7	96%	2e-06	61%	XP_005075189.1

☐	PREDICTED: alpha-1-acid glycopı	53.7	53.7	93%	2e-06	59%	XP_007094388.1
☐	PREDICTED: alpha-1-acid glycopı	53.2	53.2	89%	3e-06	65%	XP_006979617.1
☐	PREDICTED: LOW QUALITY PRO	52.8	52.8	100%	4e-06	59%	XP_006109685.1
☐	PREDICTED: alpha-1-acid glycopı	52.4	52.4	100%	5e-06	59%	XP_006917195.1
☐	PREDICTED: alpha-1-acid glycopı	52.0	52.0	93%	7e-06	63%	XP_008588096.1
☐	PREDICTED: alpha-1-acid glycopı	52.0	52.0	93%	8e-06	59%	XP_010586317.1
☐	PREDICTED: LOW QUALITY PRO	51.1	51.1	100%	1e-05	66%	XP_005880984.1
☐	PREDICTED: alpha-1-acid glycopı	50.7	50.7	100%	2e-05	59%	XP_004595034.1
☐	PREDICTED: alpha-1-acid glycopı	50.3	50.3	96%	2e-05	64%	XP_004718018.1
☐	mCG7142, isoform CRA_b [Mus m	50.3	50.3	100%	2e-05	62%	EDL31111.1
☐	PREDICTED: alpha-1-acid glycopı	50.3	50.3	96%	3e-05	57%	XP_005352666.1
☐	alpha-1-acid glycoprotein precursc	50.3	50.3	100%	3e-05	62%	AAB67844.1
☐	alpha-1-acid glycoprotein 1 precur	50.3	50.3	100%	3e-05	62%	NP_032794.1
☐	PREDICTED: alpha-1-acid glycopı	50.3	50.3	96%	3e-05	64%	XP_004712638.1
☐	RecName: Full=Alpha-1-acid glyco	50.3	50.3	100%	3e-05	62%	P21352.1
☐	Orosomucoid 1 [Mus musculus]	50.3	50.3	100%	3e-05	62%	AAH12725.1
☐	mCG7142, isoform CRA_e [Mus m	50.3	50.3	100%	3e-05	62%	EDL31114.1
☐	PREDICTED: alpha-1-acid glycopı	49.8	49.8	100%	3e-05	62%	XP_006099427.1
☐	PREDICTED: alpha-1-acid glycopı	49.4	49.4	93%	5e-05	67%	XP_010995686.1
☐	PREDICTED: alpha-1-acid glycopı	49.4	49.4	93%	5e-05	67%	XP_006186090.1
☐	PREDICTED: alpha-1-acid glycopı	49.4	49.4	93%	5e-05	63%	XP_003407551.1
☐	PREDICTED: alpha-1-acid glycopı	49.0	49.0	93%	5e-05	63%	XP_005880983.1
☐	PREDICTED: alpha-1-acid glycopı	48.6	48.6	93%	9e-05	63%	XP_001488199.1
☐	alpha-1 acid glycoprotein [Sus scr	48.1	48.1	93%	1e-04	59%	AAA30983.1
☐	PREDICTED: alpha-1-acid glycopı	48.1	48.1	93%	1e-04	59%	XP_005660423.1
☐	PREDICTED: alpha-1-acid glycopı	48.1	48.1	86%	1e-04	64%	XP_006108237.1
☐	PREDICTED: alpha-1-acid glycopı	48.1	48.1	93%	1e-04	59%	XP_005660428.1
☐	Alpha-1-acid glycoprotein 1 [Heter	47.3	47.3	96%	2e-04	64%	EHB03307.1
☐	PREDICTED: alpha-1-acid glycopı	47.3	47.3	96%	2e-04	64%	XP_004885278.1
☐	PREDICTED: alpha-1-acid glycopı	47.3	47.3	100%	2e-04	59%	XP_007449796.1
☐	PREDICTED: alpha-1-acid glycopı	46.9	46.9	100%	3e-04	62%	XP_006142835.1
☐	Alpha-1-acid glycoprotein 2 [Tupai	46.9	46.9	100%	3e-04	62%	ELW70613.1
☐	alpha-1-acid glycoprotein [Mus mu	46.4	46.4	89%	3e-04	62%	AAA91745.1
☐	alpha-1 acid glycoprotein [Capra h	46.4	46.4	100%	4e-04	55%	CAL48252.1

Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

ORM1_REYQTRQDQCIYNTTYLNVQRE_NonMod

RID B9PB9HTK01R (Expires on 01-14 15:38 pm)

Query ID lcl|134291
Description None
Molecule type amino acid
Query Length 22

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

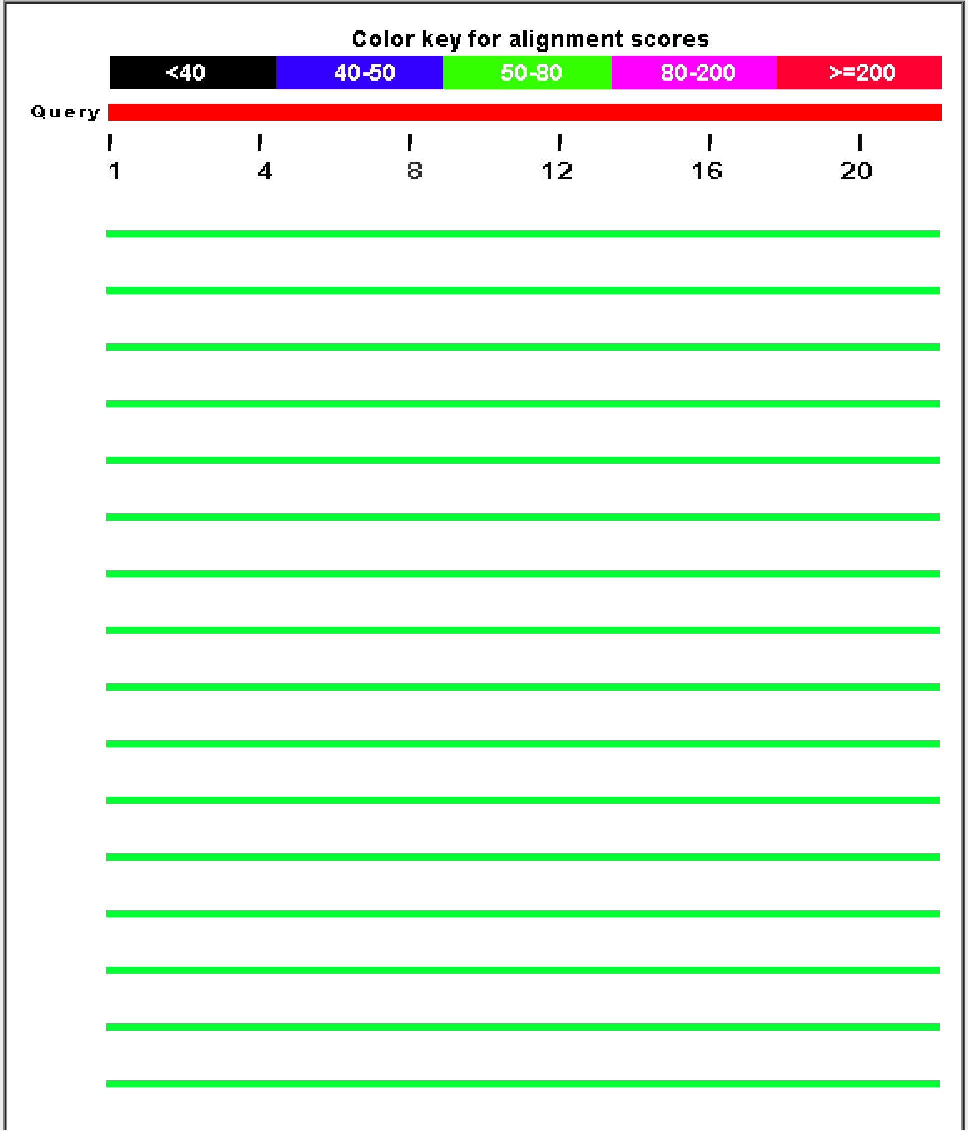
Graphic Summary

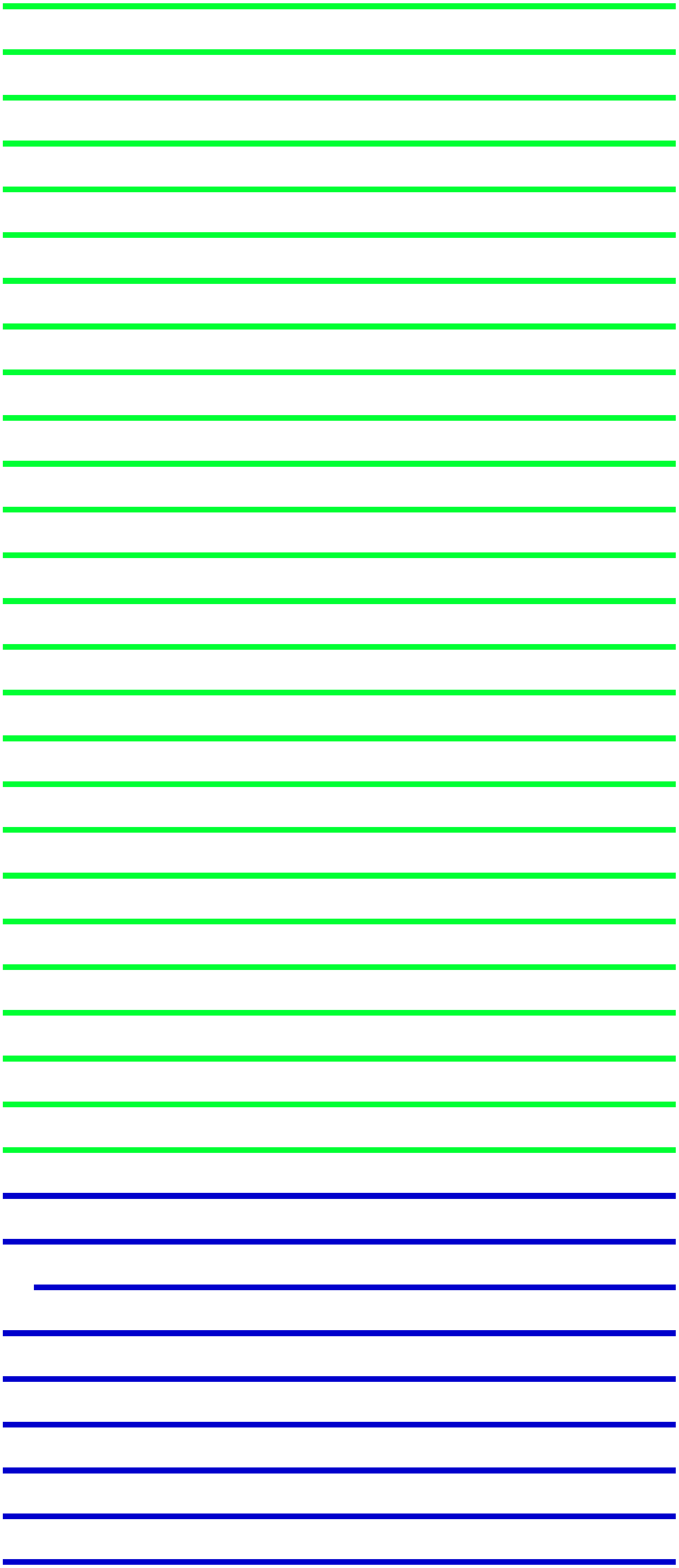
Show Conserved Domains

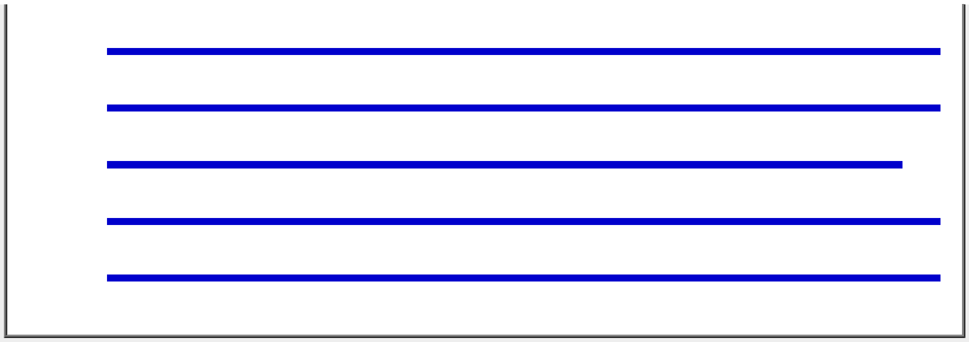
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	protein,alpha1 acid glyco [Homo sapiens]	79.1	79.1	100%	2e-15	100%	gi|229386|720005A
☐	Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein [Ho	79.1	79.1	100%	2e-15	100%	gi|285803540|3KQ0_A
☐	Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein [Ho	79.1	79.1	100%	2e-15	100%	gi|215794600|3BX6_A
☐	ORM1 [synthetic construct]	79.1	79.1	100%	2e-15	100%	gi|649120278|AIC54852.1
☐	Orosomucoid 1 [Homo sapiens]	79.1	79.1	100%	2e-15	100%	gi|219519923|AAI43315.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	79.1	79.1	100%	2e-15	100%	gi|1197209|CAA29229.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltNam	79.1	79.1	100%	2e-15	100%	gi|112877|P02763.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	79.1	79.1	100%	2e-15	100%	gi|167857790|NP_000598.2
☐	orosomucoid 1 [synthetic construct]	79.1	79.1	100%	2e-15	100%	gi|54696406|AAV38575.1
☐	orosomucoid 1 [synthetic construct]	79.1	79.1	100%	2e-15	100%	gi|54696404|AAV38574.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	74.9	74.9	100%	6e-14	95%	gi|426362801|XP_004048543.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein	74.9	74.9	100%	6e-14	95%	gi|694936727|XP_009455427.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform 1 [Nomascus leu	74.9	74.9	100%	6e-14	95%	gi|332229827|XP_003264088.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Pongo abelii]	74.9	74.9	100%	6e-14	95%	gi|297685191|XP_002820180.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like isoform 2 [Macaca m	73.6	73.6	100%	2e-13	91%	gi|109110480|XP_001100289.1
☐	Alpha-1-acid glycoprotein 1 [Macaca mulatta]	73.6	73.6	100%	2e-13	91%	gi|355567499|EHH23840.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Chlorocebus sabaeus]	73.6	73.6	100%	2e-13	91%	gi|635071762|XP_007966502.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X3 [Macaca fasci	70.6	70.6	100%	2e-12	86%	gi|544492702|XP_005581033.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Macaca fasci	70.6	70.6	100%	2e-12	86%	gi|544492700|XP_005581032.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Macaca fasci	70.6	70.6	100%	2e-12	86%	gi|544492698|XP_005581031.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Papio anubis]	69.8	69.8	100%	3e-12	86%	gi|685591954|XP_009186482.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Rhinopithecus roxellana]	67.7	67.7	100%	2e-11	82%	gi|724859712|XP_010368793.1
☐	Chain A, Crystal Structure Of The A Variant Of Human Alpha1-Acid	66.4	66.4	100%	5e-11	82%	gi|323714404|3APU_A
☐	ORM2 [synthetic construct]	66.4	66.4	100%	5e-11	82%	gi|649120282|AIC54853.1
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	66.4	66.4	100%	5e-11	82%	gi|29170378|CAA29873.2
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	66.4	66.4	100%	5e-11	82%	gi|4505529|NP_000599.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	66.4	66.4	100%	5e-11	82%	gi|426362807|XP_004048546.1
☐	ORM2 [Homo sapiens]	66.4	66.4	100%	5e-11	82%	gi|48145977|CAG33211.1
☐							

	PREDICTED: alpha-1-acid glycoprotein 2-like [Pan troglodytes]	66.4	66.4	100%	5e-11	82%	gi|694988125|XP_520209.3
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein	66.4	66.4	100%	6e-11	82%	gi|675802504|XP_008957108.1
☐	unnamed protein product [Homo sapiens]	63.8	63.8	100%	4e-10	77%	gi|189053338|BAG35159.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Callithrix jacchus]	58.3	58.3	100%	3e-08	77%	gi|296229919|XP_002760492.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variega	54.9	54.9	100%	4e-07	73%	gi|667321193|XP_008588097.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Galeopterus variegatus]	54.9	54.9	100%	4e-07	73%	gi|667321187|XP_008588094.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Elephantulus edwardii]	54.5	54.5	100%	5e-07	73%	gi|585676946|XP_006890779.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Saimiri boliviensis bolivie	54.1	54.1	100%	7e-07	68%	gi|403266135|XP_003925252.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	53.7	53.7	100%	1e-06	73%	gi|344271455|XP_003407553.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Otolemur garnettii]	52.0	52.0	100%	4e-06	73%	gi|395824383|XP_003785445.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Orycteropus afer afer]	51.1	51.1	100%	7e-06	73%	gi|634836563|XP_007934876.1
☐	hypothetical protein PANDA_003840 [Ailuropoda melanoleuca]	50.3	50.3	100%	1e-05	68%	gi|281339921|EFB15505.1
☐	PREDICTED: alpha-1-acid glycoprotein [Felis catus]	50.7	50.7	100%	1e-05	68%	gi|410978897|XP_003995824.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ailuropoda melanoleu	50.3	50.3	100%	1e-05	68%	gi|301760029|XP_002915823.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Nannospalax galili]	49.0	49.0	100%	4e-05	68%	gi|674051046|XP_008831764.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Trichechus manatus latir	49.0	49.0	100%	4e-05	68%	gi|471363692|XP_004372401.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Chrysochloris asiatica]	48.6	48.6	95%	5e-05	67%	gi|586470389|XP_006865789.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Panthera tigris altaica]	48.1	48.1	100%	7e-05	64%	gi|591337606|XP_007094388.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Canis lupus f	47.3	47.3	100%	1e-04	64%	gi|545518002|XP_005627010.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Canis lupus f	47.3	47.3	100%	1e-04	64%	gi|345777714|XP_003431634.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variega	46.9	46.9	100%	2e-04	68%	gi|667321190|XP_008588096.1
☐	Alpha-1-acid glycoprotein [Myotis davidii]	46.4	46.4	100%	2e-04	68%	gi|432095447|ELK26646.1
☐	alpha-1-acid glycoprotein precursor [Rattus norvegicus]	46.0	46.0	100%	3e-04	68%	gi|16757980|NP_445740.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Trichechus manatus	46.0	46.0	100%	3e-04	64%	gi|471419404|XP_004391192.1
☐	alpha-1-acid glycoprotein [Mus musculus]	45.6	45.6	100%	4e-04	59%	gi|387176|AAA91744.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Erinaceus europaeus]	45.6	45.6	95%	5e-04	67%	gi|617619058|XP_007526815.1
☐	alpha-1-acid glycoprotein (AGP) precursor [Mus caroli]	45.6	45.6	100%	5e-04	59%	gi|309098|AAA37197.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltNam	45.6	45.6	100%	5e-04	59%	gi|112879|P21350.1
☐	alpha-1-acid glycoprotein 2 precursor [Mus musculus]	45.6	45.6	100%	5e-04	59%	gi|6754950|NP_035146.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Mustela putorius fur	44.8	44.8	100%	8e-04	64%	gi|512022336|XP_004828368.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Echinops telfairi]	44.8	44.8	100%	9e-04	68%	gi|507712754|XP_004718018.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	44.8	44.8	100%	9e-04	64%	gi|671034105|XP_008707882.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	44.8	44.8	100%	9e-04	64%	gi|671034103|XP_008707881.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Echinops telfairi]	44.8	44.8	100%	9e-04	68%	gi|507689354|XP_004712638.1
☐	Alpha-1-acid glycoprotein 1 [Cricetulus griseus]	43.9	43.9	95%	0.002	62%	gi|344250545|EGW06649.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Cricetulus griseus]	43.9	43.9	95%	0.002	62%	gi|354482623|XP_003503497.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	43.9	43.9	100%	0.002	59%	gi|344271457|XP_003407554.1
☐	alpha-1-acid glycoprotein 1 [Cricetulus griseus]	43.9	43.9	95%	0.002	62%	gi|537238399|ERE86355.1
☐	alpha-1-acid glycoprotein 1 [Cricetulus griseus]	43.9	43.9	95%	0.002	62%	gi|537238398|ERE86354.1
☐	PREDICTED: LOW QUALITY PROTEIN: orosomucoid 1 [Myotis luc	43.5	43.5	100%	0.002	64%	gi|558172686|XP_006109685.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	43.5	43.5	100%	0.002	59%	gi|731463853|XP_010586317.1
☐	alpha-1 acid glycoprotein [Sus scrofa]	42.6	42.6	100%	0.004	64%	gi|164302|AAA30983.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Sus scrofa]	42.6	42.6	100%	0.004	64%	gi|545804155|XP_005660423.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	42.6	42.6	100%	0.004	68%	gi|344271451|XP_003407551.1
☐	PREDICTED: alpha-1-acid glycoprotein isoform X1 [Sus scrofa]	42.6	42.6	100%	0.004	64%	gi|545804166|XP_005660428.1

☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	41.8	41.8	100%	0.008	64%	gi|558213870|XP_006108237.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X2 [Tupaia c	41.4	41.4	100%	0.011	64%	gi|562826345|XP_006142836.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Peromyscus manicula	40.9	40.9	95%	0.015	62%	gi|589933663|XP_006979617.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Microtus ochrogaster]	40.9	40.9	95%	0.015	62%	gi|532017828|XP_005352666.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Myotis brandtii]	40.5	40.5	100%	0.018	64%	gi|554578831|XP_005880983.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Trichechus manatus la	40.5	40.5	100%	0.021	59%	gi|471419478|XP_004391229.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Myotis lucifugus]	40.5	40.5	100%	0.022	64%	gi|558172690|XP_006099428.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Pteropus alecto]	40.1	40.1	100%	0.029	59%	gi|586524471|XP_006917195.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Jaculus jaculus]	39.7	39.7	95%	0.039	62%	gi|507557995|XP_004662736.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	39.7	39.7	100%	0.039	64%	gi|558172682|XP_006099427.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	39.7	39.7	100%	0.039	64%	gi|558172624|XP_006099415.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Tarsius syrichta]	39.2	39.2	100%	0.053	64%	gi|640798447|XP_008055404.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Equus caballus]	38.8	38.8	100%	0.073	59%	gi|149738494|XP_001488199.1
☐	alpha-1 acid glycoprotein [Capra hircus]	38.4	38.4	86%	0.097	63%	gi|123953929|CAL48252.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ovis aries]	38.4	38.4	86%	0.100	63%	gi|426219649|XP_004004031.1
☐	alpha 1 acid glycoprotein precursor [Capra hircus]	38.4	38.4	86%	0.100	63%	gi|550822232|NP_001272559.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein	38.4	38.4	100%	0.10	68%	gi|554578835|XP_005880984.1
☐	mCG7142, isoform CRA_b [Mus musculus]	38.0	38.0	100%	0.13	64%	gi|148699164|EDL31111.1
☐	RecName: Full=Alpha-1-acid glycoprotein 3; Short=AGP 3; AltNam	38.0	38.0	100%	0.14	55%	gi|2497693|Q63805.1
☐	alpha-1-acid glycoprotein 3 precursor [Mus musculus]	38.0	38.0	100%	0.14	55%	gi|62548316|NP_038651.2
☐	alpha-1-acid glycoprotein precursor [Mus caroli]	38.0	38.0	100%	0.14	64%	gi|309100|AAB67844.1
☐	alpha-1-acid glycoprotein 1 precursor [Mus musculus]	38.0	38.0	100%	0.14	64%	gi|6679182|NP_032794.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Condylura cristata]	38.0	38.0	90%	0.14	60%	gi|507933524|XP_004677999.1
☐	RecName: Full=Alpha-1-acid glycoprotein 8; Short=AGP 8; AltNam	38.0	38.0	100%	0.14	64%	gi|112883|P21352.1
☐	Orosomucoid 1 [Mus musculus]	38.0	38.0	100%	0.14	64%	gi|15215270|AAH12725.1
☐	PREDICTED: alpha-1-acid glycoprotein 3 isoform X5 [Mus musculu	38.0	38.0	100%	0.14	55%	gi|568926184|XP_006537733.1
☐	Orm3 protein [Mus musculus]	38.0	38.0	100%	0.14	55%	gi|219519434|AAI45560.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

protein,alpha1 acid glyco

Sequence ID: gi|229386|prf||720005A **Length:** 182 **Number of Matches:** 1

Related Information

Range 1: 64 to 85 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.1 bits(179)	2e-15	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1    REYQTRQDQCIYNTTYLNVQRE  22
           REYQTRQDQCIYNTTYLNVQRE
Sbjct  64   REYQTRQDQCIYNTTYLNVQRE  85
```

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Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein

Sequence ID: gi|285803540|pdb|3KQ0|A **Length:** 192 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 63 to 84 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.1 bits(179)	2e-15	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1    REYQTRQDQCIYNTTYLNVQRE  22
```

```
                  REYQTRQDQCIYNTTYLNVQRE
Sbjct  63  REYQTRQDQCIYNTTYLNVQRE  84
```

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Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein

Sequence ID: gi|215794600|pdb|3BX6|A **Length:** 192 **Number of Matches:** 1

Related Information

Range 1: 63 to 84 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.1 bits(179)	2e-15	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1   REYQTRQDQCIYNTTYLNVQRE  22
           REYQTRQDQCIYNTTYLNVQRE
Sbjct  63  REYQTRQDQCIYNTTYLNVQRE  84
```

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ORM1, partial [synthetic construct]

Sequence ID: gi|649120278|gb|AIC54852.1| **Length:** 201 **Number of Matches:** 1

Related Information

Range 1: 81 to 102 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.1 bits(179)	2e-15	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1    REYQTRQDQCIYNTTYLNVQRE  22
            REYQTRQDQCIYNTTYLNVQRE
Sbjct  81   REYQTRQDQCIYNTTYLNVQRE  102
```

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Orosomucoid 1 [Homo sapiens]

Sequence ID: gi|219519923|gb|AAI43315.1| **Length:** 201 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 81 to 102 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.1 bits(179)	2e-15	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1    REYQTRQDQCIYNTTYLNVQRE  22
            REYQTRQDQCIYNTTYLNVQRE
Sbjct  81   REYQTRQDQCIYNTTYLNVQRE  102
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

ORM1_REYQTRQDQCIYNTTYLNVQRENGTISRY_NonMod

RID	B9PEWVX501R (Expires on 01-14 15:39 pm)		
Query ID	lcl|194606	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	29	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

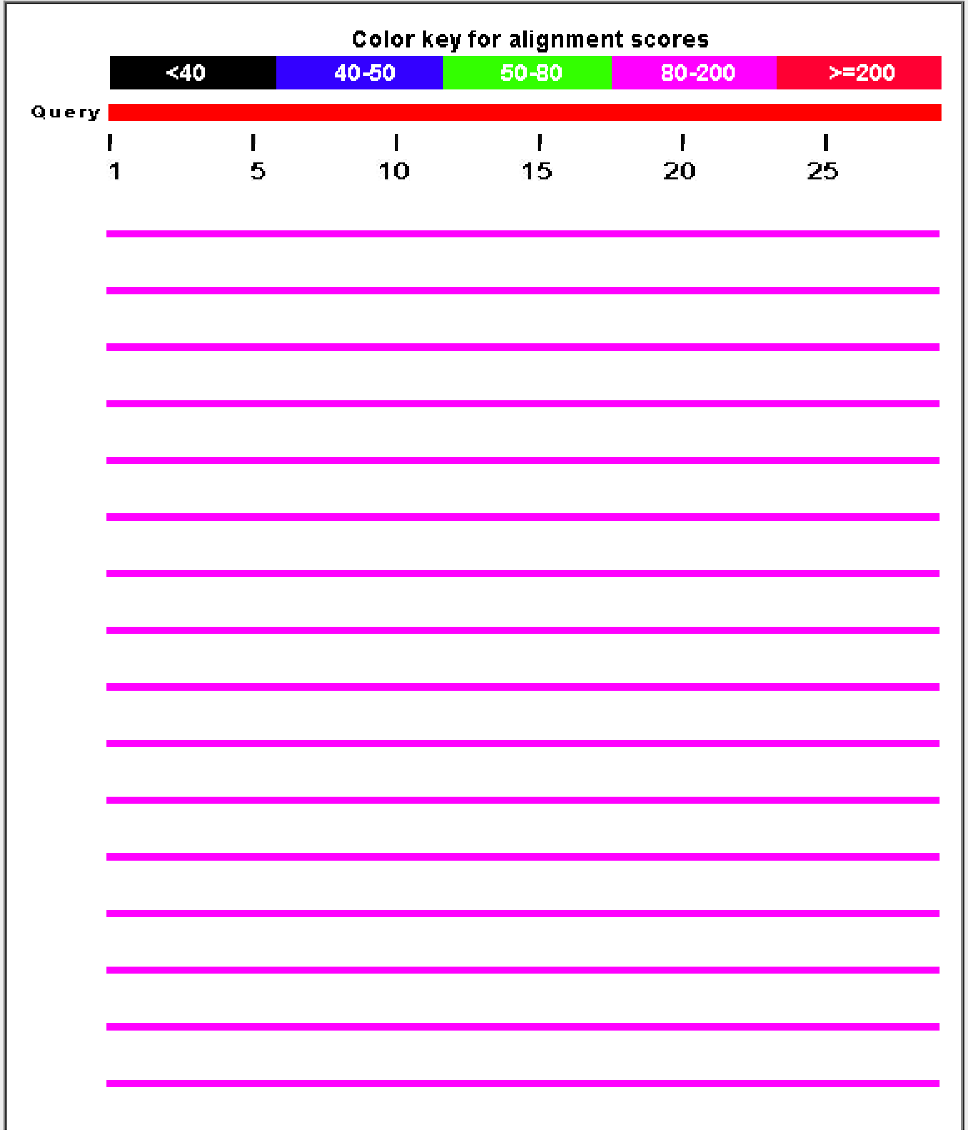
Graphic Summary

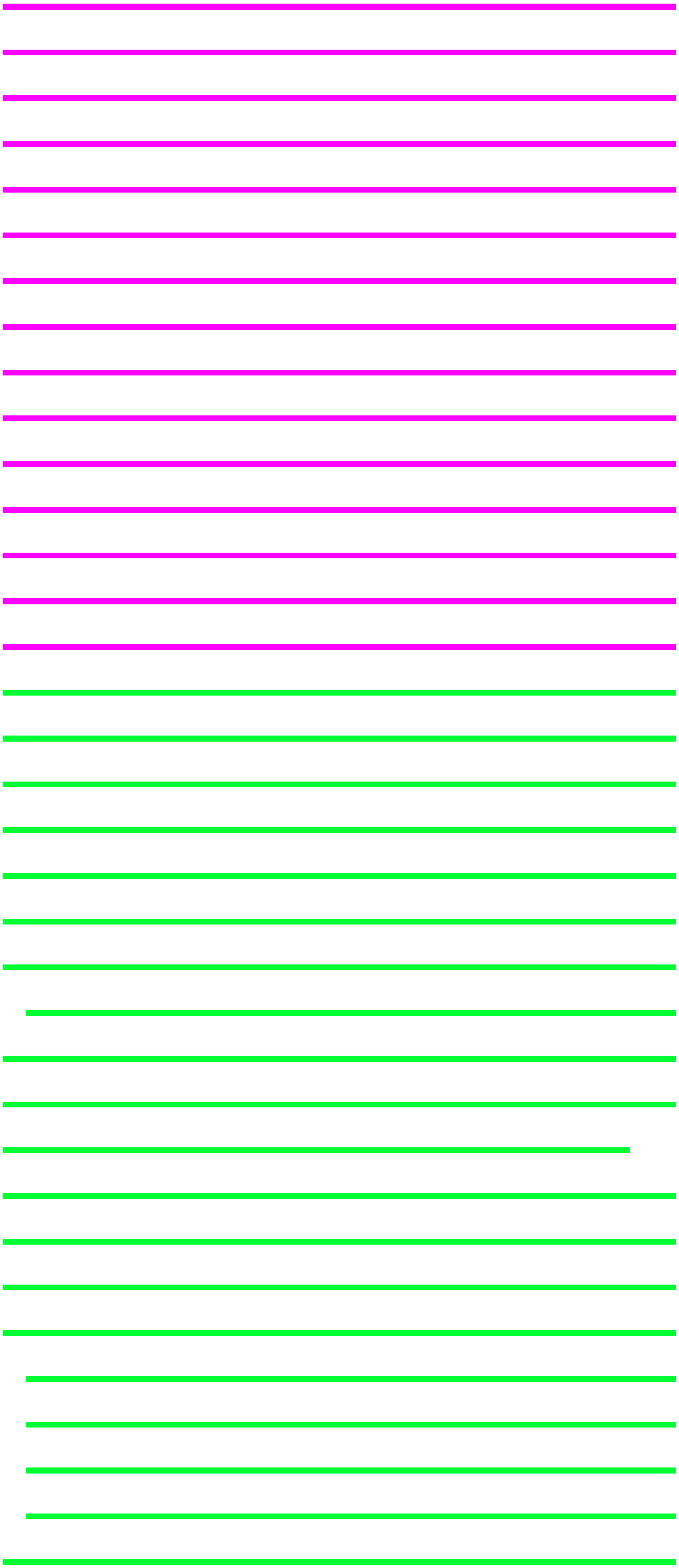
Show Conserved Domains

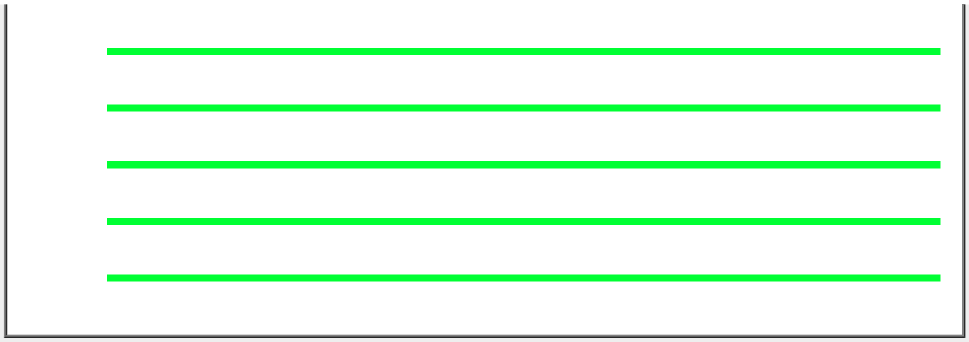
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	protein,alpha1 acid glyco [Homo sapiens]	101	101	100%	7e-23	100%	gi|229386|720005A
☐	Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein [Ho	101	101	100%	8e-23	100%	gi|285803540|3KQ0_A
☐	Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein [Hc	101	101	100%	8e-23	100%	gi|215794600|3BX6_A
☐	ORM1 [synthetic construct]	101	101	100%	8e-23	100%	gi|649120278|AIC54852.1
☐	Orosomucoid 1 [Homo sapiens]	101	101	100%	8e-23	100%	gi|219519923|AAI43315.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	101	101	100%	8e-23	100%	gi|1197209|CAA29229.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltNam	101	101	100%	8e-23	100%	gi|112877|P02763.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	101	101	100%	8e-23	100%	gi|167857790|NP_000598.2
☐	orosomucoid 1 [synthetic construct]	101	101	100%	8e-23	100%	gi|54696406|AAV38575.1
☐	orosomucoid 1 [synthetic construct]	101	101	100%	8e-23	100%	gi|54696404|AAV38574.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	97.3	97.3	100%	2e-21	97%	gi|426362801|XP_004048543.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Pongo abelii]	97.3	97.3	100%	2e-21	97%	gi|297685191|XP_002820180.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Chlorocebus sabaeus]	96.1	96.1	100%	7e-21	93%	gi|635071762|XP_007966502.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein	94.8	94.8	100%	2e-20	93%	gi|694936727|XP_009455427.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform 1 [Nomascus leu	94.8	94.8	100%	2e-20	93%	gi|332229827|XP_003264088.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like isoform 2 [Macaca m	92.7	92.7	100%	1e-19	90%	gi|109110480|XP_001100289.1
☐	Alpha-1-acid glycoprotein 1 [Macaca mulatta]	92.7	92.7	100%	1e-19	90%	gi|355567499|EHH23840.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X3 [Macaca fasci	89.7	89.7	100%	1e-18	86%	gi|544492702|XP_005581033.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Macaca fasci	89.7	89.7	100%	1e-18	86%	gi|544492700|XP_005581032.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Macaca fasci	89.7	89.7	100%	1e-18	86%	gi|544492698|XP_005581031.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Papio anubis]	88.9	88.9	100%	2e-18	86%	gi|685591954|XP_009186482.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Rhinopithecus roxellana]	86.7	86.7	100%	1e-17	83%	gi|724859712|XP_010368793.1
☐	Chain A, Crystal Structure Of The A Variant Of Human Alpha1-Acid	86.3	86.3	100%	2e-17	83%	gi|323714404|3APU_A
☐	ORM2 [synthetic construct]	86.3	86.3	100%	2e-17	83%	gi|649120282|AIC54853.1
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	86.3	86.3	100%	2e-17	83%	gi|29170378|CAA29873.2
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	86.3	86.3	100%	2e-17	83%	gi|4505529|NP_000599.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	86.3	86.3	100%	2e-17	83%	gi|426362807|XP_004048546.1
☐	ORM2 [Homo sapiens]	86.3	86.3	100%	2e-17	83%	gi|48145977|CAG33211.1
☐							

	PREDICTED: alpha-1-acid glycoprotein 2-like [Pan troglodytes]	86.3	86.3	100%	2e-17	83%	gi|694988125|XP_520209.3
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein	86.3	86.3	100%	2e-17	83%	gi|675802504|XP_008957108.1
☐	unnamed protein product [Homo sapiens]	83.8	83.8	100%	1e-16	79%	gi|189053338|BAG35159.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Callithrix jacchus]	74.0	74.0	100%	3e-13	76%	gi|296229919|XP_002760492.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Otolemur garnettii]	71.0	71.0	100%	3e-12	76%	gi|395824383|XP_003785445.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Saimiri boliviensis bolivie	69.8	69.8	100%	8e-12	69%	gi|403266135|XP_003925252.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	68.9	68.9	100%	2e-11	72%	gi|344271455|XP_003407553.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Trichechus manatus latir	67.7	67.7	100%	4e-11	72%	gi|471363692|XP_004372401.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variega	67.2	67.2	100%	5e-11	69%	gi|667321193|XP_008588097.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Galeopterus variegatus]	67.2	67.2	100%	6e-11	69%	gi|667321187|XP_008588094.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Chrysochloris asiatica]	67.2	67.2	96%	6e-11	71%	gi|586470389|XP_006865789.1
☐	hypothetical protein PANDA_003840 [Ailuropoda melanoleuca]	65.5	65.5	100%	1e-10	69%	gi|281339921|EFB15505.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Orycteropus afer afer]	66.0	66.0	100%	2e-10	72%	gi|634836563|XP_007934876.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Elephantulus edwardii]	65.5	65.5	93%	2e-10	74%	gi|585676946|XP_006890779.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ailuropoda melanoleu	65.5	65.5	100%	2e-10	69%	gi|301760029|XP_002915823.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Trichechus manatus	64.7	64.7	100%	4e-10	69%	gi|471419404|XP_004391192.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Canis lupus f	63.8	63.8	100%	8e-10	66%	gi|545518002|XP_005627010.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Canis lupus f	63.8	63.8	100%	8e-10	66%	gi|345777714|XP_003431634.1
☐	Alpha-1-acid glycoprotein 1 [Cricetulus griseus]	63.0	63.0	96%	2e-09	68%	gi|344250545|EGW06649.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Cricetulus griseus]	63.0	63.0	96%	2e-09	68%	gi|354482623|XP_003503497.1
☐	alpha-1-acid glycoprotein 1 [Cricetulus griseus]	63.0	63.0	96%	2e-09	68%	gi|537238399|ERE86355.1
☐	alpha-1-acid glycoprotein 1 [Cricetulus griseus]	63.0	63.0	96%	2e-09	68%	gi|537238398|ERE86354.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	61.3	61.3	100%	6e-09	66%	gi|671034103|XP_008707881.1
☐	alpha-1-acid glycoprotein [Mus musculus]	60.9	60.9	100%	6e-09	62%	gi|387176|AAA91744.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Nannospalax galili]	60.9	60.9	100%	8e-09	66%	gi|674051046|XP_008831764.1
☐	alpha-1-acid glycoprotein (AGP) precursor [Mus caroli]	60.9	60.9	100%	8e-09	62%	gi|309098|AAA37197.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltNam	60.9	60.9	100%	8e-09	62%	gi|112879|P21350.1
☐	alpha-1-acid glycoprotein 2 precursor [Mus musculus]	60.9	60.9	100%	8e-09	62%	gi|6754950|NP_035146.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X2 [Tupaia c	60.4	60.4	100%	1e-08	69%	gi|562826345|XP_006142836.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Mustela putorius furc	60.0	60.0	100%	1e-08	66%	gi|512022336|XP_004828368.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	60.0	60.0	100%	2e-08	66%	gi|671034105|XP_008707882.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Trichechus manatus la	59.2	59.2	100%	3e-08	66%	gi|471419478|XP_004391229.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	59.2	59.2	100%	3e-08	62%	gi|344271457|XP_003407554.1
☐	Alpha-1-acid glycoprotein [Myotis davidii]	58.3	58.3	100%	4e-08	66%	gi|432095447|ELK26646.1
☐	PREDICTED: alpha-1-acid glycoprotein [Felis catus]	58.7	58.7	93%	4e-08	67%	gi|410978897|XP_003995824.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Tarsius syrichta]	57.9	57.9	100%	8e-08	69%	gi|640798447|XP_008055404.1
☐	alpha-1-acid glycoprotein precursor [Rattus norvegicus]	57.1	57.1	93%	1e-07	70%	gi|16757980|NP_445740.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Mesocricetus auratus]	56.2	56.2	96%	3e-07	64%	gi|524950349|XP_005075189.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Panthera tigris altaica]	56.2	56.2	93%	3e-07	63%	gi|591337606|XP_007094388.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Peromyscus manicula	55.8	55.8	89%	4e-07	69%	gi|589933663|XP_006979617.1
☐	PREDICTED: LOW QUALITY PROTEIN: orosomucoid 1 [Myotis luc	55.4	55.4	100%	5e-07	62%	gi|558172686|XP_006109685.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Pteropus alecto]	54.9	54.9	100%	7e-07	62%	gi|586524471|XP_006917195.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variega	54.5	54.5	93%	1e-06	67%	gi|667321190|XP_008588096.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	54.5	54.5	93%	1e-06	63%	gi|731463853|XP_010586317.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein	53.7	53.7	100%	2e-06	69%	gi|554578835|XP_005880984.1

☐	PREDICTED: alpha-1-acid glycoprotein-like [Ochotona princeps]	53.2	53.2	100%	3e-06	62%	gi|504170887|XP_004595034.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Echinops telfairi]	52.8	52.8	96%	3e-06	68%	gi|507712754|XP_004718018.1
☐	mCG7142, isoform CRA_b [Mus musculus]	52.8	52.8	100%	3e-06	66%	gi|148699164|EDL31111.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Microtus ochrogaster]	52.8	52.8	96%	4e-06	61%	gi|532017828|XP_005352666.1
☐	alpha-1-acid glycoprotein precursor [Mus caroli]	52.8	52.8	100%	4e-06	66%	gi|309100|AAB67844.1
☐	alpha-1-acid glycoprotein 1 precursor [Mus musculus]	52.8	52.8	100%	4e-06	66%	gi|6679182|NP_032794.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Echinops telfairi]	52.8	52.8	96%	4e-06	68%	gi|507689354|XP_004712638.1
☐	RecName: Full=Alpha-1-acid glycoprotein 8; Short=AGP 8; AltNam	52.8	52.8	100%	4e-06	66%	gi|112883|P21352.1
☐	Orosomucoid 1 [Mus musculus]	52.8	52.8	100%	4e-06	66%	gi|15215270|AAH12725.1
☐	mCG7142, isoform CRA_e [Mus musculus]	52.8	52.8	100%	4e-06	66%	gi|148699167|EDL31114.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Camelus ferus]	52.0	52.0	93%	7e-06	70%	gi|560919741|XP_006186090.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	52.0	52.0	93%	7e-06	67%	gi|344271451|XP_003407551.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Myotis brandtii]	51.5	51.5	93%	7e-06	67%	gi|554578831|XP_005880983.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	51.5	51.5	100%	9e-06	62%	gi|558172682|XP_006099427.1
☐	alpha-1 acid glycoprotein [Sus scrofa]	50.7	50.7	93%	2e-05	63%	gi|164302|AAA30983.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Sus scrofa]	50.7	50.7	93%	2e-05	63%	gi|545804155|XP_005660423.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	50.7	50.7	86%	2e-05	68%	gi|558213870|XP_006108237.1
☐	PREDICTED: alpha-1-acid glycoprotein isoform X1 [Sus scrofa]	50.7	50.7	93%	2e-05	63%	gi|545804166|XP_005660428.1
☐	Alpha-1-acid glycoprotein 1 [Heterocephalus glaber]	49.8	49.8	96%	3e-05	68%	gi|351700388|EHB03307.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Heterocephalus glaber]	49.8	49.8	96%	3e-05	68%	gi|512843596|XP_004885278.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Lipotes vexillifer]	49.8	49.8	100%	3e-05	62%	gi|602728729|XP_007449796.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X1 [Tupaia c	49.4	49.4	100%	4e-05	66%	gi|562826343|XP_006142835.1
☐	Alpha-1-acid glycoprotein 2 [Tupaia chinensis]	49.4	49.4	100%	4e-05	66%	gi|444730223|ELW70613.1
☐	alpha-1-acid glycoprotein [Mus musculus]	49.0	49.0	89%	5e-05	65%	gi|553922|AAA91745.1
☐	alpha-1 acid glycoprotein [Capra hircus]	49.0	49.0	100%	6e-05	59%	gi|123953929|CAL48252.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Jaculus jaculus]	49.0	49.0	93%	6e-05	63%	gi|507557995|XP_004662736.1
☐	alpha 1 acid glycoprotein precursor [Capra hircus]	49.0	49.0	100%	6e-05	59%	gi|550822232|NP_001272559.1

⊖ Alignments

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protein,alpha1 acid glyco

Sequence ID: gi|229386|prf||720005A **Length:** 182 **Number of Matches:** 1

Related Information

Range 1: 64 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
101 bits(232)	7e-23	29/29(100%)	29/29(100%)	0/29(0%)

```
Query  1    REYQTRQDQCIYNTTYLNVQRENGTISRY  29
            REYQTRQDQCIYNTTYLNVQRENGTISRY
Sbjct  64   REYQTRQDQCIYNTTYLNVQRENGTISRY  92
```

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Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein

Sequence ID: gi|285803540|pdb|3KQ0|A **Length:** 192 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 63 to 91 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
101 bits(232)	8e-23	29/29(100%)	29/29(100%)	0/29(0%)

```
Query  1    REYQTRQDQCIYNTTYLNVQRENGTISRY  29
```

```
               REYQTRQDQCIYNTTYLNVQRENGTISRY
Sbjct  63  REYQTRQDQCIYNTTYLNVQRENGTISRY  91
```

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Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein

Sequence ID: gi|215794600|pdb|3BX6|A **Length:** 192 **Number of Matches:** 1

Related Information

Range 1: 63 to 91 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
101 bits(232)	8e-23	29/29(100%)	29/29(100%)	0/29(0%)

```
Query  1    REYQTRQDQCIYNTTYLNVQRENGTISRY  29
            REYQTRQDQCIYNTTYLNVQRENGTISRY
Sbjct  63   REYQTRQDQCIYNTTYLNVQRENGTISRY  91
```

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ORM1, partial [synthetic construct]

Sequence ID: gi|649120278|gb|AIC54852.1| **Length:** 201 **Number of Matches:** 1

Related Information

Range 1: 81 to 109 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
101 bits(232)	8e-23	29/29(100%)	29/29(100%)	0/29(0%)

```
Query  1    REYQTRQDQCIYNTTYLNVQRENGTISRY  29
            REYQTRQDQCIYNTTYLNVQRENGTISRY
Sbjct  81   REYQTRQDQCIYNTTYLNVQRENGTISRY  109
```

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Orosomucoid 1 [Homo sapiens]

Sequence ID: gi|219519923|gb|AAI43315.1| **Length:** 201 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 81 to 109 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
101 bits(232)	8e-23	29/29(100%)	29/29(100%)	0/29(0%)

```
Query  1    REYQTRQDQCIYNTTYLNVQRENGTISRY  29
            REYQTRQDQCIYNTTYLNVQRENGTISRY
Sbjct  81   REYQTRQDQCIYNTTYLNVQRENGTISRY  109
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVJXPWWN01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download   YouTube How to read this page   Blast report description

ORM1_RQDQCIYDTTYLNVQRE_Mod

RID BVJXPWWN01R (Expires on 01-21 10:29 am)

Query ID lcl|240488
Description None
Molecule type amino acid
Query Length 17

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

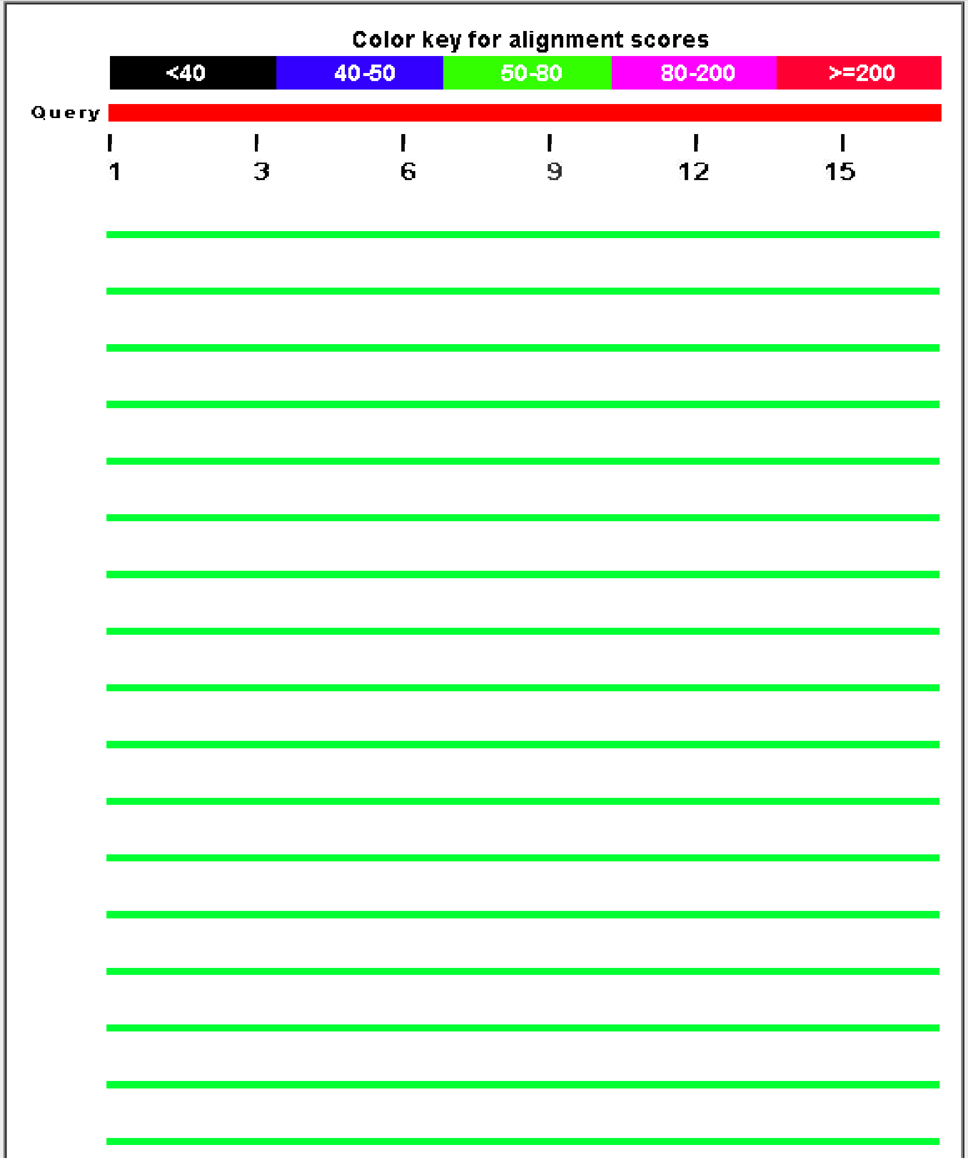
⊟ Graphic Summary

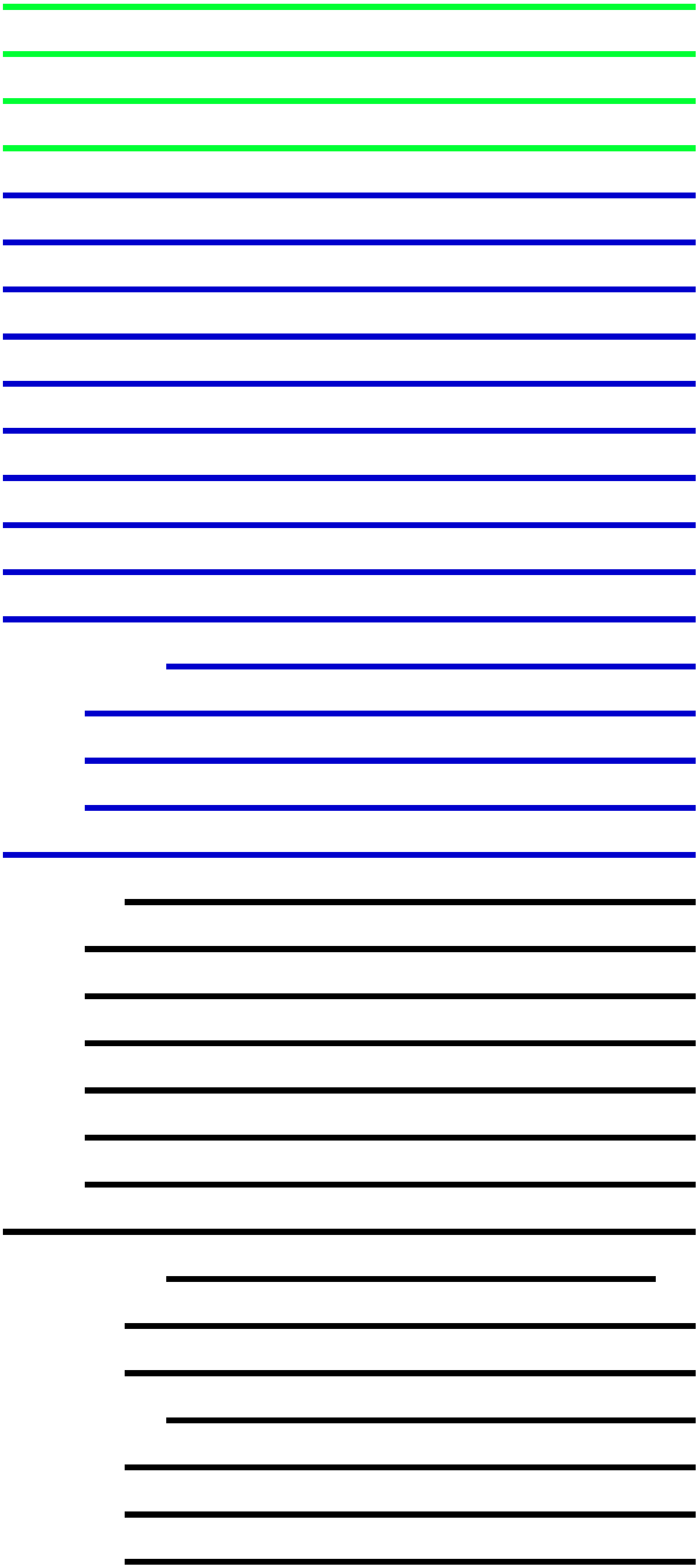
⊟ Show Conserved Domains

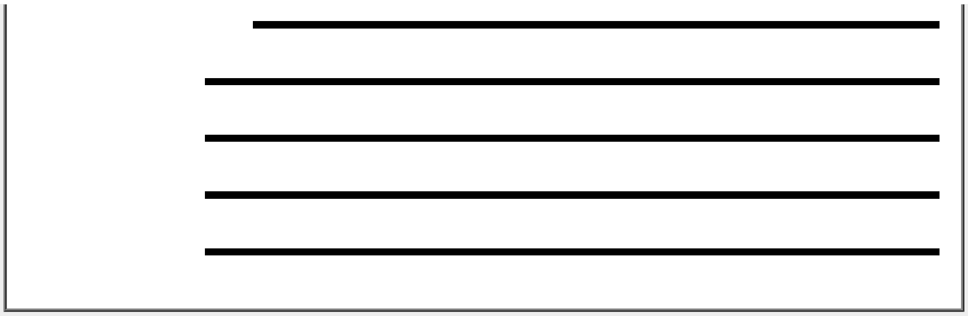
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	protein,alpha1 acid glyco [Homo sapiens]	59.2	59.2	100%	7e-09	94%	720005A
☐	Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein [Homo sapien	59.2	59.2	100%	7e-09	94%	3KQ0_A
☐	Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein [Homo sapien	59.2	59.2	100%	7e-09	94%	3BX6_A
☐	ORM1 [synthetic construct]	59.2	59.2	100%	8e-09	94%	AIC54852.1
☐	Orosomucoid 1 [Homo sapiens]	59.2	59.2	100%	8e-09	94%	AAI43315.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	59.2	59.2	100%	8e-09	94%	CAA29229.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltName: Full=Oro	59.2	59.2	100%	8e-09	94%	P02763.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	59.2	59.2	100%	8e-09	94%	NP_000598.2
☐	orosomucoid 1 [synthetic construct]	59.2	59.2	100%	8e-09	94%	AAV38575.1
☐	orosomucoid 1 [synthetic construct]	59.2	59.2	100%	8e-09	94%	AAV38574.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	54.9	54.9	100%	2e-07	88%	XP_004048543.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 1 [Pan tro	54.9	54.9	100%	2e-07	88%	XP_009455427.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform 1 [Nomascus leucogenys]	54.9	54.9	100%	2e-07	88%	XP_003264088.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Pongo abelii]	54.9	54.9	100%	2e-07	88%	XP_002820180.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X3 [Macaca fascicularis]	53.7	53.7	100%	6e-07	82%	XP_005581033.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like isoform 2 [Macaca mulatta]	53.7	53.7	100%	6e-07	82%	XP_001100289.1
☐	Alpha-1-acid glycoprotein 1 [Macaca mulatta]	53.7	53.7	100%	6e-07	82%	EHH23840.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Chlorocebus sabaeus]	53.7	53.7	100%	6e-07	82%	XP_007966502.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Macaca fascicularis]	53.7	53.7	100%	6e-07	82%	XP_005581032.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Macaca fascicularis]	53.7	53.7	100%	6e-07	82%	XP_005581031.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Rhinopithecus roxellana]	50.7	50.7	100%	6e-06	76%	XP_010368793.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Papio anubis]	49.8	49.8	100%	1e-05	76%	XP_009186482.1
☐	Chain A, Crystal Structure Of The A Variant Of Human Alpha1-Acid Glycoprot	46.4	46.4	100%	2e-04	71%	3APU_A
☐	ORM2 [synthetic construct]	46.4	46.4	100%	2e-04	71%	AIC54853.1
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	46.4	46.4	100%	2e-04	71%	CAA29873.2
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	46.4	46.4	100%	2e-04	71%	NP_000599.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	46.4	46.4	100%	2e-04	71%	XP_004048546.1
☐	ORM2 [Homo sapiens]	46.4	46.4	100%	2e-04	71%	CAG33211.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Pan troglodytes]	46.4	46.4	100%	2e-04	71%	XP_520209.3

☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 2 [Pan pa	46.4	46.4	100%	2e-04	71%	XP_008957108.1
☐	unnamed protein product [Homo sapiens]	43.9	43.9	100%	0.001	65%	BAG35159.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Callithrix jacchus]	42.6	42.6	76%	0.003	85%	XP_002760492.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	41.8	41.8	88%	0.006	73%	XP_003407553.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Panthera tigris altaica]	41.4	41.4	88%	0.008	67%	XP_007094388.1
☐	PREDICTED: alpha-1-acid glycoprotein [Felis catus]	41.4	41.4	88%	0.008	67%	XP_003995824.1
☐	Alpha-1-acid glycoprotein [Myotis davidii]	40.5	40.5	100%	0.013	59%	ELK26646.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Elephantulus edwardii]	38.8	38.8	82%	0.054	71%	XP_006890779.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variegatus]	38.0	38.0	88%	0.10	67%	XP_008588097.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variegatus]	38.0	38.0	88%	0.10	67%	XP_008588096.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Galeopterus variegatus]	38.0	38.0	88%	0.10	67%	XP_008588094.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Canis lupus familiaris]	38.0	38.0	88%	0.10	60%	XP_005627010.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Canis lupus familiaris]	38.0	38.0	88%	0.10	60%	XP_003431634.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Saimiri boliviensis boliviensis]	37.5	37.5	88%	0.14	60%	XP_003925252.1
☐	PREDICTED: LOW QUALITY PROTEIN: orosomucoid 1 [Myotis lucifugus]	37.5	37.5	100%	0.14	55%	XP_006109685.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Erinaceus europaeus]	36.7	36.7	70%	0.26	75%	XP_007526815.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Chrysochloris asiatica]	36.3	36.3	82%	0.36	64%	XP_006865789.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	36.3	36.3	82%	0.36	64%	XP_003407554.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Mustela putorius furo]	35.8	35.8	76%	0.47	69%	XP_004828368.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Orycteropus afer afer]	35.8	35.8	82%	0.50	71%	XP_007934876.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Trichechus manatus latirostris]	35.8	35.8	82%	0.50	64%	XP_004391229.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Trichechus manatus latirostris]	35.8	35.8	82%	0.50	64%	XP_004391192.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Trichechus manatus latirostris]	35.8	35.8	82%	0.50	64%	XP_004372401.1
☐	hypothetical protein PANDA_003840 [Ailuropoda melanoleuca]	35.4	35.4	88%	0.59	60%	EFB15505.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	35.4	35.4	88%	0.68	60%	XP_008707882.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	35.4	35.4	88%	0.68	60%	XP_008707881.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ailuropoda melanoleuca]	35.4	35.4	88%	0.68	60%	XP_002915823.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Otolemur garnettii]	35.4	35.4	88%	0.69	67%	XP_003785445.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Myotis brandtii]	34.6	34.6	100%	1.1	55%	XP_005880983.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Equus caballus]	34.6	34.6	88%	1.3	67%	XP_001488199.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	33.7	33.7	82%	2.4	71%	XP_003407551.1
☐	alpha-1-acid glycoprotein precursor [Rattus norvegicus]	32.9	32.9	88%	4.5	67%	NP_445740.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X2 [Tupaia chinensis]	32.5	32.5	88%	6.1	60%	XP_006142836.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Echinops telfairi]	32.0	32.0	82%	8.1	71%	XP_004718018.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	32.0	32.0	88%	8.3	60%	XP_006108237.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	32.0	32.0	88%	8.3	67%	XP_006099427.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Echinops telfairi]	32.0	32.0	82%	8.3	71%	XP_004712638.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Myotis lucifugus]	32.0	32.0	88%	8.5	60%	XP_006099428.1
☐	alpha-1-acid glycoprotein [Mus musculus]	31.6	31.6	88%	11	53%	AAA91744.1
☐	alpha-1-acid glycoprotein (AGP) precursor [Mus caroli]	31.6	31.6	88%	11	53%	AAA37197.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltName: Full=Or	31.6	31.6	88%	11	53%	P21350.1
☐	alpha-1-acid glycoprotein 2 precursor [Mus musculus]	31.6	31.6	88%	11	53%	NP_035146.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 1-like [My	31.6	31.6	82%	11	71%	XP_005880984.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	31.6	31.6	82%	12	57%	XP_010586317.1
☐	hypothetical protein RMCBS344292_16064 [Rhizopus microsporus]	31.6	31.6	88%	12	62%	CEJ02047.1

☐	hypothetical protein RO3G_15781 [Rhizopus delemar RA 99-880]	31.6	31.6	88%	12	62%	EIE91070.1
☐	hypothetical protein RMATCC62417_12957 [Rhizopus microsporus]	31.6	31.6	88%	12	62%	CEG78329.1
☐	hypothetical protein RMATCC62417_02511 [Rhizopus microsporus]	31.6	31.6	88%	12	62%	CEG65807.1
☐	hypothetical protein, conserved in Plasmodium species [Plasmodium knowles	31.6	31.6	70%	12	75%	XP_002260651.1
☐	MerR family transcriptional regulator [Vibrio genomosp. F10]	31.2	31.2	82%	15	67%	WP_026026605.1
☐	hypothetical protein [Vibrio genomosp. F10]	31.2	31.2	82%	15	67%	WP_017035912.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Nannospalax galili]	31.2	31.2	94%	15	56%	XP_008831764.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Pteropus alecto]	31.2	31.2	94%	15	50%	XP_006917195.1
☐	Alpha-1-acid glycoprotein [Pteropus alecto]	31.2	31.2	94%	16	50%	ELK08232.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Tarsius syrichta]	30.8	30.8	88%	21	60%	XP_008055404.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	30.8	30.8	88%	21	60%	XP_006108236.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	30.8	30.8	88%	21	60%	XP_006099413.1
☐	alpha-1-acid glycoprotein [Mus musculus]	30.3	30.3	88%	27	60%	AAA91745.1
☐	mCG7142, isoform CRA_b [Mus musculus]	30.3	30.3	88%	29	60%	EDL31111.1
☐	alpha-1-acid glycoprotein precursor [Mus caroli]	30.3	30.3	88%	29	60%	AAB67844.1
☐	alpha-1-acid glycoprotein 1 precursor [Mus musculus]	30.3	30.3	88%	29	60%	NP_032794.1
☐	RecName: Full=Alpha-1-acid glycoprotein 8; Short=AGP 8; AltName: Full=Orc	30.3	30.3	88%	29	60%	P21352.1
☐	Orosomucoid 1 [Mus musculus]	30.3	30.3	88%	29	60%	AAH12725.1
☐	mCG7142, isoform CRA_e [Mus musculus]	30.3	30.3	88%	29	60%	EDL31114.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	29.9	29.9	88%	40	60%	XP_006099415.1
☐	ribonuclease HII [Staphylococcus pseudintermedius]	29.9	29.9	88%	40	67%	WP_037543184.1
☐	ribonuclease HII [Staphylococcus pseudintermedius]	29.9	29.9	88%	40	67%	WP_014614093.1
☐	ribonuclease HII [Staphylococcus pseudintermedius]	29.9	29.9	88%	40	67%	WP_015729038.1
☐	hypothetical protein JCM19039_2109 [Geomicrobium sp. JCM 19039]	29.9	29.9	70%	40	71%	GAK12341.1
☐	hypothetical protein M437DRAFT_89004 [Aureobasidium melanogenum CBS	29.9	29.9	52%	41	89%	KEQ58021.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ceratotherium simum simum]	29.5	29.5	100%	54	41%	XP_004423793.1

⊟ Alignments

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protein,alpha1 acid glyco

Sequence ID: prf||720005A **Length:** 182 **Number of Matches:** 1

Related Information

Range 1: 69 to 85 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
59.2 bits(132)	7e-09	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   RQDQCIYDTTYLNVQRE  17
           RQDQCIY+TTYLNVQRE
Sbjct  69  RQDQCIYNTTYLNVQRE  85
```

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Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein

Sequence ID: pdb|3KQ0|A **Length:** 192 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 68 to 84 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
59.2 bits(132)	7e-09	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   RQDQCIYDTTYLNVQRE  17
           RQDQCIY+TTYLNVQRE
Sbjct  68  RQDQCIYNTTYLNVQRE  84
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein

Sequence ID: pdb|3BX6|A **Length:** 192 **Number of Matches:** 1

Related Information

Range 1: 68 to 84 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
59.2 bits(132)	7e-09	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   RQDQCIYDTTYLNVQRE  17
           RQDQCIY+TTYLNVQRE
Sbjct  68  RQDQCIYNTTYLNVQRE  84
```

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ORM1, partial [synthetic construct]

Sequence ID: gb|AIC54852.1| **Length:** 201 **Number of Matches:** 1

Related Information

Range 1: 86 to 102 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
59.2 bits(132)	8e-09	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1    RQDQCIYDTTYLNVQRE  17
            RQDQCIY+TTYLNVQRE
Sbjct  86   RQDQCIYNTTYLNVQRE  102
```

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Orosomucoid 1 [Homo sapiens]

Sequence ID: gb|AAI43315.1| **Length:** 201 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 86 to 102 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
59.2 bits(132)	8e-09	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1    RQDQCIYDTTYLNVQRE  17
            RQDQCIY+TTYLNVQRE
Sbjct  86   RQDQCIYNTTYLNVQRE  102
```

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Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download How to read this page Blast report description

ORM1_RQDQCIYDTTYLNVQREDGTISRY_Mod

RID BVJY9U0K01R (Expires on 01-21 10:30 am)

Query ID lcl|247790
Description None
Molecule type amino acid
Query Length 24

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

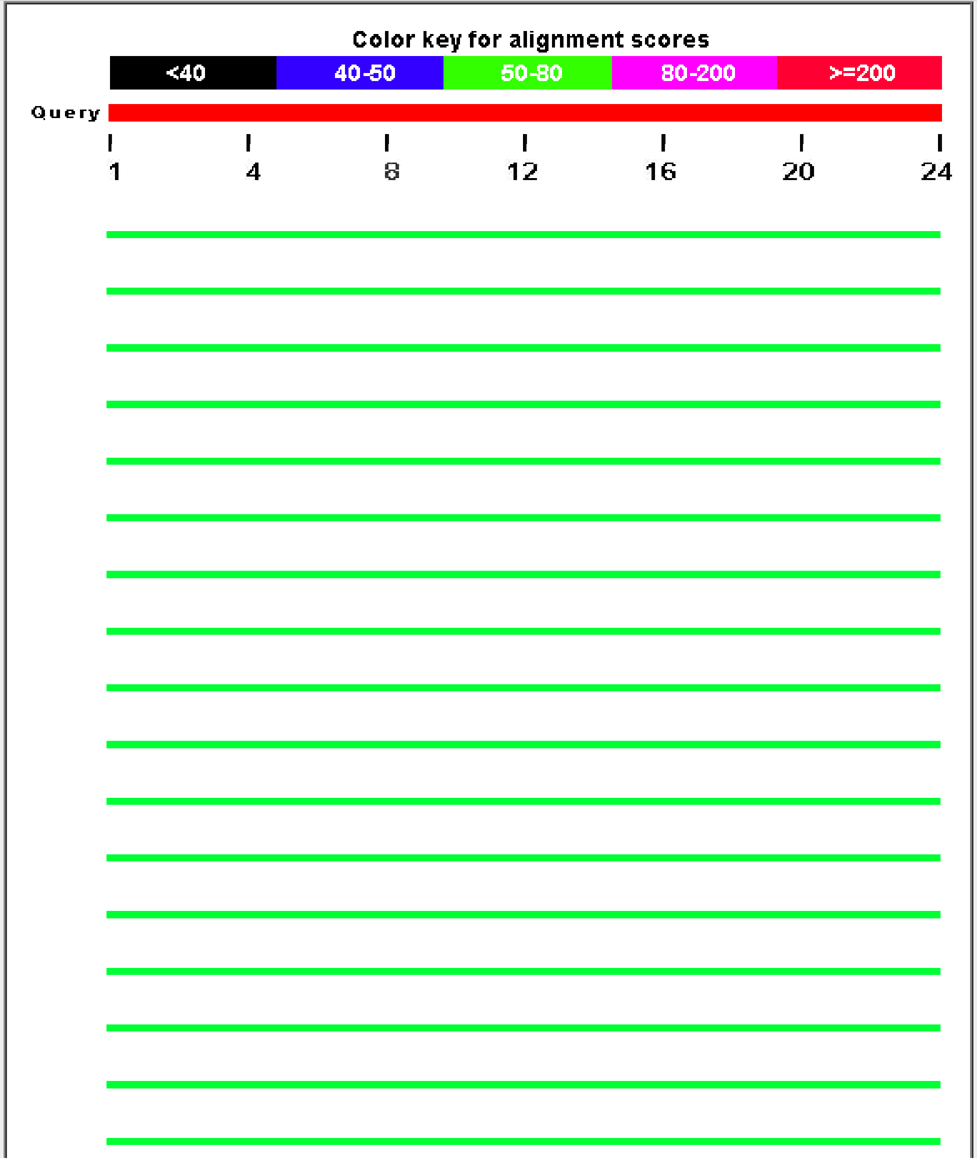
Graphic Summary

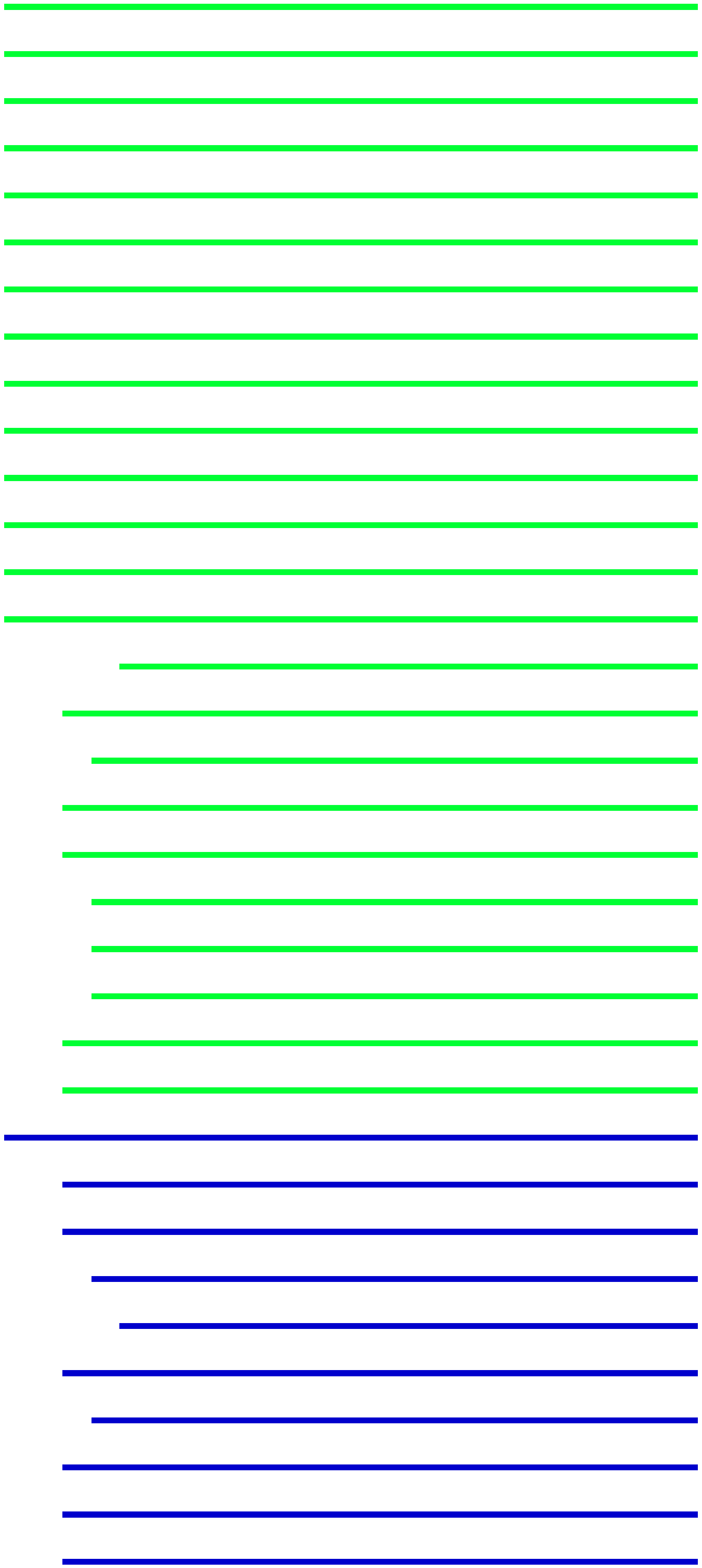
Show Conserved Domains

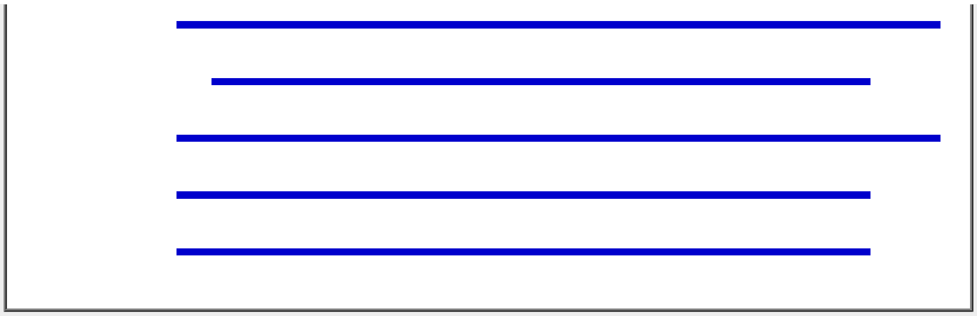
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	protein,alpha1 acid glyco [Homo sapiens]	79.1	79.1	100%	3e-15	92%	720005A
☐	Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein [Homo sapien	79.1	79.1	100%	3e-15	92%	3KQ0_A
☐	Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein [Homo sapier	79.1	79.1	100%	3e-15	92%	3BX6_A
☐	ORM1 [synthetic construct]	79.1	79.1	100%	3e-15	92%	AIC54852.1
☐	Orosomucoid 1 [Homo sapiens]	79.1	79.1	100%	3e-15	92%	AAI43315.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	79.1	79.1	100%	3e-15	92%	CAA29229.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltName: Full=Orc	79.1	79.1	100%	3e-15	92%	P02763.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	79.1	79.1	100%	3e-15	92%	NP_000598.2
☐	orosomucoid 1 [synthetic construct]	79.1	79.1	100%	3e-15	92%	AAV38575.1
☐	orosomucoid 1 [synthetic construct]	79.1	79.1	100%	3e-15	92%	AAV38574.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	74.9	74.9	100%	8e-14	88%	XP_004048543.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Pongo abelii]	74.9	74.9	100%	8e-14	88%	XP_002820180.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Chlorocebus sabaeus]	73.6	73.6	100%	2e-13	83%	XP_007966502.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 1 [Pan tro	72.3	72.3	100%	6e-13	83%	XP_009455427.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform 1 [Nomascus leucogenys]	72.3	72.3	100%	6e-13	83%	XP_003264088.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X3 [Macaca fascicularis]	70.2	70.2	100%	3e-12	79%	XP_005581033.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like isoform 2 [Macaca mulatta]	70.2	70.2	100%	3e-12	79%	XP_001100289.1
☐	Alpha-1-acid glycoprotein 1 [Macaca mulatta]	70.2	70.2	100%	3e-12	79%	EHH23840.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Macaca fascicularis]	70.2	70.2	100%	3e-12	79%	XP_005581032.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Macaca fascicularis]	70.2	70.2	100%	3e-12	79%	XP_005581031.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Rhinopithecus roxellana]	67.2	67.2	100%	3e-11	75%	XP_010368793.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Papio anubis]	66.4	66.4	100%	7e-11	75%	XP_009186482.1
☐	Chain A, Crystal Structure Of The A Variant Of Human Alpha1-Acid Glycoprot	63.8	63.8	100%	5e-10	71%	3APU_A
☐	ORM2 [synthetic construct]	63.8	63.8	100%	5e-10	71%	AIC54853.1
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	63.8	63.8	100%	5e-10	71%	CAA29873.2
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	63.8	63.8	100%	5e-10	71%	NP_000599.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	63.8	63.8	100%	5e-10	71%	XP_004048546.1
☐	ORM2 [Homo sapiens]	63.8	63.8	100%	5e-10	71%	CAG33211.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Pan troglodytes]	63.8	63.8	100%	5e-10	71%	XP_520209.3

☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 2 [Pan pa	63.8	63.8	100%	6e-10	71%	XP_008957108.1
☐	unnamed protein product [Homo sapiens]	61.3	61.3	100%	4e-09	67%	BAG35159.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Callithrix jacchus]	55.8	55.8	83%	3e-07	75%	XP_002760492.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	54.5	54.5	91%	7e-07	68%	XP_003407553.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Chrysochloris asiatica]	52.4	52.4	87%	3e-06	67%	XP_006865789.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Canis lupus familiaris]	52.0	52.0	91%	5e-06	59%	XP_005627010.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Canis lupus familiaris]	52.0	52.0	91%	5e-06	59%	XP_003431634.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Trichechus manatus latirostris]	52.0	52.0	87%	5e-06	67%	XP_004391229.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Trichechus manatus latirostris]	52.0	52.0	87%	5e-06	67%	XP_004391192.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Trichechus manatus latirostris]	52.0	52.0	87%	5e-06	67%	XP_004372401.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Otolemur garnettii]	52.0	52.0	91%	5e-06	68%	XP_003785445.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Saimiri boliviensis boliviensis]	50.7	50.7	91%	1e-05	59%	XP_003925252.1
☐	Alpha-1-acid glycoprotein [Myotis davidii]	49.8	49.8	100%	2e-05	55%	ELK26646.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	49.4	49.4	91%	3e-05	59%	XP_008707881.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X2 [Tupaia chinensis]	49.0	49.0	91%	5e-05	64%	XP_006142836.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	49.0	49.0	87%	5e-05	62%	XP_003407554.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Mustela putorius furo]	48.6	48.6	83%	6e-05	65%	XP_004828368.1
☐	hypothetical protein PANDA_003840 [Ailuropoda melanoleuca]	48.1	48.1	91%	6e-05	59%	EFB15505.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Orycteropus afer afer]	48.1	48.1	87%	9e-05	67%	XP_007934876.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	48.1	48.1	91%	9e-05	59%	XP_008707882.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ailuropoda melanoleuca]	48.1	48.1	91%	9e-05	59%	XP_002915823.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variegatus]	47.7	47.7	91%	1e-04	59%	XP_008588097.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Galeopterus variegatus]	47.7	47.7	91%	1e-04	59%	XP_008588094.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Elephantulus edwardii]	47.3	47.3	79%	2e-04	68%	XP_006890779.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Tarsius syrichta]	46.9	46.9	91%	2e-04	64%	XP_008055404.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Panthera tigris altaica]	46.9	46.9	83%	2e-04	60%	XP_007094388.1
☐	PREDICTED: alpha-1-acid glycoprotein [Felis catus]	46.9	46.9	83%	2e-04	60%	XP_003995824.1
☐	PREDICTED: LOW QUALITY PROTEIN: orosomucoid 1 [Myotis lucifugus]	46.9	46.9	100%	2e-04	52%	XP_006109685.1
☐	alpha-1-acid glycoprotein [Mus musculus]	44.3	44.3	91%	0.001	55%	AAA91744.1
☐	alpha-1-acid glycoprotein (AGP) precursor [Mus caroli]	44.3	44.3	91%	0.002	55%	AAA37197.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltName: Full=Or	44.3	44.3	91%	0.002	55%	P21350.1
☐	alpha-1-acid glycoprotein 2 precursor [Mus musculus]	44.3	44.3	91%	0.002	55%	NP_035146.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 1-like [My	44.3	44.3	87%	0.002	67%	XP_005880984.1
☐	Alpha-1-acid glycoprotein 1 [Cricetulus griseus]	43.9	43.9	95%	0.002	57%	EGW06649.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Cricetulus griseus]	43.9	43.9	95%	0.002	57%	XP_003503497.1
☐	alpha-1-acid glycoprotein 1 [Cricetulus griseus]	43.9	43.9	95%	0.002	57%	ERE86355.1
☐	alpha-1-acid glycoprotein 1 [Cricetulus griseus]	43.9	43.9	95%	0.002	57%	ERE86354.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Pteropus alecto]	43.5	43.5	95%	0.003	52%	XP_006917195.1
☐	Alpha-1-acid glycoprotein [Pteropus alecto]	43.5	43.5	95%	0.003	52%	ELK08232.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Myotis brandtii]	43.1	43.1	91%	0.003	56%	XP_005880983.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variegatus]	43.1	43.1	83%	0.004	60%	XP_008588096.1
☐	alpha-1-acid glycoprotein [Mus musculus]	42.6	42.6	91%	0.004	59%	AAA91745.1
☐	mCG7142, isoform CRA_b [Mus musculus]	42.6	42.6	91%	0.005	59%	EDL31111.1
☐	alpha-1-acid glycoprotein precursor [Mus caroli]	42.6	42.6	91%	0.005	59%	AAB67844.1
☐	alpha-1-acid glycoprotein 1 precursor [Mus musculus]	42.6	42.6	91%	0.005	59%	NP_032794.1

☐	RecName: Full=Alpha-1-acid glycoprotein 8; Short=AGP 8; AltName: Full=Orc	42.6	42.6	91%	0.005	59%	P21352.1
☐	Orosomucoid 1 [Mus musculus]	42.6	42.6	91%	0.005	59%	AAH12725.1
☐	mCG7142, isoform CRA_e [Mus musculus]	42.6	42.6	91%	0.005	59%	EDL31114.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Mesocricetus auratus]	42.2	42.2	83%	0.007	60%	XP_005075189.1
☐	alpha-1-acid glycoprotein precursor [Rattus norvegicus]	41.4	41.4	83%	0.013	65%	NP_445740.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	41.4	41.4	91%	0.014	59%	XP_006099427.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Nannospalax galili]	40.5	40.5	95%	0.025	52%	XP_008831764.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Equus caballus]	40.5	40.5	83%	0.025	65%	XP_001488199.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	40.5	40.5	79%	0.025	63%	XP_003407551.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	40.1	40.1	79%	0.036	58%	XP_010586317.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Camelus dromedarius]	39.7	39.7	83%	0.047	65%	XP_010995686.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Camelus ferus]	39.7	39.7	83%	0.047	65%	XP_006186090.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ochotona princeps]	39.2	39.2	95%	0.064	52%	XP_004595034.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	39.2	39.2	83%	0.064	60%	XP_006108236.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	39.2	39.2	83%	0.064	60%	XP_006099413.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Vicugna pacos]	38.8	38.8	79%	0.087	68%	XP_006211428.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Peromyscus maniculatus bairdii]	38.4	38.4	87%	0.12	57%	XP_006979617.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	38.4	38.4	75%	0.12	61%	XP_006108237.1
☐	Alpha-1-acid glycoprotein 1 [Heterocephalus glaber]	37.5	37.5	87%	0.21	62%	EHB03307.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Heterocephalus glaber]	37.5	37.5	87%	0.21	62%	XP_004885278.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Echinops telfairi]	37.5	37.5	83%	0.22	65%	XP_004718018.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Echinops telfairi]	37.5	37.5	83%	0.22	65%	XP_004712638.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Heterocephalus glaber]	37.5	37.5	87%	0.23	62%	XP_004849700.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Mustela putorius furo]	37.1	37.1	83%	0.28	55%	XP_004807875.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Mustela putorius furo]	37.1	37.1	83%	0.29	55%	XP_004774102.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Erinaceus europaeus]	37.1	37.1	75%	0.31	61%	XP_007526815.1

⊟ Alignments

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protein,alpha1 acid glyco

Sequence ID: prf||720005A **Length:** 182 **Number of Matches:** 1

Related Information

Range 1: 69 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.1 bits(179)	3e-15	22/24(92%)	24/24(100%)	0/24(0%)

```
Query  1   RQDQCIYDTTYLNVQREDGTISRY  24
           RQDQCIY+TTYLNVQRE+GTISRY
Sbjct  69  RQDQCIYNTTYLNVQRENGTISRY  92
```

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Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein

Sequence ID: pdb|3KQ0|A **Length:** 192 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 68 to 91 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.1 bits(179)	3e-15	22/24(92%)	24/24(100%)	0/24(0%)

```
Query  1   RQDQCIYDTTYLNVQREDGTISRY  24
           RQDQCIY+TTYLNVQRE+GTISRY
Sbjct  68  RQDQCIYNTTYLNVQRENGTISRY  91
```

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Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein

Sequence ID: pdb|3BX6|A **Length:** 192 **Number of Matches:** 1

Related Information

Range 1: 68 to 91 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.1 bits(179)	3e-15	22/24(92%)	24/24(100%)	0/24(0%)

```
Query  1   RQDQCIYDTTYLNVQREDGTISRY  24
           RQDQCIY+TTYLNVQRE+GTISRY
Sbjct  68  RQDQCIYNTTYLNVQRENGTISRY  91
```

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ORM1, partial [synthetic construct]

Sequence ID: gb|AIC54852.1| **Length:** 201 **Number of Matches:** 1

Related Information

Range 1: 86 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.1 bits(179)	3e-15	22/24(92%)	24/24(100%)	0/24(0%)

```
Query  1    RQDQCIYDTTYLNVQREDGTISRY  24
            RQDQCIY+TTYLNVQRE+GTISRY
Sbjct  86   RQDQCIYNTTYLNVQRENGTISRY  109
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Orosomucoid 1 [Homo sapiens]

Sequence ID: gb|AAI43315.1| **Length:** 201 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 86 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.1 bits(179)	3e-15	22/24(92%)	24/24(100%)	0/24(0%)

```
Query  1    RQDQCIYDTTYLNVQREDGTISRY  24
            RQDQCIY+TTYLNVQRE+GTISRY
Sbjct  86   RQDQCIYNTTYLNVQRENGTISRY  109
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BVJY0J8W01R**

Your search parameters were adjusted to search for a short input sequence.

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ORM1_RQDQCIYDTTYLNVQRENGTISRY_Mod

RID BVJY0J8W01R (Expires on 01-21 10:30 am)

Query ID lcl|158570
Description None
Molecule type amino acid
Query Length 24

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

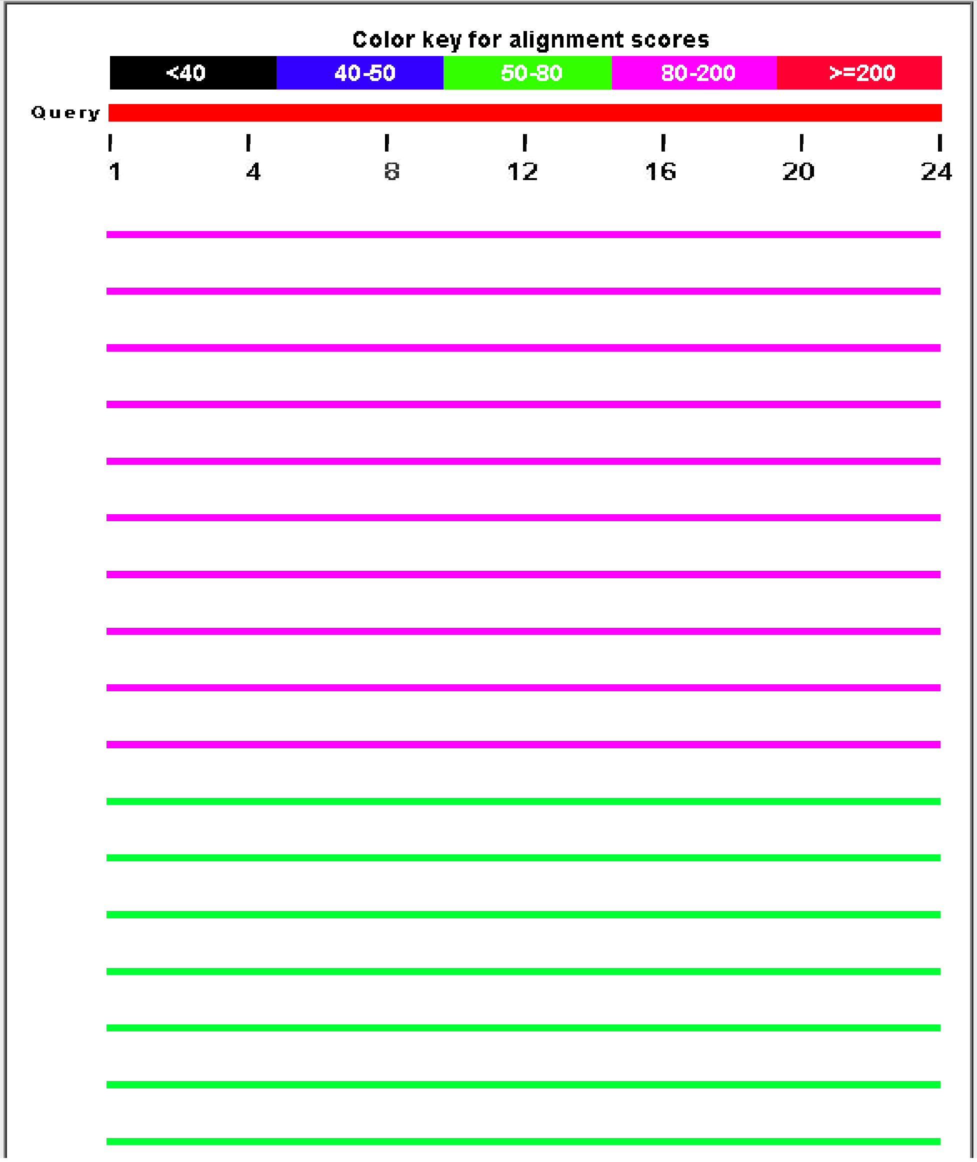
⊟Graphic Summary

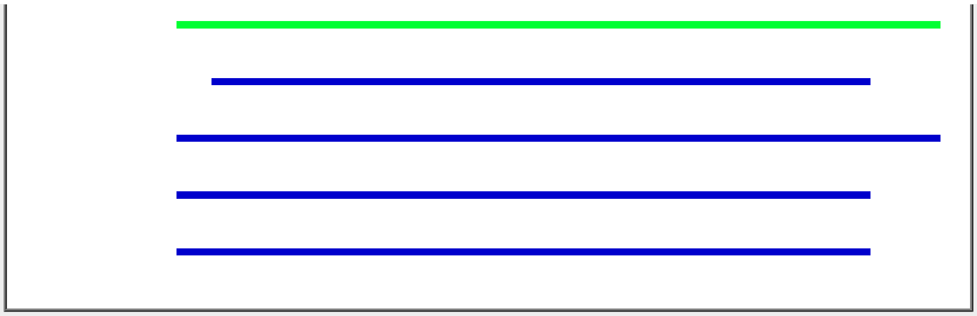
⊟Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	protein,alpha1 acid glyco [Homo sapiens]	81.7	81.7	100%	3e-16	96%	720005A
☐	Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein [Homo sapien	81.7	81.7	100%	4e-16	96%	3KQ0_A
☐	Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein [Homo sapier	81.7	81.7	100%	4e-16	96%	3BX6_A
☐	ORM1 [synthetic construct]	81.7	81.7	100%	4e-16	96%	AIC54852.1
☐	Orosomucoid 1 [Homo sapiens]	81.7	81.7	100%	4e-16	96%	AAI43315.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	81.7	81.7	100%	4e-16	96%	CAA29229.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltName: Full=Orc	81.7	81.7	100%	4e-16	96%	P02763.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	81.7	81.7	100%	4e-16	96%	NP_000598.2
☐	orosomucoid 1 [synthetic construct]	81.7	81.7	100%	4e-16	96%	AAV38575.1
☐	orosomucoid 1 [synthetic construct]	81.7	81.7	100%	4e-16	96%	AAV38574.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	77.4	77.4	100%	1e-14	92%	XP_004048543.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Pongo abelii]	77.4	77.4	100%	1e-14	92%	XP_002820180.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Chlorocebus sabaeus]	76.1	76.1	100%	3e-14	88%	XP_007966502.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 1 [Pan tro	74.9	74.9	100%	8e-14	88%	XP_009455427.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform 1 [Nomascus leucogenys]	74.9	74.9	100%	8e-14	88%	XP_003264088.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X3 [Macaca fascicularis]	72.7	72.7	100%	4e-13	83%	XP_005581033.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like isoform 2 [Macaca mulatta]	72.7	72.7	100%	4e-13	83%	XP_001100289.1
☐	Alpha-1-acid glycoprotein 1 [Macaca mulatta]	72.7	72.7	100%	4e-13	83%	EHH23840.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Macaca fascicularis]	72.7	72.7	100%	4e-13	83%	XP_005581032.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Macaca fascicularis]	72.7	72.7	100%	5e-13	83%	XP_005581031.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Rhinopithecus roxellana]	69.8	69.8	100%	5e-12	79%	XP_010368793.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Papio anubis]	68.9	68.9	100%	9e-12	79%	XP_009186482.1
☐	Chain A, Crystal Structure Of The A Variant Of Human Alpha1-Acid Glycoprot	66.4	66.4	100%	6e-11	75%	3APU_A
☐	ORM2 [synthetic construct]	66.4	66.4	100%	7e-11	75%	AIC54853.1
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	66.4	66.4	100%	7e-11	75%	CAA29873.2
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	66.4	66.4	100%	7e-11	75%	NP_000599.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	66.4	66.4	100%	7e-11	75%	XP_004048546.1
☐	ORM2 [Homo sapiens]	66.4	66.4	100%	7e-11	75%	CAG33211.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Pan troglodytes]	66.4	66.4	100%	7e-11	75%	XP_520209.3

☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 2 [Pan pa	66.4	66.4	100%	8e-11	75%	XP_008957108.1
☐	unnamed protein product [Homo sapiens]	63.8	63.8	100%	5e-10	71%	BAG35159.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Callithrix jacchus]	58.3	58.3	83%	4e-08	80%	XP_002760492.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	57.1	57.1	91%	1e-07	73%	XP_003407553.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Chrysochloris asiatica]	54.9	54.9	87%	5e-07	71%	XP_006865789.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Canis lupus familiaris]	54.5	54.5	91%	7e-07	64%	XP_005627010.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Canis lupus familiaris]	54.5	54.5	91%	7e-07	64%	XP_003431634.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Trichechus manatus latirostris]	54.5	54.5	87%	7e-07	71%	XP_004391229.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Trichechus manatus latirostris]	54.5	54.5	87%	7e-07	71%	XP_004391192.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Trichechus manatus latirostris]	54.5	54.5	87%	7e-07	71%	XP_004372401.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Otolemur garnettii]	54.5	54.5	91%	7e-07	73%	XP_003785445.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Saimiri boliviensis boliviensis]	53.2	53.2	91%	2e-06	64%	XP_003925252.1
☐	Alpha-1-acid glycoprotein [Myotis davidii]	52.4	52.4	100%	3e-06	59%	ELK26646.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	52.0	52.0	91%	5e-06	64%	XP_008707881.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X2 [Tupaia chinensis]	51.5	51.5	91%	7e-06	68%	XP_006142836.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	51.5	51.5	87%	7e-06	67%	XP_003407554.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Mustela putorius furo]	51.1	51.1	83%	8e-06	70%	XP_004828368.1
☐	hypothetical protein PANDA_003840 [Ailuropoda melanoleuca]	50.7	50.7	91%	9e-06	64%	EFB15505.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Orycteropus afer afer]	50.7	50.7	87%	1e-05	71%	XP_007934876.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	50.7	50.7	91%	1e-05	64%	XP_008707882.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ailuropoda melanoleuca]	50.7	50.7	91%	1e-05	64%	XP_002915823.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variegatus]	50.3	50.3	91%	2e-05	64%	XP_008588097.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Galeopterus variegatus]	50.3	50.3	91%	2e-05	64%	XP_008588094.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Elephantulus edwardii]	49.8	49.8	79%	2e-05	74%	XP_006890779.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Tarsius syrichta]	49.4	49.4	91%	3e-05	68%	XP_008055404.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Panthera tigris altaica]	49.4	49.4	83%	3e-05	65%	XP_007094388.1
☐	PREDICTED: alpha-1-acid glycoprotein [Felis catus]	49.4	49.4	83%	3e-05	65%	XP_003995824.1
☐	PREDICTED: LOW QUALITY PROTEIN: orosomucoid 1 [Myotis lucifugus]	49.4	49.4	100%	3e-05	55%	XP_006109685.1
☐	alpha-1-acid glycoprotein [Mus musculus]	46.9	46.9	91%	2e-04	59%	AAA91744.1
☐	alpha-1-acid glycoprotein (AGP) precursor [Mus caroli]	46.9	46.9	91%	2e-04	59%	AAA37197.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltName: Full=Or	46.9	46.9	91%	2e-04	59%	P21350.1
☐	alpha-1-acid glycoprotein 2 precursor [Mus musculus]	46.9	46.9	91%	2e-04	59%	NP_035146.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 1-like [My	46.9	46.9	87%	2e-04	71%	XP_005880984.1
☐	Alpha-1-acid glycoprotein 1 [Cricetulus griseus]	46.4	46.4	95%	3e-04	61%	EGW06649.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Cricetulus griseus]	46.4	46.4	95%	3e-04	61%	XP_003503497.1
☐	alpha-1-acid glycoprotein 1 [Cricetulus griseus]	46.4	46.4	95%	3e-04	61%	ERE86355.1
☐	alpha-1-acid glycoprotein 1 [Cricetulus griseus]	46.4	46.4	95%	3e-04	61%	ERE86354.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Pteropus alecto]	46.0	46.0	95%	4e-04	57%	XP_006917195.1
☐	Alpha-1-acid glycoprotein [Pteropus alecto]	46.0	46.0	95%	4e-04	57%	ELK08232.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Myotis brandtii]	45.6	45.6	91%	5e-04	59%	XP_005880983.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variegatus]	45.6	45.6	83%	6e-04	65%	XP_008588096.1
☐	alpha-1-acid glycoprotein [Mus musculus]	45.2	45.2	91%	6e-04	64%	AAA91745.1
☐	mCG7142, isoform CRA_b [Mus musculus]	45.2	45.2	91%	8e-04	64%	EDL31111.1
☐	alpha-1-acid glycoprotein precursor [Mus caroli]	45.2	45.2	91%	8e-04	64%	AAB67844.1
☐	alpha-1-acid glycoprotein 1 precursor [Mus musculus]	45.2	45.2	91%	8e-04	64%	NP_032794.1

☐	RecName: Full=Alpha-1-acid glycoprotein 8; Short=AGP 8; AltName: Full=Orc	45.2	45.2	91%	8e-04	64%	P21352.1
☐	Orosomucoid 1 [Mus musculus]	45.2	45.2	91%	8e-04	64%	AAH12725.1
☐	mCG7142, isoform CRA_e [Mus musculus]	45.2	45.2	91%	8e-04	64%	EDL31114.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Mesocricetus auratus]	44.8	44.8	83%	0.001	65%	XP_005075189.1
☐	alpha-1-acid glycoprotein precursor [Rattus norvegicus]	43.9	43.9	83%	0.002	70%	NP_445740.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	43.9	43.9	91%	0.002	64%	XP_006099427.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Nannospalax galili]	43.1	43.1	95%	0.004	57%	XP_008831764.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	43.1	43.1	79%	0.004	68%	XP_003407551.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	42.6	42.6	79%	0.006	63%	XP_010586317.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Camelus dromedarius]	42.2	42.2	83%	0.007	70%	XP_010995686.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Camelus ferus]	42.2	42.2	83%	0.007	70%	XP_006186090.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ochotona princeps]	41.8	41.8	95%	0.010	57%	XP_004595034.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Equus caballus]	41.8	41.8	83%	0.010	65%	XP_001488199.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	41.8	41.8	83%	0.010	65%	XP_006108236.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	41.8	41.8	83%	0.010	65%	XP_006099413.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Vicugna pacos]	41.4	41.4	79%	0.013	74%	XP_006211428.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Peromyscus maniculatus bairdii]	40.9	40.9	87%	0.018	62%	XP_006979617.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	40.9	40.9	75%	0.018	67%	XP_006108237.1
☐	Alpha-1-acid glycoprotein 1 [Heterocephalus glaber]	40.1	40.1	87%	0.031	67%	EHB03307.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Heterocephalus glaber]	40.1	40.1	87%	0.032	67%	XP_004885278.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Echinops telfairi]	40.1	40.1	83%	0.033	70%	XP_004718018.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Echinops telfairi]	40.1	40.1	83%	0.034	70%	XP_004712638.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Heterocephalus glaber]	40.1	40.1	87%	0.035	67%	XP_004849700.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Mustela putorius furo]	39.7	39.7	83%	0.042	60%	XP_004807875.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Mustela putorius furo]	39.7	39.7	83%	0.044	60%	XP_004774102.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Erinaceus europaeus]	39.7	39.7	75%	0.047	67%	XP_007526815.1

⊟ Alignments

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protein,alpha1 acid glyco

Sequence ID: prf||720005A **Length:** 182 **Number of Matches:** 1

Related Information

Range 1: 69 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	3e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1   RQDQCIYDTTYLNVQRENGTISRY  24
           RQDQCIY+TTYLNVQRENGTISRY
Sbjct  69  RQDQCIYNTTYLNVQRENGTISRY  92
```

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Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein

Sequence ID: pdb|3KQ0|A **Length:** 192 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 68 to 91 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	4e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1   RQDQCIYDTTYLNVQRENGTISRY  24
           RQDQCIY+TTYLNVQRENGTISRY
Sbjct  68  RQDQCIYNTTYLNVQRENGTISRY  91
```

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Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein

Sequence ID: pdb|3BX6|A **Length:** 192 **Number of Matches:** 1

Related Information

Range 1: 68 to 91 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	4e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1   RQDQCIYDTTYLNVQRENGTISRY  24
           RQDQCIY+TTYLNVQRENGTISRY
Sbjct  68  RQDQCIYNTTYLNVQRENGTISRY  91
```

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ORM1, partial [synthetic construct]

Sequence ID: gb|AIC54852.1| **Length:** 201 **Number of Matches:** 1

Related Information

Range 1: 86 to 109 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	4e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    RQDQCIYDTTYLNVQRENGTISRY  24
            RQDQCIY+TTYLNVQRENGTISRY
Sbjct  86   RQDQCIYNTTYLNVQRENGTISRY  109
```

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Orosomucoid 1 [Homo sapiens]

Sequence ID: gb|AAI43315.1| **Length:** 201 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 86 to 109 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	4e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    RQDQCIYDTTYLNVQRENGTISRY  24
            RQDQCIY+TTYLNVQRENGTISRY
Sbjct  86   RQDQCIYNTTYLNVQRENGTISRY  109
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BBHJEEAU01R

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How to read this page Blast report description

ORM1_RQDQCIYNTTYLNVQRE_NonMod

RID BBHJEEAU01R (Expires on 01-15 08:28 am)

Query ID	lcl|199850
Description	None
Molecule type	amino acid
Query Length	17

Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

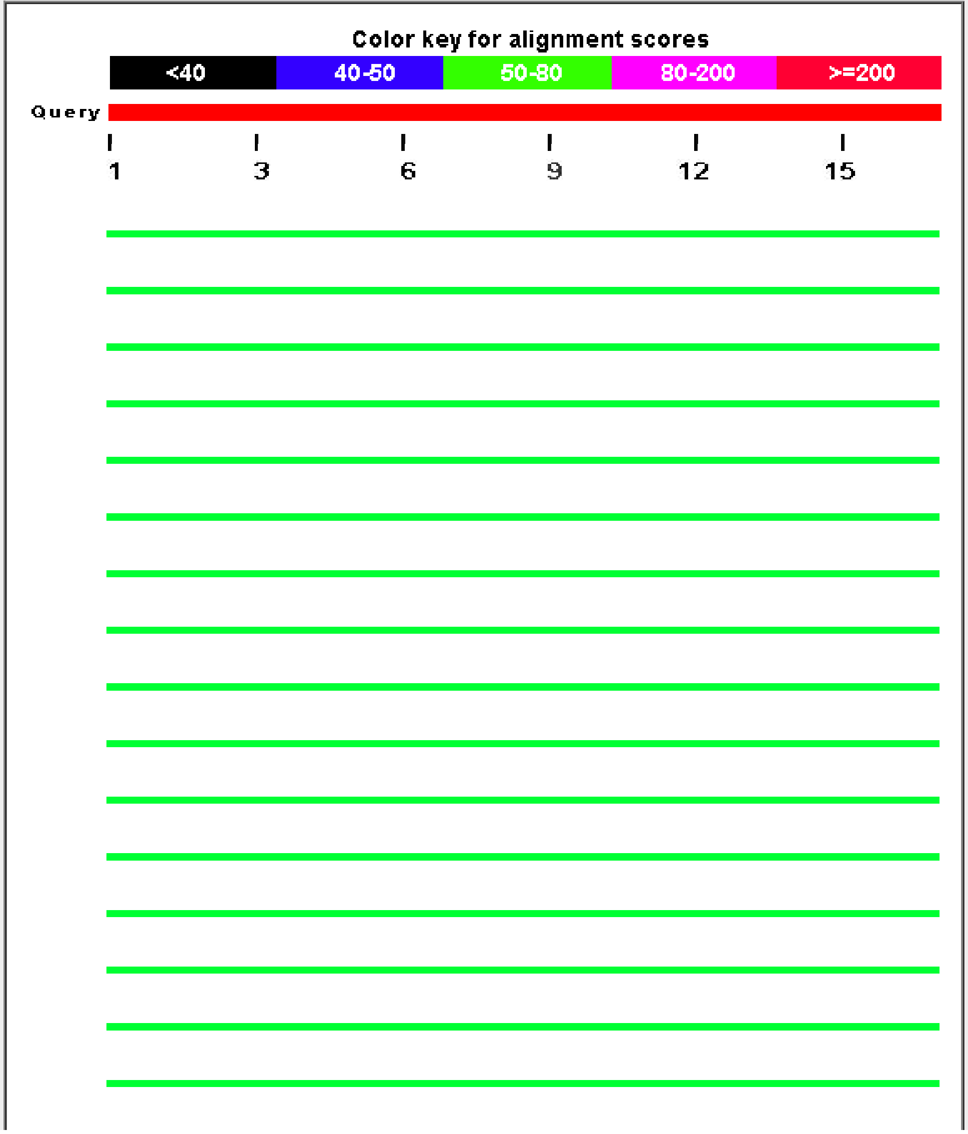
Graphic Summary

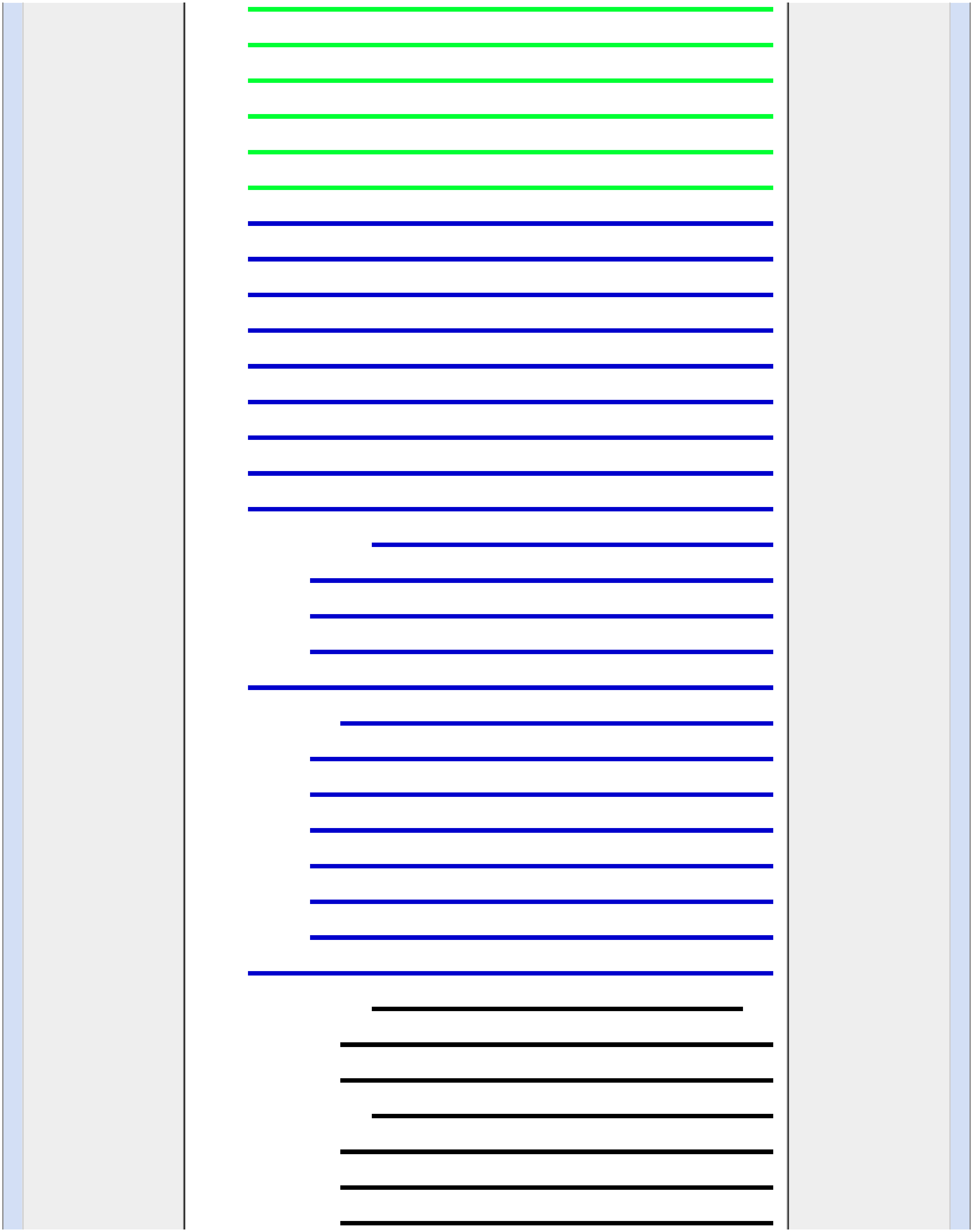
Show Conserved Domains

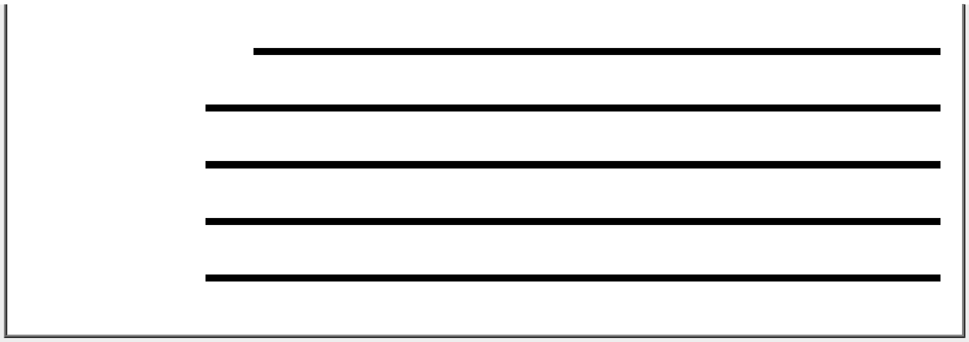
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	protein,alpha1 acid glyco [Homo sapiens]	61.7	61.7	100%	9e-10	100%	gi|229386|720005A
☐	Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein [Ho	61.7	61.7	100%	9e-10	100%	gi|285803540|3KQ0_A
☐	Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein [Hc	61.7	61.7	100%	9e-10	100%	gi|215794600|3BX6_A
☐	ORM1 [synthetic construct]	61.7	61.7	100%	1e-09	100%	gi|649120278|AIC54852.1
☐	Orosomucoid 1 [Homo sapiens]	61.7	61.7	100%	1e-09	100%	gi|219519923|AAI43315.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	61.7	61.7	100%	1e-09	100%	gi|1197209|CAA29229.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltNam	61.7	61.7	100%	1e-09	100%	gi|112877|P02763.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	61.7	61.7	100%	1e-09	100%	gi|167857790|NP_000598.2
☐	orosomucoid 1 [synthetic construct]	61.7	61.7	100%	1e-09	100%	gi|54696406|AAV38575.1
☐	orosomucoid 1 [synthetic construct]	61.7	61.7	100%	1e-09	100%	gi|54696404|AAV38574.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla	57.5	57.5	100%	3e-08	94%	gi|426362801|XP_004048543.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein	57.5	57.5	100%	3e-08	94%	gi|694936727|XP_009455427.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform 1 [Nomascus leu	57.5	57.5	100%	3e-08	94%	gi|332229827|XP_003264088.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Pongo abelii]	57.5	57.5	100%	3e-08	94%	gi|297685191|XP_002820180.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X3 [Macaca fasci	56.2	56.2	100%	7e-08	88%	gi|544492702|XP_005581033.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like isoform 2 [Macaca m	56.2	56.2	100%	7e-08	88%	gi|109110480|XP_001100289.1
☐	Alpha-1-acid glycoprotein 1 [Macaca mulatta]	56.2	56.2	100%	7e-08	88%	gi|355567499|EHH23840.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Chlorocebus sabaeus]	56.2	56.2	100%	8e-08	88%	gi|635071762|XP_007966502.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Macaca fasci	56.2	56.2	100%	8e-08	88%	gi|544492700|XP_005581032.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Macaca fasci	56.2	56.2	100%	8e-08	88%	gi|544492698|XP_005581031.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Rhinopithecus roxellana]	53.2	53.2	100%	8e-07	82%	gi|724859712|XP_010368793.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Papio anubis]	52.4	52.4	100%	2e-06	82%	gi|685591954|XP_009186482.1
☐	Chain A, Crystal Structure Of The A Variant Of Human Alpha1-Acid	49.0	49.0	100%	2e-05	76%	gi|323714404|3APU_A
☐	ORM2 [synthetic construct]	49.0	49.0	100%	2e-05	76%	gi|649120282|AIC54853.1
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	49.0	49.0	100%	2e-05	76%	gi|29170378|CAA29873.2
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	49.0	49.0	100%	2e-05	76%	gi|4505529|NP_000599.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla	49.0	49.0	100%	2e-05	76%	gi|426362807|XP_004048546.1
☐	ORM2 [Homo sapiens]	49.0	49.0	100%	2e-05	76%	gi|48145977|CAG33211.1
☐							

	PREDICTED: alpha-1-acid glycoprotein 2-like [Pan troglodytes]	49.0	49.0	100%	2e-05	76%	gi|694988125|XP_520209.3
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein	49.0	49.0	100%	2e-05	76%	gi|675802504|XP_008957108.1
☐	unnamed protein product [Homo sapiens]	46.4	46.4	100%	2e-04	71%	gi|189053338|BAG35159.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Callithrix jacchus]	45.2	45.2	76%	4e-04	92%	gi|296229919|XP_002760492.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	44.3	44.3	88%	8e-04	80%	gi|344271455|XP_003407553.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Panthera tigris altaica]	43.9	43.9	88%	0.001	73%	gi|591337606|XP_007094388.1
☐	PREDICTED: alpha-1-acid glycoprotein [Felis catus]	43.9	43.9	88%	0.001	73%	gi|410978897|XP_003995824.1
☐	Alpha-1-acid glycoprotein [Myotis davidii]	43.1	43.1	100%	0.002	64%	gi|432095447|ELK26646.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Elephantulus edwardii]	41.4	41.4	82%	0.007	79%	gi|585676946|XP_006890779.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variega	40.5	40.5	88%	0.014	73%	gi|667321193|XP_008588097.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variega	40.5	40.5	88%	0.014	73%	gi|667321190|XP_008588096.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Galeopterus variegatus]	40.5	40.5	88%	0.014	73%	gi|667321187|XP_008588094.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Canis lupus f	40.5	40.5	88%	0.014	67%	gi|545518002|XP_005627010.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Canis lupus f	40.5	40.5	88%	0.014	67%	gi|345777714|XP_003431634.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Saimiri boliviensis bolivie	40.1	40.1	88%	0.020	67%	gi|403266135|XP_003925252.1
☐	PREDICTED: LOW QUALITY PROTEIN: orosomucoid 1 [Myotis luc	40.1	40.1	100%	0.020	59%	gi|558172686|XP_006109685.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Erinaceus europaeus]	39.2	39.2	70%	0.037	83%	gi|617619058|XP_007526815.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Chrysochloris asiatica]	38.8	38.8	82%	0.051	71%	gi|586470389|XP_006865789.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	38.8	38.8	82%	0.051	71%	gi|344271457|XP_003407554.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Mustela putorius furo	38.4	38.4	76%	0.065	77%	gi|512022336|XP_004828368.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Orycteropus afer afer]	38.4	38.4	82%	0.070	79%	gi|634836563|XP_007934876.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Trichechus manatus la	38.4	38.4	82%	0.071	71%	gi|471419478|XP_004391229.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Trichechus manatus	38.4	38.4	82%	0.071	71%	gi|471419404|XP_004391192.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Trichechus manatus latir	38.4	38.4	82%	0.071	71%	gi|471363692|XP_004372401.1
☐	hypothetical protein PANDA_003840 [Ailuropoda melanoleuca]	38.0	38.0	88%	0.081	67%	gi|281339921|EFB15505.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	38.0	38.0	88%	0.097	67%	gi|671034105|XP_008707882.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	38.0	38.0	88%	0.097	67%	gi|671034103|XP_008707881.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ailuropoda melanoleu	38.0	38.0	88%	0.097	67%	gi|301760029|XP_002915823.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Otolemur garnettii]	38.0	38.0	88%	0.098	73%	gi|395824383|XP_003785445.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Myotis brandtii]	37.1	37.1	100%	0.16	59%	gi|554578831|XP_005880983.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	36.3	36.3	82%	0.34	79%	gi|344271451|XP_003407551.1
☐	alpha-1-acid glycoprotein precursor [Rattus norvegicus]	35.4	35.4	88%	0.64	73%	gi|16757980|NP_445740.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X2 [Tupaia c	35.0	35.0	88%	0.88	67%	gi|562826345|XP_006142836.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Echinops telfairi]	34.6	34.6	82%	1.2	79%	gi|507712754|XP_004718018.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	34.6	34.6	88%	1.2	67%	gi|558213870|XP_006108237.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Echinops telfairi]	34.6	34.6	82%	1.2	79%	gi|507689354|XP_004712638.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Myotis lucifugus]	34.6	34.6	88%	1.2	67%	gi|558172690|XP_006099428.1
☐	alpha-1-acid glycoprotein [Mus musculus]	34.1	34.1	88%	1.5	60%	gi|387176|AAA91744.1
☐	alpha-1-acid glycoprotein (AGP) precursor [Mus caroli]	34.1	34.1	88%	1.6	60%	gi|309098|AAA37197.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltNam	34.1	34.1	88%	1.6	60%	gi|112879|P21350.1
☐	alpha-1-acid glycoprotein 2 precursor [Mus musculus]	34.1	34.1	88%	1.6	60%	gi|6754950|NP_035146.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein	34.1	34.1	82%	1.6	79%	gi|554578835|XP_005880984.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	34.1	34.1	82%	1.7	64%	gi|731463853|XP_010586317.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Nannospalax galili]	33.7	33.7	94%	2.2	63%	gi|674051046|XP_008831764.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Pteropus alecto]	33.7	33.7	94%	2.2	56%	gi|586524471|XP_006917195.1

☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	33.7	33.7	88%	2.2	67%	gi|558172682|XP_006099427.1
☐	Alpha-1-acid glycoprotein [Pteropus alecto]	33.7	33.7	94%	2.3	56%	gi|431900791|ELK08232.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Tarsius syrichta]	33.3	33.3	88%	3.1	67%	gi|640798447|XP_008055404.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	33.3	33.3	88%	3.1	67%	gi|558213865|XP_006108236.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	33.3	33.3	88%	3.1	67%	gi|558172615|XP_006099413.1
☐	alpha-1-acid glycoprotein [Mus musculus]	32.9	32.9	88%	3.7	67%	gi|553922|AAA91745.1
☐	mCG7142, isoform CRA_b [Mus musculus]	32.9	32.9	88%	4.1	67%	gi|148699164|EDL31111.1
☐	alpha-1-acid glycoprotein precursor [Mus caroli]	32.9	32.9	88%	4.2	67%	gi|309100|AAB67844.1
☐	alpha-1-acid glycoprotein 1 precursor [Mus musculus]	32.9	32.9	88%	4.2	67%	gi|6679182|NP_032794.1
☐	RecName: Full=Alpha-1-acid glycoprotein 8; Short=AGP 8; AltNam	32.9	32.9	88%	4.2	67%	gi|112883|P21352.1
☐	Orosomucoid 1 [Mus musculus]	32.9	32.9	88%	4.2	67%	gi|15215270|AAH12725.1
☐	mCG7142, isoform CRA_e [Mus musculus]	32.9	32.9	88%	4.2	67%	gi|148699167|EDL31114.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	32.5	32.5	88%	5.7	67%	gi|558172624|XP_006099415.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Equus caballus]	32.0	32.0	88%	7.8	60%	gi|149738494|XP_001488199.1
☐	Protein C44E4.1, isoform c [Caenorhabditis elegans]	32.0	32.0	88%	8.5	48%	gi|25143932|NP_740838.1
☐	protein C44E4.1a [imported] - Caenorhabditis elegans [Caenorhabd	32.0	32.0	88%	8.6	48%	gi|25395263|D87757
☐	Protein C44E4.1, isoform a [Caenorhabditis elegans]	32.0	32.0	88%	8.6	48%	gi|453224247|NP_491407.2
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Mustela putorius fur	31.2	31.2	88%	14	60%	gi|511980019|XP_004807875.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Mustela putorius furo]	31.2	31.2	88%	14	60%	gi|511909351|XP_004774102.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Odobenus rosmarus d	30.8	30.8	70%	20	69%	gi|472354697|XP_004397008.1
☐	integrase [Metascardovia criceti]	30.8	30.8	58%	20	80%	gi|516876710|WP_018142749.1
☐	hypothetical protein [Paenibacillus sp. PAMC 26794]	30.8	30.8	70%	21	75%	gi|516288323|WP_017691630.1
☐	histidine kinase [Paenibacillus sp. FSL R5-192]	30.8	30.8	70%	21	75%	gi|573536452|ETT35445.1
☐	histidine kinase [Paenibacillus sp. FSL H7-689]	30.8	30.8	70%	21	75%	gi|573550874|ETT49673.1
☐	alpha-1 acid glycoprotein [Sus scrofa]	30.3	30.3	88%	27	60%	gi|164302|AAA30983.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Sus scrofa]	30.3	30.3	88%	27	60%	gi|545804155|XP_005660423.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Sorex araneus]	30.3	30.3	88%	27	53%	gi|505855571|XP_004621196.1

Alignments

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protein,alpha1 acid glyco

Sequence ID: gi|229386|prf||720005A **Length:** 182 **Number of Matches:** 1

Related Information

Range 1: 69 to 85 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.7 bits(138)	9e-10	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RQDQCIYNTTYLNVQRE  17
            RQDQCIYNTTYLNVQRE
Sbjct  69   RQDQCIYNTTYLNVQRE  85
```

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Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein

Sequence ID: gi|285803540|pdb|3KQ0|A **Length:** 192 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 68 to 84 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.7 bits(138)	9e-10	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RQDQCIYNTTYLNVQRE  17
```

```
                RQDQCIYNTTYLNVQRE
Sbjct  68  RQDQCIYNTTYLNVQRE  84
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein

Sequence ID: gi|215794600|pdb|3BX6|A **Length:** 192 **Number of Matches:** 1

Related Information

Range 1: 68 to 84 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.7 bits(138)	9e-10	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RQDQCIYNTTYLNVQRE  17
            RQDQCIYNTTYLNVQRE
Sbjct  68  RQDQCIYNTTYLNVQRE  84
```

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ORM1, partial [synthetic construct]

Sequence ID: gi|649120278|gb|AIC54852.1| **Length:** 201 **Number of Matches:** 1

Related Information

Range 1: 86 to 102 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.7 bits(138)	1e-09	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RQDQCIYNTTYLNVQRE  17
            RQDQCIYNTTYLNVQRE
Sbjct  86   RQDQCIYNTTYLNVQRE  102
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

Orosomucoid 1 [Homo sapiens]

Sequence ID: gi|219519923|gb|AAI43315.1| **Length:** 201 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 86 to 102 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
61.7 bits(138)	1e-09	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RQDQCIYNTTYLNVQRE  17
            RQDQCIYNTTYLNVQRE
Sbjct  86   RQDQCIYNTTYLNVQRE  102
```

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVJTXX9G01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   Formatting options   Download   How to read this page   Blast report description

ORM1_RQDQCIYNTTYLNVQREDGTISRY_Mod

RID BVJTXX9G01R (Expires on 01-21 10:27 am)

Query ID	lcl|122231	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	24		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

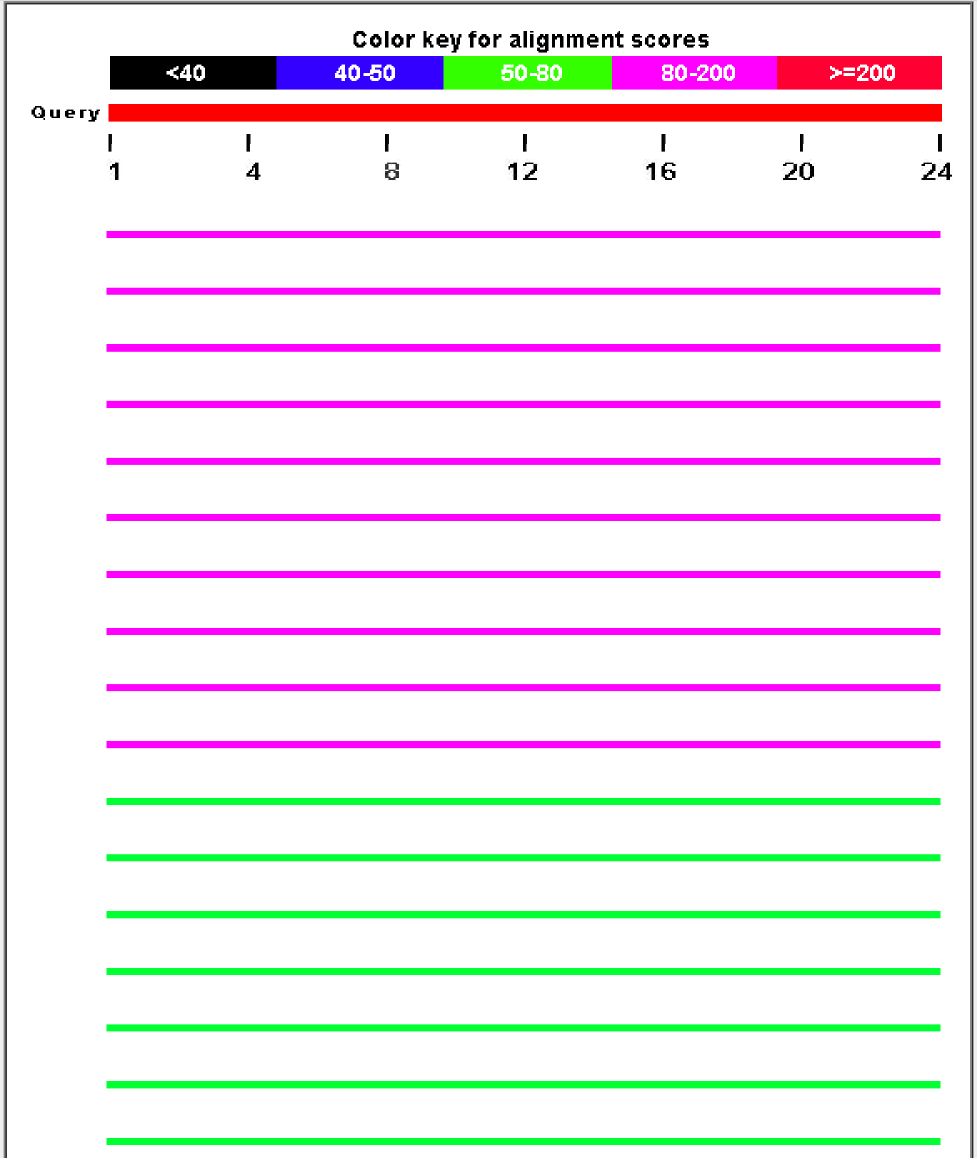
Graphic Summary

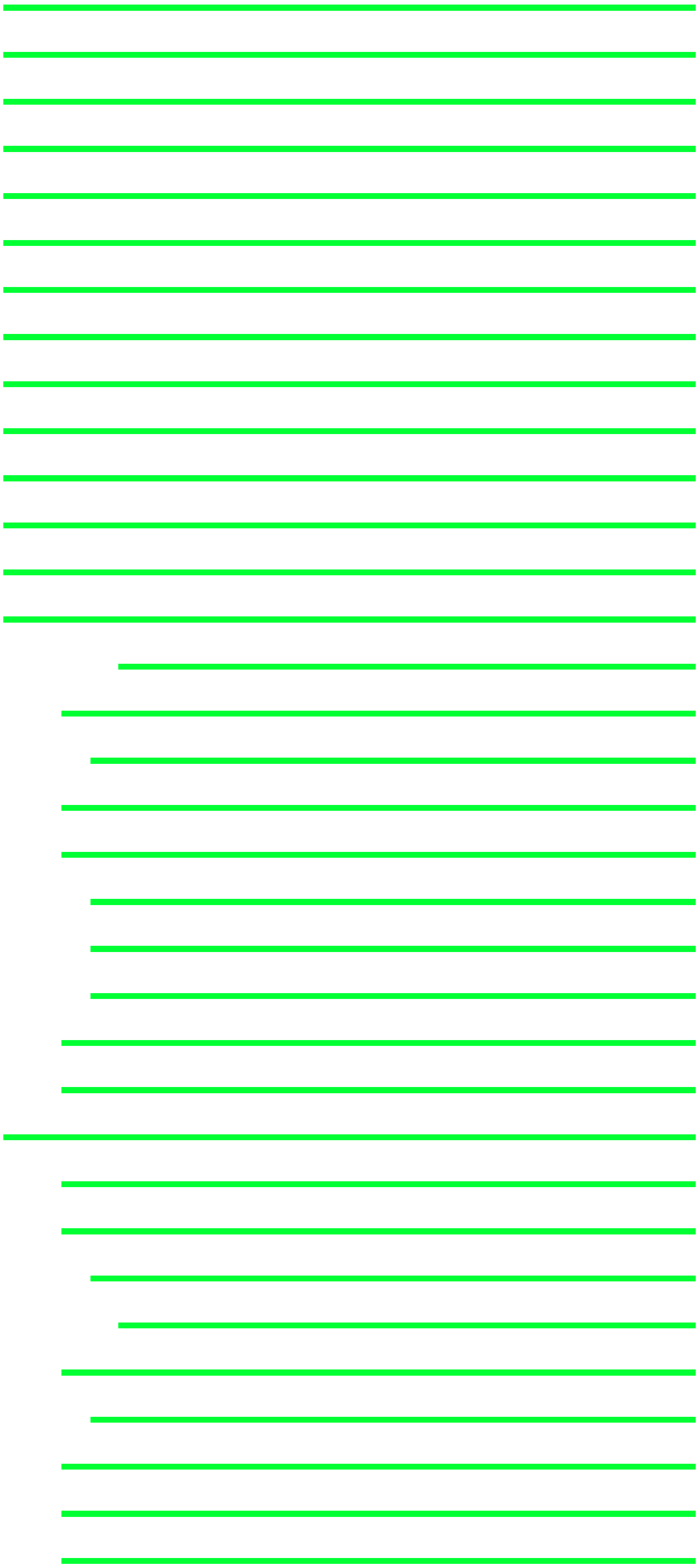
Show Conserved Domains

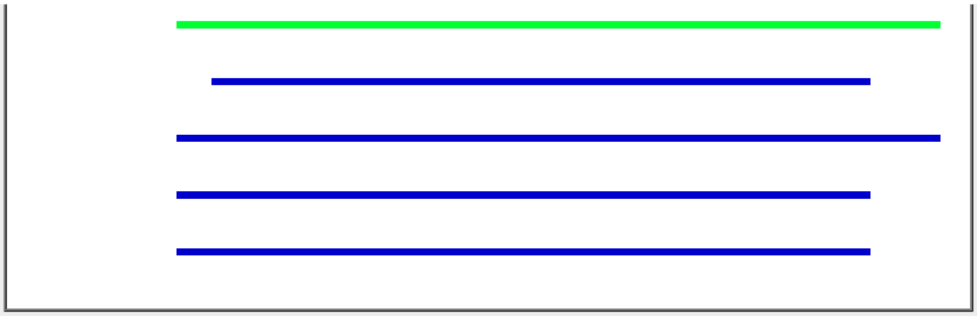
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	protein,alpha1 acid glyco [Homo sapiens]	81.7	81.7	100%	3e-16	96%	720005A
☐	Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein [Homo sapien	81.7	81.7	100%	4e-16	96%	3KQ0_A
☐	Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein [Homo sapier	81.7	81.7	100%	4e-16	96%	3BX6_A
☐	ORM1 [synthetic construct]	81.7	81.7	100%	4e-16	96%	AIC54852.1
☐	Orosomucoid 1 [Homo sapiens]	81.7	81.7	100%	4e-16	96%	AAI43315.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	81.7	81.7	100%	4e-16	96%	CAA29229.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltName: Full=Orc	81.7	81.7	100%	4e-16	96%	P02763.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	81.7	81.7	100%	4e-16	96%	NP_000598.2
☐	orosomucoid 1 [synthetic construct]	81.7	81.7	100%	4e-16	96%	AAV38575.1
☐	orosomucoid 1 [synthetic construct]	81.7	81.7	100%	4e-16	96%	AAV38574.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	77.4	77.4	100%	1e-14	92%	XP_004048543.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Pongo abelii]	77.4	77.4	100%	1e-14	92%	XP_002820180.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Chlorocebus sabaeus]	76.1	76.1	100%	3e-14	88%	XP_007966502.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 1 [Pan tro	74.9	74.9	100%	8e-14	88%	XP_009455427.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform 1 [Nomascus leucogenys]	74.9	74.9	100%	8e-14	88%	XP_003264088.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X3 [Macaca fascicularis]	72.7	72.7	100%	4e-13	83%	XP_005581033.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like isoform 2 [Macaca mulatta]	72.7	72.7	100%	4e-13	83%	XP_001100289.1
☐	Alpha-1-acid glycoprotein 1 [Macaca mulatta]	72.7	72.7	100%	4e-13	83%	EHH23840.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Macaca fascicularis]	72.7	72.7	100%	4e-13	83%	XP_005581032.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Macaca fascicularis]	72.7	72.7	100%	5e-13	83%	XP_005581031.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Rhinopithecus roxellana]	69.8	69.8	100%	5e-12	79%	XP_010368793.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Papio anubis]	68.9	68.9	100%	9e-12	79%	XP_009186482.1
☐	Chain A, Crystal Structure Of The A Variant Of Human Alpha1-Acid Glycoprot	66.4	66.4	100%	6e-11	75%	3APU_A
☐	ORM2 [synthetic construct]	66.4	66.4	100%	7e-11	75%	AIC54853.1
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	66.4	66.4	100%	7e-11	75%	CAA29873.2
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	66.4	66.4	100%	7e-11	75%	NP_000599.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	66.4	66.4	100%	7e-11	75%	XP_004048546.1
☐	ORM2 [Homo sapiens]	66.4	66.4	100%	7e-11	75%	CAG33211.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Pan troglodytes]	66.4	66.4	100%	7e-11	75%	XP_520209.3

☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 2 [Pan pa	66.4	66.4	100%	8e-11	75%	XP_008957108.1
☐	unnamed protein product [Homo sapiens]	63.8	63.8	100%	5e-10	71%	BAG35159.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Callithrix jacchus]	58.3	58.3	83%	4e-08	80%	XP_002760492.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	57.1	57.1	91%	1e-07	73%	XP_003407553.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Chrysochloris asiatica]	54.9	54.9	87%	5e-07	71%	XP_006865789.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Canis lupus familiaris]	54.5	54.5	91%	7e-07	64%	XP_005627010.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Canis lupus familiaris]	54.5	54.5	91%	7e-07	64%	XP_003431634.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Trichechus manatus latirostris]	54.5	54.5	87%	7e-07	71%	XP_004391229.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Trichechus manatus latirostris]	54.5	54.5	87%	7e-07	71%	XP_004391192.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Trichechus manatus latirostris]	54.5	54.5	87%	7e-07	71%	XP_004372401.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Otolemur garnettii]	54.5	54.5	91%	7e-07	73%	XP_003785445.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Saimiri boliviensis boliviensis]	53.2	53.2	91%	2e-06	64%	XP_003925252.1
☐	Alpha-1-acid glycoprotein [Myotis davidii]	52.4	52.4	100%	3e-06	59%	ELK26646.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	52.0	52.0	91%	5e-06	64%	XP_008707881.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X2 [Tupaia chinensis]	51.5	51.5	91%	7e-06	68%	XP_006142836.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	51.5	51.5	87%	7e-06	67%	XP_003407554.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Mustela putorius furo]	51.1	51.1	83%	8e-06	70%	XP_004828368.1
☐	hypothetical protein PANDA_003840 [Ailuropoda melanoleuca]	50.7	50.7	91%	9e-06	64%	EFB15505.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Orycteropus afer afer]	50.7	50.7	87%	1e-05	71%	XP_007934876.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	50.7	50.7	91%	1e-05	64%	XP_008707882.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ailuropoda melanoleuca]	50.7	50.7	91%	1e-05	64%	XP_002915823.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variegatus]	50.3	50.3	91%	2e-05	64%	XP_008588097.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Galeopterus variegatus]	50.3	50.3	91%	2e-05	64%	XP_008588094.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Elephantulus edwardii]	49.8	49.8	79%	2e-05	74%	XP_006890779.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Tarsius syrichta]	49.4	49.4	91%	3e-05	68%	XP_008055404.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Panthera tigris altaica]	49.4	49.4	83%	3e-05	65%	XP_007094388.1
☐	PREDICTED: alpha-1-acid glycoprotein [Felis catus]	49.4	49.4	83%	3e-05	65%	XP_003995824.1
☐	PREDICTED: LOW QUALITY PROTEIN: orosomucoid 1 [Myotis lucifugus]	49.4	49.4	100%	3e-05	55%	XP_006109685.1
☐	alpha-1-acid glycoprotein [Mus musculus]	46.9	46.9	91%	2e-04	59%	AAA91744.1
☐	alpha-1-acid glycoprotein (AGP) precursor [Mus caroli]	46.9	46.9	91%	2e-04	59%	AAA37197.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltName: Full=Or	46.9	46.9	91%	2e-04	59%	P21350.1
☐	alpha-1-acid glycoprotein 2 precursor [Mus musculus]	46.9	46.9	91%	2e-04	59%	NP_035146.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein 1-like [My	46.9	46.9	87%	2e-04	71%	XP_005880984.1
☐	Alpha-1-acid glycoprotein 1 [Cricetulus griseus]	46.4	46.4	95%	3e-04	61%	EGW06649.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Cricetulus griseus]	46.4	46.4	95%	3e-04	61%	XP_003503497.1
☐	alpha-1-acid glycoprotein 1 [Cricetulus griseus]	46.4	46.4	95%	3e-04	61%	ERE86355.1
☐	alpha-1-acid glycoprotein 1 [Cricetulus griseus]	46.4	46.4	95%	3e-04	61%	ERE86354.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Pteropus alecto]	46.0	46.0	95%	4e-04	57%	XP_006917195.1
☐	Alpha-1-acid glycoprotein [Pteropus alecto]	46.0	46.0	95%	4e-04	57%	ELK08232.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Myotis brandtii]	45.6	45.6	91%	5e-04	59%	XP_005880983.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variegatus]	45.6	45.6	83%	6e-04	65%	XP_008588096.1
☐	alpha-1-acid glycoprotein [Mus musculus]	45.2	45.2	91%	6e-04	64%	AAA91745.1
☐	mCG7142, isoform CRA_b [Mus musculus]	45.2	45.2	91%	8e-04	64%	EDL31111.1
☐	alpha-1-acid glycoprotein precursor [Mus caroli]	45.2	45.2	91%	8e-04	64%	AAB67844.1
☐	alpha-1-acid glycoprotein 1 precursor [Mus musculus]	45.2	45.2	91%	8e-04	64%	NP_032794.1

☐	RecName: Full=Alpha-1-acid glycoprotein 8; Short=AGP 8; AltName: Full=Orc	45.2	45.2	91%	8e-04	64%	P21352.1
☐	Orosomucoid 1 [Mus musculus]	45.2	45.2	91%	8e-04	64%	AAH12725.1
☐	mCG7142, isoform CRA_e [Mus musculus]	45.2	45.2	91%	8e-04	64%	EDL31114.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Mesocricetus auratus]	44.8	44.8	83%	0.001	65%	XP_005075189.1
☐	alpha-1-acid glycoprotein precursor [Rattus norvegicus]	43.9	43.9	83%	0.002	70%	NP_445740.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Nannospalax galili]	43.1	43.1	95%	0.004	57%	XP_008831764.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	43.1	43.1	91%	0.004	59%	XP_006099427.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	43.1	43.1	79%	0.004	68%	XP_003407551.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	42.6	42.6	79%	0.006	63%	XP_010586317.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Camelus dromedarius]	42.2	42.2	83%	0.007	70%	XP_010995686.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Camelus ferus]	42.2	42.2	83%	0.007	70%	XP_006186090.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ochotona princeps]	41.8	41.8	95%	0.010	57%	XP_004595034.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	41.8	41.8	83%	0.010	65%	XP_006108236.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	41.8	41.8	83%	0.010	65%	XP_006099413.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Vicugna pacos]	41.4	41.4	79%	0.013	74%	XP_006211428.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Peromyscus maniculatus bairdii]	40.9	40.9	87%	0.018	62%	XP_006979617.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	40.9	40.9	75%	0.018	67%	XP_006108237.1
☐	Alpha-1-acid glycoprotein 1 [Heterocephalus glaber]	40.1	40.1	87%	0.031	67%	EHB03307.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Heterocephalus glaber]	40.1	40.1	87%	0.032	67%	XP_004885278.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Echinops telfairi]	40.1	40.1	83%	0.033	70%	XP_004718018.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Echinops telfairi]	40.1	40.1	83%	0.034	70%	XP_004712638.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Heterocephalus glaber]	40.1	40.1	87%	0.035	67%	XP_004849700.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Mustela putorius furo]	39.7	39.7	83%	0.042	60%	XP_004807875.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Mustela putorius furo]	39.7	39.7	83%	0.044	60%	XP_004774102.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Erinaceus europaeus]	39.7	39.7	75%	0.047	67%	XP_007526815.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X1 [Tupaia chinensis]	39.7	39.7	91%	0.047	64%	XP_006142835.1

⊟ Alignments

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protein,alpha1 acid glyco

Sequence ID: prf||720005A **Length:** 182 **Number of Matches:** 1

Related Information

Range 1: 69 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	3e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1   RQDQCIYNTTYLNVQREDGTISRY  24
           RQDQCIYNTTYLNVQRE+GTISRY
Sbjct  69  RQDQCIYNTTYLNVQRENGTISRY  92
```

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Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein

Sequence ID: pdb|3KQ0|A **Length:** 192 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 68 to 91 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	4e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    RQDQCIYNTTYLNVQREDGTISRY  24
            RQDQCIYNTTYLNVQRE+GTISRY
Sbjct  68   RQDQCIYNTTYLNVQRENGTISRY  91
```

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Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein

Sequence ID: pdb|3BX6|A **Length:** 192 **Number of Matches:** 1

Related Information

Range 1: 68 to 91 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	4e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    RQDQCIYNTTYLNVQREDGTISRY  24
            RQDQCIYNTTYLNVQRE+GTISRY
Sbjct  68   RQDQCIYNTTYLNVQRENGTISRY  91
```

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ORM1, partial [synthetic construct]

Sequence ID: gb|AIC54852.1| **Length:** 201 **Number of Matches:** 1

Related Information

Range 1: 86 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	4e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1     RQDQCIYNTTYLNVQREDGTISRY  24
             RQDQCIYNTTYLNVQRE+GTISRY
Sbjct  86    RQDQCIYNTTYLNVQRENGTISRY  109
```

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Orosomucoid 1 [Homo sapiens]

Sequence ID: gb|AAI43315.1| **Length:** 201 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 86 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
81.7 bits(185)	4e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1     RQDQCIYNTTYLNVQREDGTISRY  24
             RQDQCIYNTTYLNVQRE+GTISRY
Sbjct  86    RQDQCIYNTTYLNVQRENGTISRY  109
```

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - BBJ2CMB401R

Your search parameters were adjusted to search for a short input sequence.

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How to read this page | Blast report description

ORM1_RQDQCIYNTTYLNVQRENGTISRY_NonMod

RID BBJ2CMB401R (Expires on 01-15 08:37 am)

Query ID	lcl|218060	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	24		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

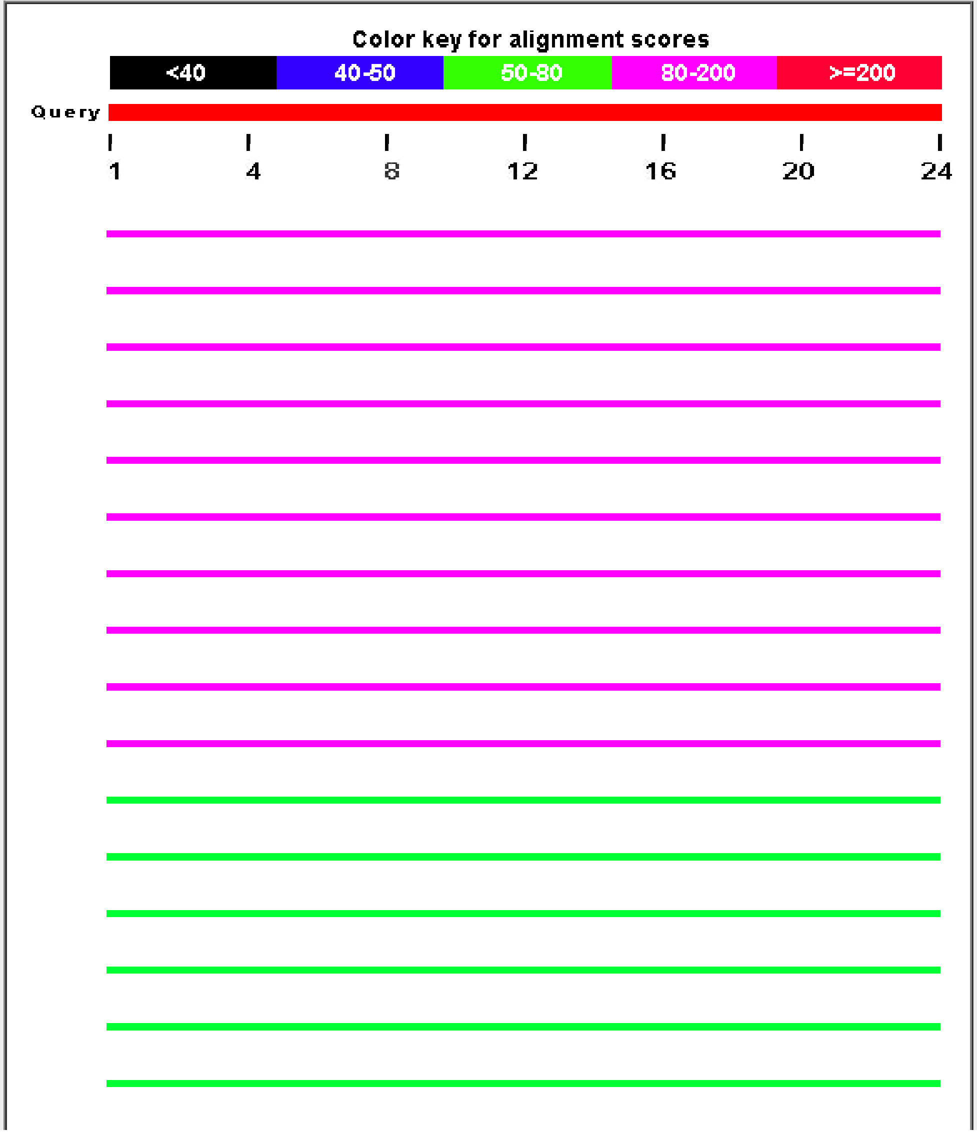
Graphic Summary

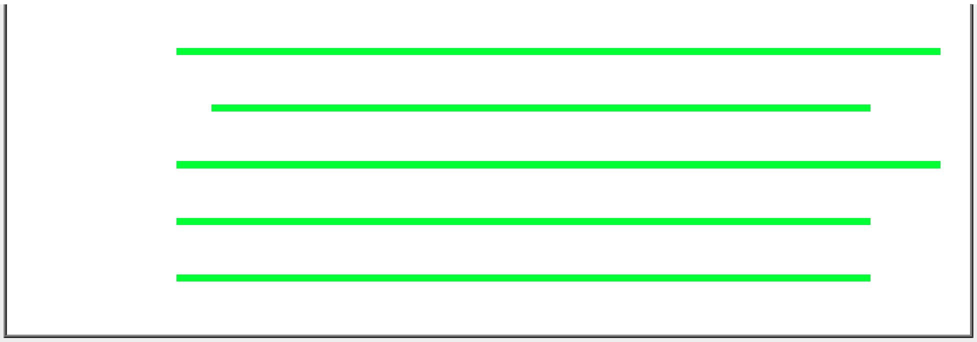
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	protein,alpha1 acid glyco [Homo sapiens]	84.2	84.2	100%	4e-17	100%	gi|229386|720005A
☐	Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein [Ho	84.2	84.2	100%	4e-17	100%	gi|285803540|3KQ0_A
☐	Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein [Hc	84.2	84.2	100%	4e-17	100%	gi|215794600|3BX6_A
☐	ORM1 [synthetic construct]	84.2	84.2	100%	4e-17	100%	gi|649120278|AIC54852.1
☐	Orosomucoid 1 [Homo sapiens]	84.2	84.2	100%	4e-17	100%	gi|219519923|AAI43315.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	84.2	84.2	100%	4e-17	100%	gi|1197209|CAA29229.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltNam	84.2	84.2	100%	4e-17	100%	gi|112877|P02763.1
☐	alpha-1-acid glycoprotein 1 precursor [Homo sapiens]	84.2	84.2	100%	4e-17	100%	gi|167857790|NP_000598.2
☐	orosomucoid 1 [synthetic construct]	84.2	84.2	100%	4e-17	100%	gi|54696406|AAV38575.1
☐	orosomucoid 1 [synthetic construct]	84.2	84.2	100%	4e-17	100%	gi|54696404|AAV38574.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	80.0	80.0	100%	1e-15	96%	gi|426362801|XP_004048543.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Pongo abelii]	80.0	80.0	100%	1e-15	96%	gi|297685191|XP_002820180.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Chlorocebus sabaeus]	78.7	78.7	100%	4e-15	92%	gi|635071762|XP_007966502.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein	77.4	77.4	100%	1e-14	92%	gi|694936727|XP_009455427.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform 1 [Nomascus leu	77.4	77.4	100%	1e-14	92%	gi|332229827|XP_003264088.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X3 [Macaca fasci	75.3	75.3	100%	5e-14	88%	gi|544492702|XP_005581033.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like isoform 2 [Macaca m	75.3	75.3	100%	5e-14	88%	gi|109110480|XP_001100289.1
☐	Alpha-1-acid glycoprotein 1 [Macaca mulatta]	75.3	75.3	100%	5e-14	88%	gi|355567499|EHH23840.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Macaca fasci	75.3	75.3	100%	6e-14	88%	gi|544492700|XP_005581032.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Macaca fasci	75.3	75.3	100%	6e-14	88%	gi|544492698|XP_005581031.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Rhinopithecus roxellana]	72.3	72.3	100%	6e-13	83%	gi|724859712|XP_010368793.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Papio anubis]	71.5	71.5	100%	1e-12	83%	gi|685591954|XP_009186482.1
☐	Chain A, Crystal Structure Of The A Variant Of Human Alpha1-Acid	68.9	68.9	100%	8e-12	79%	gi|323714404|3APU_A
☐	ORM2 [synthetic construct]	68.9	68.9	100%	8e-12	79%	gi|649120282|AIC54853.1
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	68.9	68.9	100%	8e-12	79%	gi|29170378|CAA29873.2
☐	alpha-1-acid glycoprotein 2 precursor [Homo sapiens]	68.9	68.9	100%	8e-12	79%	gi|4505529|NP_000599.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Gorilla gorilla gorilla]	68.9	68.9	100%	8e-12	79%	gi|426362807|XP_004048546.1
☐	ORM2 [Homo sapiens]	68.9	68.9	100%	8e-12	79%	gi|48145977|CAG33211.1
☐							

	PREDICTED: alpha-1-acid glycoprotein 2-like [Pan troglodytes]	68.9	68.9	100%	8e-12	79%	gi|694988125|XP_520209.3
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein	68.9	68.9	100%	1e-11	79%	gi|675802504|XP_008957108.1
☐	unnamed protein product [Homo sapiens]	66.4	66.4	100%	6e-11	75%	gi|189053338|BAG35159.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Callithrix jacchus]	60.9	60.9	83%	5e-09	85%	gi|296229919|XP_002760492.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	59.6	59.6	91%	1e-08	77%	gi|344271455|XP_003407553.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Chrysochloris asiatica]	57.5	57.5	87%	7e-08	76%	gi|586470389|XP_006865789.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X2 [Canis lupus f	57.1	57.1	91%	9e-08	68%	gi|545518002|XP_005627010.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 isoform X1 [Canis lupus f	57.1	57.1	91%	9e-08	68%	gi|345777714|XP_003431634.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Trichechus manatus la	57.1	57.1	87%	9e-08	76%	gi|471419478|XP_004391229.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Trichechus manatus	57.1	57.1	87%	9e-08	76%	gi|471419404|XP_004391192.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Trichechus manatus latir	57.1	57.1	87%	9e-08	76%	gi|471363692|XP_004372401.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Otolemur garnettii]	57.1	57.1	91%	9e-08	77%	gi|395824383|XP_003785445.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Saimiri boliviensis bolivie	55.8	55.8	91%	2e-07	68%	gi|403266135|XP_003925252.1
☐	Alpha-1-acid glycoprotein [Myotis davidii]	54.9	54.9	100%	3e-07	62%	gi|432095447|ELK26646.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	54.5	54.5	91%	6e-07	68%	gi|671034103|XP_008707881.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X2 [Tupaia c	54.1	54.1	91%	9e-07	73%	gi|562826345|XP_006142836.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	54.1	54.1	87%	9e-07	71%	gi|344271457|XP_003407554.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Mustela putorius fur	53.7	53.7	83%	1e-06	75%	gi|512022336|XP_004828368.1
☐	hypothetical protein PANDA_003840 [Ailuropoda melanoleuca]	53.2	53.2	91%	1e-06	68%	gi|281339921|EFB15505.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Orycteropus afer afer]	53.2	53.2	87%	2e-06	76%	gi|634836563|XP_007934876.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ursus maritimus]	53.2	53.2	91%	2e-06	68%	gi|671034105|XP_008707882.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ailuropoda melanoleu	53.2	53.2	91%	2e-06	68%	gi|301760029|XP_002915823.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variega	52.8	52.8	91%	2e-06	68%	gi|667321193|XP_008588097.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Galeopterus variegatus]	52.8	52.8	91%	2e-06	68%	gi|667321187|XP_008588094.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Elephantulus edwardii]	52.4	52.4	79%	3e-06	79%	gi|585676946|XP_006890779.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Tarsius syrichta]	52.0	52.0	91%	4e-06	73%	gi|640798447|XP_008055404.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Panthera tigris altaica]	52.0	52.0	83%	4e-06	70%	gi|591337606|XP_007094388.1
☐	PREDICTED: alpha-1-acid glycoprotein [Felis catus]	52.0	52.0	83%	4e-06	70%	gi|410978897|XP_003995824.1
☐	PREDICTED: LOW QUALITY PROTEIN: orosomucoid 1 [Myotis luc	52.0	52.0	100%	5e-06	59%	gi|558172686|XP_006109685.1
☐	alpha-1-acid glycoprotein [Mus musculus]	49.4	49.4	91%	3e-05	64%	gi|387176|AAA91744.1
☐	alpha-1-acid glycoprotein (AGP) precursor [Mus caroli]	49.4	49.4	91%	3e-05	64%	gi|309098|AAA37197.1
☐	RecName: Full=Alpha-1-acid glycoprotein 1; Short=AGP 1; AltNam	49.4	49.4	91%	3e-05	64%	gi|112879|P21350.1
☐	alpha-1-acid glycoprotein 2 precursor [Mus musculus]	49.4	49.4	91%	3e-05	64%	gi|6754950|NP_035146.1
☐	PREDICTED: LOW QUALITY PROTEIN: alpha-1-acid glycoprotein	49.4	49.4	87%	3e-05	76%	gi|554578835|XP_005880984.1
☐	Alpha-1-acid glycoprotein 1 [Cricetulus griseus]	49.0	49.0	95%	4e-05	65%	gi|344250545|EGW06649.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Cricetulus griseus]	49.0	49.0	95%	4e-05	65%	gi|354482623|XP_003503497.1
☐	alpha-1-acid glycoprotein 1 [Cricetulus griseus]	49.0	49.0	95%	4e-05	65%	gi|537238399|ERE86355.1
☐	alpha-1-acid glycoprotein 1 [Cricetulus griseus]	49.0	49.0	95%	4e-05	65%	gi|537238398|ERE86354.1
☐	PREDICTED: alpha-1-acid glycoprotein 2 [Pteropus alecto]	48.6	48.6	95%	6e-05	61%	gi|586524471|XP_006917195.1
☐	Alpha-1-acid glycoprotein [Pteropus alecto]	48.6	48.6	95%	6e-05	61%	gi|431900791|ELK08232.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Myotis brandtii]	48.1	48.1	91%	6e-05	63%	gi|554578831|XP_005880983.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Galeopterus variega	48.1	48.1	83%	8e-05	70%	gi|667321190|XP_008588096.1
☐	alpha-1-acid glycoprotein [Mus musculus]	47.7	47.7	91%	8e-05	68%	gi|553922|AAA91745.1
☐	mCG7142, isoform CRA_b [Mus musculus]	47.7	47.7	91%	1e-04	68%	gi|148699164|EDL31111.1
☐	alpha-1-acid glycoprotein precursor [Mus caroli]	47.7	47.7	91%	1e-04	68%	gi|309100|AAB67844.1

☐	alpha-1-acid glycoprotein 1 precursor [Mus musculus]	47.7	47.7	91%	1e-04	68%	gi|6679182|NP_032794.1
☐	RecName: Full=Alpha-1-acid glycoprotein 8; Short=AGP 8; AltNam	47.7	47.7	91%	1e-04	68%	gi|112883|P21352.1
☐	Orosomucoid 1 [Mus musculus]	47.7	47.7	91%	1e-04	68%	gi|15215270|AAH12725.1
☐	mCG7142, isoform CRA_e [Mus musculus]	47.7	47.7	91%	1e-04	68%	gi|148699167|EDL31114.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Mesocricetus auratus]	47.3	47.3	83%	2e-04	70%	gi|524950349|XP_005075189.1
☐	alpha-1-acid glycoprotein precursor [Rattus norvegicus]	46.4	46.4	83%	3e-04	75%	gi|16757980|NP_445740.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Nannospalax galili]	45.6	45.6	95%	5e-04	61%	gi|674051046|XP_008831764.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	45.6	45.6	91%	5e-04	64%	gi|558172682|XP_006099427.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	45.6	45.6	79%	6e-04	74%	gi|344271451|XP_003407551.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Loxodonta africana]	45.2	45.2	79%	8e-04	68%	gi|731463853|XP_010586317.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Camelus ferus]	44.8	44.8	83%	0.001	75%	gi|560919741|XP_006186090.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Ochotona princeps]	44.3	44.3	95%	0.001	61%	gi|504170887|XP_004595034.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	44.3	44.3	83%	0.001	70%	gi|558213865|XP_006108236.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	44.3	44.3	83%	0.001	70%	gi|558172615|XP_006099413.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Vicugna pacos]	43.9	43.9	79%	0.002	79%	gi|560978319|XP_006211428.1
☐	PREDICTED: alpha-1-acid glycoprotein-like [Peromyscus manicula	43.5	43.5	87%	0.003	67%	gi|589933663|XP_006979617.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like [Myotis lucifugus]	43.5	43.5	75%	0.003	72%	gi|558213870|XP_006108237.1
☐	Alpha-1-acid glycoprotein 1 [Heterocephalus glaber]	42.6	42.6	87%	0.004	71%	gi|351700388|EHB03307.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Heterocephalus glaber]	42.6	42.6	87%	0.005	71%	gi|512843596|XP_004885278.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Echinops telfairi]	42.6	42.6	83%	0.005	75%	gi|507712754|XP_004718018.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Echinops telfairi]	42.6	42.6	83%	0.005	75%	gi|507689354|XP_004712638.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Heterocephalus glaber]	42.6	42.6	87%	0.005	71%	gi|512975244|XP_004849700.1
☐	PREDICTED: alpha-1-acid glycoprotein 1-like [Mustela putorius fur	42.2	42.2	83%	0.006	65%	gi|511980019|XP_004807875.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Mustela putorius furo]	42.2	42.2	83%	0.006	65%	gi|511909351|XP_004774102.1
☐	PREDICTED: alpha-1-acid glycoprotein 1 [Erinaceus europaeus]	42.2	42.2	75%	0.007	72%	gi|617619058|XP_007526815.1
☐	PREDICTED: alpha-1-acid glycoprotein 2-like isoform X1 [Tupaia c	42.2	42.2	91%	0.007	68%	gi|562826343|XP_006142835.1
☐	Alpha-1-acid glycoprotein 2 [Tupaia chinensis]	42.2	42.2	91%	0.007	68%	gi|444730223|ELW70613.1

⊖ Alignments

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protein,alpha1 acid glyco

Sequence ID: gi|229386|prf||720005A **Length:** 182 **Number of Matches:** 1

Related Information

Range 1: 69 to 92 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.2 bits(191)	4e-17	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    RQDQCIYNTTYLNVQRENGTISRY  24
            RQDQCIYNTTYLNVQRENGTISRY
Sbjct  69   RQDQCIYNTTYLNVQRENGTISRY  92
```

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Chain A, Crystal Structure Of Human Alpha1-Acid Glycoprotein

Sequence ID: gi|285803540|pdb|3KQ0|A **Length:** 192 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 68 to 91 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.2 bits(191)	4e-17	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    RQDQCIYNTTYLNVQRENGTISRY  24
```

```
               RQDQCIYNTTYLNVQRENGTISRY
Sbjct  68   RQDQCIYNTTYLNVQRENGTISRY  91
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of Human Alpha 1 Acid Glycoprotein

Sequence ID: gi|215794600|pdb|3BX6|A **Length:** 192 **Number of Matches:** 1

Related Information

Range 1: 68 to 91 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.2 bits(191)	4e-17	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    RQDQCIYNTTYLNVQRENGTISRY  24
            RQDQCIYNTTYLNVQRENGTISRY
Sbjct  68   RQDQCIYNTTYLNVQRENGTISRY  91
```

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ORM1, partial [synthetic construct]

Sequence ID: gi|649120278|gb|AIC54852.1| **Length:** 201 **Number of Matches:** 1

Related Information

Range 1: 86 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.2 bits(191)	4e-17	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1     RQDQCIYNTTYLNVQRENGTISRY  24
             RQDQCIYNTTYLNVQRENGTISRY
Sbjct  86    RQDQCIYNTTYLNVQRENGTISRY  109
```

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Orosomucoid 1 [Homo sapiens]

Sequence ID: gi|219519923|gb|AAI43315.1| **Length:** 201 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 86 to 109 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.2 bits(191)	4e-17	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1     RQDQCIYNTTYLNVQRENGTISRY  24
             RQDQCIYNTTYLNVQRENGTISRY
Sbjct  86    RQDQCIYNTTYLNVQRENGTISRY  109
```

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVK0FNEX01R

Your search parameters were adjusted to search for a short input sequence.

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PI16_KSLPNFPDTSATADATGGRA_Mod

RID BVK0FNEX01R (Expires on 01-21 10:31 am)

Query ID lcl|267278
Description None
Molecule type amino acid
Query Length 20

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

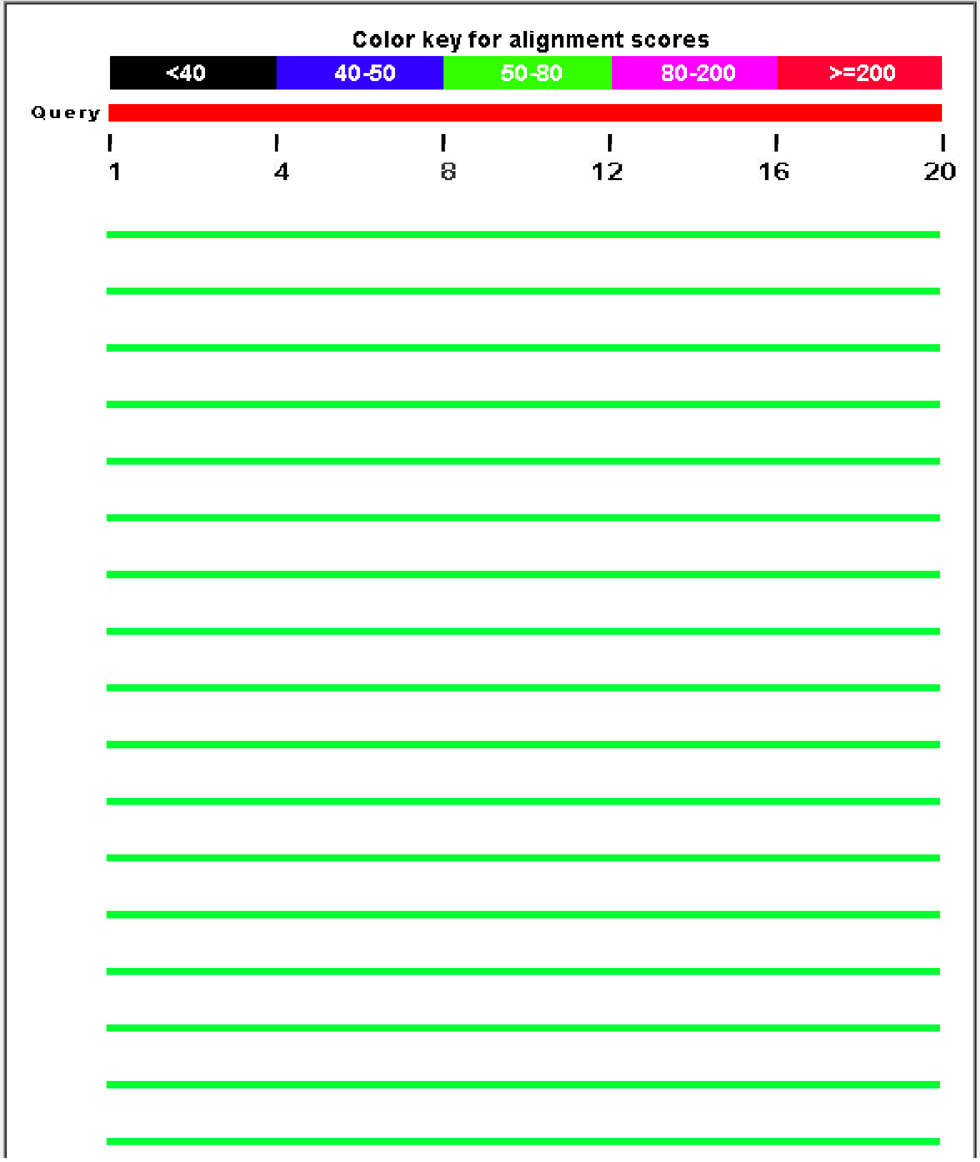
Graphic Summary

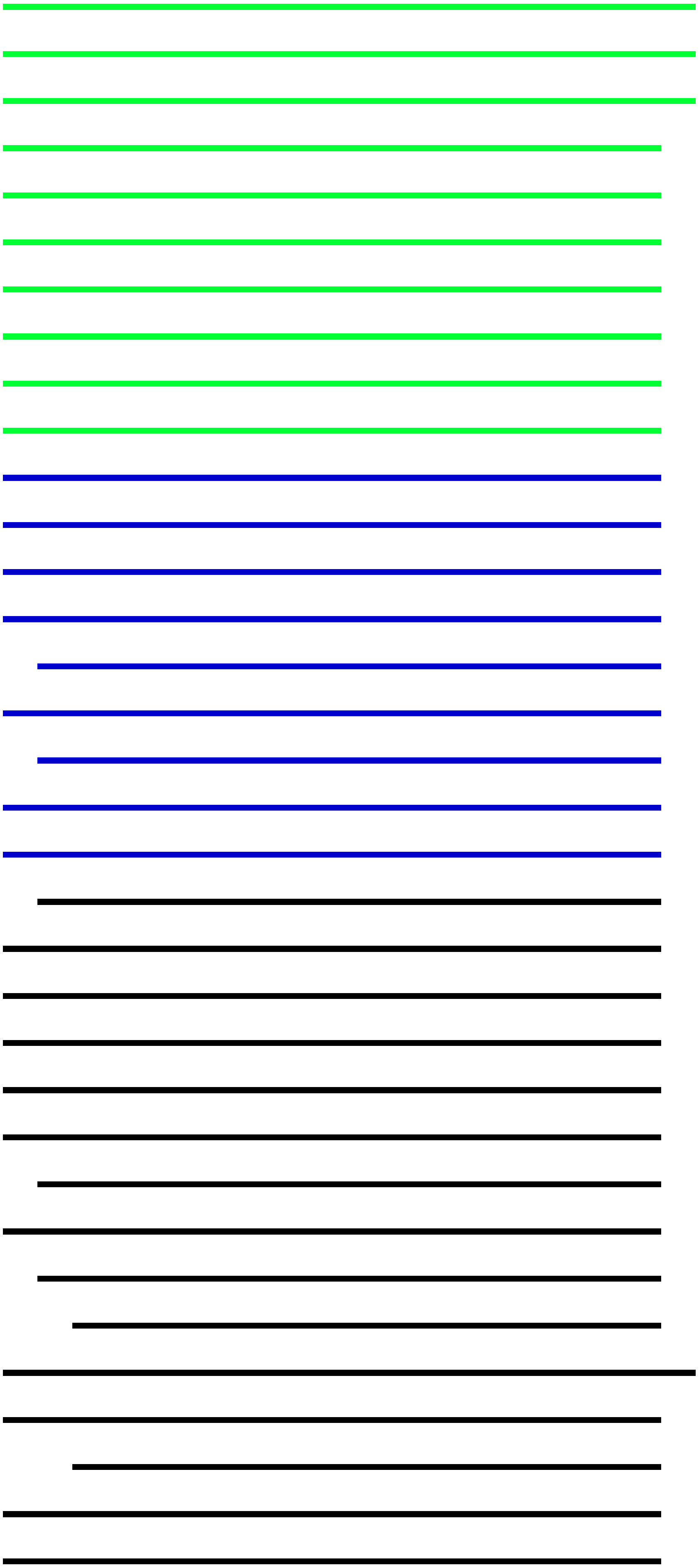
Show Conserved Domains

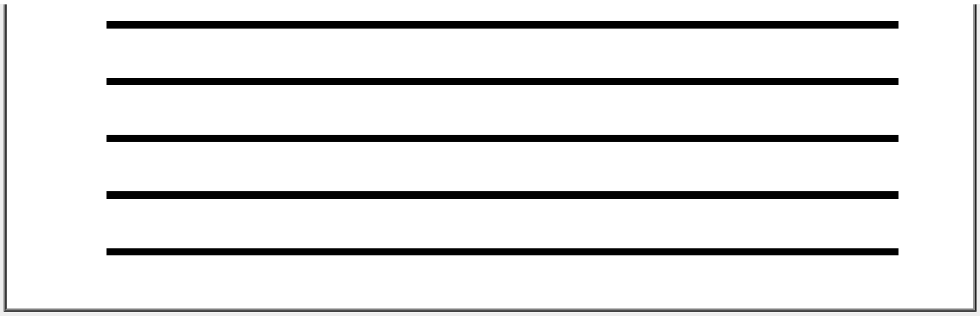
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊖ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	57.5	57.5	100%	5e-08	90%	BAG63555.1
☐	unnamed protein product [Homo sapiens]	57.5	57.5	100%	5e-08	90%	BAG64856.1
☐	unnamed protein product [Homo sapiens]	57.5	57.5	100%	5e-08	90%	BAG35648.1
☐	peptidase inhibitor 16 precursor [Homo sapiens]	57.5	57.5	100%	5e-08	90%	NP_699201.2
☐	PREDICTED: peptidase inhibitor 16 isoform 1 [Gorilla gorilla gorilla]	57.5	57.5	100%	5e-08	90%	XP_004043978.1
☐	unnamed protein product [Homo sapiens]	57.5	57.5	100%	5e-08	90%	BAC11640.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Pan paniscus]	57.5	57.5	100%	5e-08	90%	XP_008970553.1
☐	PREDICTED: peptidase inhibitor 16 [Pongo abelii]	57.5	57.5	100%	5e-08	90%	XP_003776875.1
☐	peptidase inhibitor 16 precursor [Pan troglodytes]	57.5	57.5	100%	5e-08	90%	NP_001267303.1
☐	Peptidase inhibitor 16 [Homo sapiens]	57.5	57.5	100%	5e-08	90%	AAH35634.2
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Pan troglodytes]	57.5	57.5	100%	5e-08	90%	XP_009449371.1
☐	peptidase inhibitor 16, isoform CRA_a [Homo sapiens]	57.5	57.5	100%	5e-08	90%	EAX03923.1
☐	PREDICTED: peptidase inhibitor 16 isoform X3 [Chlorocebus sabaeus]	54.1	54.1	100%	7e-07	85%	XP_007970953.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Chlorocebus sabaeus]	54.1	54.1	100%	7e-07	85%	XP_007970951.1
☐	PREDICTED: peptidase inhibitor 16 [Nomascus leucogenys]	53.2	53.2	100%	1e-06	85%	XP_003276952.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Papio anubis]	53.2	53.2	100%	1e-06	85%	XP_009203298.1
☐	PREDICTED: peptidase inhibitor 16 [Rhinopithecus roxellana]	52.8	52.8	100%	2e-06	85%	XP_010388006.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Macaca fascicularis]	52.8	52.8	100%	2e-06	85%	XP_005553197.1
☐	hypothetical protein EGK_14847 [Macaca mulatta]	52.8	52.8	100%	2e-06	85%	EHH18280.1
☐	peptidase inhibitor 16 precursor [Macaca mulatta]	52.8	52.8	100%	2e-06	85%	NP_001253247.1
☐	PREDICTED: LOW QUALITY PROTEIN: peptidase inhibitor 16 [Callithrix jacc	52.0	52.0	95%	4e-06	84%	XP_008992599.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Saimiri boliviensis boliviensis	52.0	52.0	95%	4e-06	84%	XP_010332401.1
☐	PREDICTED: peptidase inhibitor 16 [Myotis davidii]	51.5	51.5	95%	5e-06	89%	XP_006759097.1
☐	Peptidase inhibitor 16 [Myotis brandtii]	50.3	50.3	95%	1e-05	84%	EPQ01732.1
☐	PREDICTED: peptidase inhibitor 16 [Myotis brandtii]	50.3	50.3	95%	1e-05	84%	XP_005856781.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Galeopterus variegatus]	50.3	50.3	95%	1e-05	84%	XP_008566645.1
☐	PREDICTED: peptidase inhibitor 16 [Myotis lucifugus]	50.3	50.3	95%	1e-05	84%	XP_006107008.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Equus caballus]	48.6	48.6	95%	5e-05	84%	XP_001917971.2
☐	PREDICTED: peptidase inhibitor 16 [Eptesicus fuscus]	47.7	47.7	95%	1e-04	79%	XP_008150183.1

☐	PREDICTED: peptidase inhibitor 16 [Tarsius syrichta]	46.9	46.9	95%	2e-04	79%	XP_008062768.1
☐	PREDICTED: peptidase inhibitor 16 [Ceratotherium simum simum]	43.9	43.9	95%	0.002	79%	XP_004424519.1
☐	PREDICTED: peptidase inhibitor 16 [Orycteropus afer afer]	41.8	41.8	90%	0.008	78%	XP_007937600.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Nannospalax galili]	40.9	40.9	95%	0.016	74%	XP_008838284.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Mesocricetus auratus]	40.5	40.5	90%	0.021	78%	XP_005084971.1
☐	PREDICTED: LOW QUALITY PROTEIN: peptidase inhibitor 16 [Ursus maritim	40.1	40.1	95%	0.029	74%	XP_008691702.1
☐	PREDICTED: peptidase inhibitor 16-like [Ailuropoda melanoleuca]	40.1	40.1	95%	0.029	74%	XP_002930583.1
☐	PREDICTED: peptidase inhibitor 16 [Microtus ochrogaster]	39.7	39.7	90%	0.040	78%	XP_005360513.1
☐	PREDICTED: peptidase inhibitor 16-like [Leptonychotes weddellii]	37.5	37.5	95%	0.18	74%	XP_006736333.1
☐	PREDICTED: peptidase inhibitor 16-like [Leptonychotes weddellii]	37.5	37.5	95%	0.19	74%	XP_006736335.1
☐	PREDICTED: peptidase inhibitor 16 [Panthera tigris altaica]	37.5	37.5	95%	0.19	68%	XP_007085400.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Felis catus]	37.5	37.5	95%	0.19	68%	XP_006931722.1
☐	PREDICTED: peptidase inhibitor 16 [Odobenus rosmarus divergens]	37.5	37.5	95%	0.19	74%	XP_004409837.1
☐	PREDICTED: peptidase inhibitor 16 [Otolemur garnettii]	37.5	37.5	90%	0.19	72%	XP_003789199.1
☐	PREDICTED: peptidase inhibitor 16 [Octodon degus]	37.1	37.1	95%	0.26	68%	XP_004624495.1
☐	PREDICTED: peptidase inhibitor 16 [Erinaceus europaeus]	35.4	35.4	90%	0.89	72%	XP_007517881.1
☐	rCG60935 [Rattus norvegicus]	34.6	34.6	85%	1.6	71%	EDL96962.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Tupaia chinensis]	34.6	34.6	100%	1.6	70%	XP_006148688.1
☐	PREDICTED: peptidase inhibitor 16 [Ochotona princeps]	34.6	34.6	95%	1.6	63%	XP_004590384.1
☐	peptidase inhibitor 16 precursor [Rattus norvegicus]	34.6	34.6	85%	1.7	71%	NP_001163952.1
☐	PREDICTED: peptidase inhibitor 16 isoform X2 [Bos taurus]	34.1	34.1	95%	2.2	68%	XP_010816416.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Bison bison bison]	34.1	34.1	95%	2.2	68%	XP_010846978.1
☐	peptidase inhibitor 16 precursor [Bos taurus]	34.1	34.1	95%	2.2	68%	NP_001019658.1
☐	PREDICTED: peptidase inhibitor 16 [Bos mutus]	34.1	34.1	95%	2.2	68%	XP_005907794.1
☐	peptidase inhibitor 16 precursor [Camelus ferus]	33.7	33.7	95%	3.0	68%	EPY72881.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Lipotes vexillifer]	33.7	33.7	95%	3.1	68%	XP_007467342.1
☐	PREDICTED: peptidase inhibitor 16 [Vicugna pacos]	33.7	33.7	95%	3.1	68%	XP_006202118.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Camelus ferus]	33.7	33.7	95%	3.1	68%	XP_006195354.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Balaenoptera acutorostrata s	33.7	33.7	95%	3.1	68%	XP_007198004.1
☐	PREDICTED: peptidase inhibitor 16 [Physeter catodon]	33.7	33.7	95%	3.1	68%	XP_007105444.1
☐	PREDICTED: peptidase inhibitor 16 isoform 1 [Tursiops truncatus]	33.7	33.7	95%	3.1	68%	XP_004324065.1
☐	PREDICTED: peptidase inhibitor 16 isoform 1 [Orcinus orca]	33.7	33.7	95%	3.1	68%	XP_004267706.1
☐	PREDICTED: peptidase inhibitor 16 [Chrysochloris asiatica]	33.7	33.7	90%	3.1	67%	XP_006860637.1
☐	peptidase inhibitor 16 [Mus musculus]	32.9	32.9	90%	5.7	67%	EDL22615.1
☐	peptidase inhibitor 16 precursor [Sus scrofa]	32.9	32.9	95%	5.7	68%	NP_001230456.1
☐	Pi16 protein [Mus musculus]	32.9	32.9	90%	5.7	67%	AAH39124.1
☐	cysteine-rich protease inhibitor [Mus musculus]	32.9	32.9	90%	5.7	67%	BAB03398.1
☐	RecName: Full=Peptidase inhibitor 16; Short=PI-16; AltName: Full=Cysteine-r	32.9	32.9	90%	5.7	67%	Q9ET66.1
☐	peptidase inhibitor 16 precursor [Mus musculus]	32.9	32.9	90%	5.7	67%	NP_076223.3
☐	PREDICTED: LOW QUALITY PROTEIN: peptidase inhibitor 16 [Cavia porcell	32.9	32.9	95%	5.7	63%	XP_003473716.2
☐	NADH-quinone oxidoreductase subunit E [Hyphomonas polymorpha PS728]	32.0	32.0	85%	10	63%	KCZ97754.1
☐	hypothetical protein [Streptomyces exfoliatus]	31.6	31.6	75%	14	75%	WP_024758634.1
☐	hypothetical protein HMPREF1624_02308 [Sporothrix schenckii ATCC 58251	31.6	31.6	60%	15	83%	ERT01071.1
☐	hypothetical protein [Deinococcus aquatilis]	31.6	31.6	65%	15	85%	WP_019009558.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Bubalus bubalis]	31.2	31.2	95%	20	63%	XP_006050482.1

☐	N-succinyldiaminopimelate aminotransferase [Mycobacterium avium]	30.8	30.8	70%	23	73%	WP_033721577.1
☐	hypothetical protein [Xanthobacteraceae bacterium 501b]	30.8	30.8	75%	26	65%	WP_018963918.1
☐	protein phnH [Ancylobacter sp. FA202]	30.8	30.8	75%	26	65%	WP_026221082.1
☐	possible N-succinyldiaminopimelate aminotransferase [Mycobacterium parasc	30.8	30.8	70%	27	73%	WP_007168466.1
☐	PREDICTED: peptidase inhibitor 16 [Trichechus manatus latirostris]	30.8	30.8	85%	27	65%	XP_004379471.1
☐	hypothetical protein [Sphaerotilus natans]	30.8	30.8	70%	27	73%	WP_037483745.1
☐	PREDICTED: uncharacterized protein LOC101454915 [Ceratitis capitata]	30.8	30.8	80%	28	69%	XP_004526076.1
☐	hypothetical protein NEMVEDRAFT_v1g222466 [Nematostella vectensis]	30.3	30.3	70%	37	67%	XP_001621007.1
☐	hypothetical protein NEMVEDRAFT_v1g225176 [Nematostella vectensis]	30.3	30.3	70%	38	67%	XP_001618412.1
☐	PREDICTED: peptidase inhibitor 16 isoformX1 [Canis lupus familiaris]	30.3	30.3	80%	38	69%	XP_538890.2
☐	PREDICTED: peptidase inhibitor 16 [Ictidomys tridecemlineatus]	30.3	30.3	95%	38	63%	XP_005318805.1
☐	hypothetical protein NEMVEDRAFT_v1g223650 [Nematostella vectensis]	30.3	30.3	70%	38	67%	XP_001619942.1
☐	predicted protein [Nematostella vectensis]	30.3	30.3	70%	38	67%	XP_001623494.1
☐	hypothetical protein NEMVEDRAFT_v1g222313 [Nematostella vectensis]	30.3	30.3	70%	38	67%	XP_001621153.1
☐	hypothetical protein L484_012927 [Morus notabilis]	30.3	30.3	70%	38	73%	XP_010092586.1
☐	hypothetical protein NEMVEDRAFT_v1g222415 [Nematostella vectensis]	30.3	30.3	70%	38	67%	XP_001621055.1
☐	predicted protein [Nematostella vectensis]	30.3	30.3	70%	38	67%	XP_001623496.1
☐	predicted protein [Nematostella vectensis]	30.3	30.3	70%	38	67%	XP_001625772.1
☐	similar to DNA polymerase zeta catalytic subunit [Botryotinia fuckeliana T4]	30.3	30.3	70%	38	71%	CCD54747.1
☐	hypothetical protein BC1G_15151 [Botryotinia fuckeliana B05.10]	30.3	30.3	70%	38	71%	XP_001546441.1
☐	hypothetical protein [Curvibacter lanceolatus]	29.9	29.9	75%	51	67%	WP_019578416.1
☐	PREDICTED: peptidase inhibitor 16 [Pantholops hodgsonii]	29.9	29.9	95%	52	63%	XP_005964334.1
☐	PREDICTED: peptidase inhibitor 16 [Capra hircus]	29.9	29.9	95%	52	63%	XP_005696333.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Chinchilla lanigera]	29.9	29.9	95%	52	63%	XP_005389688.1
☐	hypothetical protein NECHADRAFT_38494 [Nectria haematococca mpVI 77-1	29.9	29.9	55%	52	83%	XP_003052195.1
☐	hypothetical protein [Halorubrum californiense]	29.5	29.5	50%	71	90%	WP_008440609.1

Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG63555.1| **Length:** 234 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 167 to 186 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.5 bits(128)	5e-08	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KSLPNFPDTSATADATGGRA  20
            KSLPNFP+TSATA+ATGGRA
Sbjct  167  KSLPNFPNTSATANATGGRA  186
```

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unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG64856.1| **Length:** 315 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 248 to 267 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.5 bits(128)	5e-08	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KSLPNFPDTSATADATGGRA  20
            KSLPNFP+TSATA+ATGGRA
Sbjct  248  KSLPNFPNTSATANATGGRA  267
```

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unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG35648.1| **Length:** 428 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 361 to 380 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.5 bits(128)	5e-08	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KSLPNFPDTSATADATGGRA  20
            KSLPNFP+TSATA+ATGGRA
Sbjct  361  KSLPNFPNTSATANATGGRA  380
```

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peptidase inhibitor 16 precursor [Homo sapiens]

Sequence ID: ref|NP_699201.2| **Length:** 463 **Number of Matches:** 1

See 5 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 396 to 415 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.5 bits(128)	5e-08	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KSLPNFPDTSATADATGGRA  20
            KSLPNFP+TSATA+ATGGRA
Sbjct  396  KSLPNFPNTSATANATGGRA  415
```

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PREDICTED: peptidase inhibitor 16 isoform 1 [Gorilla gorilla gorilla]

Sequence ID: ref|XP_004043978.1| **Length:** 463 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 396 to 415 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.5 bits(128)	5e-08	18/20(90%)	20/20(100%)	0/20(0%)

```
Query  1    KSLPNFPDTSATADATGGRA  20
            KSLPNFP+TSATA+ATGGRA
Sbjct  396  KSLPNFPNTSATANATGGRA  415
```

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BBJ6AW0P01R**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

PI16_KSLPNFPNTSATANATGGRA_NonMod

RID BBJ6AW0P01R (Expires on 01-15 08:39 am)

Query ID lcl|257909
Description None
Molecule type amino acid
Query Length 20

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

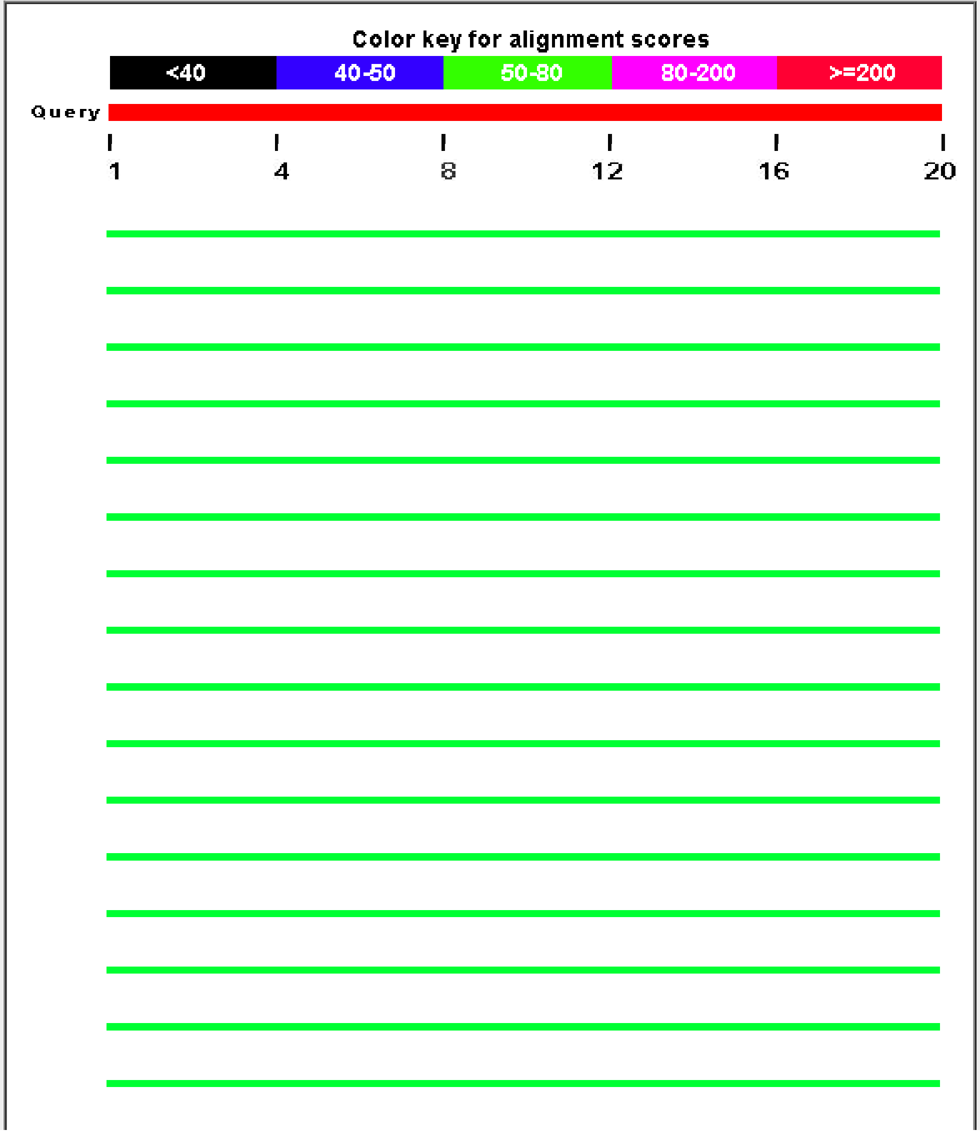
Graphic Summary

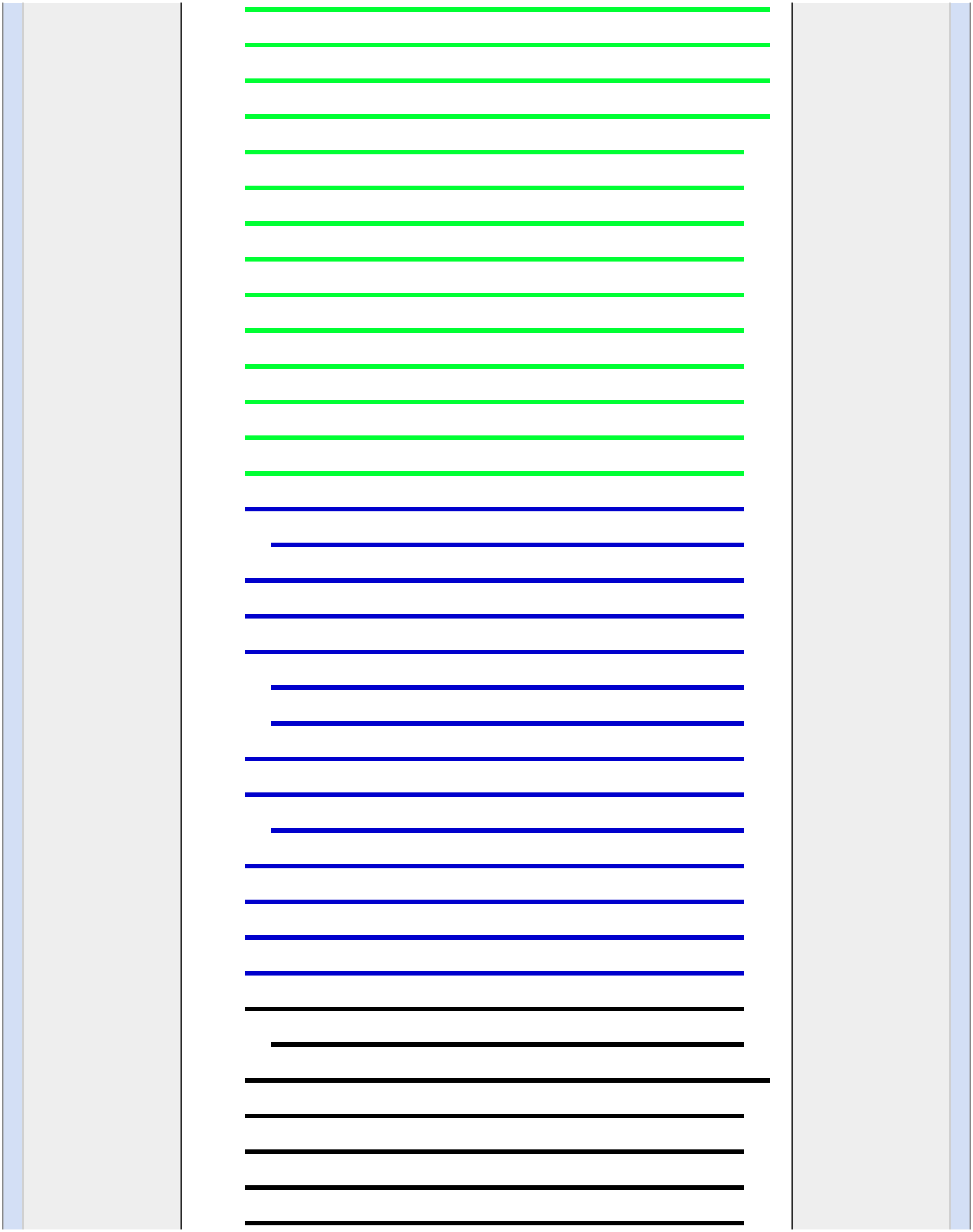
Show Conserved Domains

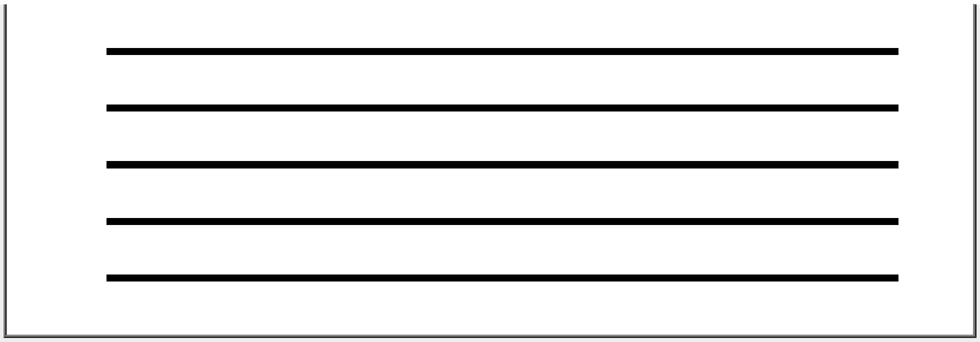
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	unnamed protein product [Homo sapiens]	62.6	62.6	100%	8e-10	100%	gi|194378780|BAG63555.1
☐	unnamed protein product [Homo sapiens]	62.6	62.6	100%	9e-10	100%	gi|194384166|BAG64856.1
☐	unnamed protein product [Homo sapiens]	62.6	62.6	100%	9e-10	100%	gi|189053482|BAG35648.1
☐	peptidase inhibitor 16 precursor [Homo sapiens]	62.6	62.6	100%	9e-10	100%	gi|70780384|NP_699201.2
☐	PREDICTED: peptidase inhibitor 16 isoform 1 [Gorilla gorilla gorilla	62.6	62.6	100%	9e-10	100%	gi|426352977|XP_004043978.1
☐	unnamed protein product [Homo sapiens]	62.6	62.6	100%	9e-10	100%	gi|22761577|BAC11640.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Pan paniscus]	62.6	62.6	100%	9e-10	100%	gi|675750658|XP_008970553.1
☐	PREDICTED: peptidase inhibitor 16 [Pongo abelii]	62.6	62.6	100%	9e-10	100%	gi|395737189|XP_003776875.1
☐	peptidase inhibitor 16 precursor [Pan troglodytes]	62.6	62.6	100%	9e-10	100%	gi|525342653|NP_001267303.1
☐	Peptidase inhibitor 16 [Homo sapiens]	62.6	62.6	100%	9e-10	100%	gi|112180443|AAH35634.2
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Pan troglodytes]	62.6	62.6	100%	9e-10	100%	gi|694916015|XP_009449371.1
☐	peptidase inhibitor 16, isoform CRA_a [Homo sapiens]	62.6	62.6	100%	9e-10	100%	gi|119624328|EAX03923.1
☐	PREDICTED: peptidase inhibitor 16 isoform X3 [Chlorocebus sabae	59.2	59.2	100%	1e-08	95%	gi|635095459|XP_007970953.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Chlorocebus sabae	59.2	59.2	100%	1e-08	95%	gi|635095455|XP_007970951.1
☐	PREDICTED: peptidase inhibitor 16 [Nomascus leucogenys]	58.3	58.3	100%	3e-08	95%	gi|332255663|XP_003276952.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Papio anubis]	58.3	58.3	100%	3e-08	95%	gi|685536357|XP_009203298.1
☐	PREDICTED: peptidase inhibitor 16 [Rhinopithecus roxellana]	57.9	57.9	100%	4e-08	95%	gi|724947508|XP_010388006.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Macaca fasciculari	57.9	57.9	100%	4e-08	95%	gi|544428280|XP_005553197.1
☐	hypothetical protein EGK_14847 [Macaca mulatta]	57.9	57.9	100%	4e-08	95%	gi|355561648|EHH18280.1
☐	peptidase inhibitor 16 precursor [Macaca mulatta]	57.9	57.9	100%	4e-08	95%	gi|388453293|NP_001253247.1
☐	PREDICTED: LOW QUALITY PROTEIN: peptidase inhibitor 16 [Ca	57.1	57.1	95%	7e-08	95%	gi|675652418|XP_008992599.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Saimiri boliviensis	57.1	57.1	95%	7e-08	95%	gi|725556967|XP_010332401.1
☐	Peptidase inhibitor 16 [Myotis brandtii]	55.4	55.4	95%	3e-07	95%	gi|521019944|EPQ01732.1
☐	PREDICTED: peptidase inhibitor 16 [Myotis brandtii]	55.4	55.4	95%	3e-07	95%	gi|554523779|XP_005856781.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Galeopterus varieg	55.4	55.4	95%	3e-07	95%	gi|667258683|XP_008566645.1
☐	PREDICTED: peptidase inhibitor 16 [Myotis lucifugus]	55.4	55.4	95%	3e-07	95%	gi|558207906|XP_006107008.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Equus caballus]	53.7	53.7	95%	1e-06	95%	gi|545198103|XP_001917971.2
☐	PREDICTED: peptidase inhibitor 16 [Eptesicus fuscus]	52.8	52.8	95%	2e-06	89%	gi|641721000|XP_008150183.1
☐							

	PREDICTED: peptidase inhibitor 16 [Tarsius syrichta]	52.0	52.0	95%	4e-06	89%	gi|640812236|XP_008062768.1
☐	PREDICTED: peptidase inhibitor 16 [Myotis davidii]	51.5	51.5	95%	5e-06	89%	gi|584077898|XP_006759097.1
☐	PREDICTED: peptidase inhibitor 16 [Ceratotherium simum simum]	49.0	49.0	95%	3e-05	89%	gi|478500399|XP_004424519.1
☐	PREDICTED: peptidase inhibitor 16 [Orycteropus afer afer]	46.9	46.9	90%	2e-04	89%	gi|634844182|XP_007937600.1
☐	PREDICTED: LOW QUALITY PROTEIN: peptidase inhibitor 16 [Urs	45.2	45.2	95%	6e-04	84%	gi|671001670|XP_008691702.1
☐	PREDICTED: peptidase inhibitor 16-like [Ailuropoda melanoleuca]	45.2	45.2	95%	6e-04	84%	gi|301791231|XP_002930583.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Nannospalax galili]	45.2	45.2	95%	6e-04	79%	gi|674062972|XP_008838284.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Mesocricetus aurat	44.8	44.8	90%	9e-04	83%	gi|524970206|XP_005084971.1
☐	PREDICTED: peptidase inhibitor 16 [Microtus ochrogaster]	43.9	43.9	90%	0.002	83%	gi|532035229|XP_005360513.1
☐	PREDICTED: peptidase inhibitor 16 [Panthera tigris altaica]	42.6	42.6	95%	0.004	79%	gi|591318271|XP_007085400.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Felis catus]	42.6	42.6	95%	0.004	79%	gi|586986384|XP_006931722.1
☐	PREDICTED: peptidase inhibitor 16 [Otolemur garnettii]	42.6	42.6	90%	0.004	83%	gi|395832276|XP_003789199.1
☐	PREDICTED: peptidase inhibitor 16-like [Leptonychotes weddellii]	41.4	41.4	95%	0.010	79%	gi|585168534|XP_006736333.1
☐	PREDICTED: peptidase inhibitor 16-like [Leptonychotes weddellii]	41.4	41.4	95%	0.010	79%	gi|585168539|XP_006736335.1
☐	PREDICTED: peptidase inhibitor 16 [Octodon degus]	41.4	41.4	95%	0.011	74%	gi|507618080|XP_004624495.1
☐	PREDICTED: peptidase inhibitor 16 [Odobenus rosmarus divergens	41.4	41.4	95%	0.011	79%	gi|472380880|XP_004409837.1
☐	PREDICTED: peptidase inhibitor 16 [Ochotona princeps]	39.7	39.7	95%	0.038	74%	gi|504157725|XP_004590384.1
☐	PREDICTED: peptidase inhibitor 16 [Chrysochloris asiatica]	38.8	38.8	90%	0.072	78%	gi|586459954|XP_006860637.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Tupaia chinensis]	38.4	38.4	100%	0.096	75%	gi|562839023|XP_006148688.1
☐	peptidase inhibitor 16 precursor [Bos taurus]	38.4	38.4	95%	0.096	74%	gi|66792752|NP_001019658.1
☐	PREDICTED: peptidase inhibitor 16 [Bos mutus]	38.4	38.4	95%	0.096	74%	gi|555992031|XP_005907794.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Bos taurus]	38.4	38.4	95%	0.097	74%	gi|529002755|XP_005223367.1
☐	peptidase inhibitor 16 precursor [Camelus ferus]	38.0	38.0	95%	0.13	74%	gi|528753222|EPY72881.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Lipotes vexillifer]	38.0	38.0	95%	0.13	74%	gi|602714250|XP_007467342.1
☐	PREDICTED: peptidase inhibitor 16 [Vicugna pacos]	38.0	38.0	95%	0.13	74%	gi|560959329|XP_006202118.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Camelus ferus]	38.0	38.0	95%	0.13	74%	gi|560939134|XP_006195354.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Balaenoptera acut	38.0	38.0	95%	0.13	74%	gi|594626758|XP_007198004.1
☐	PREDICTED: peptidase inhibitor 16 [Physeter catodon]	38.0	38.0	95%	0.13	74%	gi|593718128|XP_007105444.1
☐	PREDICTED: peptidase inhibitor 16 isoform 1 [Tursiops truncatus]	38.0	38.0	95%	0.13	74%	gi|470637507|XP_004324065.1
☐	PREDICTED: peptidase inhibitor 16 isoform 1 [Orcinus orca]	38.0	38.0	95%	0.13	74%	gi|465996930|XP_004267706.1
☐	rCG60935 [Rattus norvegicus]	37.1	37.1	85%	0.24	76%	gi|149043511|EDL96962.1
☐	peptidase inhibitor 16 precursor [Rattus norvegicus]	37.1	37.1	85%	0.24	76%	gi|281427227|NP_001163952.1
☐	PREDICTED: LOW QUALITY PROTEIN: peptidase inhibitor 16 [Ca	37.1	37.1	95%	0.25	68%	gi|514468581|XP_003473716.2
☐	PREDICTED: peptidase inhibitor 16 [Trichechus manatus latirostris	35.8	35.8	85%	0.61	76%	gi|471388850|XP_004379471.1
☐	peptidase inhibitor 16 [Mus musculus]	35.4	35.4	90%	0.83	72%	gi|148690668|EDL22615.1
☐	PREDICTED: peptidase inhibitor 16 [Erinaceus europaeus]	35.4	35.4	90%	0.84	72%	gi|617578354|XP_007517881.1
☐	PREDICTED: peptidase inhibitor 16 [Ictidomys tridecemlineatus]	35.4	35.4	95%	0.84	74%	gi|532065895|XP_005318805.1
☐	Pi16 protein [Mus musculus]	35.4	35.4	90%	0.84	72%	gi|24657486|AAH39124.1
☐	cysteine-rich protease inhibitor [Mus musculus]	35.4	35.4	90%	0.84	72%	gi|9558454|BAB03398.1
☐	RecName: Full=Peptidase inhibitor 16; Short=PI-16; AltName: Full=	35.4	35.4	90%	0.84	72%	gi|81868436|Q9ET66.1
☐	peptidase inhibitor 16 precursor [Mus musculus]	35.4	35.4	90%	0.84	72%	gi|116089320|NP_076223.3
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Bubalus bubalis]	35.4	35.4	95%	0.84	68%	gi|594052332|XP_006050482.1
☐	PREDICTED: peptidase inhibitor 16 isoformX1 [Canis lupus familiar	34.1	34.1	80%	2.1	75%	gi|73972735|XP_538890.2
☐	PREDICTED: peptidase inhibitor 16 [Pantholops hodgsonii]	34.1	34.1	95%	2.1	68%	gi|556737488|XP_005964334.1
☐	PREDICTED: peptidase inhibitor 16 [Capra hircus]	34.1	34.1	95%	2.1	68%	gi|548516991|XP_005696333.1

☐	PREDICTED: peptidase inhibitor 16 [Loxodonta africana]	34.1	34.1	90%	2.1	72%	gi|344264366|XP_003404263.1
☐	peptidase inhibitor 16 precursor [Sus scrofa]	33.7	33.7	95%	2.9	68%	gi|343488483|NP_001230456.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Chinchilla lanigera]	32.5	32.5	95%	7.3	68%	gi|533150911|XP_005389688.1
☐	PREDICTED: peptidase inhibitor 16 [Jaculus jaculus]	32.0	32.0	80%	10	63%	gi|507531495|XP_004649825.1
☐	predicted protein [Trichoderma reesei QM6a]	30.8	30.8	60%	26	83%	gi|589097893|XP_006960969.1
☐	hypothetical protein M419DRAFT_93886 [Trichoderma reesei RUT	30.8	30.8	60%	26	83%	gi|572283336|ETS06310.1
☐	PREDICTED: peptidase inhibitor 16 [Ovis aries]	30.8	30.8	95%	26	63%	gi|426250221|XP_004018836.1
☐	PREDICTED: uncharacterized protein LOC101454915 [Ceratitis ca	30.8	30.8	80%	26	69%	gi|498967489|XP_004526076.1
☐	PREDICTED: uncharacterized protein LOC101174950 [Oryzias lati	30.8	30.8	70%	26	79%	gi|432916756|XP_004079368.1
☐	proline:sodium symporter [Butyrivibrio sp. XPD2006]	30.3	30.3	85%	36	72%	gi|551022094|WP_022766253.1
☐	PREDICTED: probable E3 ubiquitin-protein ligase DTX2 [Apaloderm	29.9	29.9	60%	48	75%	gi|699615497|XP_009875239.1
☐	PREDICTED: zinc finger protein MAGPIE-like [Cucumis sativus]	29.9	29.9	65%	49	77%	gi|449532260|XP_004173100.1
☐	PREDICTED: zinc finger protein MAGPIE-like [Cucumis sativus]	29.9	29.9	65%	49	77%	gi|449462075|XP_004148767.1
☐	hypothetical protein BC1G_06910 [Botryotinia fuckeliana B05.10]	29.9	29.9	80%	49	57%	gi|154309979|XP_001554322.1
☐	PREDICTED: peptidase inhibitor 16 isoform X5 [Mustela putorius fu	29.9	29.9	65%	49	77%	gi|511948881|XP_004792893.1
☐	PREDICTED: peptidase inhibitor 16 [Pteropus alecto]	29.9	29.9	65%	49	77%	gi|586544516|XP_006907375.1
☐	hypothetical protein SBOR_7154 [Sclerotinia borealis F-4157]	29.9	29.9	80%	49	57%	gi|563292000|ESZ92459.1
☐	similar to carboxylesterase (secreted protein) [Botryotinia fuckeliana	29.9	29.9	80%	49	57%	gi|347836165|CCD50737.1
☐	PREDICTED: peptidase inhibitor 16 isoform X1 [Mustela putorius fu	29.9	29.9	65%	49	77%	gi|511948873|XP_004792889.1
☐	missing-in-metastasis, isoform L [Drosophila melanogaster]	29.9	29.9	65%	50	69%	gi|442622599|NP_001260748.1
☐	missing-in-metastasis, isoform J [Drosophila melanogaster]	29.9	29.9	65%	50	69%	gi|386767186|NP_001246159.1
☐	missing-in-metastasis, isoform F [Drosophila melanogaster]	29.9	29.9	65%	50	69%	gi|320543600|NP_001188869.1
☐	predicted protein [Fibroporia radiculosa]	29.5	29.5	80%	65	63%	gi|403411774|CCL98474.1
☐	hypothetical protein [Rhizobium leguminosarum]	29.5	29.5	60%	66	83%	gi|489682491|WP_003586713.1
☐	hypothetical protein P656_3637 [Acinetobacter baumannii UH1620	29.5	29.5	55%	67	82%	gi|571654387|ETQ45334.1
☐	hypothetical protein P647_3903 [Acinetobacter baumannii UH1220	29.5	29.5	55%	67	82%	gi|571613566|ETQ05804.1
☐	hypothetical protein [Tannerella sp. 6_1_58FAA_CT1]	29.5	29.5	60%	68	69%	gi|496675283|WP_009317773.1

⊖ Alignments

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194378780|dbj|BAG63555.1| **Length:** 234 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 167 to 186 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	8e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KSLPNFPNTSATANATGGRA  20
            KSLPNFPNTSATANATGGRA
Sbjct  167  KSLPNFPNTSATANATGGRA  186
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194384166|dbj|BAG64856.1| **Length:** 315 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 248 to 267 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	9e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KSLPNFPNTSATANATGGRA  20
```

```
                 KSLPNFPNTSATANATGGRA
Sbjct  248  KSLPNFPNTSATANATGGRA  267
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|189053482|dbj|BAG35648.1| **Length:** 428 **Number of Matches:** 1

Range 1: 361 to 380 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	9e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KSLPNFPNTSATANATGGRA  20
            KSLPNFPNTSATANATGGRA
Sbjct  361  KSLPNFPNTSATANATGGRA  380
```

Related Information

Gene - associated gene details

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peptidase inhibitor 16 precursor [Homo sapiens]

Sequence ID: gi|70780384|ref|NP_699201.2| **Length:** 463 **Number of Matches:** 1

See 5 more title(s)

Range 1: 396 to 415 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	9e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KSLPNFPNTSATANATGGRA  20
            KSLPNFPNTSATANATGGRA
Sbjct  396  KSLPNFPNTSATANATGGRA  415
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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PREDICTED: peptidase inhibitor 16 isoform 1 [Gorilla gorilla gorilla]

Sequence ID: gi|426352977|ref|XP_004043978.1| **Length:** 463 **Number of Matches:** 1

See 1 more title(s)

Range 1: 396 to 415 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	9e-10	20/20(100%)	20/20(100%)	0/20(0%)

```
Query  1    KSLPNFPNTSATANATGGRA  20
            KSLPNFPNTSATANATGGRA
Sbjct  396  KSLPNFPNTSATANATGGRA  415
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVKD2MV401R

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PIGR_KYAGRADLTNFPENGTFVVNIAQLSQDDSGRY_Mod

RID BVKD2MV401R (Expires on 01-21 10:38 am)

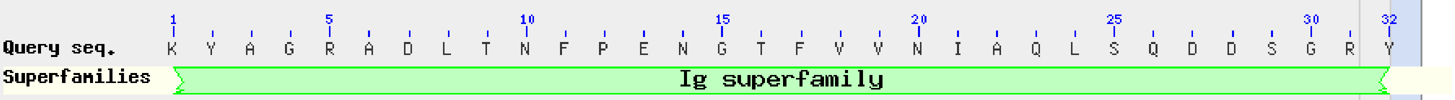
Query ID	lcl|365699	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	32		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

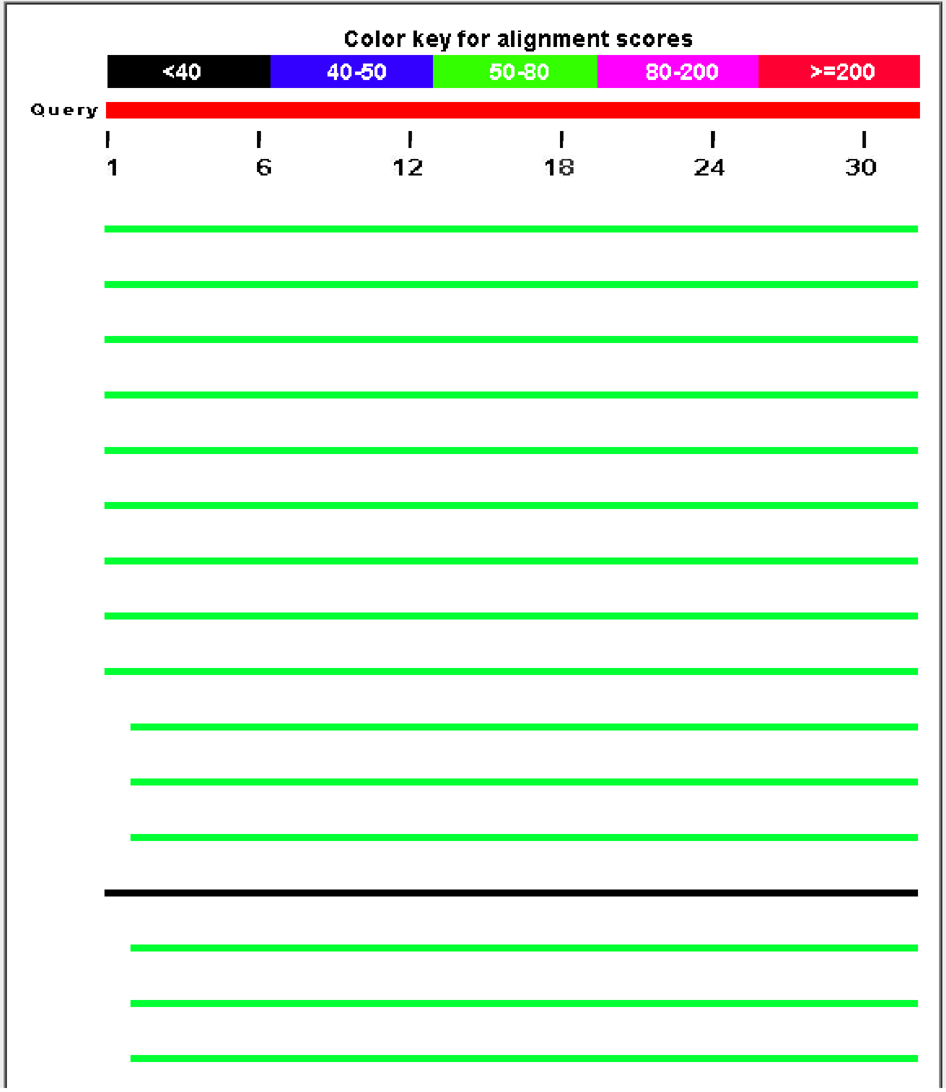
Show Conserved Domains

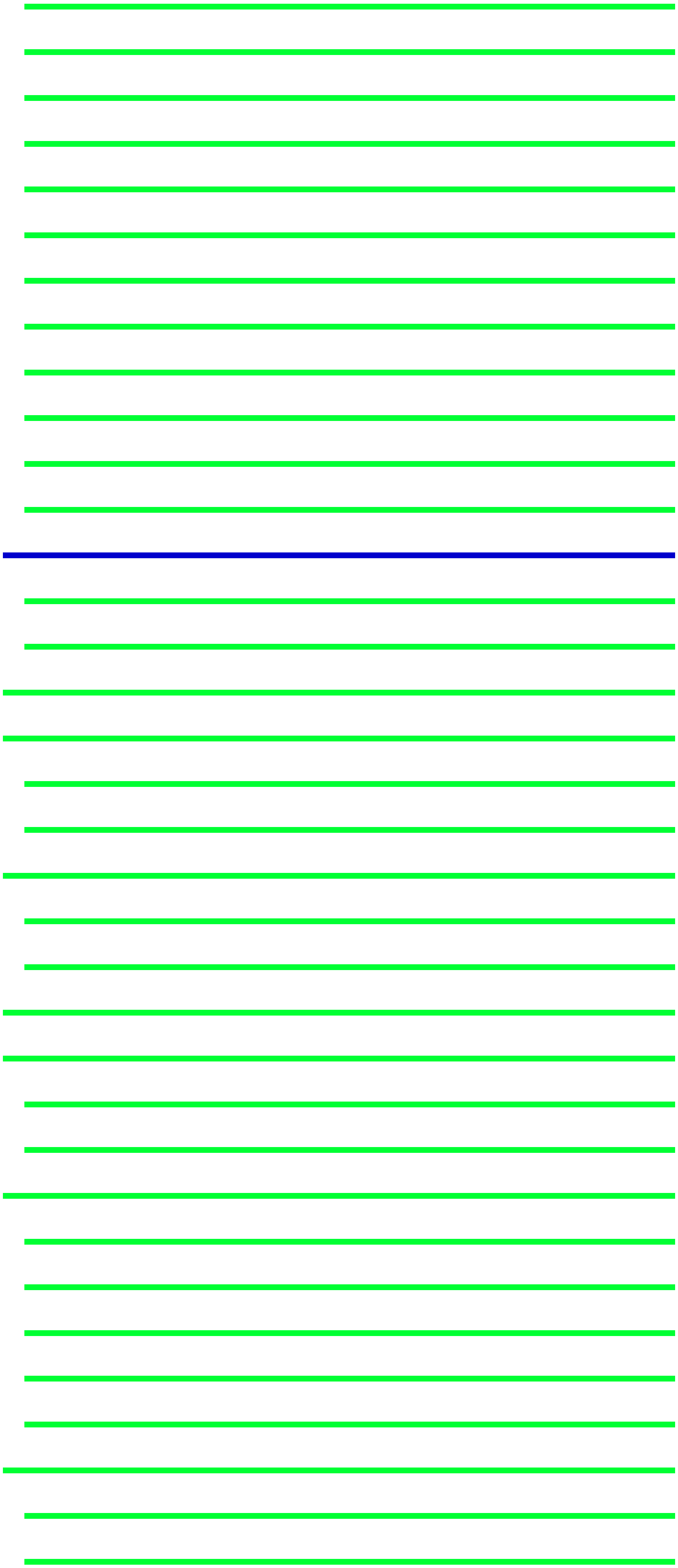
Putative conserved domains have been detected, click on the image below for detailed results.

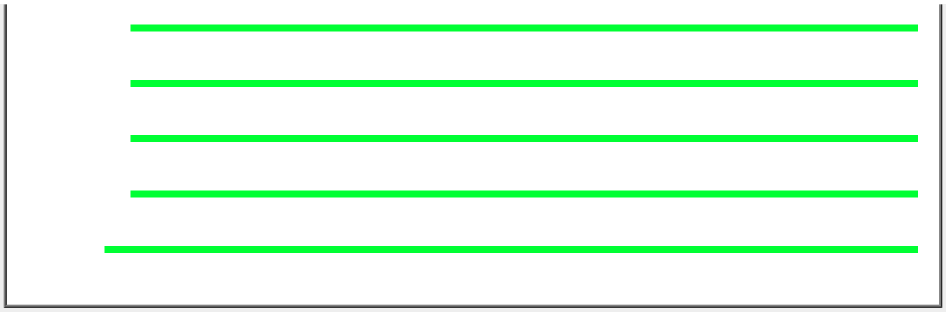


Distribution of 107 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of A Ligand-Binding Domain Of The Human Polym	68.6	68.6	100%	2e-13	97%	1XED_A
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Gorilla gorilla gor	68.2	68.2	100%	5e-12	97%	XP_004028344.1
☐	transmembrane secretory component [Homo sapiens]	68.2	68.2	100%	5e-12	97%	AAB20203.1
☐	poly-Ig receptor [Homo sapiens]	68.2	68.2	100%	5e-12	97%	AAA36102.1
☐	polymeric immunoglobulin receptor precursor [Homo sapiens]	68.2	68.2	100%	5e-12	97%	NP_002635.2
☐	PREDICTED: polymeric immunoglobulin receptor [Pan troglodytes]	68.2	68.2	100%	6e-12	97%	XP_514153.3
☐	Chain A, Solution Structure Of Human Secretory Component [Homo sapiens]	67.8	67.8	100%	6e-12	97%	2OCW_A
☐	PREDICTED: polymeric immunoglobulin receptor [Pan paniscus]	68.2	68.2	100%	6e-12	97%	XP_003822957.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Homo sapiens]	68.2	68.2	100%	6e-12	97%	XP_005273220.1
☐	hypothetical protein [Pongo abelii]	64.7	64.7	96%	1e-10	94%	CAH91352.1
☐	polymeric immunoglobulin receptor precursor [Pongo abelii]	64.7	64.7	96%	1e-10	94%	NP_001125098.1
☐	PREDICTED: polymeric immunoglobulin receptor [Callithrix jacchus]	62.8	62.8	96%	4e-10	90%	XP_002760783.1
☐	PREDICTED: polymeric immunoglobulin receptor [Rhinopithecus roxellana]	62.8	95.5	100%	5e-10	87%	XP_010363960.1
☐	PREDICTED: polymeric immunoglobulin receptor [Chlorocebus sabaeus]	62.4	62.4	96%	6e-10	90%	XP_007986846.1
☐	PREDICTED: polymeric immunoglobulin receptor-like [Galeopterus variegatus	59.3	59.3	96%	6e-10	81%	XP_008563367.1
☐	PREDICTED: polymeric immunoglobulin receptor [Papio anubis]	62.4	62.4	96%	6e-10	90%	XP_003893238.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Macaca fascicu	62.4	62.4	96%	6e-10	90%	XP_005540721.1
☐	hypothetical protein EGM_01447 [Macaca fascicularis]	62.4	62.4	96%	6e-10	90%	EHH50590.1
☐	PREDICTED: polymeric immunoglobulin receptor [Macaca mulatta]	62.4	62.4	96%	6e-10	90%	XP_001083307.2
☐	hypothetical protein EGK_01717 [Macaca mulatta]	62.4	62.4	96%	6e-10	90%	EHH15602.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Macaca fascicu	62.4	62.4	96%	7e-10	90%	XP_005540720.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Nomascus leuco	61.6	61.6	96%	1e-09	90%	XP_003273022.1
☐	PREDICTED: polymeric immunoglobulin receptor [Saimiri boliviensis boliviens	60.8	60.8	96%	2e-09	87%	XP_003930479.1
☐	PREDICTED: polymeric immunoglobulin receptor [Nannospalax galili]	59.3	59.3	96%	8e-09	84%	XP_008821506.1
☐	PREDICTED: polymeric immunoglobulin receptor [Otolemur garnettii]	58.2	58.2	96%	2e-08	81%	XP_003792254.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Ictidomys tridec	57.4	57.4	96%	3e-08	81%	XP_005329533.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Ictidomys tridec	57.4	57.4	96%	3e-08	81%	XP_005329532.1
☐	PREDICTED: polymeric immunoglobulin receptor [Camelus ferus]	57.4	57.4	96%	4e-08	74%	XP_006182326.1
☐	polymeric immunoglobulin receptor precursor [Camelus ferus]	57.4	101	100%	4e-08	74%	EQB78114.1
☐	PREDICTED: polymeric immunoglobulin receptor [Camelus bactrianus]	57.0	57.0	96%	4e-08	74%	XP_010961553.1

☐	PREDICTED: polymeric immunoglobulin receptor [Vicugna pacos]	57.0	57.0	96%	5e-08	74%	XP_006215522.1
☐	Chain A, Crystal Structure Of The 1st Ig Domain From Mouse Polymeric Immu	53.5	53.5	100%	6e-08	69%	4NOB_A
☐	PREDICTED: polymeric immunoglobulin receptor [Microtus ochrogaster]	56.6	56.6	100%	7e-08	75%	XP_005348371.1
☐	PREDICTED: polymeric immunoglobulin receptor [Tarsius syrichta]	55.8	55.8	96%	1e-07	77%	XP_008062620.1
☐	PREDICTED: polymeric immunoglobulin receptor [Leptonychotes weddellii]	55.8	55.8	96%	1e-07	77%	XP_006730466.1
☐	PREDICTED: polymeric immunoglobulin receptor [Peromyscus maniculatus b	55.5	55.5	100%	2e-07	75%	XP_006996902.1
☐	PREDICTED: polymeric immunoglobulin receptor [Bubalus bubalis]	54.7	54.7	96%	3e-07	74%	XP_006043871.1
☐	PREDICTED: polymeric immunoglobulin receptor [Tupaia chinensis]	54.3	54.3	96%	4e-07	74%	XP_006159345.1
☐	polymeric immunoglobulin receptor [Mus musculus]	53.9	53.9	100%	5e-07	69%	AAA67440.1
☐	polymeric immunoglobulin receptor precursor [Mus musculus]	53.9	53.9	100%	5e-07	69%	NP_035212.2
☐	PREDICTED: polymeric immunoglobulin receptor [Jaculus jaculus]	53.5	53.5	96%	7e-07	71%	XP_004663511.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Ovis aries]	53.5	53.5	96%	8e-07	71%	XP_004013622.1
☐	polymeric immunoglobulin receptor isoform 1 [Cricetulus griseus]	53.5	94.3	100%	8e-07	66%	ERE73918.1
☐	PREDICTED: polymeric immunoglobulin receptor [Capra hircus]	53.5	53.5	96%	8e-07	71%	XP_005690475.1
☐	PREDICTED: polymeric immunoglobulin receptor [Pantholops hodgsonii]	53.5	53.5	96%	8e-07	71%	XP_005967001.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 2 [Ovis aries]	53.5	53.5	96%	8e-07	71%	XP_004013623.1
☐	PREDICTED: polymeric immunoglobulin receptor [Felis catus]	53.1	53.1	96%	9e-07	74%	XP_006943006.1
☐	PREDICTED: polymeric immunoglobulin receptor [Panthera tigris altaica]	53.1	53.1	96%	1e-06	74%	XP_007096344.1
☐	PREDICTED: LOW QUALITY PROTEIN: polymeric immunoglobulin receptor i	53.1	53.1	100%	1e-06	66%	XP_007607970.1
☐	TPA: polymeric immunoglobulin receptor precursor [Bos taurus]	53.1	53.1	96%	1e-06	71%	DAA21480.1
☐	polymeric immunoglobulin receptor precursor [Bos taurus]	53.1	53.1	96%	1e-06	71%	NP_776568.1
☐	PREDICTED: polymeric immunoglobulin receptor [Bison bison bison]	53.1	53.1	96%	1e-06	71%	XP_010852516.1
☐	RecName: Full=Polymeric immunoglobulin receptor; Short=PIgR; Short=Poly-	52.8	52.8	96%	1e-06	71%	P81265.1
☐	PREDICTED: LOW QUALITY PROTEIN: polymeric immunoglobulin receptor		52.8	52.8	96%	1e-06	71%	XP_005891711.1
☐	PIGR protein [Bos taurus]	52.8	52.8	96%	1e-06	71%	AAI49033.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Cricetulus grise	52.8	52.8	100%	1e-06	66%	XP_003497773.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Mesocricetus au	52.8	52.8	100%	2e-06	69%	XP_005079920.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Cricetulus grise	52.8	52.8	100%	2e-06	66%	XP_003497772.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Mesocricetus au	52.8	52.8	100%	2e-06	69%	XP_005079919.1
☐	Polymeric immunoglobulin receptor [Cricetulus griseus]	52.4	52.4	100%	2e-06	66%	EGW00964.1
☐	polymeric immunoglobulin receptor precursor [Rattus norvegicus]	52.4	52.4	100%	2e-06	66%	NP_036855.3
☐	polymeric immunoglobulin receptor [Rattus norvegicus]	52.4	52.4	100%	2e-06	66%	EDM09843.1
☐	PREDICTED: polymeric immunoglobulin receptor [Ursus maritimus]	51.2	51.2	96%	5e-06	71%	XP_008683298.1
☐	PREDICTED: polymeric immunoglobulin receptor [Ceratotherium simum simu	51.2	51.2	96%	5e-06	71%	XP_004425146.1
☐	PREDICTED: polymeric immunoglobulin receptor [Lipotes vexillifer]	50.8	50.8	96%	6e-06	68%	XP_007470777.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Dasypus novemc	50.8	83.9	100%	7e-06	68%	XP_004470111.1
☐	PREDICTED: polymeric immunoglobulin receptor [Physeter catodon]	50.8	50.8	96%	7e-06	68%	XP_007105526.1
☐	polymeric immunoglobulin receptor precursor [Equus caballus]	50.4	50.4	96%	8e-06	74%	NP_001271468.1
☐	PREDICTED: polymeric immunoglobulin receptor [Equus przewalskii]	50.4	50.4	96%	8e-06	74%	XP_008539949.1
☐	PREDICTED: polymeric immunoglobulin receptor [Equus caballus]	50.4	50.4	96%	8e-06	74%	XP_001492348.2
☐	PREDICTED: polymeric immunoglobulin receptor [Odobenus rosmarus diverg	50.4	50.4	96%	1e-05	71%	XP_004415592.1
☐	PREDICTED: polymeric immunoglobulin receptor [Tursiops truncatus]	50.4	50.4	96%	1e-05	68%	XP_004319136.1
☐	PREDICTED: polymeric immunoglobulin receptor [Orcinus orca]	50.4	50.4	96%	1e-05	68%	XP_004282467.1
☐	polymeric immunoglobulin receptor [Canis lupus familiaris]	49.7	49.7	96%	1e-05	65%	AAL91653.1
☐	PREDICTED: polymeric immunoglobulin receptor [Balaenoptera acutorostrata	50.1	50.1	96%	1e-05	68%	XP_007171624.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Orycteropus afe	50.1	50.1	96%	1e-05	68%	XP_007951362.1

☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Orycteropus afe	50.1	50.1	96%	1e-05	68%	XP_007951355.1
☐	PREDICTED: polymeric immunoglobulin receptor [Elephantulus edwardii]	49.7	49.7	96%	2e-05	68%	XP_006888060.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Mustela putoriu	49.7	49.7	96%	2e-05	71%	XP_004788608.1
☐	polymeric immunoglobulin receptor precursor [Canis lupus familiaris]	49.3	49.3	96%	2e-05	65%	NP_001274081.1
☐	polymeric immunoglobulin receptor precursor [Sus scrofa]	49.3	49.3	96%	2e-05	68%	NP_999324.1
☐	PREDICTED: polymeric immunoglobulin receptor [Mustela putorius furo]	49.3	49.3	96%	2e-05	71%	XP_004756245.1
☐	Polymeric immunoglobulin receptor [Pteropus alecto]	48.5	48.5	96%	4e-05	65%	ELK03287.1
☐	PREDICTED: polymeric immunoglobulin receptor [Pteropus alecto]	48.5	87.8	96%	5e-05	65%	XP_006922980.1
☐	PREDICTED: polymeric immunoglobulin receptor [Octodon degus]	47.8	47.8	96%	7e-05	65%	XP_004641251.1
☐	PREDICTED: polymeric immunoglobulin receptor [Echinops telfairi]	48.1	48.1	100%	7e-05	66%	XP_004700183.1
☐	PREDICTED: polymeric immunoglobulin receptor [Myotis davidii]	47.8	47.8	96%	8e-05	61%	XP_006754443.1
☐	PREDICTED: polymeric immunoglobulin receptor [Erinaceus europaeus]	47.4	47.4	96%	1e-04	65%	XP_007523168.1
☐	PREDICTED: polymeric immunoglobulin receptor [Eptesicus fuscus]	47.4	47.4	96%	1e-04	61%	XP_008152394.1
☐	PREDICTED: polymeric immunoglobulin receptor [Chinchilla lanigera]	46.6	46.6	96%	2e-04	65%	XP_005375465.1
☐	High affinity immunoglobulin alpha and immunoglobulin mu Fc receptor [Tupa	46.2	46.2	100%	2e-04	59%	ELW47757.1
☐	PREDICTED: LOW QUALITY PROTEIN: polymeric immunoglobulin receptor-	46.6	46.6	96%	2e-04	65%	XP_004610232.1
☐	PREDICTED: polymeric immunoglobulin receptor [Monodelphis domestica]	46.2	82.8	100%	2e-04	56%	XP_007481356.1
☐	PREDICTED: polymeric immunoglobulin receptor [Sarcophilus harrisii]	46.2	80.9	100%	3e-04	53%	XP_003767679.1
☐	PREDICTED: high affinity immunoglobulin alpha and immunoglobulin mu Fc r	45.8	45.8	100%	3e-04	56%	XP_004425251.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Heterocephalus	45.4	45.4	96%	4e-04	61%	XP_004862115.1
☐	Polymeric immunoglobulin receptor [Heterocephalus glaber]	45.4	45.4	96%	5e-04	61%	EHB11027.1
☐	PREDICTED: high affinity immunoglobulin alpha and immunoglobulin mu Fc r	45.1	45.1	100%	5e-04	56%	XP_010961590.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Heterocephalus	45.4	45.4	96%	5e-04	61%	XP_004862114.1
☐	PREDICTED: polymeric immunoglobulin receptor [Heterocephalus glaber]	45.4	45.4	96%	5e-04	61%	XP_004897444.1

⊟ Alignments

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Chain A, Crystal Structure Of A Ligand-Binding Domain Of The Human Polymeric Ig Receptor, Pigr

Sequence ID: pdb|1XED|A **Length:** 117 **Number of Matches:** 1

▷ See 5 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 59 to 90 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
68.6 bits(166)	2e-13	Composition-based stats.	31/32(97%)	32/32(100%)	0/32(0%)

```
Query  1    KYAGRADLTNFPENGTFVVNIAQLSQDDSGRY  32
            KYAGRA+LTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  59   KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  90
```

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PREDICTED: polymeric immunoglobulin receptor isoform 1 [Gorilla gorilla gorilla]

Sequence ID: ref|XP_004028344.1| **Length:** 764 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 77 to 108 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
68.2 bits(165)	5e-12	Compositional matrix adjust.	31/32(97%)	32/32(100%)	0/32(0%)

```
Query  1     KYAGRADLTNFPENGTFVVNIAQLSQDDSGRY  32
             KYAGRA+LTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  77    KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  108
```

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transmembrane secretory component [Homo sapiens]

Sequence ID: gb|AAB20203.1| **Length:** 764 **Number of Matches:** 1

See 3 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 77 to 108 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
68.2 bits(165)	5e-12	Compositional matrix adjust.	31/32(97%)	32/32(100%)	0/32(0%)

```
Query  1    KYAGRADLTNFPENGTFVVNIAQLSQDDSGRY  32
            KYAGRA+LTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  77   KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  108
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

poly-Ig receptor, partial [Homo sapiens]

Sequence ID: gb|AAA36102.1| **Length:** 693 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 6 to 37 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
68.2 bits(165)	5e-12	Compositional matrix adjust.	31/32(97%)	32/32(100%)	0/32(0%)

```
Query  1   KYAGRADLTNFPENGTFVVNIAQLSQDDSGRY  32
           KYAGRA+LTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  6   KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  37
```

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polymeric immunoglobulin receptor precursor [Homo sapiens]

Sequence ID: ref|NP_002635.2| **Length:** 764 **Number of Matches:** 1

See 8 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 77 to 108 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
68.2 bits(165)	5e-12	Compositional matrix adjust.	31/32(97%)	32/32(100%)	0/32(0%)

```
Query  1    KYAGRADLTNFPENGTFVVNIAQLSQDDSGRY  32
            KYAGRA+LTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  77   KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  108
```

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PIGR_KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY_NonMod

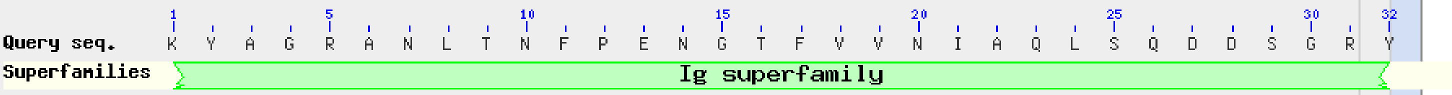
RID	BBJ7M71J014 (Expires on 01-15 08:40 am)		
Query ID	lcl|96038	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	32		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

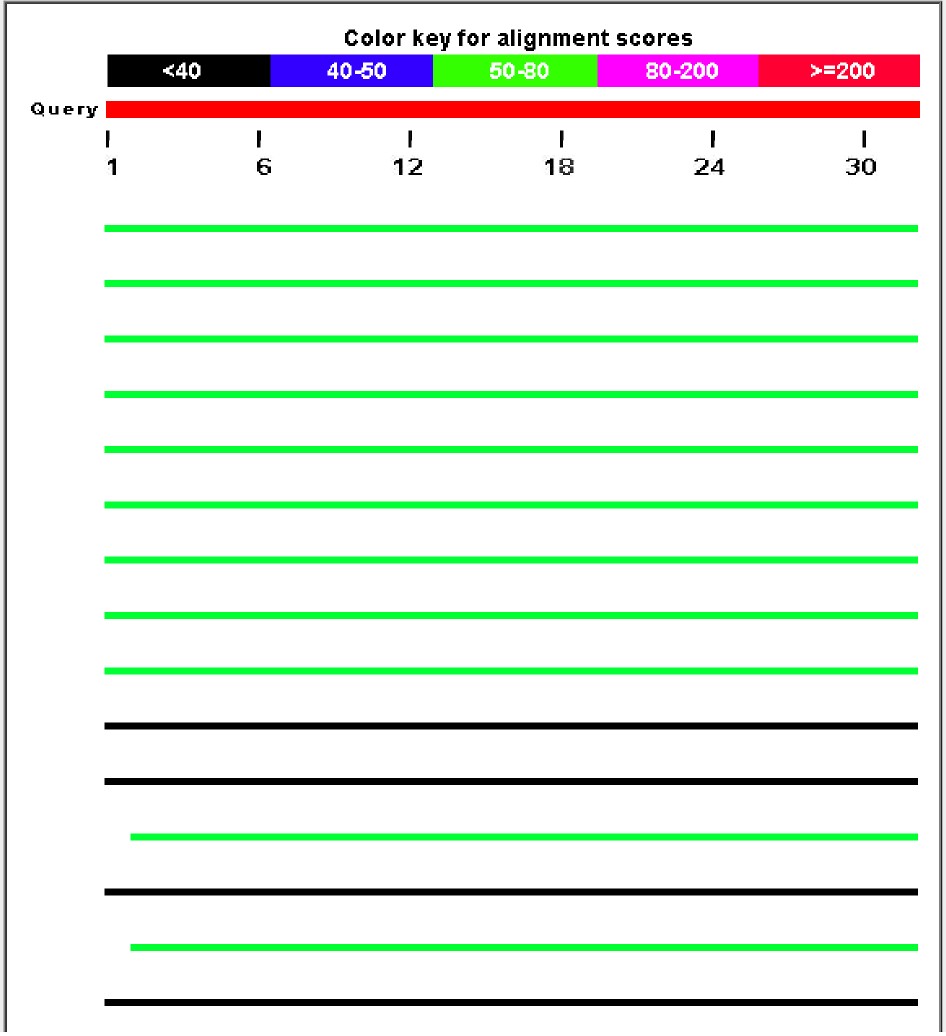
Show Conserved Domains

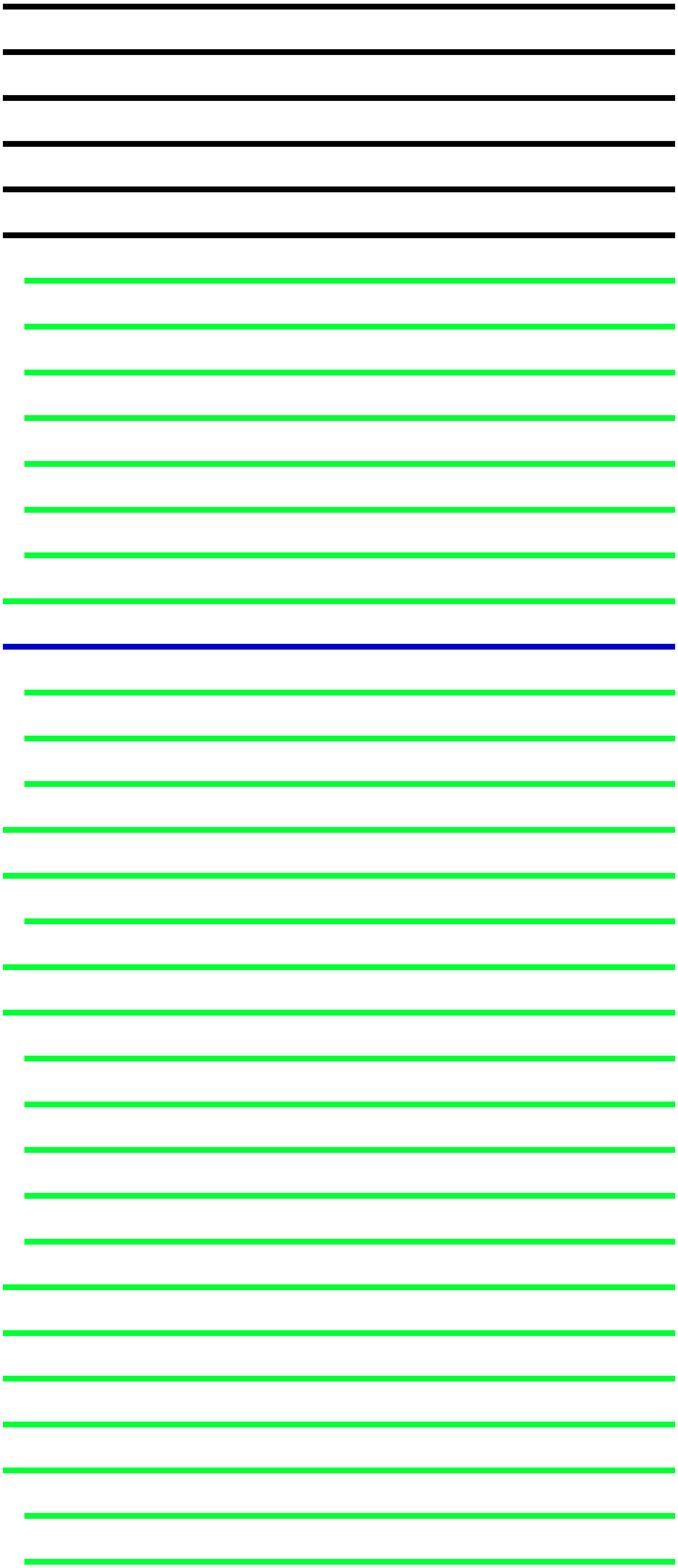
Putative conserved domains have been detected, click on the image below for detailed results.

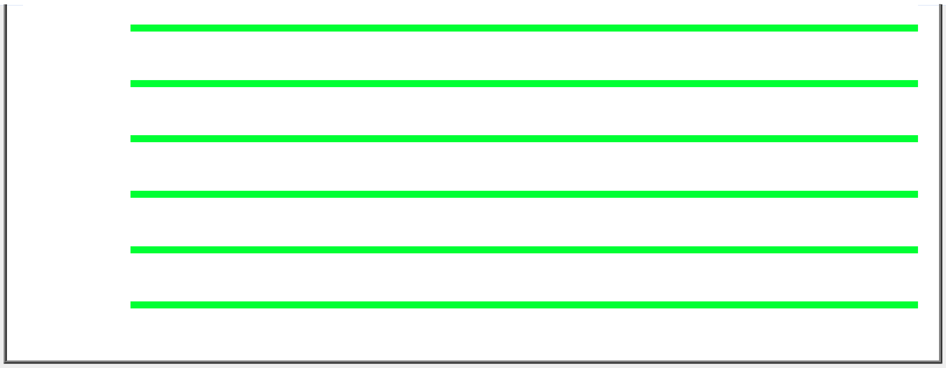


Distribution of 117 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of A Ligand-Binding Domain Of The Hur	68.9	68.9	100%	1e-13	100%	gi|56967075|1XED_A
☐	Chain A, Solution Structure Of Human Secretory Component [Homo	68.9	68.9	100%	2e-12	100%	gi|146387599|2OCW_A
☐	poly-Ig receptor [Homo sapiens]	68.9	68.9	100%	3e-12	100%	gi|514366|AAA36102.1
☐	polymeric immunoglobulin receptor precursor [Homo sapiens]	68.9	68.9	100%	3e-12	100%	gi|31377806|NP_002635.2
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Gorilla	68.9	102	100%	3e-12	100%	gi|426333562|XP_004028344.1
☐	transmembrane secretory component [Homo sapiens]	68.9	68.9	100%	3e-12	100%	gi|238236|AAB20203.1
☐	PREDICTED: polymeric immunoglobulin receptor [Pan paniscus]	68.9	68.9	100%	3e-12	100%	gi|397504777|XP_003822957.1
☐	PREDICTED: polymeric immunoglobulin receptor [Pan troglodytes]	68.9	68.9	100%	3e-12	100%	gi|332811741|XP_514153.3
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Homo	68.9	68.9	100%	3e-12	100%	gi|530366266|XP_005273220.1
☐	hypothetical protein [Pongo abelii]	65.5	98.6	100%	5e-11	97%	gi|55729233|CAH91352.1
☐	polymeric immunoglobulin receptor precursor [Pongo abelii]	65.5	98.6	100%	5e-11	97%	gi|197102290|NP_001125098.1
☐	PREDICTED: polymeric immunoglobulin receptor [Callithrix jacchus	63.9	63.9	96%	2e-10	94%	gi|296230617|XP_002760783.1
☐	PREDICTED: polymeric immunoglobulin receptor [Macaca mulatta]	63.5	96.3	100%	2e-10	94%	gi|297280921|XP_001083307.2
☐	PREDICTED: polymeric immunoglobulin receptor [Chlorocebus sab	63.5	63.5	96%	2e-10	94%	gi|635130940|XP_007986846.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Maca	63.5	96.3	100%	2e-10	94%	gi|544399911|XP_005540721.1
☐	PREDICTED: polymeric immunoglobulin receptor [Papio anubis]	63.5	96.3	100%	2e-10	94%	gi|402857385|XP_003893238.1
☐	hypothetical protein EGM_01447 [Macaca fascicularis]	63.5	96.3	100%	2e-10	94%	gi|355745965|EHH50590.1
☐	hypothetical protein EGK_01717 [Macaca mulatta]	63.5	96.3	100%	2e-10	94%	gi|355558822|EHH15602.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Maca	63.5	96.3	100%	2e-10	94%	gi|544399909|XP_005540720.1
☐	PREDICTED: polymeric immunoglobulin receptor [Rhinopithecus ro	63.2	95.9	100%	3e-10	90%	gi|724836419|XP_010363960.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Nomas	62.8	95.9	100%	4e-10	94%	gi|332247745|XP_003273022.1
☐	PREDICTED: polymeric immunoglobulin receptor-like [Galeopterus	58.9	58.9	96%	7e-10	84%	gi|667345587|XP_008563367.1
☐	PREDICTED: polymeric immunoglobulin receptor [Saimiri boliviensi	61.2	61.2	96%	1e-09	90%	gi|403277678|XP_003930479.1
☐	PREDICTED: polymeric immunoglobulin receptor [Nannospalax gal	59.3	59.3	96%	7e-09	87%	gi|674096299|XP_008821506.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Ictido	58.2	58.2	96%	2e-08	84%	gi|532087641|XP_005329532.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Ictido	58.2	58.2	96%	2e-08	84%	gi|532087643|XP_005329533.1
☐	PREDICTED: polymeric immunoglobulin receptor [Camelus ferus]	57.8	57.8	96%	2e-08	77%	gi|560912075|XP_006182326.1
☐	PREDICTED: polymeric immunoglobulin receptor [Vicugna pacos]	57.8	57.8	96%	2e-08	77%	gi|560986671|XP_006215522.1
☐	Chain A, Crystal Structure Of The 1st Ig Domain From Mouse Polyr	54.7	54.7	100%	3e-08	72%	gi|563321008|4NOB_A

☐	polymeric immunoglobulin receptor precursor [Camelus ferus]	57.8	101	100%	3e-08	77%	gi|530667813|EQB78114.1
☐	PREDICTED: polymeric immunoglobulin receptor [Tarsius syrichta]	57.0	57.0	96%	4e-08	81%	gi|640811957|XP_008062620.1
☐	PREDICTED: polymeric immunoglobulin receptor [Otolemur garnett	57.0	57.0	96%	4e-08	81%	gi|395838714|XP_003792254.1
☐	PREDICTED: polymeric immunoglobulin receptor [Leptonychotes w	56.6	56.6	96%	6e-08	81%	gi|585156277|XP_006730466.1
☐	PREDICTED: polymeric immunoglobulin receptor [Peromyscus mar	56.6	56.6	100%	6e-08	78%	gi|589968826|XP_006996902.1
☐	PREDICTED: polymeric immunoglobulin receptor [Microtus ochroga	55.5	55.5	100%	2e-07	75%	gi|532009108|XP_005348371.1
☐	PREDICTED: polymeric immunoglobulin receptor [Bubalus bubalis]	55.1	55.1	96%	2e-07	77%	gi|594038508|XP_006043871.1
☐	polymeric immunoglobulin receptor [Mus musculus]	54.7	54.7	100%	3e-07	72%	gi|458422|AAA67440.1
☐	polymeric immunoglobulin receptor precursor [Mus musculus]	54.7	54.7	100%	3e-07	72%	gi|31981570|NP_035212.2
☐	PREDICTED: polymeric immunoglobulin receptor [Tupaia chinensis	54.7	54.7	96%	3e-07	77%	gi|562862054|XP_006159345.1
☐	PREDICTED: polymeric immunoglobulin receptor [Pantholops hodg	53.9	53.9	96%	5e-07	74%	gi|556742966|XP_005967001.1
☐	PREDICTED: polymeric immunoglobulin receptor [Capra hircus]	53.9	53.9	96%	5e-07	74%	gi|548497730|XP_005690475.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Ovis ai	53.9	53.9	96%	5e-07	74%	gi|426239425|XP_004013622.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 2 [Ovis ai	53.9	53.9	96%	5e-07	74%	gi|426239427|XP_004013623.1
☐	PREDICTED: LOW QUALITY PROTEIN: polymeric immunoglobulin	53.5	53.5	100%	7e-07	69%	gi|625233654|XP_007607970.1
☐	Polymeric immunoglobulin receptor [Cricetulus griseus]	53.5	53.5	100%	7e-07	69%	gi|344244860|EGW00964.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Crice	53.5	53.5	100%	7e-07	69%	gi|354471083|XP_003497773.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Crice	53.5	53.5	100%	7e-07	69%	gi|354471081|XP_003497772.1
☐	polymeric immunoglobulin receptor isoform 1 [Cricetulus griseus]	53.5	93.6	100%	8e-07	69%	gi|537169305|ERE73918.1
☐	PREDICTED: LOW QUALITY PROTEIN: polymeric immunoglobulin	53.1	53.1	96%	1e-06	74%	gi|555959201|XP_005891711.1
☐	TPA: polymeric immunoglobulin receptor precursor [Bos taurus]	53.1	53.1	96%	1e-06	74%	gi|296479365|DAA21480.1
☐	polymeric immunoglobulin receptor precursor [Bos taurus]	52.8	52.8	96%	1e-06	74%	gi|32189338|NP_776568.1
☐	RecName: Full=Polymeric immunoglobulin receptor; Short=PIgR; S	52.8	52.8	96%	1e-06	74%	gi|3914346|P81265.1
☐	PIGR protein [Bos taurus]	52.8	52.8	96%	1e-06	74%	gi|151555693|AAI49033.1
☐	PREDICTED: polymeric immunoglobulin receptor [Panthera tigris a	52.4	52.4	96%	2e-06	74%	gi|591341842|XP_007096344.1
☐	PREDICTED: polymeric immunoglobulin receptor [Felis catus]	52.4	52.4	96%	2e-06	74%	gi|587018664|XP_006943006.1
☐	PREDICTED: polymeric immunoglobulin receptor [Ursus maritimus]	52.4	52.4	96%	2e-06	74%	gi|670984407|XP_008683298.1
☐	PREDICTED: polymeric immunoglobulin receptor [Ceratotherium si	52.4	52.4	96%	2e-06	74%	gi|478501668|XP_004425146.1
☐	PREDICTED: polymeric immunoglobulin receptor [Lipotes vexillifer]	51.6	51.6	96%	3e-06	71%	gi|602721248|XP_007470777.1
☐	PREDICTED: polymeric immunoglobulin receptor [Physeter catodoı	51.6	51.6	96%	3e-06	71%	gi|593718296|XP_007105526.1
☐	PREDICTED: polymeric immunoglobulin receptor [Equus przewalsk	51.6	51.6	96%	3e-06	77%	gi|664764562|XP_008539949.1
☐	PREDICTED: polymeric immunoglobulin receptor [Equus caballus]	51.6	51.6	96%	3e-06	77%	gi|194210251|XP_001492348.2
☐	polymeric immunoglobulin receptor precursor [Equus caballus]	51.6	51.6	96%	3e-06	77%	gi|548961809|NP_001271468.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Meso	51.6	51.6	100%	3e-06	69%	gi|524959951|XP_005079920.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Meso	51.6	51.6	100%	3e-06	69%	gi|524959949|XP_005079919.1
☐	PREDICTED: polymeric immunoglobulin receptor [Tursiops truncatu	51.2	51.2	96%	4e-06	71%	gi|470622594|XP_004319136.1
☐	PREDICTED: polymeric immunoglobulin receptor [Odobenus rosma	51.2	51.2	96%	4e-06	74%	gi|472392635|XP_004415592.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Dasypı	51.2	83.9	100%	4e-06	71%	gi|488560131|XP_004470111.1
☐	PREDICTED: polymeric immunoglobulin receptor [Orcinus orca]	51.2	51.2	96%	4e-06	71%	gi|466071278|XP_004282467.1
☐	PREDICTED: polymeric immunoglobulin receptor [Balaenoptera acı	51.2	51.2	96%	4e-06	71%	gi|594636460|XP_007171624.1
☐	PREDICTED: polymeric immunoglobulin receptor [Jaculus jaculus]	51.2	51.2	96%	4e-06	71%	gi|507559576|XP_004663511.1
☐	polymeric immunoglobulin receptor precursor [Rattus norvegicus]	51.2	51.2	100%	4e-06	66%	gi|501354879|NP_036855.3
☐	polymeric immunoglobulin receptor [Rattus norvegicus]	51.2	51.2	100%	4e-06	66%	gi|149058686|EDM09843.1
☐	polymeric immunoglobulin receptor [Canis lupus familiaris]	50.4	50.4	96%	5e-06	68%	gi|19715659|AAL91653.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Oryct	50.8	50.8	96%	6e-06	71%	gi|634826802|XP_007951362.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Oryct	50.8	50.8	96%	6e-06	71%	gi|634826799|XP_007951355.1

☐	polymeric immunoglobulin receptor precursor [Sus scrofa]	50.4	50.4	96%	8e-06	71%	gi|47523406|NP_999324.1
☐	polymeric immunoglobulin receptor precursor [Canis lupus familiaris	50.4	50.4	96%	8e-06	68%	gi|560891934|NP_001274081.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Muste	50.1	50.1	96%	1e-05	74%	gi|511939572|XP_004788608.1
☐	PREDICTED: polymeric immunoglobulin receptor [Mustela putorius	50.1	50.1	96%	1e-05	74%	gi|511871244|XP_004756245.1
☐	PREDICTED: polymeric immunoglobulin receptor [Echinops telfairi]	49.3	49.3	100%	2e-05	69%	gi|507635434|XP_004700183.1
☐	PREDICTED: polymeric immunoglobulin receptor [Elephantulus edv	48.5	48.5	96%	4e-05	68%	gi|585666892|XP_006888060.1
☐	Polymeric immunoglobulin receptor [Pteropus alecto]	48.5	48.5	96%	4e-05	68%	gi|431892859|ELK03287.1
☐	PREDICTED: polymeric immunoglobulin receptor [Pteropus alecto]	48.5	86.6	96%	4e-05	68%	gi|586536225|XP_006922980.1
☐	PREDICTED: polymeric immunoglobulin receptor [Chinchilla lanige	48.1	48.1	96%	5e-05	68%	gi|533120059|XP_005375465.1
☐	PREDICTED: polymeric immunoglobulin receptor [Octodon degus]	47.8	47.8	96%	7e-05	65%	gi|507688344|XP_004641251.1
☐	PREDICTED: polymeric immunoglobulin receptor [Myotis davidii]	47.8	47.8	96%	7e-05	65%	gi|584068124|XP_006754443.1
☐	PREDICTED: polymeric immunoglobulin receptor [Sarcophilus harr	47.4	81.2	100%	9e-05	56%	gi|395531218|XP_003767679.1
☐	PREDICTED: polymeric immunoglobulin receptor [Monodelphis dor	47.4	83.9	100%	9e-05	59%	gi|611989136|XP_007481356.1
☐	PREDICTED: polymeric immunoglobulin receptor [Eptesicus fuscus	47.4	47.4	96%	9e-05	65%	gi|641724928|XP_008152394.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Heter	47.0	47.0	96%	1e-04	65%	gi|513001195|XP_004862115.1
☐	PREDICTED: polymeric immunoglobulin receptor [Heterocephalus	47.0	47.0	96%	1e-04	65%	gi|512893082|XP_004897444.1
☐	Polymeric immunoglobulin receptor [Heterocephalus glaber]	47.0	47.0	96%	1e-04	65%	gi|351708108|EHB11027.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Heter	47.0	47.0	96%	1e-04	65%	gi|513001193|XP_004862114.1
☐	PREDICTED: polymeric immunoglobulin receptor [Erinaceus europ	46.6	46.6	96%	2e-04	65%	gi|617602067|XP_007523168.1
☐	PREDICTED: polymeric immunoglobulin receptor [Cavia porcellus]	46.6	46.6	96%	2e-04	71%	gi|348578097|XP_003474820.1
☐	PREDICTED: LOW QUALITY PROTEIN: polymeric immunoglobulir	45.8	45.8	96%	3e-04	65%	gi|505829866|XP_004610232.1
☐	PREDICTED: polymeric immunoglobulin receptor [Chrysochloris as	45.1	45.1	96%	6e-04	65%	gi|586450680|XP_006834271.1
☐	PREDICTED: polymeric immunoglobulin receptor [Trichechus mana	45.1	45.1	96%	6e-04	61%	gi|471369481|XP_004375257.1
☐	PREDICTED: polymeric immunoglobulin receptor [Myotis lucifugus]	44.3	44.3	96%	0.001	58%	gi|558152618|XP_006094928.1
☐	PREDICTED: polymeric immunoglobulin receptor [Myotis brandtii]	44.3	44.3	96%	0.001	58%	gi|554587770|XP_005885286.1

⊟ Alignments

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Chain A, Crystal Structure Of A Ligand-Binding Domain Of The Human Polymeric Ig Receptor, Pigr

Sequence ID: gi|56967075|pdb|1XED|A **Length:** 117 **Number of Matches:** 1

▷ See 5 more title(s)

Range 1: 59 to 90 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(167)	1e-13	32/32(100%)	32/32(100%)	0/32(0%)

```
Query  1    KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  32
            KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  59   KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  90
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Solution Structure Of Human Secretory Component

Sequence ID: gi|146387599|pdb|2OCW|A **Length:** 585 **Number of Matches:** 1

▷ See 2 more title(s)

Range 1: 59 to 90 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(167)	2e-12	32/32(100%)	32/32(100%)	0/32(0%)

```
Query  1    KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  32
            KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  59   KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  90
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

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poly-Ig receptor, partial [Homo sapiens]

Sequence ID: gi|514366|gb|AAA36102.1| **Length:** 693 **Number of Matches:** 1

Range 1: 6 to 37 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(167)	3e-12	32/32(100%)	32/32(100%)	0/32(0%)

```
Query  1    KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  32
            KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  6    KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  37
```

Related Information

Gene - associated gene details

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

polymeric immunoglobulin receptor precursor [Homo sapiens]

Sequence ID: gi|31377806|ref|NP_002635.2| **Length:** 764 **Number of Matches:** 1

▷ See 8 more title(s)

Range 1: 77 to 108 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(167)	3e-12	32/32(100%)	32/32(100%)	0/32(0%)

```
Query  1     KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  32
             KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  77    KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  108
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Download ⌄ GenPept Graphics Sort by: 0 t ▲ Previous Descriptions

PREDICTED: polymeric immunoglobulin receptor isoform 1 [Gorilla gorilla gorilla]

Sequence ID: gi|426333562|ref|XP_004028344.1| **Length:** 764 **Number of Matches:** 2

▷ See 1 more title(s)

Range 1: 77 to 108 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
68.9 bits(167)	3e-12	32/32(100%)	32/32(100%)	0/32(0%)

```
Query  1     KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  32
             KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  77    KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  108
```

Range 2: 408 to 439 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
33.1 bits(74)	6.6	15/32(47%)	20/32(62%)	0/32(0%)

```
Query  1     KYAGRANLTNFPENGTFVVNIAQLSQDDSGRY  32
             +Y GR +L    P NGTF V + QL+   D+G Y
Sbjct  408   QYEGRLSLLEEPGNGTFTVILNQLTSQDAGFY  439
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

BLAST ® Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVK220EV01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

PIGR_RANLTNFPEDGTFVVNIAQLSQDDSGRY_Mod

RID BVK220EV01R (Expires on 01-21 10:32 am)

Query ID lcl|201803
Description None
Molecule type amino acid
Query Length 28

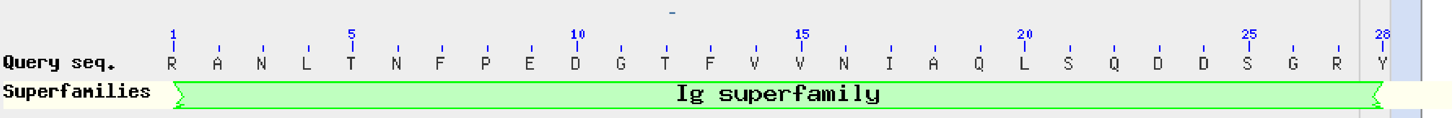
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

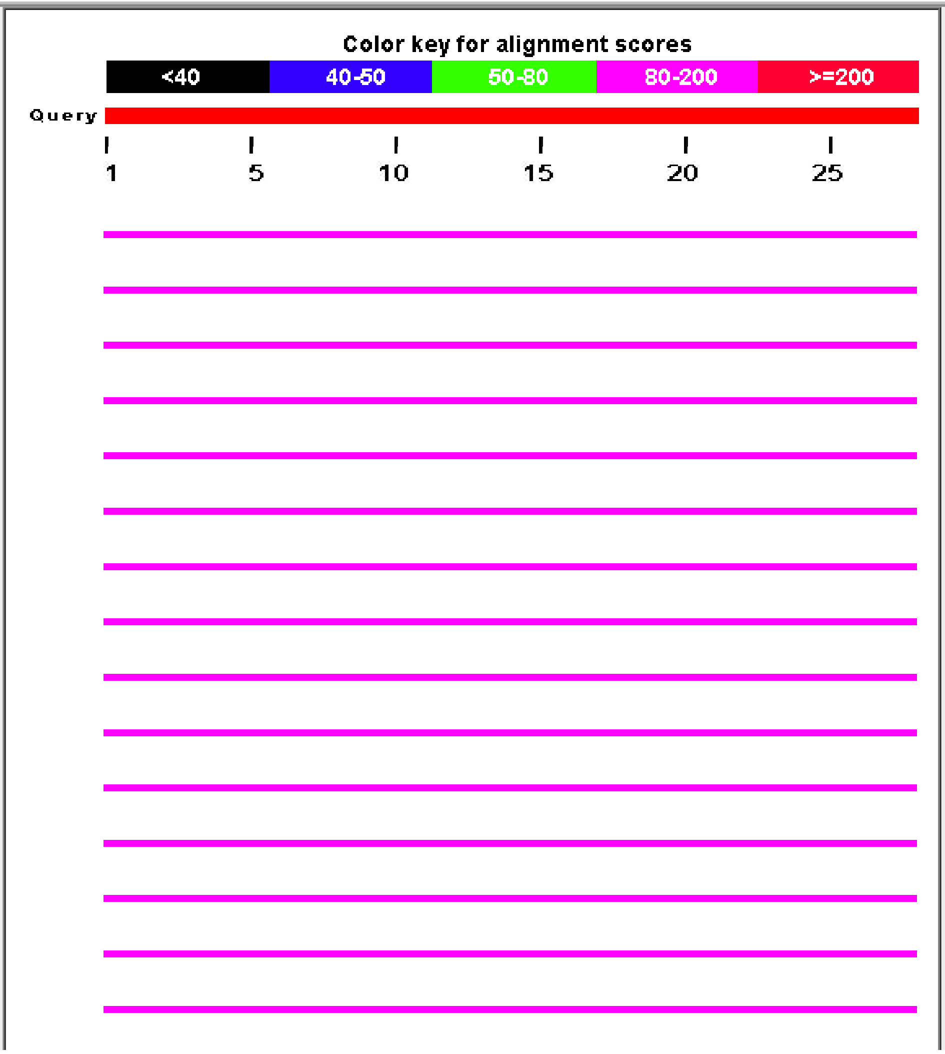
Show Conserved Domains

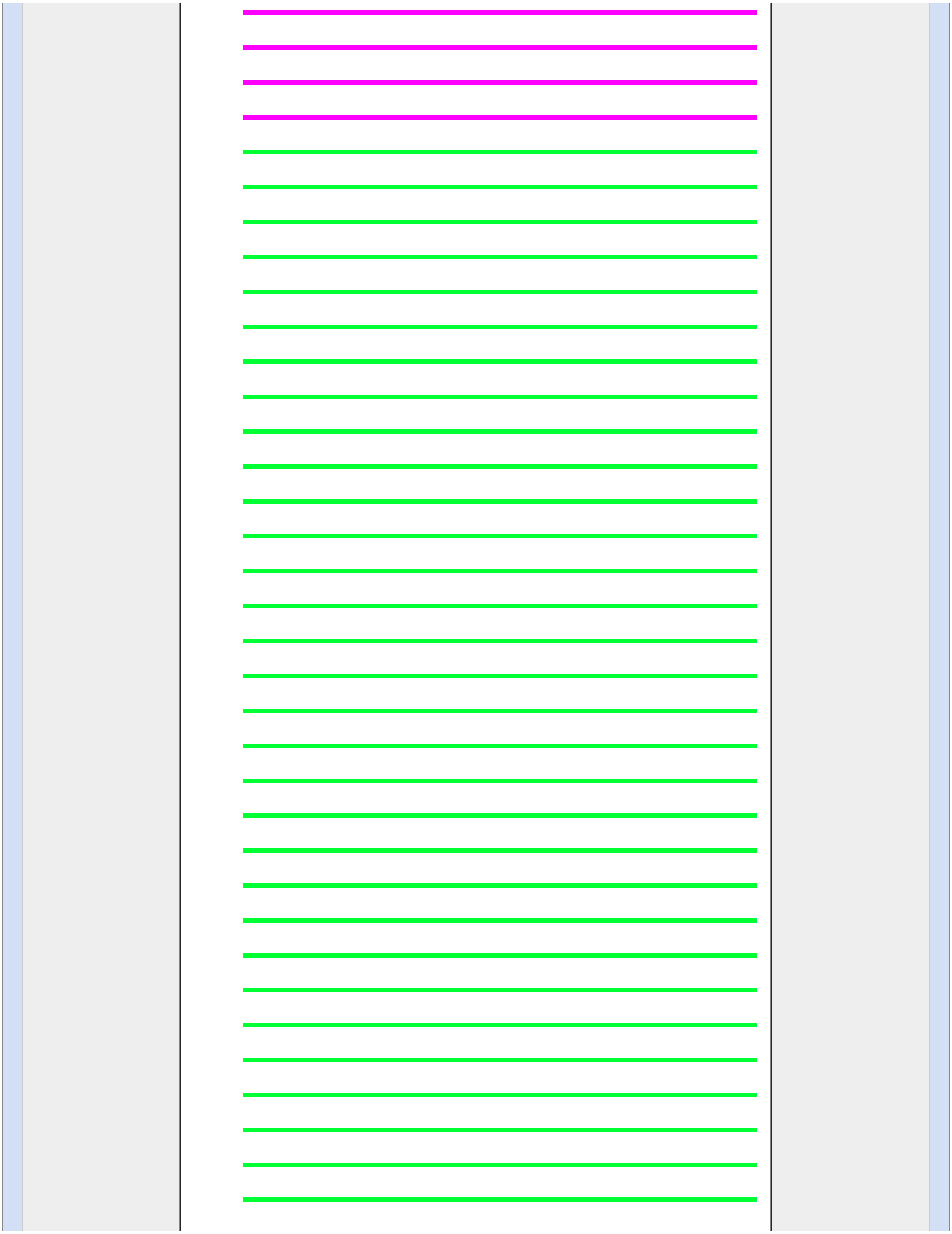
Putative conserved domains have been detected, click on the image below for detailed results.

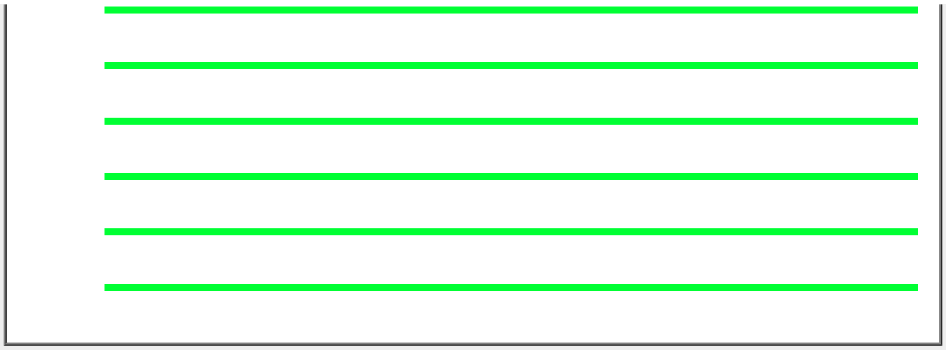


Distribution of 170 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of A Ligand-Binding Domain Of The Human Polym	89.7	89.7	100%	5e-19	96%	1XED_A
☐	Chain A, Solution Structure Of Human Secretory Component [Homo sapiens]	89.7	114	100%	2e-18	96%	2OCW_A
☐	poly-Ig receptor [Homo sapiens]	89.7	114	100%	2e-18	96%	AAA36102.1
☐	polymeric immunoglobulin receptor precursor [Homo sapiens]	89.7	114	100%	2e-18	96%	NP_002635.2
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Gorilla gorilla gor	89.7	138	100%	2e-18	96%	XP_004028344.1
☐	transmembrane secretory component [Homo sapiens]	89.7	114	100%	2e-18	96%	AAB20203.1
☐	PREDICTED: polymeric immunoglobulin receptor [Pan paniscus]	89.7	114	100%	2e-18	96%	XP_003822957.1
☐	PREDICTED: polymeric immunoglobulin receptor [Pan troglodytes]	89.7	114	100%	2e-18	96%	XP_514153.3
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Homo sapiens]	89.7	114	100%	2e-18	96%	XP_005273220.1
☐	PREDICTED: polymeric immunoglobulin receptor [Callithrix jacchus]	85.5	106	100%	5e-17	93%	XP_002760783.1
☐	hypothetical protein [Pongo abelii]	85.5	134	100%	5e-17	93%	CAH91352.1
☐	polymeric immunoglobulin receptor precursor [Pongo abelii]	85.5	134	100%	5e-17	93%	NP_001125098.1
☐	PREDICTED: polymeric immunoglobulin receptor [Macaca mulatta]	81.2	126	100%	1e-15	89%	XP_001083307.2
☐	PREDICTED: polymeric immunoglobulin receptor [Chlorocebus sabaeus]	81.2	126	100%	1e-15	89%	XP_007986846.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Macaca fascicu	81.2	126	100%	1e-15	89%	XP_005540721.1
☐	PREDICTED: polymeric immunoglobulin receptor [Papio anubis]	81.2	126	100%	1e-15	89%	XP_003893238.1
☐	hypothetical protein EGM_01447 [Macaca fascicularis]	81.2	126	100%	1e-15	89%	EHH50590.1
☐	hypothetical protein EGK_01717 [Macaca mulatta]	81.2	126	100%	1e-15	89%	EHH15602.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Macaca fascicu	81.2	126	100%	1e-15	89%	XP_005540720.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Ictidomys tridec	79.5	79.5	100%	5e-15	86%	XP_005329532.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Ictidomys tridec	79.5	79.5	100%	5e-15	86%	XP_005329533.1
☐	PREDICTED: polymeric immunoglobulin receptor-like [Galeopterus variegatus	77.8	77.8	100%	8e-15	86%	XP_008563367.1
☐	PREDICTED: polymeric immunoglobulin receptor [Rhinopithecus roxellana]	78.7	124	100%	1e-14	86%	XP_010363960.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Nomascus leucoç	78.7	127	100%	1e-14	89%	XP_003273022.1
☐	PREDICTED: polymeric immunoglobulin receptor [Saimiri boliviensis boliviens	77.4	98.4	100%	3e-14	86%	XP_003930479.1
☐	PREDICTED: polymeric immunoglobulin receptor [Nannospalax galili]	75.7	75.7	100%	1e-13	82%	XP_008821506.1
☐	PREDICTED: polymeric immunoglobulin receptor [Camelus bactrianus]	74.0	74.0	100%	4e-13	75%	XP_010961553.1
☐	PREDICTED: polymeric immunoglobulin receptor [Camelus ferus]	74.0	74.0	100%	4e-13	75%	XP_006182326.1
☐	PREDICTED: polymeric immunoglobulin receptor [Otolemur garnettii]	74.0	74.0	100%	4e-13	79%	XP_003792254.1

☐	polymeric immunoglobulin receptor precursor [Camelus ferus]	74.0	117	100%	4e-13	75%	EQB78114.1
☐	PREDICTED: polymeric immunoglobulin receptor [Vicugna pacos]	73.2	95.9	100%	7e-13	75%	XP_006215522.1
☐	PREDICTED: polymeric immunoglobulin receptor [Leptonychotes weddellii]	72.7	93.7	100%	1e-12	79%	XP_006730466.1
☐	PREDICTED: polymeric immunoglobulin receptor [Bubalus bubalis]	70.2	92.0	100%	7e-12	79%	XP_006043871.1
☐	PREDICTED: polymeric immunoglobulin receptor [Pantholops hodgsonii]	69.8	69.8	100%	1e-11	75%	XP_005967001.1
☐	PREDICTED: polymeric immunoglobulin receptor [Capra hircus]	69.8	119	100%	1e-11	75%	XP_005690475.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Ovis aries]	69.8	119	100%	1e-11	75%	XP_004013622.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 2 [Ovis aries]	69.8	119	100%	1e-11	75%	XP_004013623.1
☐	PREDICTED: polymeric immunoglobulin receptor [Tarsius syrichta]	69.4	92.9	100%	1e-11	75%	XP_008062620.1
☐	polymeric immunoglobulin receptor precursor [Bos taurus]	68.5	89.9	100%	3e-11	75%	NP_776568.1
☐	RecName: Full=Polymeric immunoglobulin receptor; Short=PIgR; Short=Poly-	68.5	89.9	100%	3e-11	75%	P81265.1
☐	PIGR protein [Bos taurus]	68.5	89.9	100%	3e-11	75%	AAI49033.1
☐	Chain A, Crystal Structure Of The 1st Ig Domain From Mouse Polymeric Immu	66.8	66.8	100%	5e-11	71%	4NOB_A
☐	PREDICTED: LOW QUALITY PROTEIN: polymeric immunoglobulin receptor	67.2	88.7	100%	7e-11	75%	XP_005891711.1
☐	TPA: polymeric immunoglobulin receptor precursor [Bos taurus]	67.2	88.7	100%	7e-11	75%	DAA21480.1
☐	PREDICTED: polymeric immunoglobulin receptor [Jaculus jaculus]	67.2	67.2	100%	7e-11	71%	XP_004663511.1
☐	PREDICTED: polymeric immunoglobulin receptor [Bison bison bison]	67.2	88.7	100%	7e-11	75%	XP_010852516.1
☐	PREDICTED: polymeric immunoglobulin receptor [Panthera tigris altaica]	66.8	87.8	100%	1e-10	71%	XP_007096344.1
☐	PREDICTED: polymeric immunoglobulin receptor [Peromyscus maniculatus b	66.8	66.8	100%	1e-10	75%	XP_006996902.1
☐	PREDICTED: polymeric immunoglobulin receptor [Felis catus]	66.8	87.8	100%	1e-10	71%	XP_006943006.1
☐	polymeric immunoglobulin receptor [Mus musculus]	66.8	87.8	100%	1e-10	71%	AAA67440.1
☐	polymeric immunoglobulin receptor precursor [Mus musculus]	66.8	87.8	100%	1e-10	71%	NP_035212.2
☐	PREDICTED: polymeric immunoglobulin receptor [Equus przewalskii]	66.0	66.0	100%	2e-10	79%	XP_008539949.1
☐	PREDICTED: polymeric immunoglobulin receptor [Equus caballus]	66.0	66.0	100%	2e-10	79%	XP_001492348.2
☐	polymeric immunoglobulin receptor precursor [Equus caballus]	66.0	66.0	100%	2e-10	79%	NP_001271468.1
☐	PREDICTED: polymeric immunoglobulin receptor [Microtus ochrogaster]	65.5	87.4	100%	3e-10	71%	XP_005348371.1
☐	PREDICTED: polymeric immunoglobulin receptor [Ursus maritimus]	64.7	85.7	100%	5e-10	71%	XP_008683298.1
☐	PREDICTED: polymeric immunoglobulin receptor [Tupaia chinensis]	64.7	64.7	100%	5e-10	71%	XP_006159345.1
☐	PREDICTED: polymeric immunoglobulin receptor [Ceratotherium simum simu	63.8	63.8	92%	1e-09	77%	XP_004425146.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Mustela putoriu	63.4	85.3	100%	1e-09	71%	XP_004788608.1
☐	PREDICTED: polymeric immunoglobulin receptor [Mustela putorius furo]	63.4	85.3	100%	1e-09	71%	XP_004756245.1
☐	PREDICTED: polymeric immunoglobulin receptor [Odobenus rosmarus diverg	63.0	83.6	100%	2e-09	71%	XP_004415592.1
☐	polymeric immunoglobulin receptor [Canis lupus familiaris]	62.6	62.6	100%	2e-09	68%	AAL91653.1
☐	polymeric immunoglobulin receptor precursor [Canis lupus familiaris]	62.6	84.0	100%	3e-09	68%	NP_001274081.1
☐	PREDICTED: polymeric immunoglobulin receptor [Lipotes vexillifer]	62.1	84.0	100%	4e-09	71%	XP_007470777.1
☐	PREDICTED: polymeric immunoglobulin receptor [Physeter catodon]	62.1	62.1	100%	4e-09	71%	XP_007105526.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Orycteropus afe	61.7	61.7	100%	5e-09	68%	XP_007951362.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Orycteropus afe	61.7	61.7	100%	5e-09	68%	XP_007951355.1
☐	polymeric immunoglobulin receptor precursor [Rattus norvegicus]	61.7	61.7	100%	5e-09	64%	NP_036855.3
☐	polymeric immunoglobulin receptor [Rattus norvegicus]	61.7	61.7	100%	5e-09	64%	EDM09843.1
☐	PREDICTED: polymeric immunoglobulin receptor [Tursiops truncatus]	61.3	61.3	100%	7e-09	71%	XP_004319136.1
☐	PREDICTED: polymeric immunoglobulin receptor [Orcinus orca]	61.3	61.3	100%	7e-09	71%	XP_004282467.1
☐	PREDICTED: polymeric immunoglobulin receptor [Balaenoptera acutorostrata	61.3	61.3	100%	7e-09	71%	XP_007171624.1
☐	PREDICTED: polymeric immunoglobulin receptor [Echinops telfairi]	60.4	81.0	100%	1e-08	71%	XP_004700183.1
☐	PREDICTED: LOW QUALITY PROTEIN: polymeric immunoglobulin receptor i	60.0	60.0	100%	2e-08	64%	XP_007607970.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Mesocricetus au	60.0	81.4	100%	2e-08	64%	XP_005079920.1

☐	Polymeric immunoglobulin receptor [Cricetulus griseus]	60.0	60.0	100%	2e-08	64%	EGW00964.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Mesocricetus au	60.0	81.4	100%	2e-08	64%	XP_005079919.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Cricetulus grise	60.0	60.0	100%	2e-08	64%	XP_003497773.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Cricetulus grise	60.0	60.0	100%	2e-08	64%	XP_003497772.1
☐	polymeric immunoglobulin receptor isoform 1 [Cricetulus griseus]	60.0	95.4	100%	2e-08	64%	ERE73918.1
☐	PREDICTED: polymeric immunoglobulin receptor [Elephantulus edwardii]	59.6	83.1	100%	3e-08	68%	XP_006888060.1
☐	polymeric immunoglobulin receptor precursor [Sus scrofa]	59.2	59.2	100%	4e-08	68%	NP_999324.1
☐	Polymeric immunoglobulin receptor [Pteropus alecto]	58.7	58.7	96%	5e-08	70%	ELK03287.1
☐	PREDICTED: polymeric immunoglobulin receptor [Pteropus alecto]	58.7	97.1	100%	5e-08	70%	XP_006922980.1
☐	PREDICTED: polymeric immunoglobulin receptor [Loxodonta africana]	57.5	57.5	100%	1e-07	68%	XP_010588572.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Dasypus novemc	57.5	78.9	100%	1e-07	68%	XP_004470111.1
☐	PREDICTED: polymeric immunoglobulin receptor [Cavia porcellus]	56.6	56.6	100%	2e-07	69%	XP_003474820.1
☐	PREDICTED: polymeric immunoglobulin receptor [Chinchilla lanigera]	56.2	82.3	100%	3e-07	68%	XP_005375465.1
☐	PREDICTED: polymeric immunoglobulin receptor [Octodon degus]	55.8	55.8	100%	5e-07	64%	XP_004641251.1
☐	PREDICTED: polymeric immunoglobulin receptor [Chrysochloris asiatica]	55.4	81.0	100%	6e-07	68%	XP_006834271.1
☐	PREDICTED: polymeric immunoglobulin receptor [Trichechus manatus latiros	55.4	55.4	100%	6e-07	68%	XP_004375257.1
☐	PREDICTED: polymeric immunoglobulin receptor [Eptesicus fuscus]	54.5	54.5	100%	1e-06	61%	XP_008152394.1
☐	PREDICTED: polymeric immunoglobulin receptor [Myotis davidii]	54.5	54.5	100%	1e-06	64%	XP_006754443.1
☐	PREDICTED: polymeric immunoglobulin receptor [Erinaceus europaeus]	54.1	54.1	100%	2e-06	61%	XP_007523168.1
☐	PREDICTED: LOW QUALITY PROTEIN: polymeric immunoglobulin receptor-	53.7	53.7	100%	2e-06	64%	XP_004610232.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Heterocephalus	52.4	52.4	100%	6e-06	64%	XP_004862115.1
☐	PREDICTED: polymeric immunoglobulin receptor [Heterocephalus glaber]	52.4	52.4	100%	6e-06	64%	XP_004897444.1
☐	Polymeric immunoglobulin receptor [Heterocephalus glaber]	52.4	52.4	100%	6e-06	64%	EHB11027.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Heterocephalus	52.4	52.4	100%	6e-06	64%	XP_004862114.1
☐	PREDICTED: polymeric immunoglobulin receptor [Myotis lucifugus]	52.0	52.0	100%	8e-06	57%	XP_006094928.1

⊟ Alignments

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Chain A, Crystal Structure Of A Ligand-Binding Domain Of The Human Polymeric Ig Receptor, Pigr

Sequence ID: pdb|1XED|A **Length:** 117 **Number of Matches:** 1

▷ See 5 more title(s)

Range 1: 63 to 90 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
89.7 bits(204)	5e-19	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    RANLTNFPEDGTFVVNIAQLSQDDSGRY  28
            RANLTNFPE+GTFVVNIAQLSQDDSGRY
Sbjct  63   RANLTNFPENGTFVVNIAQLSQDDSGRY  90
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Download GenPept Graphics **Sort by:** 0 ▼ Next ▲ Previous Descriptions

Chain A, Solution Structure Of Human Secretory Component

Sequence ID: pdb|2OCW|A **Length:** 585 **Number of Matches:** 2

▷ See 2 more title(s)

Range 1: 63 to 90 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
89.7 bits(204)	2e-18	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    RANLTNFPEDGTFVVNIAQLSQDDSGRY  28
            RANLTNFPE+GTFVVNIAQLSQDDSGRY
```

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

```
Sbjct  63   RANLTNFPENGTFVVNIAQLSQDDSGRY  90
```

Range 2: 287 to 305 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
25.2 bits(52)	5287	11/20(55%)	12/20(60%)	2/20(10%)

```
Query  10   DGTF-VVNIAQLSQDDSGRY  28
            DG F VV I  L  +D GRY
Sbjct  287  DGSFSVV-ITGLRKEDAGRY  305
```

Download GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

poly-Ig receptor, partial [Homo sapiens]

Sequence ID: gb|AAA36102.1| **Length:** 693 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 10 to 37 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
89.7 bits(204)	2e-18	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1    RANLTNFPEDGTFVVNIAQLSQDDSGRY  28
            RANLTNFPE+GTFVVNIAQLSQDDSGRY
Sbjct  10   RANLTNFPENGTFVVNIAQLSQDDSGRY  37
```

Range 2: 234 to 252 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
25.2 bits(52)	5301	11/20(55%)	12/20(60%)	2/20(10%)

```
Query  10   DGTF-VVNIAQLSQDDSGRY  28
            DG F VV I  L  +D GRY
Sbjct  234  DGSFSVV-ITGLRKEDAGRY  252
```

Download GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

polymeric immunoglobulin receptor precursor [Homo sapiens]

Sequence ID: ref|NP_002635.2| **Length:** 764 **Number of Matches:** 2

See 8 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 81 to 108 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
89.7 bits(204)	2e-18	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1     RANLTNFPEDGTFVVNIAQLSQDDSGRY  28
             RANLTNFPE+GTFVVNIAQLSQDDSGRY
Sbjct  81    RANLTNFPENGTFVVNIAQLSQDDSGRY  108
```

Range 2: 305 to 323 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
25.2 bits(52)	5308	11/20(55%)	12/20(60%)	2/20(10%)

```
Query  10   DGTF-VVNIAQLSQDDSGRY  28
            DG F VV I  L  +D GRY
Sbjct  305  DGSFSVV-ITGLRKEDAGRY  323
```

Download GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

PREDICTED: polymeric immunoglobulin receptor isoform 1 [Gorilla gorilla gorilla]

Sequence ID: ref|XP_004028344.1| **Length:** 764 **Number of Matches:** 3

See 1 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 81 to 108 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
89.7 bits(204)	2e-18	27/28(96%)	28/28(100%)	0/28(0%)

```
Query  1     RANLTNFPEDGTFVVNIAQLSQDDSGRY  28
             RANLTNFPE+GTFVVNIAQLSQDDSGRY
Sbjct  81    RANLTNFPENGTFVVNIAQLSQDDSGRY  108
```

Range 2: 305 to 323 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
25.2 bits(52)	5308	11/20(55%)	12/20(60%)	2/20(10%)

```
Query  10   DGTF-VVNIAQLSQDDSGRY  28
            DG F VV I  L  +D GRY
Sbjct  305  DGSFSVV-ITGLRKEDAGRY  323
```

Range 3: 419 to 435 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
24.0 bits(49)	14270	10/17(59%)	11/17(64%)	1/17(5%)

```
Query  8    PEDGTFVVNIAQL-SQD  23
            P +GTF V   QL SQD
Sbjct  419  PGNGTFTVILNQLTSQD  435
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download

How to read this page Blast report description

PIGR_RANLTNFPENGTFVVNIAQLSQDDSGRY_NonMod

RID BBJ8VJ0401R (Expires on 01-15 08:40 am)

Query ID lcl|375017
Description None
Molecule type amino acid
Query Length 28

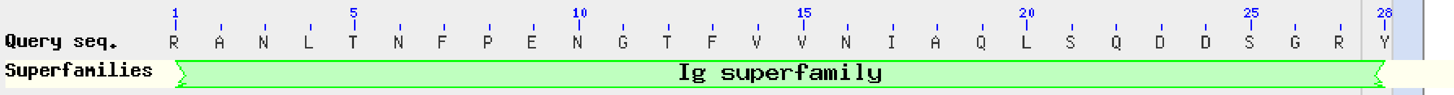
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

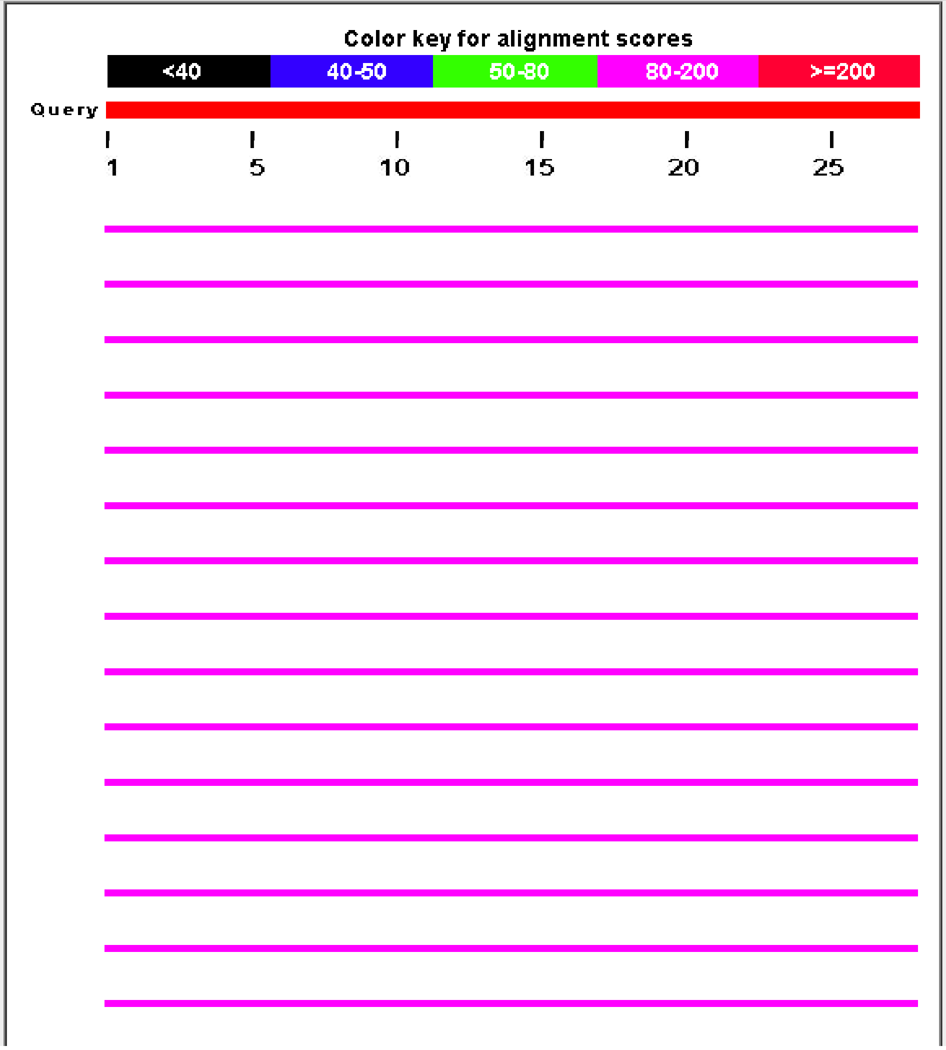
Show Conserved Domains

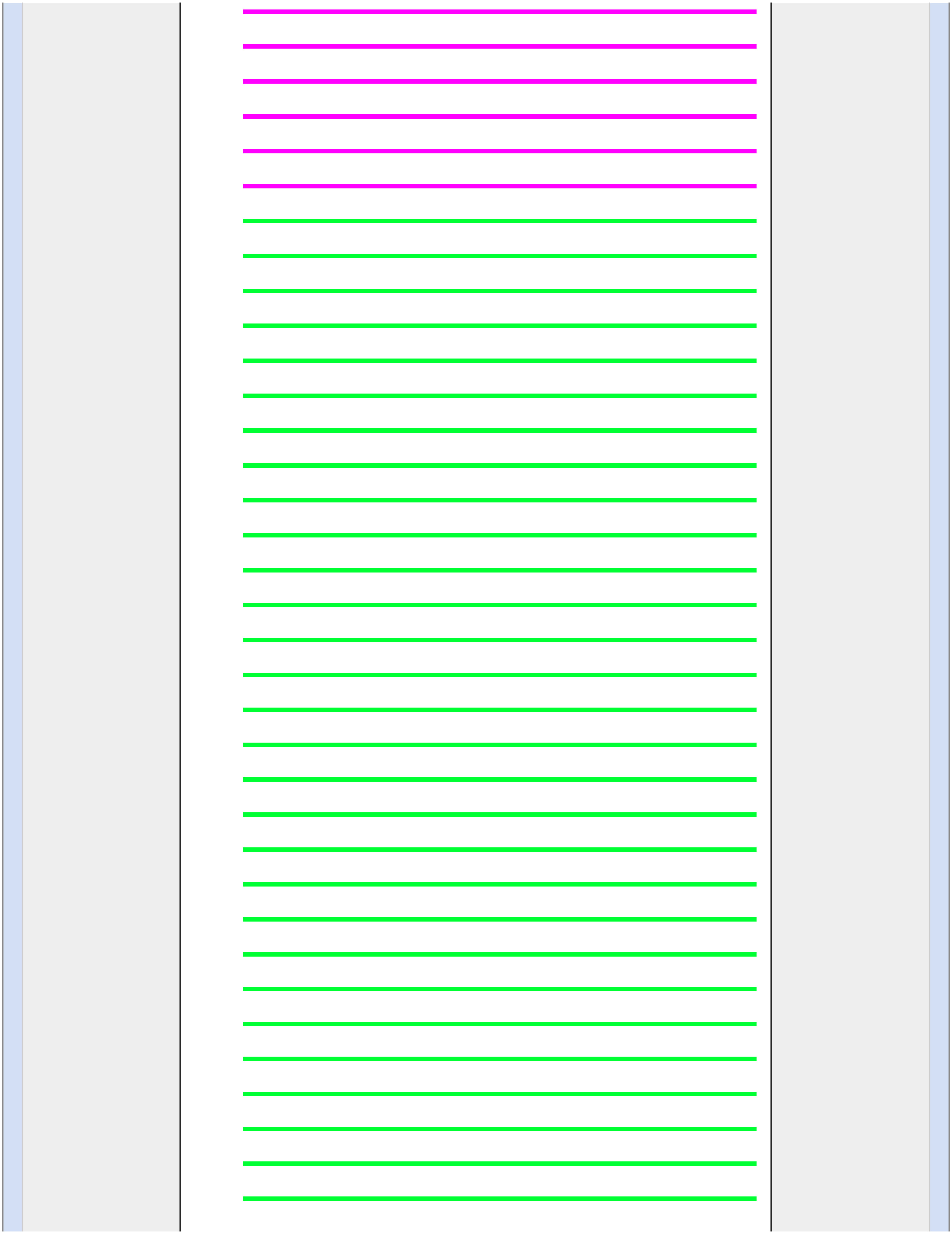
Putative conserved domains have been detected, click on the image below for detailed results.

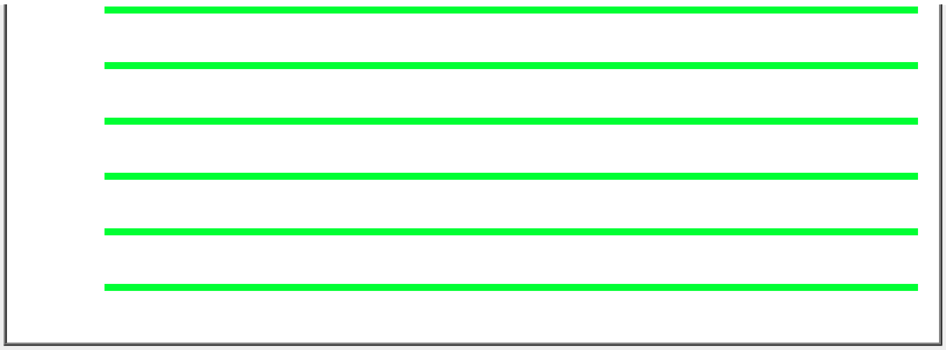


Distribution of 201 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, Crystal Structure Of A Ligand-Binding Domain Of The Hur	92.3	92.3	100%	5e-20	100%	gi|56967075|1XED_A
☐	Chain A, Solution Structure Of Human Secretory Component [Homo	92.3	114	100%	2e-19	100%	gi|146387599|2OCW_A
☐	poly-Ig receptor [Homo sapiens]	92.3	114	100%	2e-19	100%	gi|514366|AAA36102.1
☐	polymeric immunoglobulin receptor precursor [Homo sapiens]	92.3	114	100%	2e-19	100%	gi|31377806|NP_002635.2
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Gorilla	92.3	118	100%	2e-19	100%	gi|426333562|XP_004028344.1
☐	transmembrane secretory component [Homo sapiens]	92.3	114	100%	2e-19	100%	gi|238236|AAB20203.1
☐	PREDICTED: polymeric immunoglobulin receptor [Pan paniscus]	92.3	114	100%	2e-19	100%	gi|397504777|XP_003822957.1
☐	PREDICTED: polymeric immunoglobulin receptor [Pan troglodytes]	92.3	114	100%	2e-19	100%	gi|332811741|XP_514153.3
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Homo	92.3	114	100%	2e-19	100%	gi|530366266|XP_005273220.1
☐	PREDICTED: polymeric immunoglobulin receptor [Callithrix jacchus	88.0	111	100%	6e-18	96%	gi|296230617|XP_002760783.1
☐	hypothetical protein [Pongo abelii]	88.0	114	100%	6e-18	96%	gi|55729233|CAH91352.1
☐	polymeric immunoglobulin receptor precursor [Pongo abelii]	88.0	114	100%	6e-18	96%	gi|197102290|NP_001125098.1
☐	PREDICTED: polymeric immunoglobulin receptor [Macaca mulatta]	83.8	108	100%	2e-16	93%	gi|297280921|XP_001083307.2
☐	PREDICTED: polymeric immunoglobulin receptor [Chlorocebus sab	83.8	108	100%	2e-16	93%	gi|635130940|XP_007986846.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Maca	83.8	108	100%	2e-16	93%	gi|544399911|XP_005540721.1
☐	PREDICTED: polymeric immunoglobulin receptor [Papio anubis]	83.8	108	100%	2e-16	93%	gi|402857385|XP_003893238.1
☐	hypothetical protein EGM_01447 [Macaca fascicularis]	83.8	108	100%	2e-16	93%	gi|355745965|EHH50590.1
☐	hypothetical protein EGK_01717 [Macaca mulatta]	83.8	108	100%	2e-16	93%	gi|355558822|EHH15602.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Maca	83.8	108	100%	2e-16	93%	gi|544399909|XP_005540720.1
☐	PREDICTED: polymeric immunoglobulin receptor [Rhinopithecus ro	81.2	106	100%	1e-15	89%	gi|724836419|XP_010363960.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Nomas	81.2	107	100%	1e-15	93%	gi|332247745|XP_003273022.1
☐	PREDICTED: polymeric immunoglobulin receptor-like [Galeopterus	79.5	79.5	100%	2e-15	86%	gi|667345587|XP_008563367.1
☐	PREDICTED: polymeric immunoglobulin receptor [Saimiri boliviensi	80.0	103	100%	3e-15	89%	gi|403277678|XP_003930479.1
☐	PREDICTED: polymeric immunoglobulin receptor [Nannospalax gal	78.3	100	100%	1e-14	86%	gi|674096299|XP_008821506.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Ictido	77.8	99.7	100%	2e-14	86%	gi|532087641|XP_005329532.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Ictido	77.8	99.7	100%	2e-14	86%	gi|532087643|XP_005329533.1
☐	PREDICTED: polymeric immunoglobulin receptor [Camelus ferus]	76.6	76.6	100%	5e-14	79%	gi|560912075|XP_006182326.1
☐	PREDICTED: polymeric immunoglobulin receptor [Otolemur garnett	76.6	99.3	100%	5e-14	82%	gi|395838714|XP_003792254.1
☐	polymeric immunoglobulin receptor precursor [Camelus ferus]	76.6	121	100%	5e-14	79%	gi|530667813|EQB78114.1

☐	PREDICTED: polymeric immunoglobulin receptor [Vicugna pacos]	75.7	98.4	100%	9e-14	79%	gi|560986671|XP_006215522.1
☐	PREDICTED: polymeric immunoglobulin receptor [Leptonychotes w	75.3	98.8	100%	1e-13	82%	gi|585156277|XP_006730466.1
☐	PREDICTED: polymeric immunoglobulin receptor [Tarsius syrichta]	71.9	120	100%	2e-12	79%	gi|640811957|XP_008062620.1
☐	PREDICTED: polymeric immunoglobulin receptor [Bubalus bubalis]	71.9	96.3	100%	2e-12	79%	gi|594038508|XP_006043871.1
☐	PREDICTED: polymeric immunoglobulin receptor [Pantholops hodg	71.5	122	100%	3e-12	75%	gi|556742966|XP_005967001.1
☐	PREDICTED: polymeric immunoglobulin receptor [Capra hircus]	71.5	126	100%	3e-12	75%	gi|548497730|XP_005690475.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Ovis ar	71.5	126	100%	3e-12	75%	gi|426239425|XP_004013622.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 2 [Ovis ar	71.5	126	100%	3e-12	75%	gi|426239427|XP_004013623.1
☐	Chain A, Crystal Structure Of The 1st Ig Domain From Mouse Polyr	69.4	69.4	100%	7e-12	75%	gi|563321008|4NOB_A
☐	polymeric immunoglobulin receptor precursor [Bos taurus]	70.2	122	100%	7e-12	75%	gi|32189338|NP_776568.1
☐	RecName: Full=Polymeric immunoglobulin receptor; Short=PIgR; S	70.2	122	100%	7e-12	75%	gi|3914346|P81265.1
☐	PIGR protein [Bos taurus]	70.2	122	100%	7e-12	75%	gi|151555693|AAI49033.1
☐	PREDICTED: polymeric immunoglobulin receptor [Panthera tigris a	69.4	92.9	100%	1e-11	75%	gi|591341842|XP_007096344.1
☐	PREDICTED: polymeric immunoglobulin receptor [Peromyscus mar	69.4	90.8	100%	1e-11	79%	gi|589968826|XP_006996902.1
☐	PREDICTED: polymeric immunoglobulin receptor [Felis catus]	69.4	92.9	100%	1e-11	75%	gi|587018664|XP_006943006.1
☐	polymeric immunoglobulin receptor [Mus musculus]	69.4	92.9	100%	1e-11	75%	gi|458422|AAA67440.1
☐	polymeric immunoglobulin receptor precursor [Mus musculus]	69.4	92.9	100%	1e-11	75%	gi|31981570|NP_035212.2
☐	PREDICTED: LOW QUALITY PROTEIN: polymeric immunoglobulin	68.9	121	100%	2e-11	75%	gi|555959201|XP_005891711.1
☐	TPA: polymeric immunoglobulin receptor precursor [Bos taurus]	68.9	121	100%	2e-11	75%	gi|296479365|DAA21480.1
☐	PREDICTED: polymeric immunoglobulin receptor [Microtus ochroga	68.1	68.1	100%	4e-11	75%	gi|532009108|XP_005348371.1
☐	PREDICTED: polymeric immunoglobulin receptor [Equus przewalsk	67.7	89.9	100%	5e-11	79%	gi|664764562|XP_008539949.1
☐	PREDICTED: polymeric immunoglobulin receptor [Equus caballus]	67.7	89.9	100%	5e-11	79%	gi|194210251|XP_001492348.2
☐	polymeric immunoglobulin receptor precursor [Equus caballus]	67.7	89.9	100%	5e-11	79%	gi|548961809|NP_001271468.1
☐	PREDICTED: polymeric immunoglobulin receptor [Ursus maritimus]	67.2	90.8	100%	7e-11	75%	gi|670984407|XP_008683298.1
☐	PREDICTED: polymeric immunoglobulin receptor [Tupaia chinensis	67.2	113	100%	7e-11	75%	gi|562862054|XP_006159345.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Muste	66.0	90.4	100%	2e-10	75%	gi|511939572|XP_004788608.1
☐	PREDICTED: polymeric immunoglobulin receptor [Mustela putorius	66.0	90.4	100%	2e-10	75%	gi|511871244|XP_004756245.1
☐	PREDICTED: polymeric immunoglobulin receptor [Odobenus rosma	65.5	88.7	100%	3e-10	75%	gi|472392635|XP_004415592.1
☐	PREDICTED: polymeric immunoglobulin receptor [Ceratotherium si	65.5	87.8	100%	3e-10	77%	gi|478501668|XP_004425146.1
☐	PREDICTED: polymeric immunoglobulin receptor [Jaculus jaculus]	64.7	87.0	100%	5e-10	68%	gi|507559576|XP_004663511.1
☐	polymeric immunoglobulin receptor [Canis lupus familiaris]	64.3	64.3	100%	6e-10	68%	gi|19715659|AAL91653.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Oryct	64.3	108	100%	7e-10	71%	gi|634826802|XP_007951362.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Oryct	64.3	108	100%	7e-10	71%	gi|634826799|XP_007951355.1
☐	polymeric immunoglobulin receptor precursor [Canis lupus familiaris	64.3	88.2	100%	7e-10	68%	gi|560891934|NP_001274081.1
☐	polymeric immunoglobulin receptor precursor [Rattus norvegicus]	64.3	64.3	100%	7e-10	68%	gi|501354879|NP_036855.3
☐	polymeric immunoglobulin receptor [Rattus norvegicus]	64.3	64.3	100%	7e-10	68%	gi|149058686|EDM09843.1
☐	PREDICTED: polymeric immunoglobulin receptor [Lipotes vexillifer]	63.8	88.2	100%	9e-10	71%	gi|602721248|XP_007470777.1
☐	PREDICTED: polymeric immunoglobulin receptor [Physeter catodor	63.8	85.7	100%	9e-10	71%	gi|593718296|XP_007105526.1
☐	PREDICTED: polymeric immunoglobulin receptor [Tursiops truncatu	63.0	84.8	100%	2e-09	71%	gi|470622594|XP_004319136.1
☐	PREDICTED: polymeric immunoglobulin receptor [Orcinus orca]	63.0	84.8	100%	2e-09	71%	gi|466071278|XP_004282467.1
☐	PREDICTED: polymeric immunoglobulin receptor [Balaenoptera acu	63.0	85.7	100%	2e-09	71%	gi|594636460|XP_007171624.1
☐	PREDICTED: LOW QUALITY PROTEIN: polymeric immunoglobulin	62.6	84.0	100%	3e-09	68%	gi|625233654|XP_007607970.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Meso	62.6	86.5	100%	3e-09	68%	gi|524959951|XP_005079920.1
☐	Polymeric immunoglobulin receptor [Cricetulus griseus]	62.6	84.0	100%	3e-09	68%	gi|344244860|EGW00964.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Meso	62.6	86.5	100%	3e-09	68%	gi|524959949|XP_005079919.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Crice	62.6	84.0	100%	3e-09	68%	gi|354471083|XP_003497773.1

☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Crice	62.6	84.0	100%	3e-09	68%	gi|354471081|XP_003497772.1
☐	polymeric immunoglobulin receptor isoform 1 [Cricetulus griseus]	62.6	121	100%	3e-09	68%	gi|537169305|ERE73918.1
☐	polymeric immunoglobulin receptor precursor [Sus scrofa]	61.7	84.0	100%	5e-09	71%	gi|47523406|NP_999324.1
☐	Polymeric immunoglobulin receptor [Pteropus alecto]	60.4	82.3	96%	1e-08	70%	gi|431892859|ELK03287.1
☐	PREDICTED: polymeric immunoglobulin receptor [Pteropus alecto]	60.4	123	100%	1e-08	70%	gi|586536225|XP_006922980.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform 1 [Dasypı	59.2	83.1	100%	3e-08	68%	gi|488560131|XP_004470111.1
☐	PREDICTED: polymeric immunoglobulin receptor [Echinops telfairi]	58.7	101	100%	5e-08	71%	gi|507635434|XP_004700183.1
☐	PREDICTED: polymeric immunoglobulin receptor [Chinchilla lanige	58.3	84.4	100%	6e-08	68%	gi|533120059|XP_005375465.1
☐	PREDICTED: polymeric immunoglobulin receptor [Octodon degus]	57.9	57.9	100%	9e-08	64%	gi|507688344|XP_004641251.1
☐	PREDICTED: polymeric immunoglobulin receptor [Cavia porcellus]	57.5	57.5	100%	1e-07	68%	gi|348578097|XP_003474820.1
☐	PREDICTED: polymeric immunoglobulin receptor [Elephantulus edv	57.1	78.1	100%	2e-07	64%	gi|585666892|XP_006888060.1
☐	PREDICTED: polymeric immunoglobulin receptor [Chrysochloris as	57.1	107	100%	2e-07	68%	gi|586450680|XP_006834271.1
☐	PREDICTED: polymeric immunoglobulin receptor [Erinaceus europ	56.6	56.6	100%	2e-07	64%	gi|617602067|XP_007523168.1
☐	PREDICTED: polymeric immunoglobulin receptor [Eptesicus fuscus	56.2	77.2	100%	3e-07	61%	gi|641724928|XP_008152394.1
☐	PREDICTED: polymeric immunoglobulin receptor [Myotis davidii]	56.2	77.2	100%	3e-07	64%	gi|584068124|XP_006754443.1
☐	PREDICTED: LOW QUALITY PROTEIN: polymeric immunoglobulir	55.4	55.4	100%	6e-07	64%	gi|505829866|XP_004610232.1
☐	PREDICTED: polymeric immunoglobulin receptor [Loxodonta africa	54.9	54.9	100%	8e-07	64%	gi|731475646|XP_010588572.1
☐	PREDICTED: polymeric immunoglobulin receptor [Monodelphis dor	54.1	84.4	100%	2e-06	64%	gi|611989136|XP_007481356.1
☐	PREDICTED: polymeric immunoglobulin receptor [Myotis lucifugus]	53.7	74.7	100%	2e-06	57%	gi|558152618|XP_006094928.1
☐	PREDICTED: polymeric immunoglobulin receptor [Myotis brandtii]	53.7	74.7	100%	2e-06	57%	gi|554587770|XP_005885286.1
☐	Polymeric immunoglobulin receptor [Myotis brandtii]	53.7	95.7	100%	2e-06	57%	gi|521037818|EPQ19595.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X2 [Heter	53.2	53.2	100%	3e-06	64%	gi|513001195|XP_004862115.1
☐	PREDICTED: polymeric immunoglobulin receptor [Heterocephalus	53.2	53.2	100%	3e-06	64%	gi|512893082|XP_004897444.1
☐	Polymeric immunoglobulin receptor [Heterocephalus glaber]	53.2	53.2	100%	3e-06	64%	gi|351708108|EHB11027.1
☐	PREDICTED: polymeric immunoglobulin receptor isoform X1 [Heter	53.2	53.2	100%	3e-06	64%	gi|513001193|XP_004862114.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, Crystal Structure Of A Ligand-Binding Domain Of The Human Polymeric Ig Receptor, Pigr

Sequence ID: gi|56967075|pdb|1XED|A **Length:** 117 **Number of Matches:** 1

▷ See 5 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 63 to 90 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
92.3 bits(210)	5e-20	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1   RANLTNFPENGTFVVNIAQLSQDDSGRY  28
           RANLTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  63  RANLTNFPENGTFVVNIAQLSQDDSGRY  90
```

Download GenPept Graphics **Sort by:** 0 ▼ Next ▲ Previous Descriptions

Chain A, Solution Structure Of Human Secretory Component

Sequence ID: gi|146387599|pdb|2OCW|A **Length:** 585 **Number of Matches:** 2

▷ See 2 more title(s)

Related Information

Structure - 3D structure displays

Identical Proteins - Proteins identical to the subject

Range 1: 63 to 90 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
92.3 bits(210)	2e-19	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1   RANLTNFPENGTFVVNIAQLSQDDSGRY  28
           RANLTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  63  RANLTNFPENGTFVVNIAQLSQDDSGRY  90
```

Range 2: 401 to 417 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
22.3 bits(45)	49173	10/17(59%)	10/17(58%)	1/17(5%)

```
Query  8    PENGTFVVNIAQL-SQD  23
            P NGTF V   QL S D
Sbjct  401  PGNGTFTVILNQLTSRD  417
```

Download GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

poly-Ig receptor, partial [Homo sapiens]

Sequence ID: gi|514366|gb|AAA36102.1| **Length:** 693 **Number of Matches:** 2

Related Information

Gene - associated gene details

Range 1: 10 to 37 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
92.3 bits(210)	2e-19	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1   RANLTNFPENGTFVVNIAQLSQDDSGRY  28
           RANLTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  10  RANLTNFPENGTFVVNIAQLSQDDSGRY  37
```

Range 2: 348 to 364 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
22.3 bits(45)	49301	10/17(59%)	10/17(58%)	1/17(5%)

```
Query  8    PENGTFVVNIAQL-SQD  23
            P NGTF V   QL S D
Sbjct  348  PGNGTFTVILNQLTSRD  364
```

Download GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

polymeric immunoglobulin receptor precursor [Homo sapiens]

Sequence ID: gi|31377806|ref|NP_002635.2| **Length:** 764 **Number of Matches:** 2

▷ See 8 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 81 to 108 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
92.3 bits(210)	2e-19	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    RANLTNFPENGTFVVNIAQLSQDDSGRY  28
            RANLTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  81   RANLTNFPENGTFVVNIAQLSQDDSGRY  108
```

Range 2: 419 to 435 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
22.3 bits(45)	49365	10/17(59%)	10/17(58%)	1/17(5%)

```
Query  8    PENGTFVVNIAQL-SQD  23
            P NGTF V   QL S D
Sbjct  419  PGNGTFTVILNQLTSRD  435
```

Download GenPept Graphics Sort by: 0 ▼ Next ▲ Previous Descriptions

PREDICTED: polymeric immunoglobulin receptor isoform 1 [Gorilla gorilla gorilla]

Sequence ID: gi|426333562|ref|XP_004028344.1| **Length:** 764 **Number of Matches:** 2

▷ See 1 more title(s)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 81 to 108 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
92.3 bits(210)	2e-19	28/28(100%)	28/28(100%)	0/28(0%)

```
Query  1    RANLTNFPENGTFVVNIAQLSQDDSGRY  28
            RANLTNFPENGTFVVNIAQLSQDDSGRY
Sbjct  81   RANLTNFPENGTFVVNIAQLSQDDSGRY  108
```

Range 2: 419 to 435 GenPept Graphics ▼ Next Match ▲ Previous Match First Match

Score	Expect	Identities	Positives	Gaps
26.5 bits(55)	1836	11/17(65%)	11/17(64%)	1/17(5%)

```
Query  8    PENGTFVVNIAQL-SQD  23
            P NGTF V   QL SQD
Sbjct  419  PGNGTFTVILNQLTSQD  435
```

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Your search parameters were adjusted to search for a short input sequence.

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PLTP_KVSDVSCQASVSRM_Mod

RID	BVK2V5KM01R (Expires on 01-21 10:32 am)
Query ID	lcl|209639
Description	None
Molecule type	amino acid
Query Length	14

Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ ▷ Citation

Other reports: ▷ Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

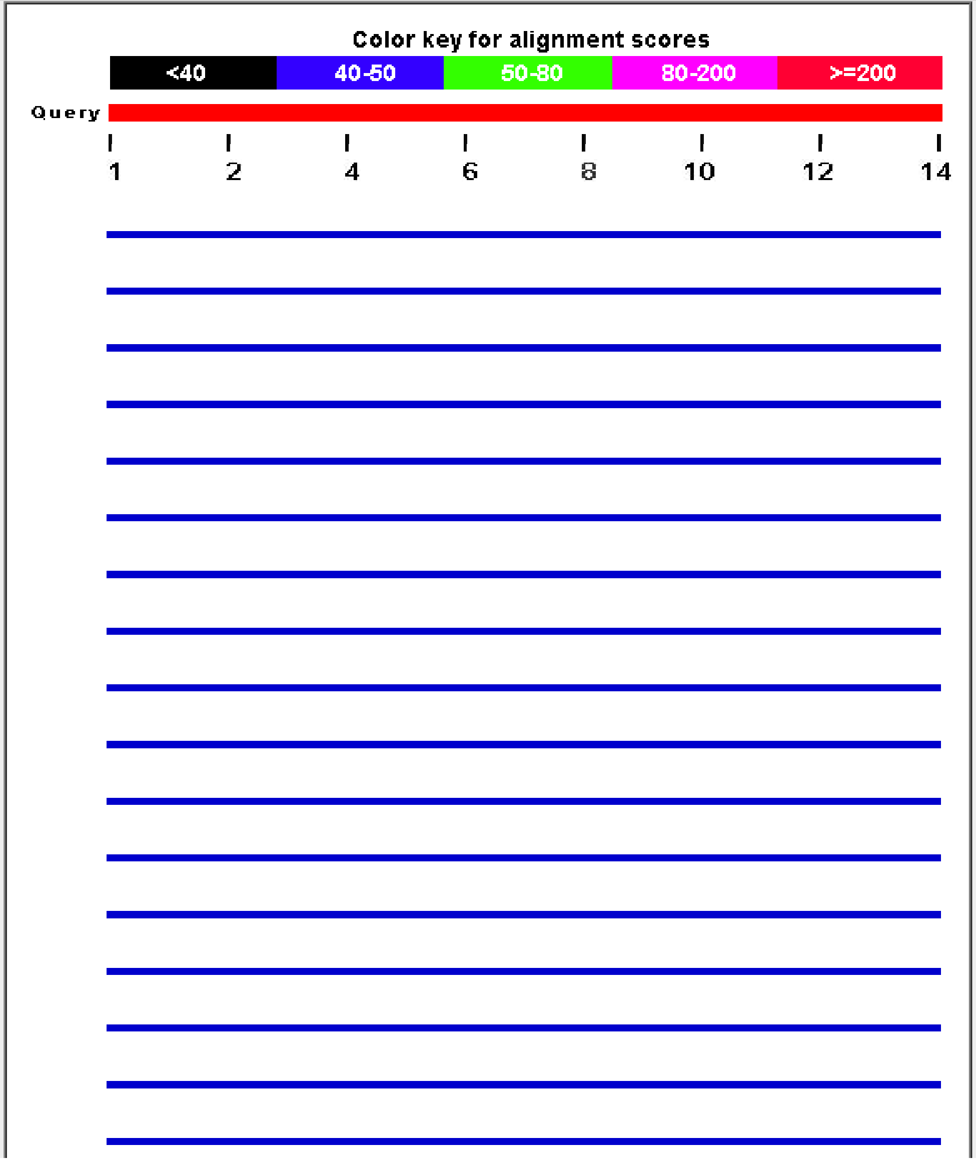
Graphic Summary

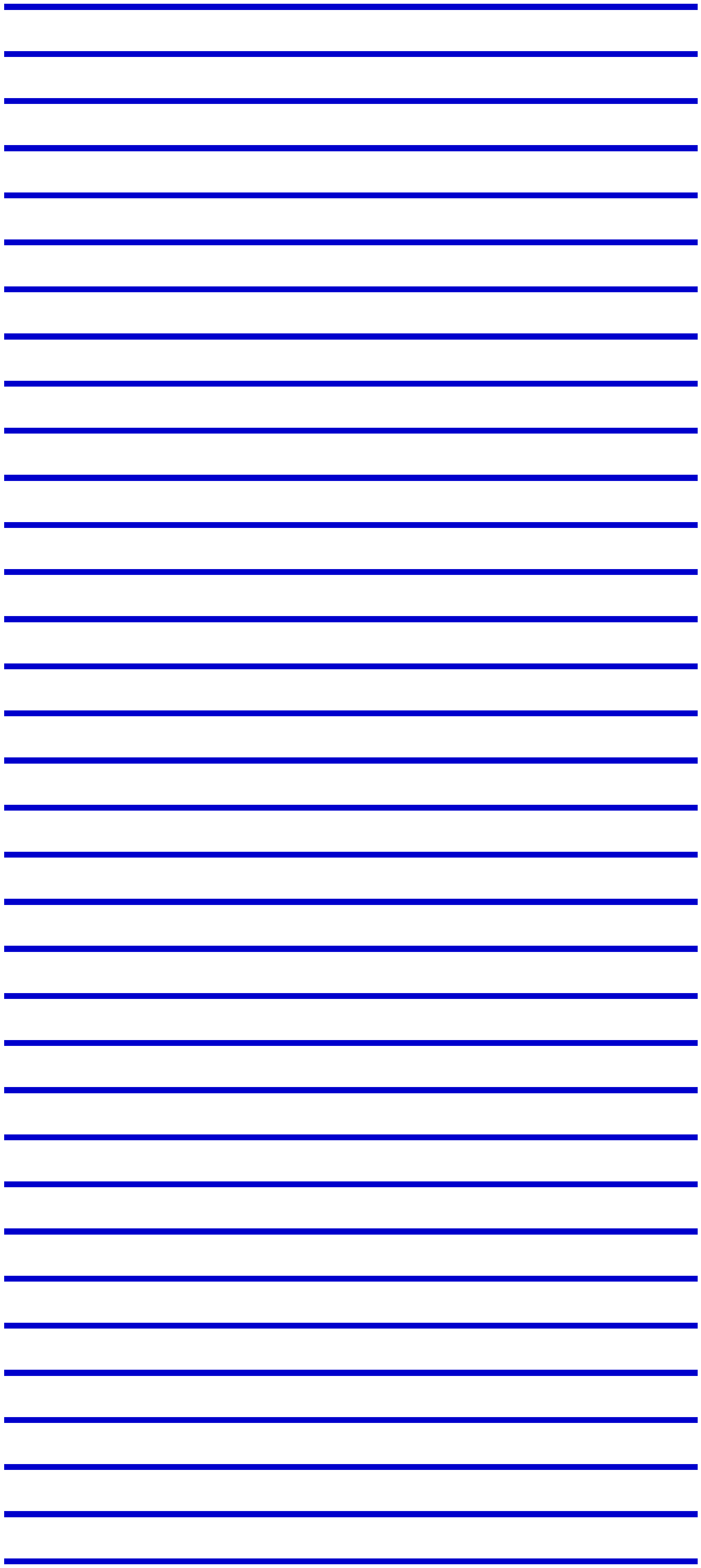
Show Conserved Domains

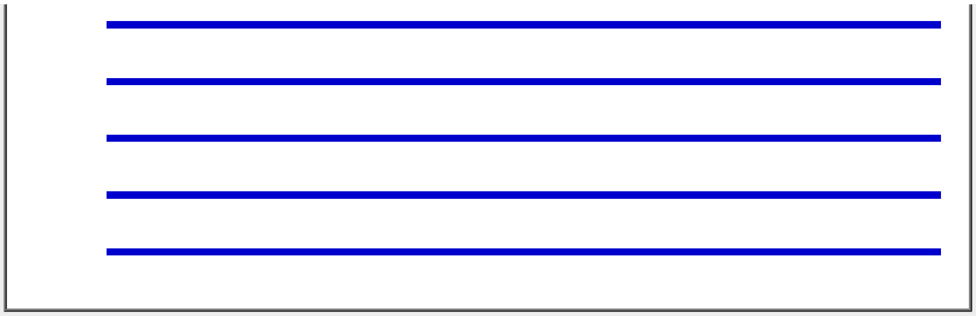
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PLTP-like protein [Bos taurus]	44.3	44.3	100%	5e-04	93%	AAW21227.1
☐	PREDICTED: phospholipid transfer protein-like isoform X1 [Sus scrofa]	44.3	44.3	100%	5e-04	93%	XP_005673034.1
☐	PREDICTED: phospholipid transfer protein-like [Leptonychotes weddellii]	44.3	44.3	100%	6e-04	93%	XP_006739837.1
☐	PREDICTED: phospholipid transfer protein isoform X3 [Pan troglodytes]	44.3	44.3	100%	7e-04	93%	XP_009435596.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Tarsius syrichta]	44.3	44.3	100%	7e-04	93%	XP_008056109.1
☐	PREDICTED: phospholipid transfer protein isoform X3 [Chlorocebus sabaeus]	44.3	44.3	100%	7e-04	93%	XP_008013799.1
☐	unnamed protein product [Homo sapiens]	44.3	44.3	100%	7e-04	93%	BAG56696.1
☐	PREDICTED: phospholipid transfer protein isoform X6 [Macaca fascicularis]	44.3	44.3	100%	7e-04	93%	XP_005569256.1
☐	phospholipid transfer protein precursor [Pan troglodytes]	44.3	44.3	100%	7e-04	93%	BAK62129.1
☐	phospholipid transfer protein isoform d [Homo sapiens]	44.3	44.3	100%	7e-04	93%	NP_001229850.1
☐	unnamed protein product [Macaca fascicularis]	44.3	44.3	100%	7e-04	93%	BAE00639.1
☐	PREDICTED: phospholipid transfer protein isoform X4 [Vicugna pacos]	44.3	44.3	100%	7e-04	93%	XP_006202544.1
☐	PREDICTED: phospholipid transfer protein isoform X4 [Camelus ferus]	44.3	44.3	100%	7e-04	93%	XP_006187692.1
☐	PREDICTED: phospholipid transfer protein isoform 4 [Ceratotherium simum si	44.3	44.3	100%	7e-04	93%	XP_004430381.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Condylura cristata]	44.3	44.3	100%	7e-04	93%	XP_004687488.1
☐	PREDICTED: phospholipid transfer protein isoform 4 [Orcinus orca]	44.3	44.3	100%	7e-04	93%	XP_004272968.1
☐	PREDICTED: phospholipid transfer protein [Callithrix jacchus]	44.3	44.3	100%	7e-04	93%	XP_008994362.1
☐	phospholipid transfer protein, isoform CRA_d [Homo sapiens]	44.3	44.3	100%	7e-04	93%	EAW75786.1
☐	PREDICTED: phospholipid transfer protein [Capra hircus]	44.3	44.3	100%	7e-04	93%	XP_005688777.1
☐	PREDICTED: phospholipid transfer protein isoform 1 [Ovis aries]	44.3	44.3	100%	7e-04	93%	XP_004014658.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Came	44.3	44.3	100%	7e-04	93%	XP_010956961.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Came	44.3	44.3	100%	7e-04	93%	XP_010976914.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Bos m	44.3	44.3	100%	7e-04	93%	XP_005897642.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Pan troglodytes]	44.3	44.3	100%	7e-04	93%	XP_009435595.1
☐	PREDICTED: phospholipid transfer protein [Rhinopithecus roxellana]	44.3	44.3	100%	7e-04	93%	XP_010382500.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Chlorocebus sabaeus]	44.3	44.3	100%	7e-04	93%	XP_008013795.1
☐	Phospholipid transfer protein [Homo sapiens]	44.3	44.3	100%	7e-04	93%	AAH19847.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Macaca fascicularis]	44.3	44.3	100%	7e-04	93%	XP_005569252.1
☐	PREDICTED: phospholipid transfer protein [Gorilla gorilla gorilla]	44.3	44.3	100%	7e-04	93%	XP_004062321.1

☐	phospholipid transfer protein isoform a precursor [Homo sapiens]	44.3	44.3	100%	7e-04	93%	NP_006218.1
☐	PREDICTED: phospholipid transfer protein [Saimiri boliviensis boliviensis]	44.3	44.3	100%	7e-04	93%	XP_003936508.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Papio	44.3	44.3	100%	7e-04	93%	XP_003904720.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Pan paniscus]	44.3	44.3	100%	7e-04	93%	XP_008949625.1
☐	Lipid transfer protein II [Macaca mulatta]	44.3	44.3	100%	7e-04	93%	EHH19636.1
☐	PREDICTED: phospholipid transfer protein [Nomascus leucogenys]	44.3	44.3	100%	7e-04	93%	XP_003253705.1
☐	PREDICTED: phospholipid transfer protein-like [Macaca mulatta]	44.3	44.3	100%	7e-04	93%	XP_002798159.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Pan troglodytes]	44.3	44.3	100%	7e-04	93%	XP_001158846.2
☐	phospholipid transfer protein isoform a precursor variant [Homo sapiens]	44.3	44.3	100%	7e-04	93%	BAD96410.1
☐	PREDICTED: phospholipid transfer protein [Heterocephalus glaber]	44.3	44.3	100%	7e-04	93%	XP_004888423.1
☐	PREDICTED: phospholipid transfer protein isoform 2 [Ovis aries]	44.3	44.3	100%	7e-04	93%	XP_004014659.1
☐	PREDICTED: phospholipid transfer protein [Ursus maritimus]	44.3	44.3	100%	7e-04	93%	XP_008696270.1
☐	hypothetical protein PANDA_018015 [Ailuropoda melanoleuca]	44.3	44.3	100%	7e-04	93%	EFB21975.1
☐	PREDICTED: phospholipid transfer protein isoformX3 [Canis lupus familiaris]	44.3	44.3	100%	7e-04	93%	XP_543027.2
☐	PREDICTED: phospholipid transfer protein isoform 1 [Otolemur garnettii]	44.3	44.3	100%	7e-04	93%	XP_003787705.1
☐	phospholipid transfer protein precursor [Sus scrofa]	44.3	44.3	100%	7e-04	93%	NP_999448.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Erinaceus europaeus]	44.3	44.3	100%	7e-04	93%	XP_007533119.1
☐	PREDICTED: phospholipid transfer protein [Balaenoptera acutorostrata scam	44.3	44.3	100%	7e-04	93%	XP_007185441.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Bubalus bubalis]	44.3	44.3	100%	7e-04	93%	XP_006051425.1
☐	PREDICTED: phospholipid transfer protein [Physeter catodon]	44.3	44.3	100%	7e-04	93%	XP_007115580.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Tupaia chinensis]	44.3	44.3	100%	7e-04	93%	XP_006158592.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Vicugna pacos]	44.3	44.3	100%	7e-04	93%	XP_006202541.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Camelus ferus]	44.3	44.3	100%	7e-04	93%	XP_006187689.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Bos taurus]	44.3	44.3	100%	7e-04	93%	XP_005214615.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Muste	44.3	44.3	100%	7e-04	93%	XP_004746370.1
☐	PREDICTED: phospholipid transfer protein isoform 1 [Ceratotherium simum si	44.3	44.3	100%	7e-04	93%	XP_004430378.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Tursio	44.3	44.3	100%	7e-04	93%	XP_004319149.1
☐	PREDICTED: phospholipid transfer protein isoform 1 [Orcinus orca]	44.3	44.3	100%	7e-04	93%	XP_004272965.1
☐	PREDICTED: phospholipid transfer protein-like [Ailuropoda melanoleuca]	44.3	44.3	100%	7e-04	93%	XP_002928111.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Lipote	44.3	44.3	100%	7e-04	93%	XP_007451697.1
☐	Phospholipid transfer protein [Tupaia chinensis]	44.3	44.3	100%	7e-04	93%	ELW48240.1
☐	PREDICTED: phospholipid transfer protein [Bison bison bison]	44.3	44.3	100%	7e-04	93%	XP_010833341.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Tupaia chinensis]	44.3	44.3	100%	7e-04	93%	XP_006158591.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Panth	44.3	44.3	100%	7e-04	93%	XP_005954715.1
☐	phospholipid transfer protein precursor [Bos taurus]	44.3	44.3	100%	7e-04	93%	NP_001030199.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Chlorocebus sabaeus	44.3	44.3	100%	7e-04	93%	XP_008013792.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Macaca fascicularis]	44.3	44.3	100%	7e-04	93%	XP_005569251.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Homo sapiens]	44.3	44.3	100%	7e-04	93%	XP_005260496.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Ictidomys tridecemline	44.3	44.3	100%	7e-04	93%	XP_005325306.1
☐	Phospholipid transfer protein [Heterocephalus glaber]	44.3	44.3	100%	7e-04	93%	EHB05309.1
☐	phospholipid transfer protein isoform 3 [Camelus ferus]	44.3	44.3	100%	7e-04	93%	EPY78753.1
☐	PREDICTED: phospholipid transfer protein isoform X4 [Canis lupus familiaris]	44.3	44.3	100%	7e-04	93%	XP_005635182.1
☐	PREDICTED: phospholipid transfer protein [Chrysochloris asiatica]	42.2	42.2	100%	0.003	86%	XP_006839396.1
☐	phospholipid transfer protein precursor [Pongo abelii]	42.2	42.2	100%	0.003	86%	NP_001127290.1
☐	PREDICTED: phospholipid transfer protein [Equus przewalskii]	41.8	41.8	100%	0.005	86%	XP_008519895.1

☐	PREDICTED: phospholipid transfer protein isoform X3 [Galeopterus variegatu	41.8	41.8	100%	0.005	86%	XP_008569812.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Galeopterus variegatu	41.8	41.8	100%	0.005	86%	XP_008569811.1
☐	PREDICTED: phospholipid transfer protein isoformX1 [Equus caballus]	41.8	41.8	100%	0.005	86%	XP_001503419.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Galeopterus variegatu	41.8	41.8	100%	0.005	86%	XP_008569810.1
☐	PREDICTED: phospholipid transfer protein [Nannospalax galili]	41.4	41.4	100%	0.006	86%	XP_008835992.1
☐	PREDICTED: phospholipid transfer protein [Jaculus jaculus]	41.4	41.4	100%	0.007	86%	XP_004663955.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Fukomys damarensis]	40.9	40.9	100%	0.009	86%	XP_010624498.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Fukomys damarensis]	40.9	40.9	100%	0.009	86%	XP_010624497.1
☐	phospholipid transfer protein [Cricetulus griseus]	40.1	40.1	100%	0.017	86%	ERE71590.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Cricetulus griseus]	40.1	40.1	100%	0.017	86%	XP_007608544.1
☐	PREDICTED: phospholipid transfer protein [Mesocricetus auratus]	40.1	40.1	100%	0.017	86%	XP_005085047.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Cricetulus griseus]	40.1	40.1	100%	0.017	86%	XP_003500579.1
☐	phospholipid transfer protein [Cricetulus griseus]	40.1	40.1	100%	0.017	86%	ERE71588.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Cricetulus griseus]	40.1	40.1	100%	0.017	86%	XP_007608543.1
☐	phospholipid transfer protein [Cricetulus griseus]	40.1	40.1	100%	0.017	86%	ERE71587.1
☐	PREDICTED: phospholipid transfer protein isoform 2 [Dasypus novemcinctus]	39.2	39.2	100%	0.033	86%	XP_004469931.1
☐	PREDICTED: phospholipid transfer protein isoform 1 [Dasypus novemcinctus]	39.2	39.2	100%	0.033	86%	XP_004469930.1
☐	PREDICTED: phospholipid transfer protein [Peromyscus maniculatus bairdii]	38.8	38.8	100%	0.045	79%	XP_006971038.1
☐	PREDICTED: phospholipid transfer protein [Panthera tigris altaica]	38.4	38.4	100%	0.063	86%	XP_007077837.1
☐	PREDICTED: phospholipid transfer protein [Felis catus]	38.4	38.4	100%	0.063	86%	XP_006929771.1
☐	unnamed protein product [Mus musculus]	38.0	38.0	100%	0.084	79%	BAE29052.1
☐	PREDICTED: phospholipid transfer protein [Ochotona princeps]	38.0	38.0	100%	0.086	86%	XP_004586137.1
☐	plasma phospholipid transfer protein [Mus musculus]	38.0	38.0	100%	0.086	79%	AAA87943.1
☐	Phospholipid transfer protein [Mus musculus]	38.0	38.0	100%	0.086	79%	AAH03782.1
☐	PREDICTED: phospholipid transfer protein [Microtus ochrogaster]	38.0	38.0	100%	0.086	79%	XP_005362957.1
☐	phospholipid transfer protein precursor [Mus musculus]	38.0	38.0	100%	0.086	79%	NP_035255.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PLTP-like protein [Bos taurus]

Sequence ID: gb|AAW21227.1| **Length:** 127 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 106 to 119 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	5e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KVSDVSCQASVSRM  14
            KVS+VSCQASVSRM
Sbjct  106  KVSNVSCQASVSRM  119
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: phospholipid transfer protein-like isoform X1 [Sus scrofa]

Sequence ID: ref|XP_005673034.1| **Length:** 162 **Number of Matches:** 1

▸ See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins

Range 1: 140 to 153 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	5e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KVSDVSCQASVSRM  14
            KVS+VSCQASVSRM
Sbjct  140  KVSNVSCQASVSRM  153
```

identical to the subject

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: phospholipid transfer protein-like [Leptonychotes weddellii]

Sequence ID: ref|XP_006739837.1| **Length:** 246 **Number of Matches:** 1

Range 1: 140 to 153 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	6e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KVSDVSCQASVSRM  14
            KVS+VSCQASVSRM
Sbjct  140  KVSNVSCQASVSRM  153
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: phospholipid transfer protein isoform X3 [Pan troglodytes]

Sequence ID: ref|XP_009435596.1| **Length:** 405 **Number of Matches:** 1

Range 1: 52 to 65 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	7e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1   KVSDVSCQASVSRM  14
           KVS+VSCQASVSRM
Sbjct  52  KVSNVSCQASVSRM  65
```

Related Information

Gene - associated gene details

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: phospholipid transfer protein isoform X2 [Tarsius syrichta]

Sequence ID: ref|XP_008056109.1| **Length:** 405 **Number of Matches:** 1

Range 1: 52 to 65 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	7e-04	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1   KVSDVSCQASVSRM  14
           KVS+VSCQASVSRM
Sbjct  52  KVSNVSCQASVSRM  65
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

BLAST ®

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Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

PLTP_KVSNVSCQASVSRM_NonMod

RID	BBJA8X3K015 (Expires on 01-15 08:41 am)		
Query ID	lcl|69692	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	14	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

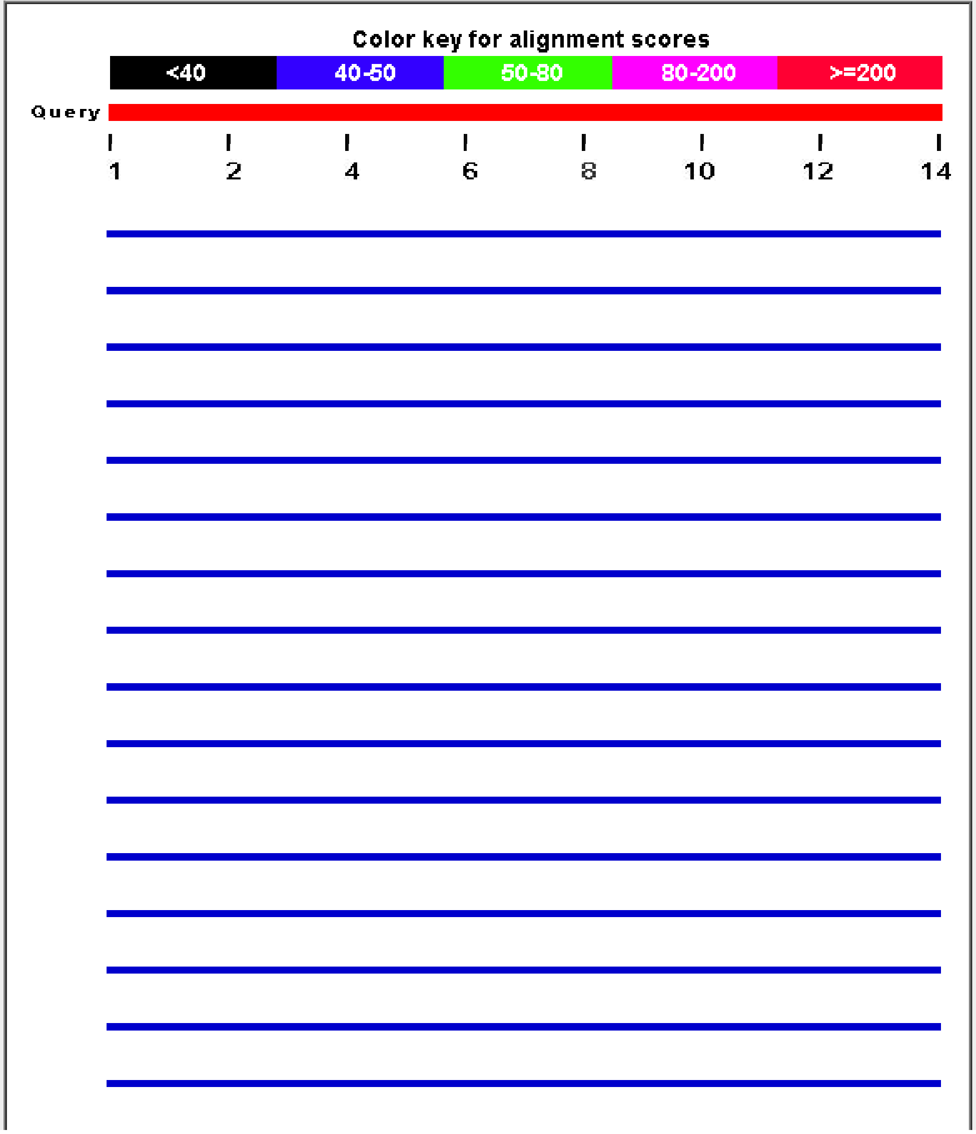
Graphic Summary

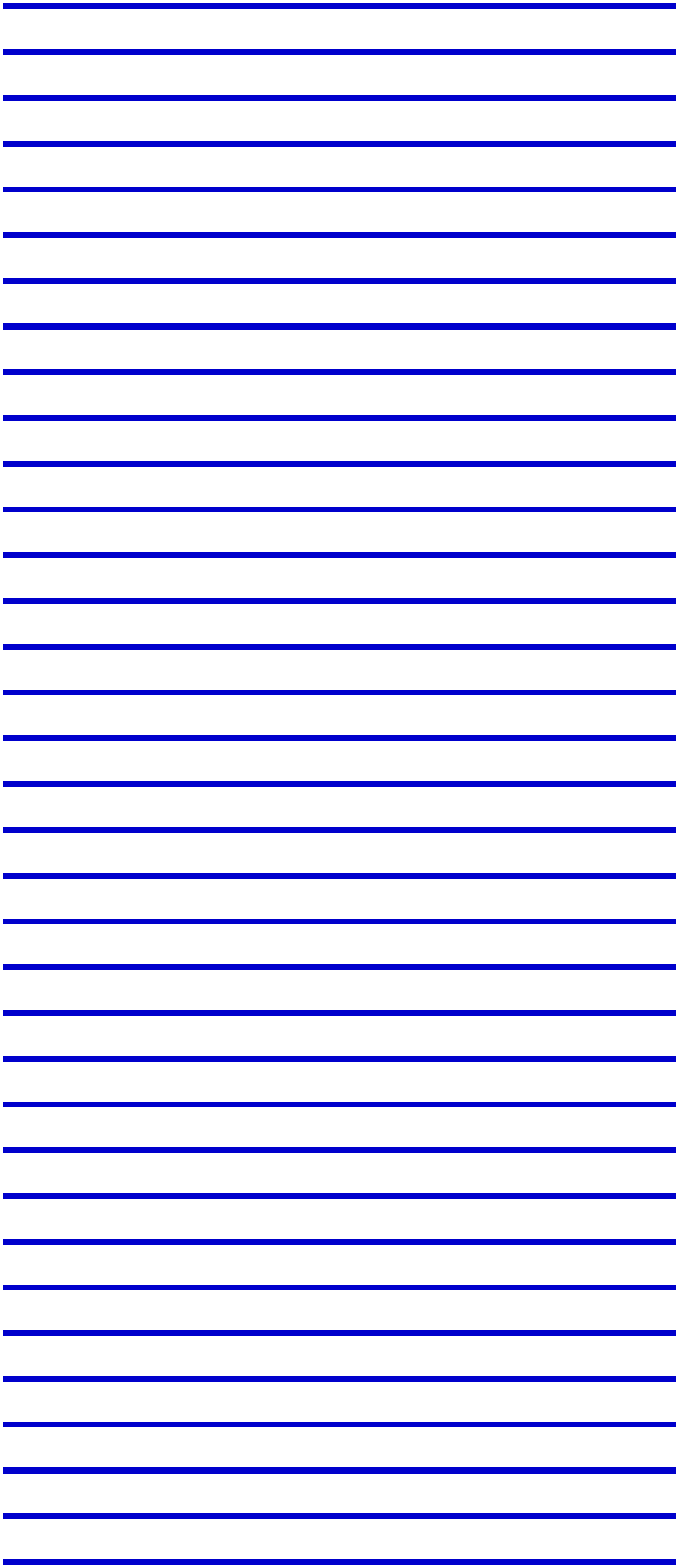
Show Conserved Domains

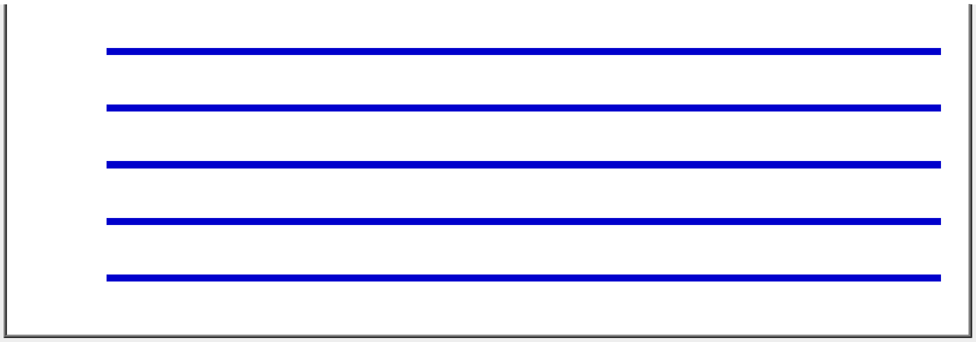
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PLTP-like protein [Bos taurus]	46.9	46.9	100%	6e-05	100%	gi|56681181|AAW21227.1
☐	PREDICTED: phospholipid transfer protein-like isoform X1 [Sus scr	46.9	46.9	100%	7e-05	100%	gi|545880919|XP_005673034.1
☐	PREDICTED: phospholipid transfer protein-like [Leptonychotes wed	46.9	46.9	100%	8e-05	100%	gi|585176105|XP_006739837.1
☐	PREDICTED: phospholipid transfer protein isoform X3 [Pan troglody	46.9	46.9	100%	9e-05	100%	gi|694979328|XP_009435596.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Tarsius syric	46.9	46.9	100%	9e-05	100%	gi|640799767|XP_008056109.1
☐	PREDICTED: phospholipid transfer protein isoform X3 [Chlorocebus	46.9	46.9	100%	9e-05	100%	gi|635020540|XP_008013799.1
☐	unnamed protein product [Homo sapiens]	46.9	46.9	100%	9e-05	100%	gi|194375502|BAG56696.1
☐	PREDICTED: phospholipid transfer protein isoform X6 [Macaca fas	46.9	46.9	100%	9e-05	100%	gi|544466131|XP_005569256.1
☐	phospholipid transfer protein precursor [Pan troglodytes]	46.9	46.9	100%	9e-05	100%	gi|343961079|BAK62129.1
☐	phospholipid transfer protein isoform d [Homo sapiens]	46.9	46.9	100%	9e-05	100%	gi|339275810|NP_001229850.1
☐	unnamed protein product [Macaca fascicularis]	46.9	46.9	100%	9e-05	100%	gi|67968557|BAE00639.1
☐	PREDICTED: phospholipid transfer protein isoform X4 [Vicugna pac	46.9	46.9	100%	9e-05	100%	gi|560960187|XP_006202544.1
☐	PREDICTED: phospholipid transfer protein isoform X4 [Camelus fer	46.9	46.9	100%	9e-05	100%	gi|560922989|XP_006187692.1
☐	PREDICTED: phospholipid transfer protein isoform 4 [Ceratotherium	46.9	46.9	100%	9e-05	100%	gi|478512237|XP_004430381.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Condylura c	46.9	46.9	100%	9e-05	100%	gi|507961913|XP_004687488.1
☐	PREDICTED: phospholipid transfer protein isoform 4 [Orcinus orca]	46.9	46.9	100%	9e-05	100%	gi|466024688|XP_004272968.1
☐	PREDICTED: phospholipid transfer protein [Callithrix jacchus]	46.9	46.9	100%	9e-05	100%	gi|675657086|XP_008994362.1
☐	phospholipid transfer protein, isoform CRA_d [Homo sapiens]	46.9	46.9	100%	9e-05	100%	gi|119596192|EAW75786.1
☐	PREDICTED: phospholipid transfer protein [Capra hircus]	46.9	46.9	100%	9e-05	100%	gi|548491933|XP_005688777.1
☐	PREDICTED: phospholipid transfer protein isoform 1 [Ovis aries]	46.9	46.9	100%	9e-05	100%	gi|426241561|XP_004014658.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer prot	46.9	46.9	100%	9e-05	100%	gi|555971257|XP_005897642.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Pan troglody	46.9	46.9	100%	9e-05	100%	gi|694979326|XP_009435595.1
☐	PREDICTED: phospholipid transfer protein [Rhinopithecus roxellana	46.9	46.9	100%	9e-05	100%	gi|724927761|XP_010382500.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Chlorocebus	46.9	46.9	100%	9e-05	100%	gi|635020538|XP_008013795.1
☐	Phospholipid transfer protein [Homo sapiens]	46.9	46.9	100%	9e-05	100%	gi|18044721|AAH19847.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Macaca fas	46.9	46.9	100%	9e-05	100%	gi|544466123|XP_005569252.1
☐	PREDICTED: phospholipid transfer protein [Gorilla gorilla gorilla]	46.9	46.9	100%	9e-05	100%	gi|426391940|XP_004062321.1
☐	phospholipid transfer protein isoform a precursor [Homo sapiens]	46.9	46.9	100%	9e-05	100%	gi|5453914|NP_006218.1
☐							

	PREDICTED: phospholipid transfer protein [Saimiri boliviensis boliv	46.9	46.9	100%	9e-05	100%	gi|403290826|XP_003936508.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer prot	46.9	46.9	100%	9e-05	100%	gi|402882376|XP_003904720.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Pan panisci	46.9	46.9	100%	9e-05	100%	gi|675783669|XP_008949625.1
☐	Lipid transfer protein II [Macaca mulatta]	46.9	46.9	100%	9e-05	100%	gi|355563074|EHH19636.1
☐	PREDICTED: phospholipid transfer protein [Nomascus leucogenys]	46.9	46.9	100%	9e-05	100%	gi|332209213|XP_003253705.1
☐	PREDICTED: phospholipid transfer protein-like [Macaca mulatta]	46.9	46.9	100%	9e-05	100%	gi|297259688|XP_002798159.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Pan troglody	46.9	46.9	100%	9e-05	100%	gi|332858594|XP_001158846.2
☐	phospholipid transfer protein isoform a precursor variant [Homo sap	46.9	46.9	100%	9e-05	100%	gi|62896939|BAD96410.1
☐	PREDICTED: phospholipid transfer protein [Heterocephalus glaber]	46.9	46.9	100%	9e-05	100%	gi|512855805|XP_004888423.1
☐	PREDICTED: phospholipid transfer protein isoform 2 [Ovis aries]	46.9	46.9	100%	9e-05	100%	gi|426241563|XP_004014659.1
☐	PREDICTED: phospholipid transfer protein [Ursus maritimus]	46.9	46.9	100%	9e-05	100%	gi|671010882|XP_008696270.1
☐	hypothetical protein PANDA_018015 [Ailuropoda melanoleuca]	46.9	46.9	100%	9e-05	100%	gi|281346391|EFB21975.1
☐	PREDICTED: phospholipid transfer protein isoformX3 [Canis lupus	46.9	46.9	100%	9e-05	100%	gi|73992532|XP_543027.2
☐	PREDICTED: phospholipid transfer protein isoform 1 [Otolemur gar	46.9	46.9	100%	9e-05	100%	gi|395829113|XP_003787705.1
☐	phospholipid transfer protein precursor [Sus scrofa]	46.9	46.9	100%	9e-05	100%	gi|47523640|NP_999448.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Erinaceus e	46.9	46.9	100%	9e-05	100%	gi|617646971|XP_007533119.1
☐	PREDICTED: phospholipid transfer protein [Balaenoptera acutorost	46.9	46.9	100%	9e-05	100%	gi|594675219|XP_007185441.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Bubalus bub	46.9	46.9	100%	9e-05	100%	gi|594054314|XP_006051425.1
☐	PREDICTED: phospholipid transfer protein [Physeter catodon]	46.9	46.9	100%	9e-05	100%	gi|593753347|XP_007115580.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Tupaia chin	46.9	46.9	100%	9e-05	100%	gi|562860414|XP_006158592.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Vicugna pac	46.9	46.9	100%	9e-05	100%	gi|560960181|XP_006202541.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Camelus fer	46.9	46.9	100%	9e-05	100%	gi|560922983|XP_006187689.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Bos taurus]	46.9	46.9	100%	9e-05	100%	gi|528973460|XP_005214615.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer prot	46.9	46.9	100%	9e-05	100%	gi|511843869|XP_004746370.1
☐	PREDICTED: phospholipid transfer protein isoform 1 [Ceratotheriun	46.9	46.9	100%	9e-05	100%	gi|478512231|XP_004430378.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer prot	46.9	46.9	100%	9e-05	100%	gi|470622636|XP_004319149.1
☐	PREDICTED: phospholipid transfer protein isoform 1 [Orcinus orca]	46.9	46.9	100%	9e-05	100%	gi|466024672|XP_004272965.1
☐	PREDICTED: phospholipid transfer protein-like [Ailuropoda melanol	46.9	46.9	100%	9e-05	100%	gi|301785379|XP_002928111.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer prot	46.9	46.9	100%	9e-05	100%	gi|602732607|XP_007451697.1
☐	Phospholipid transfer protein [Tupaia chinensis]	46.9	46.9	100%	9e-05	100%	gi|444706925|ELW48240.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Tupaia chin	46.9	46.9	100%	9e-05	100%	gi|562860412|XP_006158591.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer prot	46.9	46.9	100%	9e-05	100%	gi|556717613|XP_005954715.1
☐	phospholipid transfer protein precursor [Bos taurus]	46.9	46.9	100%	9e-05	100%	gi|78042516|NP_001030199.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Chlorocebus	46.9	46.9	100%	9e-05	100%	gi|635020536|XP_008013792.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Macaca fas	46.9	46.9	100%	9e-05	100%	gi|544466121|XP_005569251.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Homo sapie	46.9	46.9	100%	9e-05	100%	gi|530418164|XP_005260496.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Ictidomys tri	46.9	46.9	100%	9e-05	100%	gi|532079075|XP_005325306.1
☐	Phospholipid transfer protein [Heterocephalus glaber]	46.9	46.9	100%	9e-05	100%	gi|351702390|EHB05309.1
☐	phospholipid transfer protein isoform 3 [Camelus ferus]	46.9	46.9	100%	9e-05	100%	gi|528759094|EPY78753.1
☐	PREDICTED: phospholipid transfer protein isoform X4 [Canis lupus	46.9	46.9	100%	9e-05	100%	gi|545540927|XP_005635182.1
☐	PREDICTED: phospholipid transfer protein [Chrysochloris asiatica]	44.8	44.8	100%	5e-04	93%	gi|586455144|XP_006839396.1
☐	phospholipid transfer protein precursor [Pongo abelii]	44.8	44.8	100%	5e-04	93%	gi|197100925|NP_001127290.1
☐	PREDICTED: phospholipid transfer protein [Equus przewalskii]	44.3	44.3	100%	6e-04	93%	gi|664725512|XP_008519895.1
☐	PREDICTED: phospholipid transfer protein isoform X3 [Galeopterus	44.3	44.3	100%	6e-04	93%	gi|667267881|XP_008569812.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Galeopterus	44.3	44.3	100%	6e-04	93%	gi|667267878|XP_008569811.1

☐	PREDICTED: phospholipid transfer protein isoformX1 [Equus cabal	44.3	44.3	100%	6e-04	93%	gi|149733315|XP_001503419.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Galeopterus	44.3	44.3	100%	6e-04	93%	gi|667267875|XP_008569810.1
☐	PREDICTED: phospholipid transfer protein [Nannospalax galili]	43.9	43.9	100%	9e-04	93%	gi|674058816|XP_008835992.1
☐	PREDICTED: phospholipid transfer protein [Jaculus jaculus]	43.9	43.9	100%	9e-04	93%	gi|507560498|XP_004663955.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Fukomys da	43.5	43.5	100%	0.001	93%	gi|731220560|XP_010624498.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Fukomys da	43.5	43.5	100%	0.001	93%	gi|731220558|XP_010624497.1
☐	phospholipid transfer protein [Cricetulus griseus]	42.6	42.6	100%	0.002	93%	gi|537151313|ERE71590.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Cricetulus g	42.6	42.6	100%	0.002	93%	gi|625234759|XP_007608544.1
☐	PREDICTED: phospholipid transfer protein [Mesocricetus auratus]	42.6	42.6	100%	0.002	93%	gi|524970358|XP_005085047.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Cricetulus g	42.6	42.6	100%	0.002	93%	gi|354476736|XP_003500579.1
☐	phospholipid transfer protein [Cricetulus griseus]	42.6	42.6	100%	0.002	93%	gi|537151311|ERE71588.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Cricetulus g	42.6	42.6	100%	0.002	93%	gi|625234757|XP_007608543.1
☐	phospholipid transfer protein [Cricetulus griseus]	42.6	42.6	100%	0.002	93%	gi|537151310|ERE71587.1
☐	PREDICTED: phospholipid transfer protein isoform 2 [Dasypus nove	41.8	41.8	100%	0.004	93%	gi|488559570|XP_004469931.1
☐	PREDICTED: phospholipid transfer protein isoform 1 [Dasypus nove	41.8	41.8	100%	0.004	93%	gi|488559567|XP_004469930.1
☐	PREDICTED: phospholipid transfer protein [Peromyscus maniculatu	41.4	41.4	100%	0.006	86%	gi|589915411|XP_006971038.1
☐	PREDICTED: phospholipid transfer protein [Panthera tigris altaica]	40.9	40.9	100%	0.009	93%	gi|591301856|XP_007077837.1
☐	PREDICTED: phospholipid transfer protein [Felis catus]	40.9	40.9	100%	0.009	93%	gi|586980550|XP_006929771.1
☐	unnamed protein product [Mus musculus]	40.5	40.5	100%	0.011	86%	gi|74207827|BAE29052.1
☐	plasma phospholipid transfer protein [Mus musculus]	40.5	40.5	100%	0.012	86%	gi|902888|AAA87943.1
☐	Phospholipid transfer protein [Mus musculus]	40.5	40.5	100%	0.012	86%	gi|13277783|AAH03782.1
☐	PREDICTED: phospholipid transfer protein [Microtus ochrogaster]	40.5	40.5	100%	0.012	86%	gi|532040209|XP_005362957.1
☐	phospholipid transfer protein precursor [Mus musculus]	40.5	40.5	100%	0.012	86%	gi|6755112|NP_035255.1
☐	PREDICTED: phospholipid transfer protein [Trichechus manatus lat	40.5	40.5	100%	0.012	93%	gi|471360078|XP_004370611.1
☐	PREDICTED: phospholipid transfer protein [Orycteropus afer afer]	40.1	40.1	92%	0.016	92%	gi|634841511|XP_007936631.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Myotis davic	40.1	40.1	100%	0.016	86%	gi|584058185|XP_006773605.1
☐	PREDICTED: phospholipid transfer protein [Octodon degus]	39.2	39.2	100%	0.031	86%	gi|507663922|XP_004636143.1

⊖Alignments

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PLTP-like protein [Bos taurus]

Sequence ID: gi|56681181|gb|AAW21227.1| **Length:** 127 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 106 to 119 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	6e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KVSNVSCQASVSRM  14
            KVSNVSCQASVSRM
Sbjct  106  KVSNVSCQASVSRM  119
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: phospholipid transfer protein-like isoform X1 [Sus scrofa]

Sequence ID: gi|545880919|ref|XP_005673034.1| **Length:** 162 **Number of Matches:** 1

▷See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 140 to 153 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	7e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KVSNVSCQASVSRM  14
            KVSNVSCQASVSRM
Sbjct  140  KVSNVSCQASVSRM  153
```

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PREDICTED: phospholipid transfer protein-like [Leptonychotes weddellii]

Sequence ID: gi|585176105|ref|XP_006739837.1| **Length:** 246 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 140 to 153 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	8e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KVSNVSCQASVSRM  14
            KVSNVSCQASVSRM
Sbjct  140  KVSNVSCQASVSRM  153
```

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PREDICTED: phospholipid transfer protein isoform X3 [Pan troglodytes]

Sequence ID: gi|694979328|ref|XP_009435596.1| **Length:** 405 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 52 to 65 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	9e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1   KVSNVSCQASVSRM  14
           KVSNVSCQASVSRM
Sbjct  52  KVSNVSCQASVSRM  65
```

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PREDICTED: phospholipid transfer protein isoform X2 [Tarsius syrichta]

Sequence ID: gi|640799767|ref|XP_008056109.1| **Length:** 405 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 52 to 65 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	9e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1   KVSNVSCQASVSRM  14
           KVSNVSCQASVSRM
Sbjct  52  KVSNVSCQASVSRM  65
```

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BVK408EU01R**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

PLTP_RMKVSDVSCQASVSRM_Mod

RID BVK408EU01R (Expires on 01-21 10:33 am)

Query ID lcl|223370
Description None
Molecule type amino acid
Query Length 16

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

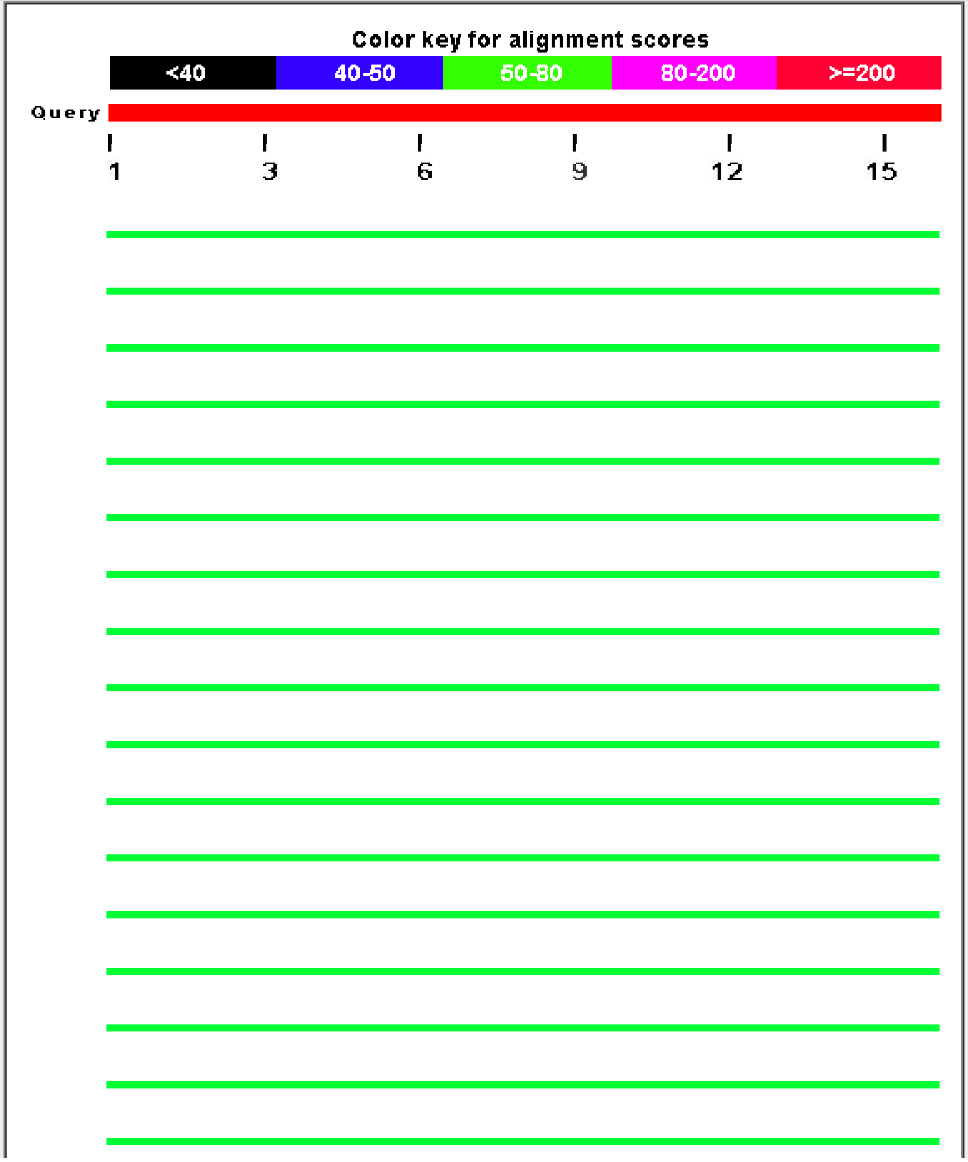
Graphic Summary

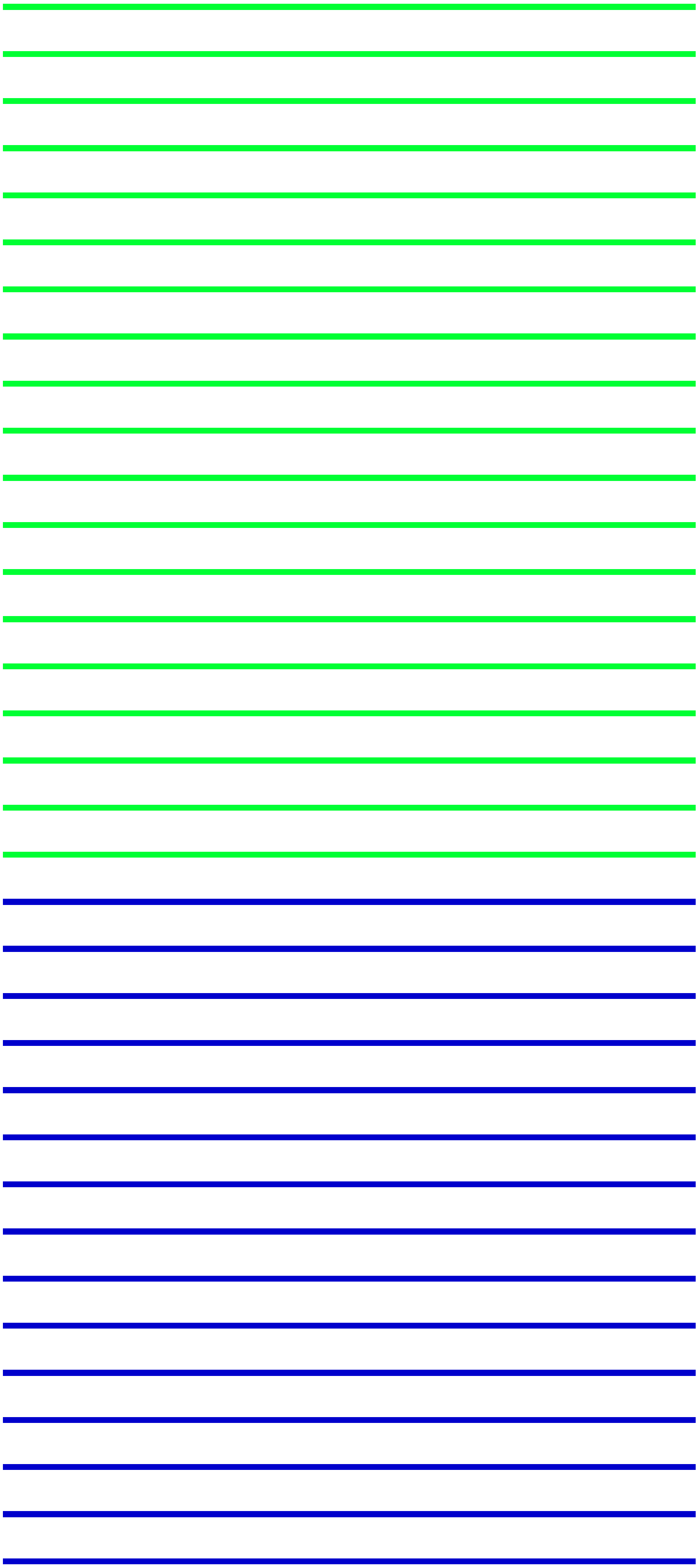
Show Conserved Domains

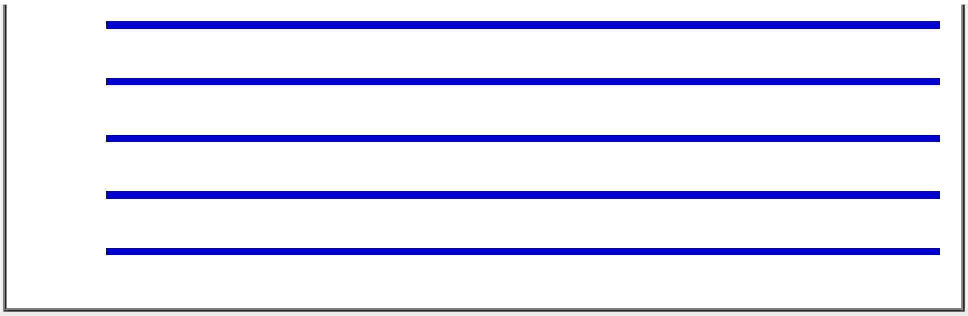
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: phospholipid transfer protein isoform X3 [Pan troglodytes]	52.4	52.4	100%	2e-06	94%	XP_009435596.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Tarsius syrichta]	52.4	52.4	100%	2e-06	94%	XP_008056109.1
☐	PREDICTED: phospholipid transfer protein isoform X3 [Chlorocebus sabaeus	52.4	52.4	100%	2e-06	94%	XP_008013799.1
☐	unnamed protein product [Homo sapiens]	52.4	52.4	100%	2e-06	94%	BAG56696.1
☐	PREDICTED: phospholipid transfer protein isoform X6 [Macaca fascicularis]	52.4	52.4	100%	2e-06	94%	XP_005569256.1
☐	phospholipid transfer protein precursor [Pan troglodytes]	52.4	52.4	100%	2e-06	94%	BAK62129.1
☐	phospholipid transfer protein isoform d [Homo sapiens]	52.4	52.4	100%	2e-06	94%	NP_001229850.1
☐	unnamed protein product [Macaca fascicularis]	52.4	52.4	100%	2e-06	94%	BAE00639.1
☐	PREDICTED: phospholipid transfer protein [Callithrix jacchus]	52.4	52.4	100%	2e-06	94%	XP_008994362.1
☐	phospholipid transfer protein, isoform CRA_d [Homo sapiens]	52.4	52.4	100%	2e-06	94%	EAW75786.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Pan troglodytes]	52.4	52.4	100%	2e-06	94%	XP_009435595.1
☐	PREDICTED: phospholipid transfer protein [Rhinopithecus roxellana]	52.4	52.4	100%	2e-06	94%	XP_010382500.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Chlorocebus sabaeus	52.4	52.4	100%	2e-06	94%	XP_008013795.1
☐	Phospholipid transfer protein [Homo sapiens]	52.4	52.4	100%	2e-06	94%	AAH19847.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Macaca fascicularis]	52.4	52.4	100%	2e-06	94%	XP_005569252.1
☐	PREDICTED: phospholipid transfer protein [Gorilla gorilla gorilla]	52.4	52.4	100%	2e-06	94%	XP_004062321.1
☐	phospholipid transfer protein isoform a precursor [Homo sapiens]	52.4	52.4	100%	2e-06	94%	NP_006218.1
☐	PREDICTED: phospholipid transfer protein [Saimiri boliviensis boliviensis]	52.4	52.4	100%	2e-06	94%	XP_003936508.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Papio	52.4	52.4	100%	2e-06	94%	XP_003904720.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Pan paniscus]	52.4	52.4	100%	2e-06	94%	XP_008949625.1
☐	Lipid transfer protein II [Macaca mulatta]	52.4	52.4	100%	2e-06	94%	EHH19636.1
☐	PREDICTED: phospholipid transfer protein [Nomascus leucogenys]	52.4	52.4	100%	2e-06	94%	XP_003253705.1
☐	PREDICTED: phospholipid transfer protein-like [Macaca mulatta]	52.4	52.4	100%	2e-06	94%	XP_002798159.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Pan troglodytes]	52.4	52.4	100%	2e-06	94%	XP_001158846.2
☐	phospholipid transfer protein isoform a precursor variant [Homo sapiens]	52.4	52.4	100%	2e-06	94%	BAD96410.1
☐	PREDICTED: phospholipid transfer protein [Heterocephalus glaber]	52.4	52.4	100%	2e-06	94%	XP_004888423.1
☐	PREDICTED: phospholipid transfer protein [Physeter catodon]	52.4	52.4	100%	2e-06	94%	XP_007115580.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Tupaia chinensis]	52.4	52.4	100%	2e-06	94%	XP_006158592.1
☐	Phospholipid transfer protein [Tupaia chinensis]	52.4	52.4	100%	2e-06	94%	ELW48240.1

☐	PREDICTED: phospholipid transfer protein isoform X1 [Tupaia chinensis]	52.4	52.4	100%	2e-06	94%	XP_006158591.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Chlorocebus sabaeus	52.4	52.4	100%	2e-06	94%	XP_008013792.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Macaca fascicularis]	52.4	52.4	100%	2e-06	94%	XP_005569251.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Homo sapiens]	52.4	52.4	100%	2e-06	94%	XP_005260496.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Ictidomys tridecemline	52.4	52.4	100%	2e-06	94%	XP_005325306.1
☐	Phospholipid transfer protein [Heterocephalus glaber]	52.4	52.4	100%	2e-06	94%	EHB05309.1
☐	phospholipid transfer protein precursor [Pongo abelii]	50.3	50.3	100%	9e-06	88%	NP_001127290.1
☐	PREDICTED: phospholipid transfer protein isoform X3 [Galeopterus variegatu	49.8	49.8	100%	1e-05	88%	XP_008569812.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Galeopterus variegatu	49.8	49.8	100%	1e-05	88%	XP_008569811.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Galeopterus variegatu	49.8	49.8	100%	1e-05	88%	XP_008569810.1
☐	PREDICTED: phospholipid transfer protein [Jaculus jaculus]	49.4	49.4	100%	2e-05	88%	XP_004663955.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Fukomys damarensis]	49.0	49.0	100%	2e-05	88%	XP_010624498.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Fukomys damarensis]	49.0	49.0	100%	2e-05	88%	XP_010624497.1
☐	PLTP-like protein [Bos taurus]	47.3	47.3	100%	6e-05	88%	AAW21227.1
☐	PREDICTED: phospholipid transfer protein-like isoform X1 [Sus scrofa]	47.3	47.3	100%	7e-05	88%	XP_005673034.1
☐	PREDICTED: phospholipid transfer protein-like [Leptonychotes weddellii]	47.3	47.3	100%	8e-05	88%	XP_006739837.1
☐	PREDICTED: phospholipid transfer protein isoform X4 [Vicugna pacos]	47.3	47.3	100%	8e-05	88%	XP_006202544.1
☐	PREDICTED: phospholipid transfer protein isoform X4 [Camelus ferus]	47.3	47.3	100%	8e-05	88%	XP_006187692.1
☐	PREDICTED: phospholipid transfer protein isoform 4 [Ceratotherium simum si	47.3	47.3	100%	8e-05	88%	XP_004430381.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Condylura cristata]	47.3	47.3	100%	9e-05	88%	XP_004687488.1
☐	PREDICTED: phospholipid transfer protein isoform 4 [Orcinus orca]	47.3	47.3	100%	9e-05	88%	XP_004272968.1
☐	PREDICTED: phospholipid transfer protein [Capra hircus]	47.3	47.3	100%	9e-05	88%	XP_005688777.1
☐	PREDICTED: phospholipid transfer protein isoform 1 [Ovis aries]	47.3	47.3	100%	9e-05	88%	XP_004014658.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Came	47.3	47.3	100%	9e-05	88%	XP_010956961.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Came	47.3	47.3	100%	9e-05	88%	XP_010976914.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Bos m	47.3	47.3	100%	9e-05	88%	XP_005897642.1
☐	PREDICTED: phospholipid transfer protein isoform 2 [Ovis aries]	47.3	47.3	100%	9e-05	88%	XP_004014659.1
☐	PREDICTED: phospholipid transfer protein [Ursus maritimus]	47.3	47.3	100%	9e-05	88%	XP_008696270.1
☐	hypothetical protein PANDA_018015 [Ailuropoda melanoleuca]	47.3	47.3	100%	9e-05	88%	EFB21975.1
☐	PREDICTED: phospholipid transfer protein isoformX3 [Canis lupus familiaris]	47.3	47.3	100%	9e-05	88%	XP_543027.2
☐	PREDICTED: phospholipid transfer protein isoform 1 [Otolemur garnettii]	47.3	47.3	100%	9e-05	88%	XP_003787705.1
☐	phospholipid transfer protein precursor [Sus scrofa]	47.3	47.3	100%	9e-05	88%	NP_999448.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Erinaceus europaeus]	47.3	47.3	100%	9e-05	88%	XP_007533119.1
☐	PREDICTED: phospholipid transfer protein [Balaenoptera acutorostrata scam	47.3	47.3	100%	9e-05	88%	XP_007185441.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Bubalus bubalis]	47.3	47.3	100%	9e-05	88%	XP_006051425.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Vicugna pacos]	47.3	47.3	100%	9e-05	88%	XP_006202541.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Camelus ferus]	47.3	47.3	100%	9e-05	88%	XP_006187689.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Bos taurus]	47.3	47.3	100%	9e-05	88%	XP_005214615.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Muste	47.3	47.3	100%	9e-05	88%	XP_004746370.1
☐	PREDICTED: phospholipid transfer protein isoform 1 [Ceratotherium simum si	47.3	47.3	100%	9e-05	88%	XP_004430378.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Tursio	47.3	47.3	100%	9e-05	88%	XP_004319149.1
☐	PREDICTED: phospholipid transfer protein isoform 1 [Orcinus orca]	47.3	47.3	100%	9e-05	88%	XP_004272965.1
☐	PREDICTED: phospholipid transfer protein-like [Ailuropoda melanoleuca]	47.3	47.3	100%	9e-05	88%	XP_002928111.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Lipote	47.3	47.3	100%	9e-05	88%	XP_007451697.1
☐	PREDICTED: phospholipid transfer protein [Bison bison bison]	47.3	47.3	100%	9e-05	88%	XP_010833341.1

☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer protein [Panth	47.3	47.3	100%	9e-05	88%	XP_005954715.1
☐	phospholipid transfer protein precursor [Bos taurus]	47.3	47.3	100%	9e-05	88%	NP_001030199.1
☐	phospholipid transfer protein isoform 3 [Camelus ferus]	47.3	47.3	100%	9e-05	88%	EPY78753.1
☐	PREDICTED: phospholipid transfer protein isoform X4 [Canis lupus familiaris]	47.3	47.3	100%	9e-05	88%	XP_005635182.1
☐	PREDICTED: phospholipid transfer protein [Ochotona princeps]	46.0	46.0	100%	2e-04	88%	XP_004586137.1
☐	PREDICTED: phospholipid transfer protein [Equus przewalskii]	44.8	44.8	100%	6e-04	81%	XP_008519895.1
☐	PREDICTED: phospholipid transfer protein [Octodon degus]	44.8	44.8	100%	6e-04	81%	XP_004636143.1
☐	PREDICTED: phospholipid transfer protein isoformX1 [Equus caballus]	44.8	44.8	100%	6e-04	81%	XP_001503419.1
☐	PREDICTED: phospholipid transfer protein [Nannospalax galili]	44.3	44.3	100%	8e-04	81%	XP_008835992.1
☐	PREDICTED: phospholipid transfer protein [Chinchilla lanigera]	43.9	43.9	100%	0.001	81%	XP_005392459.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Cavia porcellus]	43.5	43.5	100%	0.002	81%	XP_003467746.1
☐	phospholipid transfer protein [Cricetulus griseus]	43.1	43.1	100%	0.002	81%	ERE71590.1
☐	Phospholipid transfer protein [Pteropus alecto]	43.1	43.1	100%	0.002	75%	ELK04252.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Cricetulus griseus]	43.1	43.1	100%	0.002	81%	XP_007608544.1
☐	PREDICTED: phospholipid transfer protein [Mesocricetus auratus]	43.1	43.1	100%	0.002	81%	XP_005085047.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Cricetulus griseus]	43.1	43.1	100%	0.002	81%	XP_003500579.1
☐	PREDICTED: phospholipid transfer protein [Pteropus alecto]	43.1	43.1	100%	0.002	75%	XP_006921934.1
☐	phospholipid transfer protein [Cricetulus griseus]	43.1	43.1	100%	0.002	81%	ERE71588.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Cricetulus griseus]	43.1	43.1	100%	0.002	81%	XP_007608543.1
☐	phospholipid transfer protein [Cricetulus griseus]	43.1	43.1	100%	0.002	81%	ERE71587.1
☐	PREDICTED: phospholipid transfer protein [Sarcophilus harrisii]	42.6	42.6	100%	0.003	81%	XP_003757387.1
☐	PREDICTED: phospholipid transfer protein [Chrysochloris asiatica]	42.2	42.2	87%	0.004	86%	XP_006839396.1
☐	PREDICTED: phospholipid transfer protein [Peromyscus maniculatus bairdii]	41.8	41.8	100%	0.006	75%	XP_006971038.1
☐	PREDICTED: phospholipid transfer protein [Panthera tigris altaica]	41.4	41.4	100%	0.008	81%	XP_007077837.1
☐	PREDICTED: phospholipid transfer protein [Felis catus]	41.4	41.4	100%	0.008	81%	XP_006929771.1
☐	unnamed protein product [Mus musculus]	40.9	40.9	100%	0.011	75%	BAE29052.1

⊟ Alignments

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PREDICTED: phospholipid transfer protein isoform X3 [Pan troglodytes]

Sequence ID: ref|XP_009435596.1| **Length:** 405 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 50 to 65 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	2e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1   RMKVSDVSCQASVSRM  16
           RMKVS+VSCQASVSRM
Sbjct  50  RMKVSNVSCQASVSRM  65
```

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PREDICTED: phospholipid transfer protein isoform X2 [Tarsius syrichta]

Sequence ID: ref|XP_008056109.1| **Length:** 405 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 50 to 65 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	2e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RMKVSDVSCQASVSRM  16
            RMKVS+VSCQASVSRM
Sbjct  50   RMKVSNVSCQASVSRM  65
```

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PREDICTED: phospholipid transfer protein isoform X3 [Chlorocebus sabaeus]

Sequence ID: ref|XP_008013799.1| **Length:** 405 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 50 to 65 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	2e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RMKVSDVSCQASVSRM  16
            RMKVS+VSCQASVSRM
Sbjct  50   RMKVSNVSCQASVSRM  65
```

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unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG56696.1| **Length:** 405 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 50 to 65 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	2e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RMKVSDVSCQASVSRM  16
            RMKVS+VSCQASVSRM
Sbjct  50   RMKVSNVSCQASVSRM  65
```

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PREDICTED: phospholipid transfer protein isoform X6 [Macaca fascicularis]

Sequence ID: ref|XP_005569256.1| **Length:** 405 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 50 to 65 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
52.4 bits(116)	2e-06	15/16(94%)	16/16(100%)	0/16(0%)

```
Query  1    RMKVSDVSCQASVSRM  16
            RMKVS+VSCQASVSRM
Sbjct  50   RMKVSNVSCQASVSRM  65
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BE7CDYF6015**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

PLTP_RMKVSNVSCQASVSRM_NonMod

RID BE7CDYF6015 (Expires on 01-16 08:53 am)

Query ID lcl|54782
Description None
Molecule type amino acid
Query Length 16

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

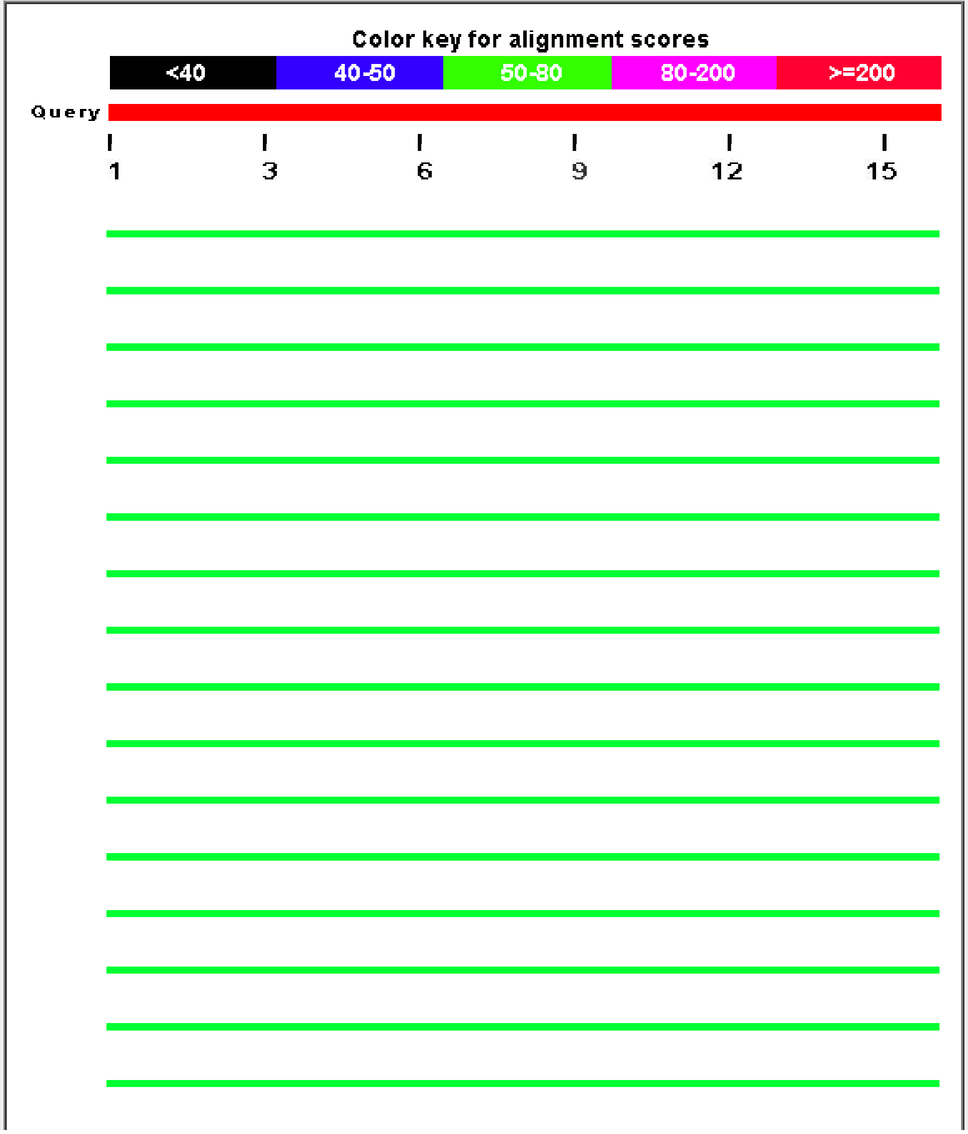
Graphic Summary

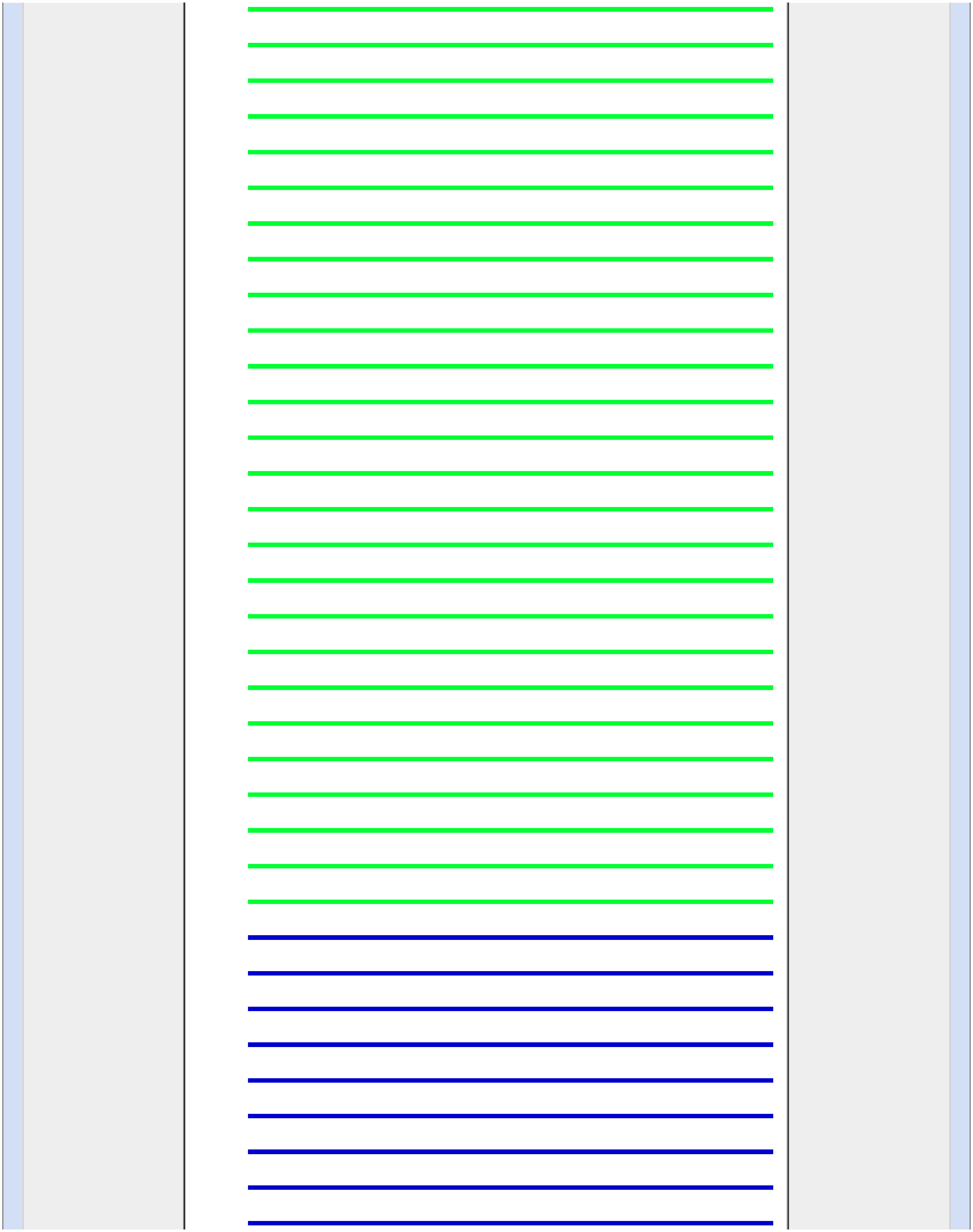
Show Conserved Domains

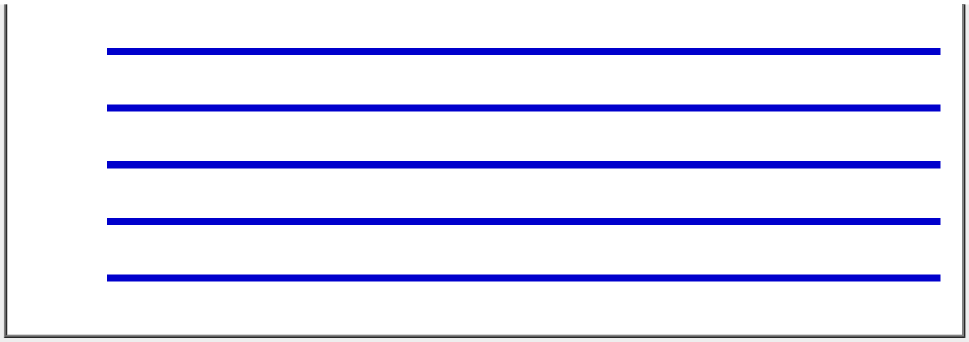
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: phospholipid transfer protein isoform X3 [Pan troglody	54.9	54.9	100%	2e-07	100%	gi|694979328|XP_009435596.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Tarsius syric	54.9	54.9	100%	2e-07	100%	gi|640799767|XP_008056109.1
☐	PREDICTED: phospholipid transfer protein isoform X3 [Chlorocebus	54.9	54.9	100%	2e-07	100%	gi|635020540|XP_008013799.1
☐	unnamed protein product [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|194375502|BAG56696.1
☐	PREDICTED: phospholipid transfer protein isoform X6 [Macaca fasc	54.9	54.9	100%	2e-07	100%	gi|544466131|XP_005569256.1
☐	phospholipid transfer protein precursor [Pan troglodytes]	54.9	54.9	100%	2e-07	100%	gi|343961079|BAK62129.1
☐	phospholipid transfer protein isoform d [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|339275810|NP_001229850.1
☐	unnamed protein product [Macaca fascicularis]	54.9	54.9	100%	2e-07	100%	gi|67968557|BAE00639.1
☐	PREDICTED: phospholipid transfer protein [Callithrix jacchus]	54.9	54.9	100%	2e-07	100%	gi|675657086|XP_008994362.1
☐	phospholipid transfer protein, isoform CRA_d [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|119596192|EAW75786.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Pan troglody	54.9	54.9	100%	2e-07	100%	gi|694979326|XP_009435595.1
☐	PREDICTED: phospholipid transfer protein [Rhinopithecus roxellana	54.9	54.9	100%	2e-07	100%	gi|724927761|XP_010382500.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Chlorocebus	54.9	54.9	100%	2e-07	100%	gi|635020538|XP_008013795.1
☐	Phospholipid transfer protein [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|18044721|AAH19847.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Macaca fasc	54.9	54.9	100%	2e-07	100%	gi|544466123|XP_005569252.1
☐	PREDICTED: phospholipid transfer protein [Gorilla gorilla gorilla]	54.9	54.9	100%	2e-07	100%	gi|426391940|XP_004062321.1
☐	phospholipid transfer protein isoform a precursor [Homo sapiens]	54.9	54.9	100%	2e-07	100%	gi|5453914|NP_006218.1
☐	PREDICTED: phospholipid transfer protein [Saimiri boliviensis boliv	54.9	54.9	100%	2e-07	100%	gi|403290826|XP_003936508.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer prot	54.9	54.9	100%	2e-07	100%	gi|402882376|XP_003904720.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Pan paniscu	54.9	54.9	100%	2e-07	100%	gi|675783669|XP_008949625.1
☐	Lipid transfer protein II [Macaca mulatta]	54.9	54.9	100%	2e-07	100%	gi|355563074|EHH19636.1
☐	PREDICTED: phospholipid transfer protein [Nomascus leucogenys]	54.9	54.9	100%	2e-07	100%	gi|332209213|XP_003253705.1
☐	PREDICTED: phospholipid transfer protein-like [Macaca mulatta]	54.9	54.9	100%	2e-07	100%	gi|297259688|XP_002798159.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Pan troglody	54.9	54.9	100%	2e-07	100%	gi|332858594|XP_001158846.2
☐	phospholipid transfer protein isoform a precursor variant [Homo sap	54.9	54.9	100%	2e-07	100%	gi|62896939|BAD96410.1
☐	PREDICTED: phospholipid transfer protein [Heterocephalus glaber]	54.9	54.9	100%	2e-07	100%	gi|512855805|XP_004888423.1
☐	PREDICTED: phospholipid transfer protein [Physeter catodon]	54.9	54.9	100%	2e-07	100%	gi|593753347|XP_007115580.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Tupaia chin	54.9	54.9	100%	2e-07	100%	gi|562860414|XP_006158592.1
☐							

	Phospholipid transfer protein [Tupaia chinensis]	54.9	54.9	100%	2e-07	100%	gi|444706925|ELW48240.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Tupaia chin	54.9	54.9	100%	2e-07	100%	gi|562860412|XP_006158591.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Chlorocebus	54.9	54.9	100%	2e-07	100%	gi|635020536|XP_008013792.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Macaca fas	54.9	54.9	100%	2e-07	100%	gi|544466121|XP_005569251.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Homo sapie	54.9	54.9	100%	2e-07	100%	gi|530418164|XP_005260496.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Ictidomys tri	54.9	54.9	100%	2e-07	100%	gi|532079075|XP_005325306.1
☐	Phospholipid transfer protein [Heterocephalus glaber]	54.9	54.9	100%	2e-07	100%	gi|351702390|EHB05309.1
☐	phospholipid transfer protein precursor [Pongo abelii]	52.8	52.8	100%	1e-06	94%	gi|197100925|NP_001127290.1
☐	PREDICTED: phospholipid transfer protein isoform X3 [Galeopterus	52.4	52.4	100%	2e-06	94%	gi|667267881|XP_008569812.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Galeopterus	52.4	52.4	100%	2e-06	94%	gi|667267878|XP_008569811.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Galeopterus	52.4	52.4	100%	2e-06	94%	gi|667267875|XP_008569810.1
☐	PREDICTED: phospholipid transfer protein [Jaculus jaculus]	52.0	52.0	100%	2e-06	94%	gi|507560498|XP_004663955.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Fukomys da	51.5	51.5	100%	3e-06	94%	gi|731220560|XP_010624498.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Fukomys da	51.5	51.5	100%	3e-06	94%	gi|731220558|XP_010624497.1
☐	PLTP-like protein [Bos taurus]	49.8	49.8	100%	8e-06	94%	gi|56681181|AAW21227.1
☐	PREDICTED: phospholipid transfer protein-like isoform X1 [Sus scr	49.8	49.8	100%	9e-06	94%	gi|545880919|XP_005673034.1
☐	PREDICTED: phospholipid transfer protein-like [Leptonychotes wed	49.8	49.8	100%	1e-05	94%	gi|585176105|XP_006739837.1
☐	PREDICTED: phospholipid transfer protein isoform X4 [Vicugna pac	49.8	49.8	100%	1e-05	94%	gi|560960187|XP_006202544.1
☐	PREDICTED: phospholipid transfer protein isoform X4 [Camelus fer	49.8	49.8	100%	1e-05	94%	gi|560922989|XP_006187692.1
☐	PREDICTED: phospholipid transfer protein isoform 4 [Ceratotheriun	49.8	49.8	100%	1e-05	94%	gi|478512237|XP_004430381.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Condylura c	49.8	49.8	100%	1e-05	94%	gi|507961913|XP_004687488.1
☐	PREDICTED: phospholipid transfer protein isoform 4 [Orcinus orca]	49.8	49.8	100%	1e-05	94%	gi|466024688|XP_004272968.1
☐	PREDICTED: phospholipid transfer protein [Capra hircus]	49.8	49.8	100%	1e-05	94%	gi|548491933|XP_005688777.1
☐	PREDICTED: phospholipid transfer protein isoform 1 [Ovis aries]	49.8	49.8	100%	1e-05	94%	gi|426241561|XP_004014658.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer prot	49.8	49.8	100%	1e-05	94%	gi|743725982|XP_010956961.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer prot	49.8	49.8	100%	1e-05	94%	gi|744560326|XP_010976914.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer prot	49.8	49.8	100%	1e-05	94%	gi|555971257|XP_005897642.1
☐	PREDICTED: phospholipid transfer protein isoform 2 [Ovis aries]	49.8	49.8	100%	1e-05	94%	gi|426241563|XP_004014659.1
☐	PREDICTED: phospholipid transfer protein [Ursus maritimus]	49.8	49.8	100%	1e-05	94%	gi|671010882|XP_008696270.1
☐	hypothetical protein PANDA_018015 [Ailuropoda melanoleuca]	49.8	49.8	100%	1e-05	94%	gi|281346391|EFB21975.1
☐	PREDICTED: phospholipid transfer protein isoformX3 [Canis lupus	49.8	49.8	100%	1e-05	94%	gi|73992532|XP_543027.2
☐	PREDICTED: phospholipid transfer protein isoform 1 [Otolemur gar	49.8	49.8	100%	1e-05	94%	gi|395829113|XP_003787705.1
☐	phospholipid transfer protein precursor [Sus scrofa]	49.8	49.8	100%	1e-05	94%	gi|47523640|NP_999448.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Erinaceus e	49.8	49.8	100%	1e-05	94%	gi|617646971|XP_007533119.1
☐	PREDICTED: phospholipid transfer protein [Balaenoptera acutorost	49.8	49.8	100%	1e-05	94%	gi|594675219|XP_007185441.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Bubalus bub	49.8	49.8	100%	1e-05	94%	gi|594054314|XP_006051425.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Vicugna pac	49.8	49.8	100%	1e-05	94%	gi|560960181|XP_006202541.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Camelus fer	49.8	49.8	100%	1e-05	94%	gi|560922983|XP_006187689.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Bos taurus]	49.8	49.8	100%	1e-05	94%	gi|528973460|XP_005214615.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer prot	49.8	49.8	100%	1e-05	94%	gi|511843869|XP_004746370.1
☐	PREDICTED: phospholipid transfer protein isoform 1 [Ceratotheriun	49.8	49.8	100%	1e-05	94%	gi|478512231|XP_004430378.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer prot	49.8	49.8	100%	1e-05	94%	gi|470622636|XP_004319149.1
☐	PREDICTED: phospholipid transfer protein isoform 1 [Orcinus orca]	49.8	49.8	100%	1e-05	94%	gi|466024672|XP_004272965.1
☐	PREDICTED: phospholipid transfer protein-like [Ailuropoda melanol	49.8	49.8	100%	1e-05	94%	gi|301785379|XP_002928111.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer prot	49.8	49.8	100%	1e-05	94%	gi|602732607|XP_007451697.1

☐	PREDICTED: phospholipid transfer protein [Bison bison bison]	49.8	49.8	100%	1e-05	94%	gi|742097445|XP_010833341.1
☐	PREDICTED: LOW QUALITY PROTEIN: phospholipid transfer prot	49.8	49.8	100%	1e-05	94%	gi|556717613|XP_005954715.1
☐	phospholipid transfer protein precursor [Bos taurus]	49.8	49.8	100%	1e-05	94%	gi|78042516|NP_001030199.1
☐	phospholipid transfer protein isoform 3 [Camelus ferus]	49.8	49.8	100%	1e-05	94%	gi|528759094|EPY78753.1
☐	PREDICTED: phospholipid transfer protein isoform X4 [Canis lupus	49.8	49.8	100%	1e-05	94%	gi|545540927|XP_005635182.1
☐	PREDICTED: phospholipid transfer protein [Equus przewalskii]	47.3	47.3	100%	8e-05	88%	gi|664725512|XP_008519895.1
☐	PREDICTED: phospholipid transfer protein [Octodon degus]	47.3	47.3	100%	9e-05	88%	gi|507663922|XP_004636143.1
☐	PREDICTED: phospholipid transfer protein isoformX1 [Equus cabal	47.3	47.3	100%	9e-05	88%	gi|149733315|XP_001503419.1
☐	PREDICTED: phospholipid transfer protein [Nannospalax galili]	46.9	46.9	100%	1e-04	88%	gi|674058816|XP_008835992.1
☐	PREDICTED: phospholipid transfer protein [Chinchilla lanigera]	46.4	46.4	100%	2e-04	88%	gi|533156934|XP_005392459.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Cavia porce	46.0	46.0	100%	2e-04	88%	gi|348563903|XP_003467746.1
☐	phospholipid transfer protein [Cricetulus griseus]	45.6	45.6	100%	3e-04	88%	gi|537151313|ERE71590.1
☐	Phospholipid transfer protein [Pteropus alecto]	45.6	45.6	100%	3e-04	81%	gi|431894452|ELK04252.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Cricetulus g	45.6	45.6	100%	3e-04	88%	gi|625234759|XP_007608544.1
☐	PREDICTED: phospholipid transfer protein [Mesocricetus auratus]	45.6	45.6	100%	3e-04	88%	gi|524970358|XP_005085047.1
☐	PREDICTED: phospholipid transfer protein isoform X2 [Cricetulus g	45.6	45.6	100%	3e-04	88%	gi|354476736|XP_003500579.1
☐	PREDICTED: phospholipid transfer protein [Pteropus alecto]	45.6	45.6	100%	3e-04	81%	gi|586534094|XP_006921934.1
☐	phospholipid transfer protein [Cricetulus griseus]	45.6	45.6	100%	3e-04	88%	gi|537151311|ERE71588.1
☐	PREDICTED: phospholipid transfer protein isoform X1 [Cricetulus g	45.6	45.6	100%	3e-04	88%	gi|625234757|XP_007608543.1
☐	phospholipid transfer protein [Cricetulus griseus]	45.6	45.6	100%	3e-04	88%	gi|537151310|ERE71587.1
☐	PREDICTED: phospholipid transfer protein [Sarcophilus harrisii]	45.2	45.2	100%	4e-04	88%	gi|395506127|XP_003757387.1
☐	PREDICTED: phospholipid transfer protein [Chrysochloris asiatica]	44.8	44.8	87%	6e-04	93%	gi|586455144|XP_006839396.1
☐	PREDICTED: phospholipid transfer protein [Peromyscus maniculatu	44.3	44.3	100%	8e-04	81%	gi|589915411|XP_006971038.1
☐	PREDICTED: phospholipid transfer protein [Panthera tigris altaica]	43.9	43.9	100%	0.001	88%	gi|591301856|XP_007077837.1
☐	PREDICTED: phospholipid transfer protein [Felis catus]	43.9	43.9	100%	0.001	88%	gi|586980550|XP_006929771.1
☐	unnamed protein product [Mus musculus]	43.5	43.5	100%	0.002	81%	gi|74207827|BAE29052.1
☐	PREDICTED: phospholipid transfer protein [Ochotona princeps]	43.5	43.5	100%	0.002	81%	gi|504147446|XP_004586137.1

⊟ Alignments

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PREDICTED: phospholipid transfer protein isoform X3 [Pan troglodytes]

Sequence ID: gi|694979328|ref|XP_009435596.1| **Length:** 405 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 50 to 65 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.9 bits(122)	2e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RMKVSNVSCQASVSRM  16
            RMKVSNVSCQASVSRM
Sbjct  50   RMKVSNVSCQASVSRM  65
```

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PREDICTED: phospholipid transfer protein isoform X2 [Tarsius syrichta]

Sequence ID: gi|640799767|ref|XP_008056109.1| **Length:** 405 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 50 to 65 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.9 bits(122)	2e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RMKVSNVSCQASVSRM  16
```

```
             RMKVSNVSCQASVSRM
Sbjct  50   RMKVSNVSCQASVSRM  65
```

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PREDICTED: phospholipid transfer protein isoform X3 [Chlorocebus sabaeus]

Sequence ID: gi|635020540|ref|XP_008013799.1| **Length:** 405 **Number of Matches:** 1

Range 1: 50 to 65 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.9 bits(122)	2e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RMKVSNVSCQASVSRM  16
            RMKVSNVSCQASVSRM
Sbjct  50   RMKVSNVSCQASVSRM  65
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194375502|dbj|BAG56696.1| **Length:** 405 **Number of Matches:** 1

Range 1: 50 to 65 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.9 bits(122)	2e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RMKVSNVSCQASVSRM  16
            RMKVSNVSCQASVSRM
Sbjct  50   RMKVSNVSCQASVSRM  65
```

Related Information

Gene - associated gene details

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PREDICTED: phospholipid transfer protein isoform X6 [Macaca fascicularis]

Sequence ID: gi|544466131|ref|XP_005569256.1| **Length:** 405 **Number of Matches:** 1

Range 1: 50 to 65 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
54.9 bits(122)	2e-07	16/16(100%)	16/16(100%)	0/16(0%)

```
Query  1    RMKVSNVSCQASVSRM  16
            RMKVSNVSCQASVSRM
Sbjct  50   RMKVSNVSCQASVSRM  65
```

Related Information

Gene - associated gene details

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Your search parameters were adjusted to search for a short input sequence.

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PON3_RVSTVYANDGSVLQGTSVASVYHGKI_Mod

RID BVK51HBY01R (Expires on 01-21 10:33 am)

Query ID	lcl|296963	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	26	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

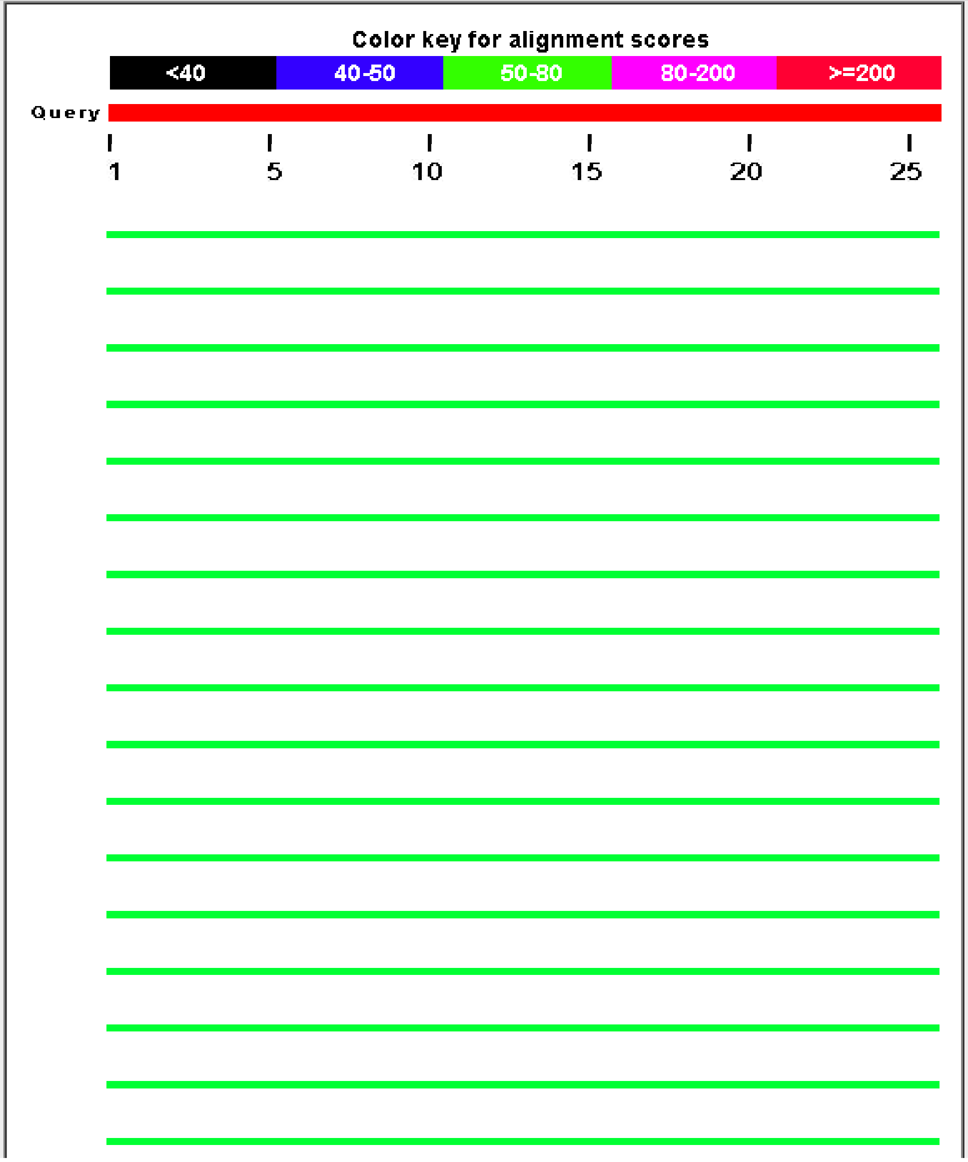
Graphic Summary

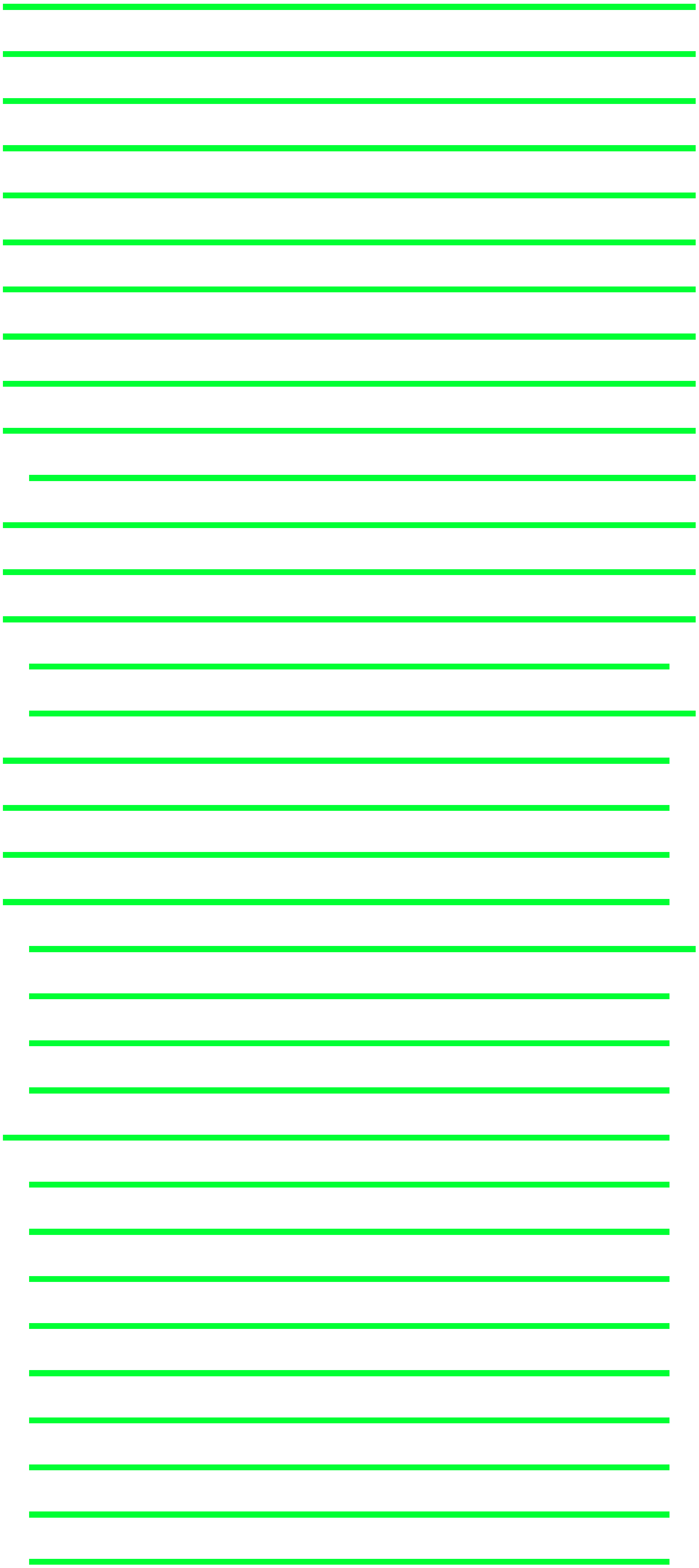
Show Conserved Domains

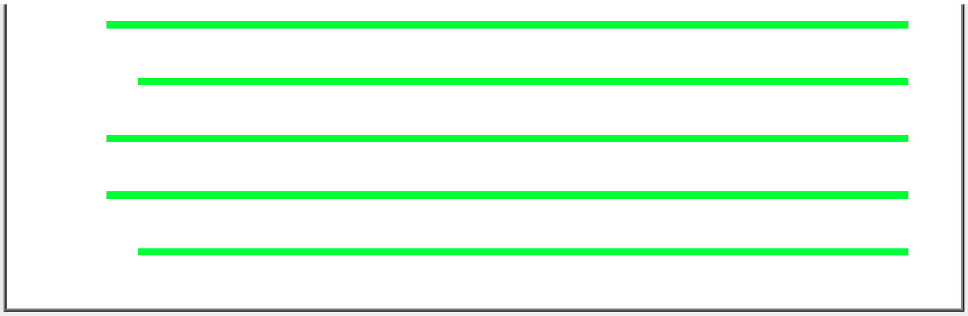
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X2 [Macaca fasciculari	79.5	79.5	100%	3e-15	96%	XP_005550232.1
☐	paraoxonase-3 [Homo sapiens]	79.5	79.5	100%	3e-15	96%	AAC41996.1
☐	Paraoxonase 3 [Homo sapiens]	79.5	79.5	100%	3e-15	96%	AAH70374.1
☐	paraoxonase PON3 variant G3G3 [synthetic construct]	79.5	79.5	100%	3e-15	96%	AAR95991.1
☐	paraoxanase-3 [Homo sapiens]	79.5	79.5	100%	3e-15	96%	AAK07629.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Gorilla gorilla gorilla]	79.5	79.5	100%	3e-15	96%	XP_004045826.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Nomascus leucogenys]	79.5	79.5	100%	3e-15	96%	XP_003252564.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Pongo abelii]	79.5	79.5	100%	3e-15	96%	XP_002818287.1
☐	PREDICTED: serum paraoxonase/lactonase 3-like [Macaca mulatta]	79.5	79.5	100%	3e-15	96%	XP_001095770.1
☐	serum paraoxonase/lactonase 3 [Homo sapiens]	79.5	79.5	100%	3e-15	96%	NP_000931.1
☐	hCG2023324, isoform CRA_c [Homo sapiens]	79.5	79.5	100%	3e-15	96%	EAW76770.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Ictidomys tridecemlineatus]	77.4	77.4	100%	2e-14	92%	XP_005331867.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X3 [Callithrix jacchus]	76.1	76.1	100%	5e-14	92%	XP_009000653.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X2 [Callithrix jacchus]	76.1	76.1	100%	5e-14	92%	XP_002751633.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Saimiri boliviensis boliviensis]	76.1	76.1	100%	5e-14	92%	XP_003921270.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X1 [Callithrix jacchus]	76.1	76.1	100%	5e-14	92%	XP_009000652.1
☐	paraoxonase PON3 variant G3A5 [synthetic construct]	75.7	75.7	100%	7e-14	92%	AAR95990.1
☐	paraoxonase PON3 variant G3H9 [synthetic construct]	75.7	75.7	100%	7e-14	92%	AAR95992.1
☐	paraoxonase PON3 variant G1A7 [synthetic construct]	75.7	75.7	100%	7e-14	92%	AAR95987.1
☐	paraoxonase PON3 variant G2C2 [synthetic construct]	75.7	75.7	100%	7e-14	92%	AAR95989.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X2 [Papio anubis]	74.9	74.9	100%	1e-13	92%	XP_009201642.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Rhinopithecus roxellana]	74.9	74.9	100%	1e-13	92%	XP_010354563.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X1 [Chlorocebus saba	74.9	74.9	100%	1e-13	92%	XP_007980302.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X1 [Papio anubis]	74.9	74.9	100%	1e-13	92%	XP_003896353.1
☐	Serum paraoxonase/lactonase 3 [Tupaia chinensis]	74.0	74.0	100%	3e-13	88%	ELW49134.1
☐	PREDICTED: LOW QUALITY PROTEIN: serum paraoxonase/lactonase 3 [Tu	74.0	74.0	100%	3e-13	88%	XP_006157556.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Fukomys damarensis]	71.5	71.5	100%	2e-12	85%	XP_010601717.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Heterocephalus glaber]	71.5	71.5	96%	2e-12	88%	XP_004875782.1
☐	paraoxonase PON3 variant G1B11 [synthetic construct]	70.6	70.6	100%	4e-12	85%	AAR95988.1

☐	PREDICTED: serum paraoxonase/lactonase 3 [Tarsius syrichta]	70.2	70.2	100%	5e-12	88%	XP_008061715.1
☐	serum paraoxonase/lactonase 3 precursor [Oryctolagus cuniculus]	70.2	70.2	100%	5e-12	85%	NP_001075547.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Trichechus manatus latirostris	69.8	69.8	92%	7e-12	92%	XP_004386195.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Chinchilla lanigera]	68.9	68.9	96%	1e-11	88%	XP_005388120.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Echinops telfairi]	67.2	67.2	96%	5e-11	84%	XP_004702728.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Otolemur garnettii]	67.2	67.2	96%	5e-11	88%	XP_003782731.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Nannospalax galili]	66.8	66.8	96%	7e-11	84%	XP_008820796.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Mesocricetus auratus]	66.8	66.8	96%	7e-11	84%	XP_005082968.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Cavia porcellus]	66.8	66.8	96%	7e-11	84%	XP_003475052.2
☐	PREDICTED: serum paraoxonase/lactonase 3 [Galeopterus variegatus]	66.4	66.4	92%	1e-10	88%	XP_008577501.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Dasypus novemcinctus]	66.4	66.4	92%	1e-10	88%	XP_004470801.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Cavia porcellus]	64.7	64.7	92%	4e-10	88%	XP_005006096.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Microtus ochrogaster]	64.7	64.7	96%	4e-10	84%	XP_005363748.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X1 [Cavia porcellus]	64.7	64.7	92%	4e-10	88%	XP_003475053.2
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Chinchilla lanigera]	64.3	64.3	92%	5e-10	88%	XP_005388121.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Octodon degus]	64.3	64.3	92%	5e-10	88%	XP_004632673.1
☐	PREDICTED: serum paraoxonase/arylesterase 1-like isoform X3 [Chrysochlo	63.8	63.8	92%	7e-10	83%	XP_006834338.1
☐	Serum paraoxonase/arylesterase 2 [Fukomys damarensis]	63.4	63.4	92%	1e-09	83%	KFO23896.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Fukomys dama	63.4	63.4	92%	1e-09	83%	XP_010601716.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X1 [Fukomys dama	63.4	63.4	92%	1e-09	83%	XP_010601714.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Panthera tigris altaica]	63.4	63.4	92%	1e-09	83%	XP_007076752.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Heterocephalus glaber]	63.4	63.4	92%	1e-09	83%	XP_004875781.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Loxodonta africana]	63.0	63.0	96%	1e-09	80%	XP_003407179.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Jaculus jaculus]	62.6	62.6	92%	2e-09	83%	XP_004656265.1
☐	PREDICTED: serum paraoxonase/lactonase 3-like [Lipotes vexillifer]	62.1	62.1	96%	2e-09	80%	XP_007467394.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Tursiops truncatus]	62.1	62.1	96%	3e-09	80%	XP_004328323.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X3 [Ursus maritimus]	62.1	62.1	92%	3e-09	83%	XP_008684490.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Physeter catodon]	62.1	62.1	96%	3e-09	80%	XP_007117402.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X1 [Ursus maritimus]	62.1	62.1	92%	3e-09	83%	XP_008684487.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Lipotes vexillifer]	62.1	62.1	96%	3e-09	80%	XP_007450717.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Orcinus orca]	62.1	62.1	96%	3e-09	80%	XP_004265625.1
☐	Pon3 protein [Mus musculus]	61.3	61.3	88%	3e-09	83%	AAH05714.1
☐	PREDICTED: serum paraoxonase/arylesterase 2-like isoform 2 [Gorilla gorilla	61.7	61.7	92%	3e-09	83%	XP_004045830.1
☐	paraoxonase 2, isoform CRA_d [Homo sapiens]	61.7	61.7	92%	4e-09	83%	EAW76766.1
☐	PREDICTED: serum paraoxonase/arylesterase 2-like isoform 1 [Gorilla gorilla	61.7	61.7	92%	4e-09	83%	XP_004045829.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Homo sapiens]	61.7	61.7	92%	4e-09	83%	XP_005250511.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Pongo abelii]	61.7	61.7	92%	4e-09	83%	XP_009241272.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X1 [Homo sapiens]	61.7	61.7	92%	4e-09	83%	XP_005250510.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X3 [Galeopterus va	61.7	61.7	92%	4e-09	83%	XP_008577500.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Orycteropus afe	61.7	61.7	92%	4e-09	83%	XP_007937984.1
☐	unnamed protein product [Homo sapiens]	61.7	61.7	92%	4e-09	83%	BAG58797.1
☐	serum paraoxonase/arylesterase 2 isoform 2 [Homo sapiens]	61.7	61.7	92%	4e-09	83%	NP_001018171.1
☐	paraoxonase nirs variant 1 [Homo sapiens]	61.7	61.7	92%	4e-09	83%	BAD89420.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Octodon degus]	61.7	61.7	84%	4e-09	86%	XP_004632934.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Loxodonta africana]	61.7	61.7	92%	4e-09	83%	XP_010585559.1

☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Galeopterus var	61.7	61.7	92%	4e-09	83%	XP_008577499.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X1 [Orycteropus afe	61.7	61.7	92%	4e-09	83%	XP_007937983.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Oryctolagus cuniculus]	61.7	61.7	92%	4e-09	83%	XP_002713838.1
☐	unnamed protein product [Homo sapiens]	61.7	61.7	92%	4e-09	83%	BAG37646.1
☐	paraoxonase [Homo sapiens]	61.7	61.7	92%	4e-09	83%	AAC27944.1
☐	paraoxonase 2 [Homo sapiens]	61.7	61.7	92%	4e-09	83%	AAC41995.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Erinaceus europaeus]	61.7	61.7	84%	4e-09	86%	XP_007538317.1
☐	RecName: Full=Serum paraoxonase/arylesterase 2; Short=PON 2; AltName:	61.7	61.7	92%	4e-09	83%	Q15165.3
☐	serum paraoxonase/arylesterase 2 precursor [Sus scrofa]	61.7	61.7	92%	4e-09	83%	NP_001116695.1
☐	serum paraoxonase/arylesterase 2 isoform 1 [Homo sapiens]	61.7	61.7	92%	4e-09	83%	NP_000296.2
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X1 [Galeopterus var	61.7	61.7	92%	4e-09	83%	XP_008577498.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Callithrix jacchu	61.7	61.7	92%	4e-09	83%	XP_002751632.1
☐	unnamed protein product [Homo sapiens]	61.7	61.7	92%	4e-09	83%	BAG59238.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform 2 [Gorilla gorilla gori	61.7	61.7	92%	4e-09	83%	XP_004045828.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Macaca fascicul	61.7	61.7	92%	4e-09	83%	XP_005550230.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Pan paniscus]	61.7	61.7	92%	4e-09	83%	XP_003809758.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Pan troglodytes	61.7	61.7	92%	4e-09	83%	XP_001170049.2
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform 2 [Nomascus leucog	61.7	61.7	92%	4e-09	83%	XP_003252566.1
☐	PREDICTED: serum paraoxonase/arylesterase 2-like isoform 1 [Macaca mula	61.7	61.7	92%	4e-09	83%	XP_001094896.2
☐	paraoxonase 2, isoform CRA_b [Homo sapiens]	61.7	61.7	92%	4e-09	83%	EAW76764.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Rhinopithecus roxellana]	61.7	61.7	92%	4e-09	83%	XP_010354564.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Chlorocebus sabaeus]	61.7	61.7	92%	4e-09	83%	XP_007980304.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform 1 [Gorilla gorilla gori	61.7	61.7	92%	4e-09	83%	XP_004045827.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Saimiri boliviensis boliviens	61.7	61.7	92%	4e-09	83%	XP_003921271.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X1 [Pan paniscus]	61.7	61.7	92%	4e-09	83%	XP_003809757.1
☐	hypothetical protein EGM_12758 [Macaca fascicularis]	61.7	61.7	92%	4e-09	83%	EHH52331.1

Alignments

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PREDICTED: serum paraoxonase/lactonase 3 isoform X2 [Macaca fascicularis]

Sequence ID: ref|XP_005550232.1| **Length:** 327 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 288 to 313 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	3e-15	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    RVSTVYANDGSVLQGTSVASVYHGKI  26
            RVSTVYAN+GSVLQGTSVASVYHGKI
Sbjct  288  RVSTVYANNGSVLQGTSVASVYHGKI  313
```

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paraoxonase-3, partial [Homo sapiens]

Sequence ID: gb|AAC41996.1| **Length:** 341 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 302 to 327 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	3e-15	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    RVSTVYANDGSVLQGTSVASVYHGKI  26
            RVSTVYAN+GSVLQGTSVASVYHGKI
Sbjct  302  RVSTVYANNGSVLQGTSVASVYHGKI  327
```

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Paraoxonase 3 [Homo sapiens]

Sequence ID: gb|AAH70374.1| **Length:** 354 **Number of Matches:** 1

See 1 more title(s)

Range 1: 315 to 340 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	3e-15	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    RVSTVYANDGSVLQGTSVASVYHGKI  26
            RVSTVYAN+GSVLQGTSVASVYHGKI
Sbjct  315  RVSTVYANNGSVLQGTSVASVYHGKI  340
```

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

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paraoxonase PON3 variant G3G3, partial [synthetic construct]

Sequence ID: gb|AAR95991.1| **Length:** 354 **Number of Matches:** 1

Range 1: 315 to 340 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	3e-15	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    RVSTVYANDGSVLQGTSVASVYHGKI  26
            RVSTVYAN+GSVLQGTSVASVYHGKI
Sbjct  315  RVSTVYANNGSVLQGTSVASVYHGKI  340
```

Related Information

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

paraoxanase-3 [Homo sapiens]

Sequence ID: gb|AAK07629.1| **Length:** 354 **Number of Matches:** 1

Range 1: 315 to 340 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
79.5 bits(180)	3e-15	25/26(96%)	26/26(100%)	0/26(0%)

```
Query  1    RVSTVYANDGSVLQGTSVASVYHGKI  26
            RVSTVYAN+GSVLQGTSVASVYHGKI
Sbjct  315  RVSTVYANNGSVLQGTSVASVYHGKI  340
```

Related Information

Gene - associated gene details

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

PON3_RVSTVYANNGSVLQGTSVASVYHGKI_NonMod

RID BE879JR0014 (Expires on 01-16 09:07 am)

Query ID lcl|34172
Description None
Molecule type amino acid
Query Length 26

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

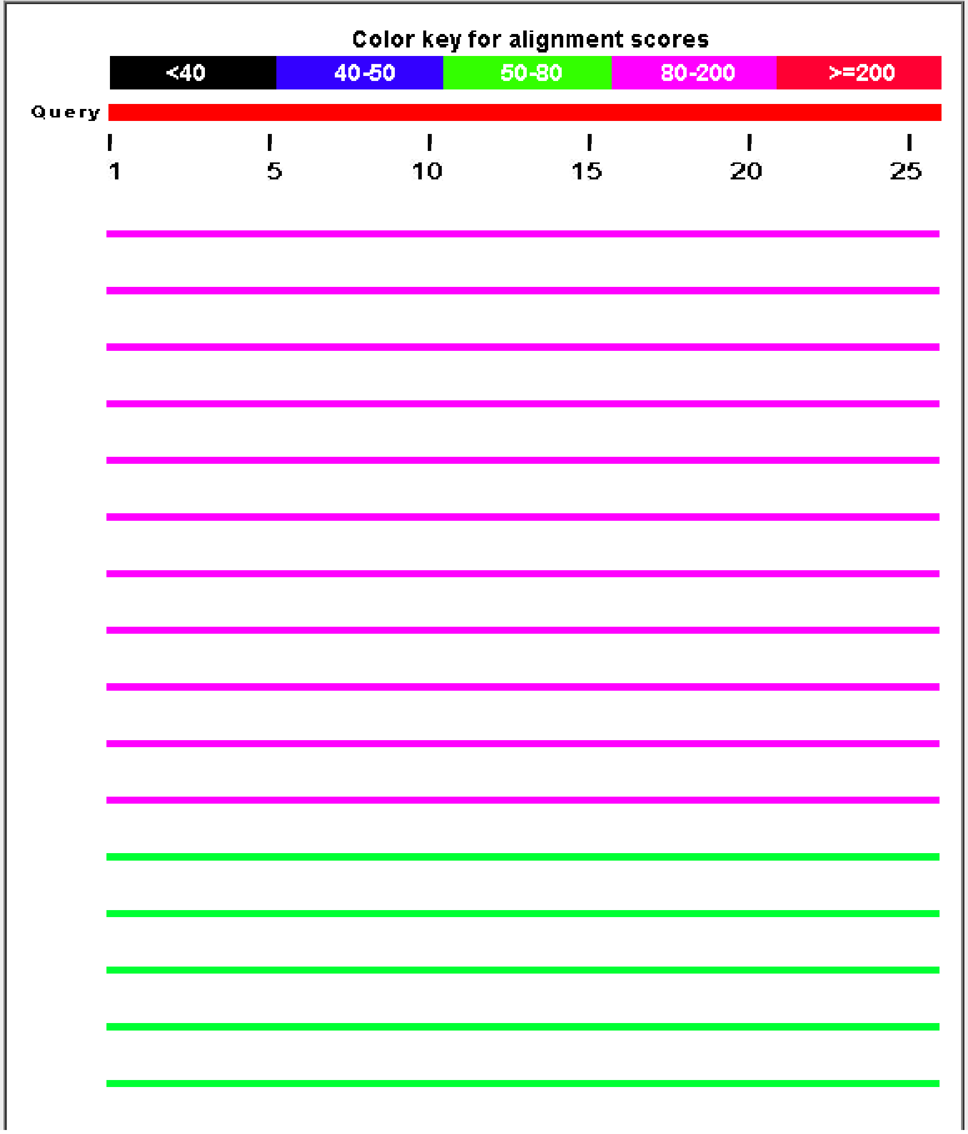
Graphic Summary

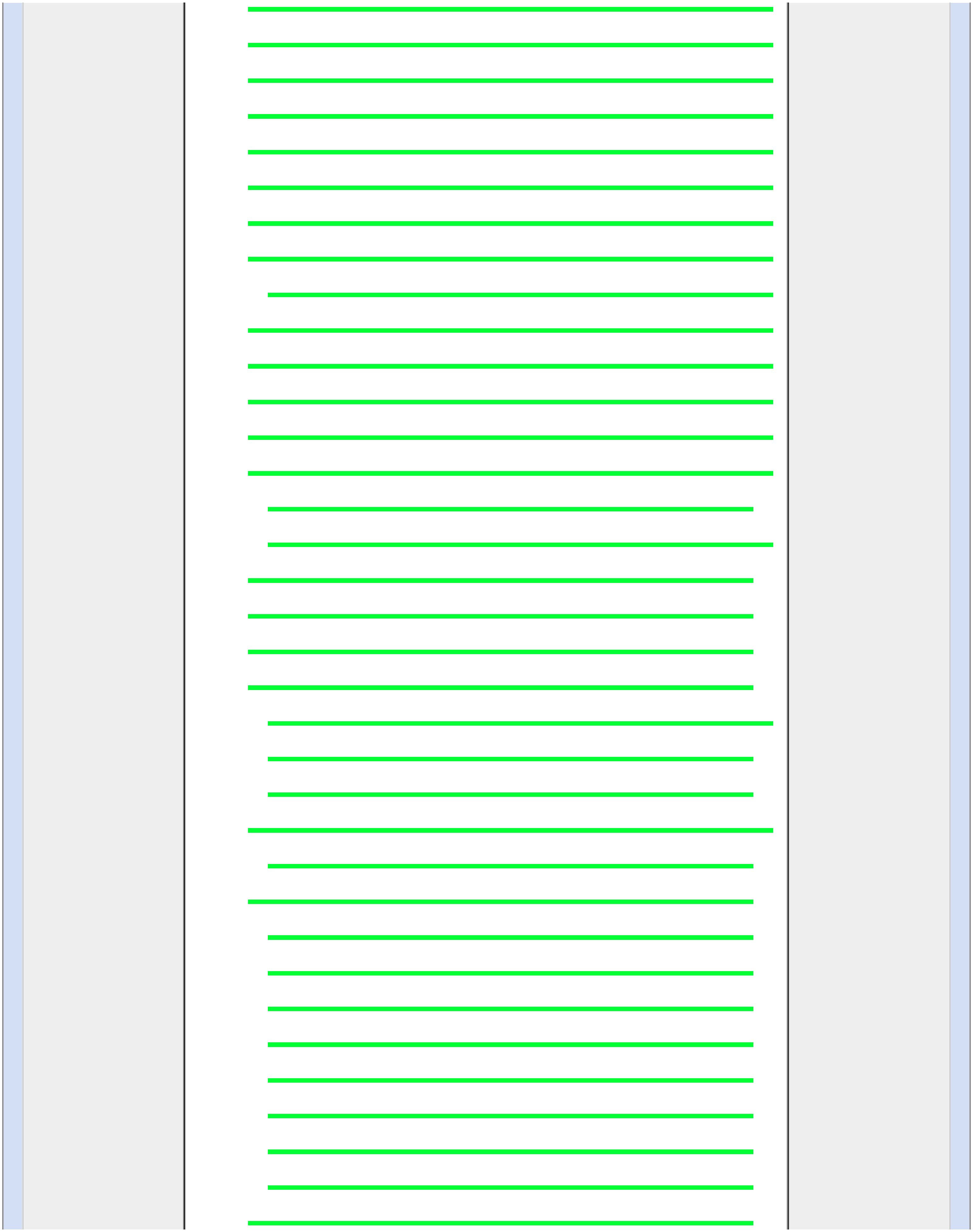
Show Conserved Domains

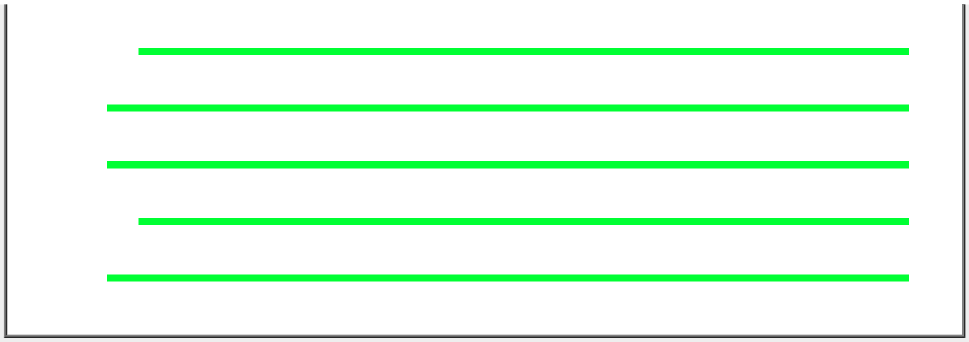
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X2 [Macaca	82.1	82.1	100%	4e-16	100%	gi|544421401|XP_005550232.1
☐	paraoxonase-3 [Homo sapiens]	82.1	82.1	100%	4e-16	100%	gi|1333634|AAC41996.1
☐	Paraoxonase 3 [Homo sapiens]	82.1	82.1	100%	4e-16	100%	gi|47682431|AAH70374.1
☐	paraoxonase PON3 variant G3G3 [synthetic construct]	82.1	82.1	100%	4e-16	100%	gi|40850554|AAR95991.1
☐	paraoxanase-3 [Homo sapiens]	82.1	82.1	100%	4e-16	100%	gi|12751374|AAK07629.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Gorilla gorilla gorilla	82.1	82.1	100%	4e-16	100%	gi|426356977|XP_004045826.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Nomascus leucoger	82.1	82.1	100%	4e-16	100%	gi|332206964|XP_003252564.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Pongo abelii]	82.1	82.1	100%	4e-16	100%	gi|297681036|XP_002818287.1
☐	PREDICTED: serum paraoxonase/lactonase 3-like [Macaca mulatta	82.1	82.1	100%	4e-16	100%	gi|109067456|XP_001095770.1
☐	serum paraoxonase/lactonase 3 [Homo sapiens]	82.1	82.1	100%	4e-16	100%	gi|29788996|NP_000931.1
☐	hCG2023324, isoform CRA_c [Homo sapiens]	82.1	82.1	100%	5e-16	100%	gi|119597176|EAW76770.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Ictidomys tridecemli	80.0	80.0	100%	2e-15	96%	gi|532092367|XP_005331867.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X3 [Callithrix	78.7	78.7	100%	6e-15	96%	gi|675673198|XP_009000653.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X2 [Callithrix	78.7	78.7	100%	6e-15	96%	gi|296209660|XP_002751633.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Saimiri boliviensis b	78.7	78.7	100%	6e-15	96%	gi|403257318|XP_003921270.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X1 [Callithrix	78.7	78.7	100%	7e-15	96%	gi|675673195|XP_009000652.1
☐	paraoxonase PON3 variant G1A7 [synthetic construct]	78.3	78.3	100%	9e-15	96%	gi|40850546|AAR95987.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X2 [Papio ar	77.4	77.4	100%	2e-14	96%	gi|685532002|XP_009201642.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Rhinopithecus roxel	77.4	77.4	100%	2e-14	96%	gi|724960789|XP_010354563.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X1 [Chloroce	77.4	77.4	100%	2e-14	96%	gi|635114722|XP_007980302.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X1 [Papio ar	77.4	77.4	100%	2e-14	96%	gi|402864178|XP_003896353.1
☐	Serum paraoxonase/lactonase 3 [Tupaia chinensis]	76.6	76.6	100%	3e-14	92%	gi|444708006|ELW49134.1
☐	PREDICTED: LOW QUALITY PROTEIN: serum paraoxonase/lactor	76.6	76.6	100%	3e-14	92%	gi|562858158|XP_006157556.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Fukomys damarens	74.0	74.0	100%	3e-13	88%	gi|731264517|XP_010601717.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Heterocephalus glal	74.0	74.0	96%	3e-13	92%	gi|512808025|XP_004875782.1
☐	paraoxonase PON3 variant G3A5 [synthetic construct]	73.2	73.2	100%	5e-13	88%	gi|40850552|AAR95990.1
☐	paraoxonase PON3 variant G3H9 [synthetic construct]	73.2	73.2	100%	5e-13	88%	gi|40850556|AAR95992.1
☐	paraoxonase PON3 variant G1B11 [synthetic construct]	73.2	73.2	100%	5e-13	88%	gi|40850548|AAR95988.1
☐							

	paraoxonase PON3 variant G2C2 [synthetic construct]	73.2	73.2	100%	5e-13	88%	gi|40850550|AAR95989.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Tarsius syrichta]	72.7	72.7	100%	7e-13	92%	gi|640810272|XP_008061715.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Trichechus manatus	72.3	72.3	92%	1e-12	96%	gi|471409235|XP_004386195.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Chinchilla lanigera]	71.5	71.5	96%	2e-12	92%	gi|533147430|XP_005388120.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Echinops telfairi]	69.8	69.8	96%	7e-12	88%	gi|507645867|XP_004702728.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Otolemur garnettii]	69.8	69.8	96%	7e-12	92%	gi|395818644|XP_003782731.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Nannospalax galili]	69.4	69.4	96%	1e-11	88%	gi|674094968|XP_008820796.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Mesocricetus auratu	69.4	69.4	96%	1e-11	88%	gi|524966130|XP_005082968.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Cavia porcellus]	69.4	69.4	96%	1e-11	88%	gi|514471180|XP_003475052.2
☐	PREDICTED: serum paraoxonase/lactonase 3 [Galeopterus variega	68.9	68.9	92%	1e-11	92%	gi|667290365|XP_008577501.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Dasypus novemcinc	68.9	68.9	92%	1e-11	92%	gi|488562159|XP_004470801.1
☐	serum paraoxonase/lactonase 3 precursor [Oryctolagus cuniculus]	67.7	67.7	100%	4e-11	81%	gi|126723032|NP_001075547.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Cavia	67.2	67.2	92%	5e-11	92%	gi|514471184|XP_005006096.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Microtus ochrogaste	67.2	67.2	96%	5e-11	88%	gi|532041816|XP_005363748.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X1 [Cavia	67.2	67.2	92%	5e-11	92%	gi|514471182|XP_003475053.2
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Chinchilla laniger	66.8	66.8	92%	7e-11	92%	gi|533147432|XP_005388121.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Octodon degus]	66.8	66.8	92%	7e-11	92%	gi|507650678|XP_004632673.1
☐	Serum paraoxonase/arylesterase 2 [Fukomys damarensis]	66.0	66.0	92%	1e-10	88%	gi|676268318|KFO23896.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Fukor	66.0	66.0	92%	1e-10	88%	gi|731264515|XP_010601716.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X1 [Fukor	66.0	66.0	92%	1e-10	88%	gi|731264513|XP_010601714.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Panthera tigris altai	66.0	66.0	92%	1e-10	88%	gi|591299463|XP_007076752.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Heterocephalus g	66.0	66.0	92%	1e-10	88%	gi|512808023|XP_004875781.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Loxodonta africana]	65.5	65.5	96%	2e-10	84%	gi|344270695|XP_003407179.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Jaculus jaculus]	65.1	65.1	92%	3e-10	88%	gi|507544585|XP_004656265.1
☐	PREDICTED: serum paraoxonase/lactonase 3-like [Lipotes vexillife	64.7	64.7	96%	3e-10	84%	gi|602714358|XP_007467394.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Tursiops truncatus]	64.7	64.7	96%	4e-10	84%	gi|470649612|XP_004328323.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X3 [Ursus m	64.7	64.7	92%	4e-10	88%	gi|670986874|XP_008684490.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Physeter catodon]	64.7	64.7	96%	4e-10	84%	gi|593757173|XP_007117402.1
☐	PREDICTED: serum paraoxonase/lactonase 3 isoform X1 [Ursus m	64.7	64.7	92%	4e-10	88%	gi|670986870|XP_008684487.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Lipotes vexillifer]	64.7	64.7	96%	4e-10	84%	gi|602730612|XP_007450717.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Orcinus orca]	64.7	64.7	96%	4e-10	84%	gi|465984490|XP_004265625.1
☐	Pon3 protein [Mus musculus]	63.8	63.8	88%	4e-10	87%	gi|13543076|AAH05714.1
☐	PREDICTED: serum paraoxonase/arylesterase 2-like isoform 2 [Go	64.3	64.3	92%	5e-10	88%	gi|426356985|XP_004045830.1
☐	paraoxonase 2, isoform CRA_d [Homo sapiens]	64.3	64.3	92%	5e-10	88%	gi|119597172|EAW76766.1
☐	PREDICTED: serum paraoxonase/arylesterase 2-like isoform 1 [Go	64.3	64.3	92%	5e-10	88%	gi|426356983|XP_004045829.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Homo	64.3	64.3	92%	5e-10	88%	gi|530386130|XP_005250511.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Pongo	64.3	64.3	92%	5e-10	88%	gi|686725757|XP_009241272.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X1 [Homo	64.3	64.3	92%	5e-10	88%	gi|530386128|XP_005250510.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X3 [Galeo	64.3	64.3	92%	5e-10	88%	gi|667290361|XP_008577500.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Oryct	64.3	64.3	92%	5e-10	88%	gi|634845273|XP_007937984.1
☐	unnamed protein product [Homo sapiens]	64.3	64.3	92%	5e-10	88%	gi|194382084|BAG58797.1
☐	serum paraoxonase/arylesterase 2 isoform 2 [Homo sapiens]	64.3	64.3	92%	5e-10	88%	gi|66529396|NP_001018171.1
☐	paraoxonase nirs variant 1 [Homo sapiens]	64.3	64.3	92%	5e-10	88%	gi|58737023|BAD89420.1
☐	PREDICTED: serum paraoxonase/lactonase 3 [Octodon degus]	64.3	64.3	84%	5e-10	91%	gi|507651723|XP_004632934.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Loxodonta africar	64.3	64.3	92%	5e-10	88%	gi|731461644|XP_010585559.1

☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Galeo	64.3	64.3	92%	5e-10	88%	gi|667290358|XP_008577499.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X1 [Oryct	64.3	64.3	92%	5e-10	88%	gi|634845270|XP_007937983.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Oryctolagus cuni	64.3	64.3	92%	5e-10	88%	gi|291394781|XP_002713838.1
☐	unnamed protein product [Homo sapiens]	64.3	64.3	92%	5e-10	88%	gi|189054815|BAG37646.1
☐	paraoxonase [Homo sapiens]	64.3	64.3	92%	5e-10	88%	gi|2228775|AAC27944.1
☐	paraoxonase 2 [Homo sapiens]	64.3	64.3	92%	5e-10	88%	gi|1333632|AAC41995.1
☐	RecName: Full=Serum paraoxonase/arylesterase 2; Short=PON 2;	64.3	64.3	92%	5e-10	88%	gi|325511384|Q15165.3
☐	serum paraoxonase/arylesterase 2 precursor [Sus scrofa]	64.3	64.3	92%	5e-10	88%	gi|178056462|NP_001116695.1
☐	serum paraoxonase/arylesterase 2 isoform 1 [Homo sapiens]	64.3	64.3	92%	5e-10	88%	gi|66529294|NP_000296.2
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X1 [Galeo	64.3	64.3	92%	5e-10	88%	gi|667290354|XP_008577498.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Callith	64.3	64.3	92%	5e-10	88%	gi|296209658|XP_002751632.1
☐	unnamed protein product [Homo sapiens]	64.3	64.3	92%	5e-10	88%	gi|194383760|BAG59238.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform 2 [Gorilla	64.3	64.3	92%	5e-10	88%	gi|426356981|XP_004045828.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Maca	64.3	64.3	92%	5e-10	88%	gi|544421397|XP_005550230.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Pan p	64.3	64.3	92%	5e-10	88%	gi|397476756|XP_003809758.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X2 [Pan tr	64.3	64.3	92%	5e-10	88%	gi|332866740|XP_001170049.2
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform 2 [Nomas	64.3	64.3	92%	5e-10	88%	gi|332206968|XP_003252566.1
☐	PREDICTED: serum paraoxonase/arylesterase 2-like isoform 1 [Ma	64.3	64.3	92%	5e-10	88%	gi|297288859|XP_001094896.2
☐	paraoxonase 2, isoform CRA_b [Homo sapiens]	64.3	64.3	92%	5e-10	88%	gi|119597170|EAW76764.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Rhinopithecus ro	64.3	64.3	92%	5e-10	88%	gi|724960791|XP_010354564.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Chlorocebus saba	64.3	64.3	92%	5e-10	88%	gi|635114726|XP_007980304.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform 1 [Gorilla	64.3	64.3	92%	5e-10	88%	gi|426356979|XP_004045827.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 [Saimiri boliviensi	64.3	64.3	92%	5e-10	88%	gi|403257320|XP_003921271.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X1 [Pan p	64.3	64.3	92%	5e-10	88%	gi|397476754|XP_003809757.1
☐	hypothetical protein EGM_12758 [Macaca fascicularis]	64.3	64.3	92%	5e-10	88%	gi|355747834|EHH52331.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform 1 [Nomas	64.3	64.3	92%	5e-10	88%	gi|332206966|XP_003252565.1
☐	PREDICTED: serum paraoxonase/arylesterase 2 isoform X1 [Pongo	64.3	64.3	92%	5e-10	88%	gi|297681032|XP_002818289.1

⊖ Alignments

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PREDICTED: serum paraoxonase/lactonase 3 isoform X2 [Macaca fascicularis]

Sequence ID: gi|544421401|ref|XP_005550232.1| **Length:** 327 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 288 to 313 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.1 bits(186)	4e-16	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    RVSTVYANNGSVLQGTSVASVYHGKI  26
            RVSTVYANNGSVLQGTSVASVYHGKI
Sbjct  288  RVSTVYANNGSVLQGTSVASVYHGKI  313
```

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paraoxonase-3, partial [Homo sapiens]

Sequence ID: gi|1333634|gb|AAC41996.1| **Length:** 341 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 302 to 327 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.1 bits(186)	4e-16	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    RVSTVYANNGSVLQGTSVASVYHGKI  26
```

```
              RVSTVYANNGSVLQGTSVASVYHGKI
Sbjct  302  RVSTVYANNGSVLQGTSVASVYHGKI  327
```

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Paraoxonase 3 [Homo sapiens]

Sequence ID: gi|47682431|gb|AAH70374.1| **Length:** 354 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 315 to 340 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.1 bits(186)	4e-16	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    RVSTVYANNGSVLQGTSVASVYHGKI  26
            RVSTVYANNGSVLQGTSVASVYHGKI
Sbjct  315  RVSTVYANNGSVLQGTSVASVYHGKI  340
```

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paraoxonase PON3 variant G3G3, partial [synthetic construct]

Sequence ID: gi|40850554|gb|AAR95991.1| **Length:** 354 **Number of Matches:** 1

Related Information

Range 1: 315 to 340 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.1 bits(186)	4e-16	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    RVSTVYANNGSVLQGTSVASVYHGKI  26
            RVSTVYANNGSVLQGTSVASVYHGKI
Sbjct  315  RVSTVYANNGSVLQGTSVASVYHGKI  340
```

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paraoxanase-3 [Homo sapiens]

Sequence ID: gi|12751374|gb|AAK07629.1| **Length:** 354 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 315 to 340 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.1 bits(186)	4e-16	26/26(100%)	26/26(100%)	0/26(0%)

```
Query  1    RVSTVYANNGSVLQGTSVASVYHGKI  26
            RVSTVYANNGSVLQGTSVASVYHGKI
Sbjct  315  RVSTVYANNGSVLQGTSVASVYHGKI  340
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVKF5JS001R

Your search parameters were adjusted to search for a short input sequence.

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SELL_KIGGIWTWVGTDKS_Mod

RID BVKF5JS001R (Expires on 01-21 10:39 am)

Query ID	lcl|320009	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	14		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

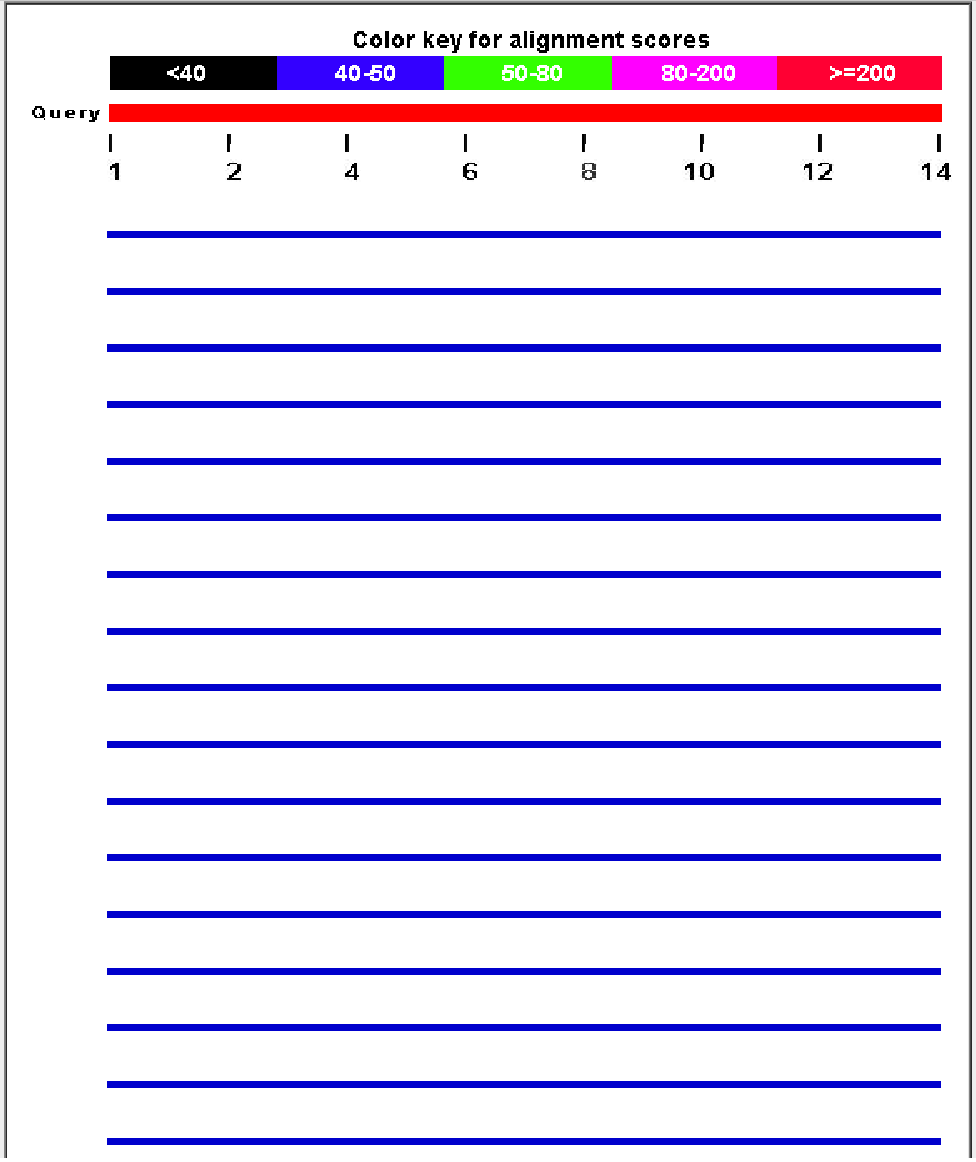
Graphic Summary

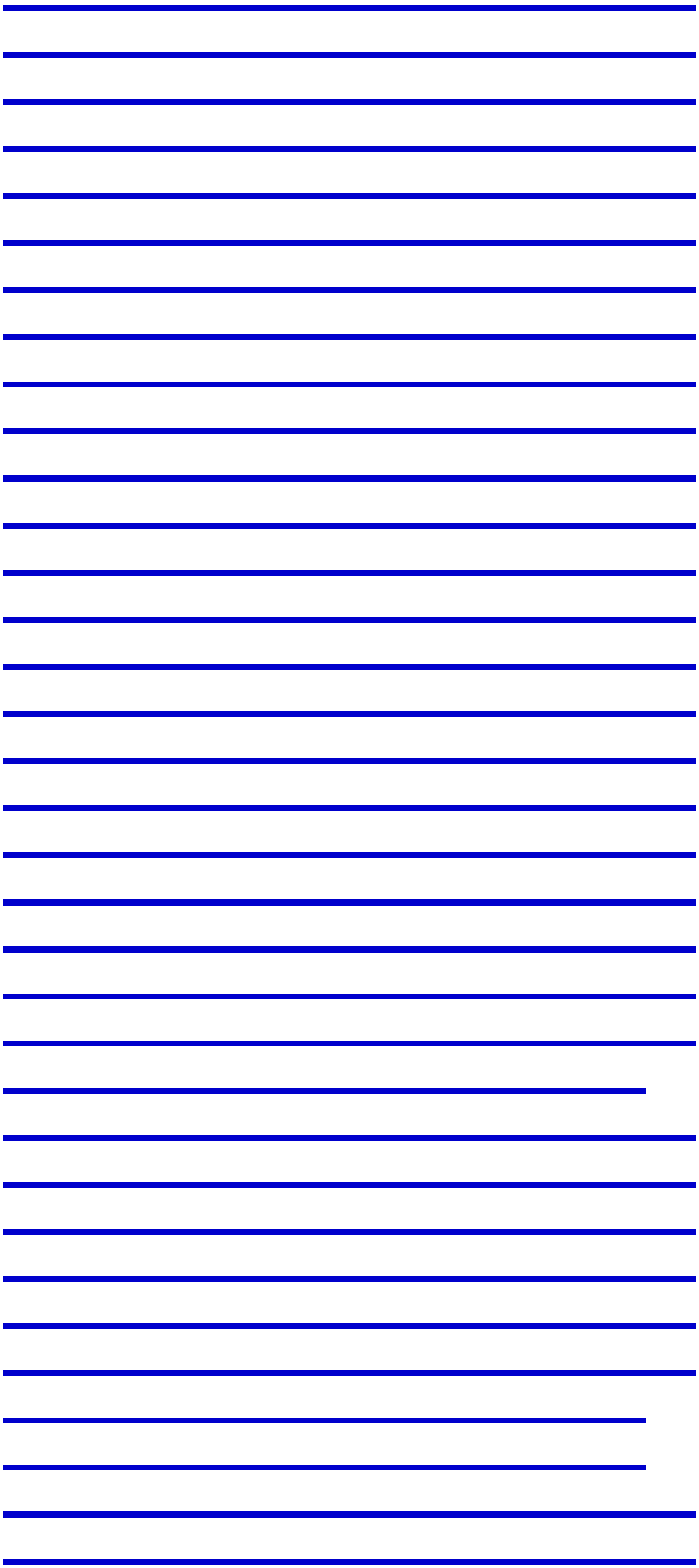
Show Conserved Domains

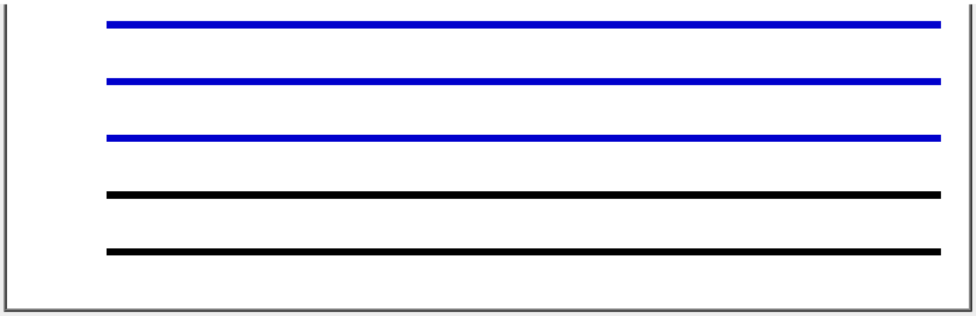
No putative conserved domains have been detected

Distribution of 105 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, L-selectin Lectin And Egf Domains [Homo sapiens]	46.9	46.9	100%	8e-05	93%	3CFW_A
☐	selectin L (lymphocyte adhesion molecule 1), isoform CRA_c [Homo sapiens]	46.9	46.9	100%	9e-05	93%	EAW90857.1
☐	PREDICTED: L-selectin isoform X2 [Macaca fascicularis]	46.9	46.9	100%	9e-05	93%	XP_005539997.1
☐	unnamed protein product [Homo sapiens]	46.9	46.9	100%	9e-05	93%	BAG60862.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Tarsius syrichta]	46.9	46.9	100%	9e-05	93%	XP_008059542.1
☐	Leu-8 antigen short form [Homo sapiens]	46.9	46.9	100%	9e-05	93%	CAB43537.1
☐	PREDICTED: L-selectin isoform X2 [Ursus maritimus]	46.9	46.9	100%	9e-05	93%	XP_008694116.1
☐	lymph node homing receptor precursor [Homo sapiens]	46.9	46.9	100%	9e-05	93%	AAC63053.1
☐	L-selectin precursor [Pan troglodytes]	46.9	46.9	100%	9e-05	93%	NP_001009074.1
☐	unnamed protein product [Homo sapiens]	46.9	46.9	100%	9e-05	93%	CAA34275.1
☐	pln homing receptor [Homo sapiens]	46.9	46.9	100%	9e-05	93%	CAA34203.1
☐	L-selectin [Papio anubis]	46.9	46.9	100%	9e-05	93%	NP_001106096.1
☐	RecName: Full=L-selectin; AltName: Full=CD62 antigen-like family member L	46.9	46.9	100%	9e-05	93%	P14151.2
☐	L-selectin precursor [Macaca mulatta]	46.9	46.9	100%	9e-05	93%	NP_001036228.1
☐	RecName: Full=L-selectin; AltName: Full=CD62 antigen-like family member L	46.9	46.9	100%	9e-05	93%	Q95235.1
☐	selectin L (lymphocyte adhesion molecule 1), isoform CRA_a [Homo sapiens]	46.9	46.9	100%	9e-05	93%	EAW90855.1
☐	SELL [synthetic construct]	46.9	46.9	100%	9e-05	93%	AIC62025.1
☐	Lymph node homing receptor [Macaca mulatta]	46.9	46.9	100%	9e-05	93%	EHH15803.1
☐	SELL protein [Homo sapiens]	46.9	46.9	100%	9e-05	93%	AAH20758.1
☐	PREDICTED: L-selectin isoform X1 [Ursus maritimus]	46.9	46.9	100%	9e-05	93%	XP_008694111.1
☐	PREDICTED: L-selectin [Rhinopithecus roxellana]	46.9	46.9	100%	9e-05	93%	XP_010359291.1
☐	PREDICTED: L-selectin [Chlorocebus sabaeus]	46.9	46.9	100%	9e-05	93%	XP_007987763.1
☐	PREDICTED: L-selectin [Callithrix jacchus]	46.9	46.9	100%	9e-05	93%	XP_002760427.1
☐	PREDICTED: L-selectin isoform X1 [Macaca fascicularis]	46.9	46.9	100%	9e-05	93%	XP_005539996.1
☐	PREDICTED: L-selectin [Gorilla gorilla gorilla]	46.9	46.9	100%	9e-05	93%	XP_004027917.1
☐	unnamed protein product [Homo sapiens]	46.9	46.9	100%	9e-05	93%	CAB43536.1
☐	PREDICTED: L-selectin [Pan paniscus]	46.9	46.9	100%	9e-05	93%	XP_003824676.1
☐	PREDICTED: L-selectin [Pongo abelii]	46.9	46.9	100%	9e-05	93%	XP_002809857.2
☐	PREDICTED: L-selectin [Nomascus leucogenys]	46.9	46.9	100%	9e-05	93%	XP_003258894.1

☐	L-selectin precursor [Homo sapiens]	46.9	46.9	100%	9e-05	93%	NP_000646.2
☐	PREDICTED: L-selectin-like [Leptonychotes weddellii]	44.3	44.3	100%	6e-04	86%	XP_006739818.1
☐	hypothetical protein PANDA_007106 [Ailuropoda melanoleuca]	44.3	44.3	100%	6e-04	86%	EFB23838.1
☐	PREDICTED: L-selectin isoform X2 [Canis lupus familiaris]	44.3	44.3	100%	6e-04	86%	XP_005622604.1
☐	PREDICTED: L-selectin isoformX1 [Canis lupus familiaris]	44.3	44.3	100%	6e-04	86%	XP_537201.2
☐	PREDICTED: L-selectin [Ceratotherium simum simum]	44.3	44.3	100%	6e-04	86%	XP_004425116.1
☐	PREDICTED: L-selectin [Odobenus rosmarus divergens]	44.3	44.3	100%	6e-04	86%	XP_004408944.1
☐	PREDICTED: L-selectin [Trichechus manatus latirostris]	44.3	44.3	100%	6e-04	86%	XP_004384151.1
☐	PREDICTED: L-selectin [Saimiri boliviensis boliviensis]	44.3	44.3	100%	7e-04	86%	XP_003925442.1
☐	PREDICTED: l-selectin-like [Ailuropoda melanoleuca]	44.3	44.3	100%	7e-04	86%	XP_002918625.1
☐	L-selectin precursor [Oryctolagus cuniculus]	43.1	43.1	100%	0.002	86%	NP_001075821.1
☐	PREDICTED: L-selectin [Sarcophilus harrisii]	41.8	41.8	92%	0.005	85%	XP_003767474.1
☐	PREDICTED: L-selectin [Erinaceus europaeus]	41.8	41.8	100%	0.005	79%	XP_007531867.1
☐	PREDICTED: L-selectin [Elephantulus edwardii]	41.4	41.4	100%	0.006	86%	XP_006887476.1
☐	PREDICTED: L-selectin [Galeopterus variegatus]	41.4	41.4	100%	0.006	86%	XP_008589968.1
☐	PREDICTED: L-selectin isoform X2 [Ornithorhynchus anatinus]	41.4	41.4	100%	0.006	86%	XP_007667058.1
☐	PREDICTED: L-selectin isoform X1 [Ornithorhynchus anatinus]	41.4	41.4	100%	0.006	86%	XP_007667057.1
☐	PREDICTED: L-selectin [Chrysochloris asiatica]	40.9	59.8	100%	0.009	79%	XP_006872694.1
☐	PREDICTED: L-selectin [Ictidomys tridecemlineatus]	40.5	40.5	92%	0.012	85%	XP_005319885.1
☐	LECAM-1 [Sigmodon hispidus]	40.5	40.5	92%	0.012	85%	AAN87893.1
☐	PREDICTED: L-selectin [Ochotona princeps]	40.5	40.5	100%	0.012	79%	XP_004589372.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Mustela putorius furo]	40.1	40.1	100%	0.017	79%	XP_004756722.1
☐	PREDICTED: L-selectin [Panthera tigris altaica]	40.1	40.1	100%	0.017	79%	XP_007077079.1
☐	L-selectin [Felis catus]	40.1	40.1	100%	0.017	79%	NP_001082779.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Mustela putorius furo]	40.1	40.1	100%	0.017	79%	XP_004799211.1
☐	PREDICTED: L-selectin isoform X2 [Balaenoptera acutorostrata scammoni]	38.8	38.8	100%	0.043	79%	XP_007172554.1
☐	PREDICTED: L-selectin [Lipotes vexillifer]	38.8	38.8	100%	0.044	79%	XP_007458185.1
☐	PREDICTED: L-selectin isoform X1 [Balaenoptera acutorostrata scammoni]	38.8	38.8	100%	0.044	79%	XP_007172553.1
☐	PREDICTED: L-selectin [Physeter catodon]	38.8	38.8	100%	0.044	79%	XP_007102109.1
☐	PREDICTED: L-selectin [Orcinus orca]	38.8	38.8	100%	0.044	79%	XP_004269787.1
☐	PREDICTED: L-selectin isoform X2 [Monodelphis domestica]	38.8	38.8	92%	0.045	85%	XP_007480808.1
☐	PREDICTED: L-selectin isoform X1 [Monodelphis domestica]	38.8	38.8	92%	0.045	85%	XP_007480807.1
☐	PREDICTED: E-selectin [Ornithorhynchus anatinus]	38.8	38.8	100%	0.046	79%	XP_007667059.1
☐	PREDICTED: L-selectin [Camelus dromedarius]	38.4	38.4	100%	0.060	71%	XP_010982785.1
☐	PREDICTED: L-selectin [Camelus bactrianus]	38.4	38.4	100%	0.060	71%	XP_010952144.1
☐	PREDICTED: L-selectin [Myotis brandtii]	38.4	38.4	100%	0.060	71%	XP_005861291.1
☐	PREDICTED: L-selectin [Echinops telfairi]	38.4	38.4	100%	0.061	71%	XP_004706892.1
☐	PREDICTED: L-selectin isoform X2 [Vicugna pacos]	38.4	38.4	100%	0.061	71%	XP_006211162.1
☐	PREDICTED: L-selectin isoform X1 [Vicugna pacos]	38.4	38.4	100%	0.061	71%	XP_006211161.1
☐	PREDICTED: L-selectin [Myotis davidii]	38.4	38.4	100%	0.061	71%	XP_006764234.1
☐	PREDICTED: L-selectin [Camelus ferus]	38.4	38.4	100%	0.061	71%	XP_006173301.1
☐	L-selectin [Myotis davidii]	38.4	38.4	100%	0.062	71%	ELK29869.1
☐	PREDICTED: L-selectin [Myotis lucifugus]	38.4	38.4	100%	0.063	71%	XP_006099687.1
☐	PREDICTED: E-selectin-like [Serinus canaria]	38.4	38.4	92%	0.064	85%	XP_009097829.1
☐	PREDICTED: P-selectin-like [Geospiza fortis]	38.4	38.4	92%	0.064	85%	XP_005426754.1

☐	PREDICTED: E-selectin [Eptesicus fuscus]	38.4	60.7	100%	0.065	71%	XP_008151404.1
☐	E-selectin [Myotis brandtii]	38.4	60.7	100%	0.065	71%	EPQ04591.1
☐	hypothetical protein CB1_000094012 [Camelus ferus]	38.4	93.5	100%	0.066	71%	EPY89559.1
☐	PREDICTED: L-selectin [Loxodonta africana]	38.0	38.0	100%	0.084	79%	XP_010593279.1
☐	P-selectin [Merops nubicus]	38.0	38.0	92%	0.087	85%	KFQ34721.1
☐	PREDICTED: E-selectin [Poecilia formosa]	38.0	38.0	100%	0.088	71%	XP_007558781.1
☐	PREDICTED: P-selectin [Merops nubicus]	38.0	38.0	92%	0.088	85%	XP_008943868.1
☐	PREDICTED: LOW QUALITY PROTEIN: P-selectin [Egretta garzetta]	38.0	38.0	92%	0.089	85%	XP_009643678.1
☐	PREDICTED: L-selectin isoform X2 [Bison bison bison]	37.5	37.5	100%	0.11	71%	XP_010835001.1
☐	PREDICTED: L-selectin isoform X3 [Capra hircus]	37.5	37.5	100%	0.11	71%	XP_005690682.1
☐	PREDICTED: L-selectin isoform X4 [Bubalus bubalis]	37.5	37.5	100%	0.11	71%	XP_006073161.1
☐	PREDICTED: L-selectin isoform X2 [Capra hircus]	37.5	37.5	100%	0.12	71%	XP_005690681.1
☐	L-selectin [Bos mutus]	37.5	37.5	100%	0.12	71%	ELR51562.1
☐	PREDICTED: L-selectin isoform X3 [Bubalus bubalis]	37.5	37.5	100%	0.12	71%	XP_006073160.1
☐	L-selectin precursor [Bos taurus]	37.5	37.5	100%	0.12	71%	NP_776607.1
☐	TPA: L-selectin [Bos taurus]	37.5	37.5	100%	0.12	71%	DAA21340.1
☐	PREDICTED: L-selectin isoform X1 [Capra hircus]	37.5	37.5	100%	0.12	71%	XP_005690680.1
☐	PREDICTED: L-selectin [Ovis aries]	37.5	37.5	100%	0.12	71%	XP_004013726.1
☐	L-selectin precursor [Sus scrofa]	37.5	37.5	100%	0.12	71%	NP_001106148.1
☐	PREDICTED: L-selectin isoform X1 [Bison bison bison]	37.5	37.5	100%	0.12	71%	XP_010835000.1
☐	PREDICTED: L-selectin [Pantholops hodgsonii]	37.5	37.5	100%	0.12	71%	XP_005973458.1
☐	PREDICTED: L-selectin [Bos mutus]	37.5	37.5	100%	0.12	71%	XP_005902444.1
☐	PREDICTED: L-selectin isoform X1 [Bos taurus]	37.5	37.5	100%	0.12	71%	XP_005216937.1
☐	PREDICTED: L-selectin [Orycteropus afer afer]	37.5	37.5	100%	0.12	71%	XP_007935972.1
☐	PREDICTED: L-selectin isoform X2 [Bubalus bubalis]	37.5	37.5	100%	0.12	71%	XP_006073159.1
☐	PREDICTED: L-selectin isoform X1 [Bubalus bubalis]	37.5	37.5	100%	0.12	71%	XP_006073158.1

⊟ Alignments

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

Chain A, L-selectin Lectin And Egf Domains

Sequence ID: pdb|3CFW|A **Length:** 164 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 55 to 68 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	8e-05	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1   KIGGIWTWVGTDKS  14
           KIGGIWTWVGT+KS
Sbjct  55  KIGGIWTWVGTNKS  68
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

selectin L (lymphocyte adhesion molecule 1), isoform CRA_c [Homo sapiens]

Sequence ID: gb|EAW90857.1| **Length:** 320 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 106 to 119 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	9e-05	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KIGGIWTWVGTDKS  14
            KIGGIWTWVGT+KS
Sbjct  106  KIGGIWTWVGTNKS  119
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: L-selectin isoform X2 [Macaca fascicularis]

Sequence ID: ref|XP_005539997.1| **Length:** 323 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 106 to 119 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	9e-05	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KIGGIWTWVGTDKS  14
            KIGGIWTWVGT+KS
Sbjct  106  KIGGIWTWVGTNKS  119
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG60862.1| **Length:** 325 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 46 to 59 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	9e-05	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1   KIGGIWTWVGTDKS  14
           KIGGIWTWVGT+KS
Sbjct  46  KIGGIWTWVGTNKS  59
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: LOW QUALITY PROTEIN: L-selectin [Tarsius syrichta]

Sequence ID: ref|XP_008059542.1| **Length:** 362 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 93 to 106 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	9e-05	13/14(93%)	14/14(100%)	0/14(0%)

```
Query  1    KIGGIWTWVGTDKS  14
            KIGGIWTWVGT+KS
Sbjct  93   KIGGIWTWVGTNKS  106
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

SELL_KIGGIWTWVGTNKS_NonMod

RID BE83R5AU015 (Expires on 01-16 09:05 am)

Query ID	lcl|60737	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	14		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

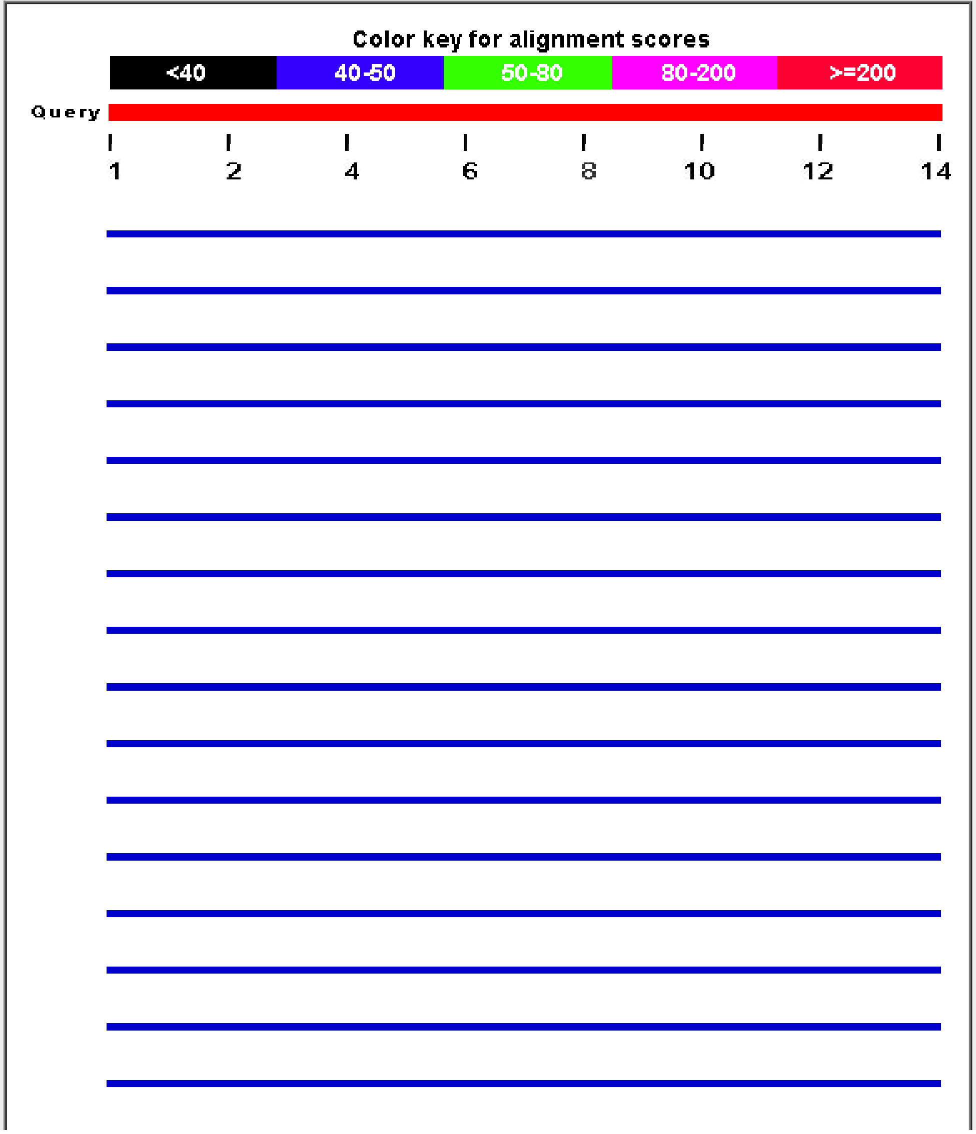
Graphic Summary

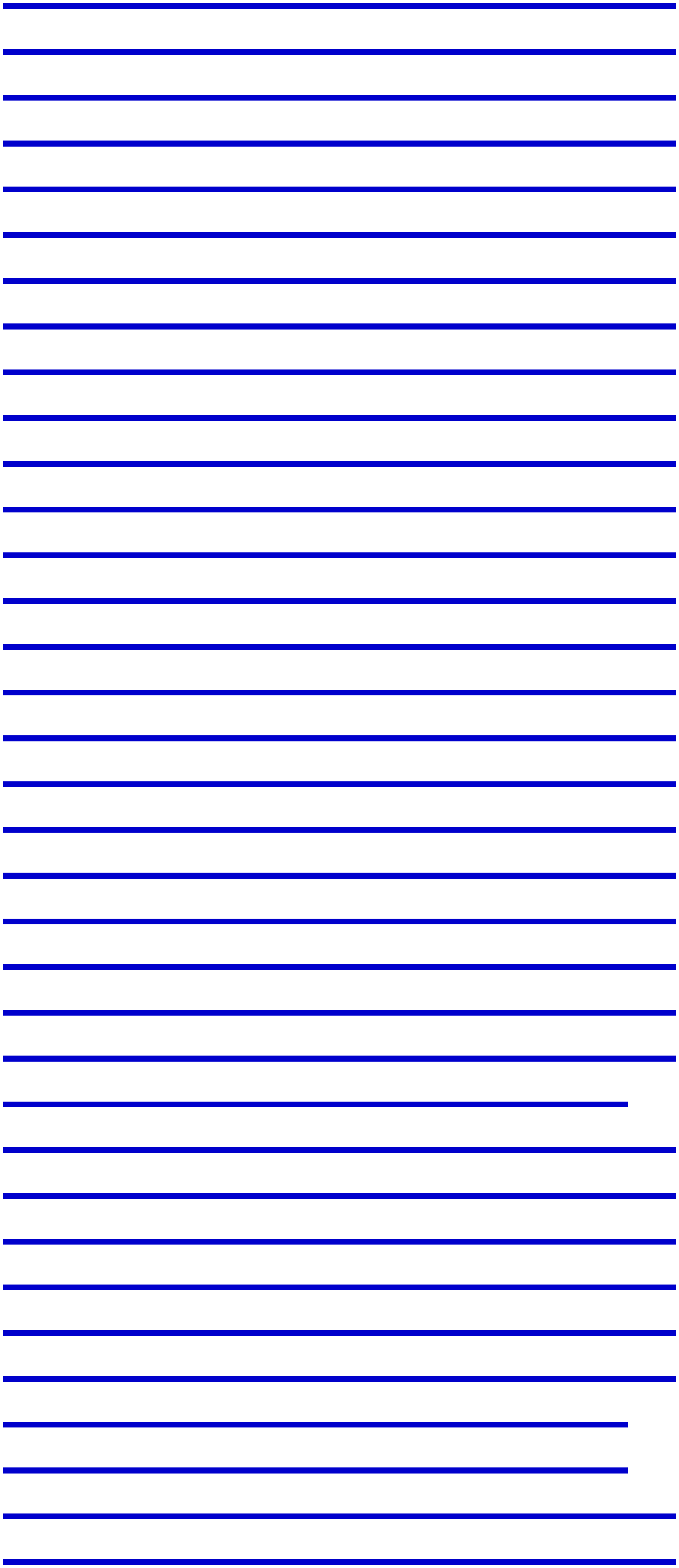
Show Conserved Domains

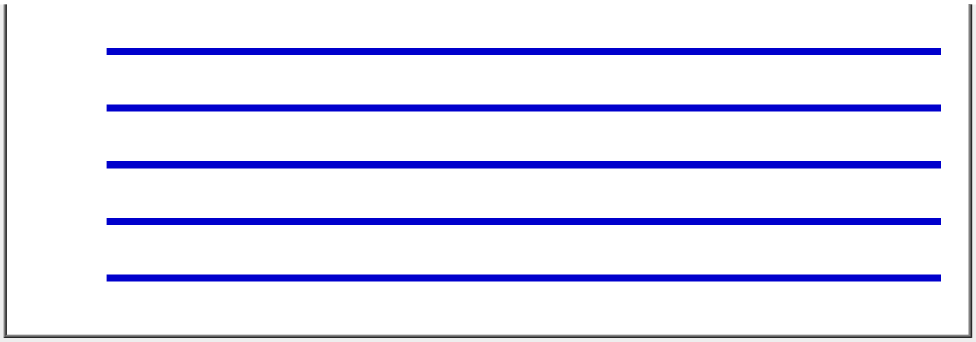
No putative conserved domains have been detected

Distribution of 105 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, L-selectin Lectin And Egf Domains [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|170292544|3CFW_A
☐	selectin L (lymphocyte adhesion molecule 1), isoform CRA_c [Hom	49.4	49.4	100%	1e-05	100%	gi|119611263|EAW90857.1
☐	PREDICTED: L-selectin isoform X2 [Macaca fascicularis]	49.4	49.4	100%	1e-05	100%	gi|544398261|XP_005539997.1
☐	unnamed protein product [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|194384912|BAG60862.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Tarsius syricht	49.4	49.4	100%	1e-05	100%	gi|640806175|XP_008059542.1
☐	Leu-8 antigen short form [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|4902830|CAB43537.1
☐	PREDICTED: L-selectin isoform X2 [Ursus maritimus]	49.4	49.4	100%	1e-05	100%	gi|670979215|XP_008694116.1
☐	lymph node homing receptor precursor [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|307134|AAC63053.1
☐	L-selectin precursor [Pan troglodytes]	49.4	49.4	100%	1e-05	100%	gi|57114019|NP_001009074.1
☐	unnamed protein product [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|34429|CAA34275.1
☐	pln homing receptor [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|38093|CAA34203.1
☐	L-selectin [Papio anubis]	49.4	49.4	100%	1e-05	100%	gi|162951976|NP_001106096.1
☐	RecName: Full=L-selectin; AltName: Full=CD62 antigen-like family	49.4	49.4	100%	1e-05	100%	gi|126178|P14151.2
☐	L-selectin precursor [Macaca mulatta]	49.4	49.4	100%	1e-05	100%	gi|112363117|NP_001036228.1
☐	RecName: Full=L-selectin; AltName: Full=CD62 antigen-like family	49.4	49.4	100%	1e-05	100%	gi|2497646|Q95235.1
☐	selectin L (lymphocyte adhesion molecule 1), isoform CRA_a [Hom	49.4	49.4	100%	1e-05	100%	gi|119611261|EAW90855.1
☐	SELL [synthetic construct]	49.4	49.4	100%	1e-05	100%	gi|649149084|AIC62025.1
☐	Lymph node homing receptor [Macaca mulatta]	49.4	49.4	100%	1e-05	100%	gi|355559023|EHH15803.1
☐	SELL protein [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|18088808|AAH20758.1
☐	PREDICTED: L-selectin isoform X1 [Ursus maritimus]	49.4	49.4	100%	1e-05	100%	gi|670979213|XP_008694111.1
☐	PREDICTED: L-selectin [Rhinopithecus roxellana]	49.4	49.4	100%	1e-05	100%	gi|724796904|XP_010359291.1
☐	PREDICTED: L-selectin [Chlorocebus sabaeus]	49.4	49.4	100%	1e-05	100%	gi|635132726|XP_007987763.1
☐	PREDICTED: L-selectin [Callithrix jacchus]	49.4	49.4	100%	1e-05	100%	gi|296229840|XP_002760427.1
☐	PREDICTED: L-selectin isoform X1 [Macaca fascicularis]	49.4	49.4	100%	1e-05	100%	gi|544398259|XP_005539996.1
☐	PREDICTED: L-selectin [Gorilla gorilla gorilla]	49.4	49.4	100%	1e-05	100%	gi|426332662|XP_004027917.1
☐	unnamed protein product [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|4902829|CAB43536.1
☐	PREDICTED: L-selectin [Pan paniscus]	49.4	49.4	100%	1e-05	100%	gi|397508469|XP_003824676.1
☐	PREDICTED: L-selectin [Pongo abelii]	49.4	49.4	100%	1e-05	100%	gi|395729434|XP_002809857.2
☐							

	PREDICTED: L-selectin [Nomascus leucogenys]	49.4	49.4	100%	1e-05	100%	gi|332219505|XP_003258894.1
☐	L-selectin precursor [Homo sapiens]	49.4	49.4	100%	1e-05	100%	gi|262206315|NP_000646.2
☐	PREDICTED: L-selectin-like [Leptonychotes weddellii]	46.9	46.9	100%	8e-05	93%	gi|585176064|XP_006739818.1
☐	hypothetical protein PANDA_007106 [Ailuropoda melanoleuca]	46.9	46.9	100%	9e-05	93%	gi|281348254|EFB23838.1
☐	PREDICTED: L-selectin isoform X2 [Canis lupus familiaris]	46.9	46.9	100%	9e-05	93%	gi|545504917|XP_005622604.1
☐	PREDICTED: L-selectin isoformX1 [Canis lupus familiaris]	46.9	46.9	100%	9e-05	93%	gi|73960664|XP_537201.2
☐	PREDICTED: L-selectin [Ceratotherium simum simum]	46.9	46.9	100%	9e-05	93%	gi|478501608|XP_004425116.1
☐	PREDICTED: L-selectin [Odobenus rosmarus divergens]	46.9	46.9	100%	9e-05	93%	gi|472379056|XP_004408944.1
☐	PREDICTED: L-selectin [Trichechus manatus latirostris]	46.9	46.9	100%	9e-05	93%	gi|471403937|XP_004384151.1
☐	PREDICTED: L-selectin [Saimiri boliviensis boliviensis]	46.9	46.9	100%	9e-05	93%	gi|403266555|XP_003925442.1
☐	PREDICTED: l-selectin-like [Ailuropoda melanoleuca]	46.9	46.9	100%	9e-05	93%	gi|301766396|XP_002918625.1
☐	L-selectin precursor [Oryctolagus cuniculus]	45.6	45.6	100%	2e-04	93%	gi|126723231|NP_001075821.1
☐	PREDICTED: L-selectin [Sarcophilus harrisii]	44.3	44.3	92%	6e-04	92%	gi|395530797|XP_003767474.1
☐	PREDICTED: L-selectin [Erinaceus europaeus]	44.3	44.3	100%	6e-04	86%	gi|617641767|XP_007531867.1
☐	PREDICTED: L-selectin [Elephantulus edwardii]	43.9	43.9	100%	9e-04	93%	gi|585664723|XP_006887476.1
☐	PREDICTED: L-selectin [Galeopterus variegatus]	43.9	43.9	100%	9e-04	93%	gi|667326711|XP_008589968.1
☐	PREDICTED: L-selectin isoform X2 [Ornithorhynchus anatinus]	43.9	43.9	100%	9e-04	93%	gi|620963547|XP_007667058.1
☐	PREDICTED: L-selectin isoform X1 [Ornithorhynchus anatinus]	43.9	43.9	100%	0.001	93%	gi|620963545|XP_007667057.1
☐	PREDICTED: L-selectin [Chrysochloris asiatica]	43.5	43.5	100%	0.001	86%	gi|586484387|XP_006872694.1
☐	PREDICTED: L-selectin [Ictidomys tridecemlineatus]	43.1	43.1	92%	0.002	92%	gi|532068085|XP_005319885.1
☐	LECAM-1 [Sigmodon hispidus]	43.1	43.1	92%	0.002	92%	gi|27372091|AAN87893.1
☐	PREDICTED: L-selectin [Ochotona princeps]	43.1	43.1	100%	0.002	86%	gi|504154850|XP_004589372.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Mustela putoriu	42.6	42.6	100%	0.002	86%	gi|511872755|XP_004756722.1
☐	PREDICTED: L-selectin [Panthera tigris altaica]	42.6	42.6	100%	0.002	86%	gi|591300224|XP_007077079.1
☐	L-selectin [Felis catus]	42.6	42.6	100%	0.002	86%	gi|148234680|NP_001082779.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Mustela putoriu	42.6	42.6	100%	0.002	86%	gi|511962048|XP_004799211.1
☐	PREDICTED: L-selectin isoform X2 [Balaenoptera acutorostrata sca	41.4	41.4	100%	0.006	86%	gi|594638526|XP_007172554.1
☐	PREDICTED: L-selectin [Lipotes vexillifer]	41.4	41.4	100%	0.006	86%	gi|602692142|XP_007458185.1
☐	PREDICTED: L-selectin isoform X1 [Balaenoptera acutorostrata sca	41.4	41.4	100%	0.006	86%	gi|594638524|XP_007172553.1
☐	PREDICTED: L-selectin [Physeter catodon]	41.4	41.4	100%	0.006	86%	gi|593711089|XP_007102109.1
☐	PREDICTED: L-selectin [Orcinus orca]	41.4	41.4	100%	0.006	86%	gi|466008816|XP_004269787.1
☐	PREDICTED: L-selectin isoform X2 [Monodelphis domestica]	41.4	41.4	92%	0.006	92%	gi|611987525|XP_007480808.1
☐	PREDICTED: L-selectin isoform X1 [Monodelphis domestica]	41.4	41.4	92%	0.006	92%	gi|611987523|XP_007480807.1
☐	PREDICTED: L-selectin [Camelus dromedarius]	40.9	40.9	100%	0.009	79%	gi|744577738|XP_010982785.1
☐	PREDICTED: L-selectin [Camelus bactrianus]	40.9	40.9	100%	0.009	79%	gi|743716948|XP_010952144.1
☐	PREDICTED: L-selectin [Myotis brandtii]	40.9	40.9	100%	0.009	79%	gi|554533070|XP_005861291.1
☐	PREDICTED: L-selectin [Echinops telfairi]	40.9	40.9	100%	0.009	79%	gi|507663676|XP_004706892.1
☐	PREDICTED: L-selectin isoform X2 [Vicugna pacos]	40.9	40.9	100%	0.009	79%	gi|560977773|XP_006211162.1
☐	PREDICTED: L-selectin isoform X1 [Vicugna pacos]	40.9	40.9	100%	0.009	79%	gi|560977771|XP_006211161.1
☐	PREDICTED: L-selectin [Myotis davidii]	40.9	40.9	100%	0.009	79%	gi|584089194|XP_006764234.1
☐	PREDICTED: L-selectin [Camelus ferus]	40.9	40.9	100%	0.009	79%	gi|560893596|XP_006173301.1
☐	L-selectin [Myotis davidii]	40.9	40.9	100%	0.009	79%	gi|432102050|ELK29869.1
☐	PREDICTED: L-selectin [Myotis lucifugus]	40.9	40.9	100%	0.009	79%	gi|558173845|XP_006099687.1
☐	PREDICTED: E-selectin [Eptesicus fuscus]	40.9	63.2	100%	0.009	79%	gi|641723183|XP_008151404.1
☐	E-selectin [Myotis brandtii]	40.9	63.2	100%	0.009	79%	gi|521022803|EPQ04591.1

☐	hypothetical protein CB1_000094012 [Camelus ferus]	40.9	96.9	100%	0.009	79%	gi|528769900|EPY89559.1
☐	PREDICTED: L-selectin [Loxodonta africana]	40.5	40.5	100%	0.012	86%	gi|731497014|XP_010593279.1
☐	PREDICTED: E-selectin [Poecilia formosa]	40.5	40.5	100%	0.013	79%	gi|617421905|XP_007558781.1
☐	PREDICTED: L-selectin isoform X2 [Bison bison bison]	40.1	40.1	100%	0.016	79%	gi|742104371|XP_010835001.1
☐	PREDICTED: L-selectin isoform X3 [Capra hircus]	40.1	40.1	100%	0.016	79%	gi|548498158|XP_005690682.1
☐	PREDICTED: L-selectin isoform X4 [Bubalus bubalis]	40.1	40.1	100%	0.017	79%	gi|594100108|XP_006073161.1
☐	PREDICTED: L-selectin isoform X2 [Capra hircus]	40.1	40.1	100%	0.017	79%	gi|548498156|XP_005690681.1
☐	L-selectin [Bos mutus]	40.1	40.1	100%	0.017	79%	gi|440900418|ELR51562.1
☐	PREDICTED: L-selectin isoform X3 [Bubalus bubalis]	40.1	40.1	100%	0.017	79%	gi|594100106|XP_006073160.1
☐	L-selectin precursor [Bos taurus]	40.1	40.1	100%	0.017	79%	gi|27901801|NP_776607.1
☐	TPA: L-selectin [Bos taurus]	40.1	40.1	100%	0.017	79%	gi|296479225|DAA21340.1
☐	PREDICTED: L-selectin isoform X1 [Capra hircus]	40.1	40.1	100%	0.017	79%	gi|548498154|XP_005690680.1
☐	PREDICTED: L-selectin [Ovis aries]	40.1	40.1	100%	0.017	79%	gi|426239637|XP_004013726.1
☐	L-selectin precursor [Sus scrofa]	40.1	40.1	100%	0.017	79%	gi|162952046|NP_001106148.1
☐	PREDICTED: L-selectin isoform X1 [Bison bison bison]	40.1	40.1	100%	0.017	79%	gi|742104367|XP_010835000.1
☐	PREDICTED: L-selectin [Pantholops hodgsonii]	40.1	40.1	100%	0.017	79%	gi|556756215|XP_005973458.1
☐	PREDICTED: L-selectin [Bos mutus]	40.1	40.1	100%	0.017	79%	gi|555981044|XP_005902444.1
☐	PREDICTED: L-selectin isoform X1 [Bos taurus]	40.1	40.1	100%	0.017	79%	gi|528979726|XP_005216937.1
☐	PREDICTED: L-selectin [Orycteropus afer afer]	40.1	40.1	100%	0.017	79%	gi|634839634|XP_007935972.1
☐	PREDICTED: L-selectin isoform X2 [Bubalus bubalis]	40.1	40.1	100%	0.017	79%	gi|594100104|XP_006073159.1
☐	PREDICTED: L-selectin isoform X1 [Bubalus bubalis]	40.1	40.1	100%	0.017	79%	gi|594100102|XP_006073158.1
☐	PREDICTED: L-selectin isoform X2 [Cricetulus griseus]	39.7	39.7	100%	0.023	86%	gi|625273173|XP_007628167.1
☐	PREDICTED: L-selectin isoform X1 [Cricetulus griseus]	39.7	39.7	100%	0.023	86%	gi|625212795|XP_007647090.1
☐	E-selectin [Odocoileus hemionus]	39.7	39.7	100%	0.024	79%	gi|13898376|AAK48710.1
☐	P-selectin-like protein [Cricetulus griseus]	39.7	73.0	100%	0.025	86%	gi|537153471|ERE72501.1
☐	unnamed protein product [Tetraodon nigroviridis]	39.2	39.2	92%	0.028	85%	gi|47179328|CAG13395.1
☐	PREDICTED: L-selectin [Microtus ochrogaster]	39.2	39.2	92%	0.032	85%	gi|532042485|XP_005364074.1

⊟ Alignments

Download ⌄ GenPept Graphics ▼ Next ▲ Previous ▲ Descriptions

Chain A, L-selectin Lectin And Egf Domains

Sequence ID: gi|170292544|pdb|3CFW|A **Length:** 164 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 55 to 68 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KIGGIWTWVGTNKS  14
            KIGGIWTWVGTNKS
Sbjct  55   KIGGIWTWVGTNKS  68
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous ▲ Descriptions

selectin L (lymphocyte adhesion molecule 1), isoform CRA_c [Homo sapiens]

Sequence ID: gi|119611263|gb|EAW90857.1| **Length:** 320 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 106 to 119 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KIGGIWTWVGTNKS  14
```

```
                KIGGIWTWVGTNKS
Sbjct  106  KIGGIWTWVGTNKS  119
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: L-selectin isoform X2 [Macaca fascicularis]

Sequence ID: gi|544398261|ref|XP_005539997.1| **Length:** 323 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 106 to 119 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KIGGIWTWVGTNKS  14
            KIGGIWTWVGTNKS
Sbjct  106  KIGGIWTWVGTNKS  119
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: gi|194384912|dbj|BAG60862.1| **Length:** 325 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 46 to 59 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1   KIGGIWTWVGTNKS  14
           KIGGIWTWVGTNKS
Sbjct  46  KIGGIWTWVGTNKS  59
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: LOW QUALITY PROTEIN: L-selectin [Tarsius syrichta]

Sequence ID: gi|640806175|ref|XP_008059542.1| **Length:** 362 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 93 to 106 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	14/14(100%)	14/14(100%)	0/14(0%)

```
Query  1    KIGGIWTWVGTNKS  14
            KIGGIWTWVGTNKS
Sbjct  93   KIGGIWTWVGTNKS  106
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVKFGK9801R

Your search parameters were adjusted to search for a short input sequence.

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SELL_RFCRDDYTDLVAIQNKA_Mod

RID BVKFGK9801R (Expires on 01-21 10:39 am)

Query ID lcl|322106
Description None
Molecule type amino acid
Query Length 17

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

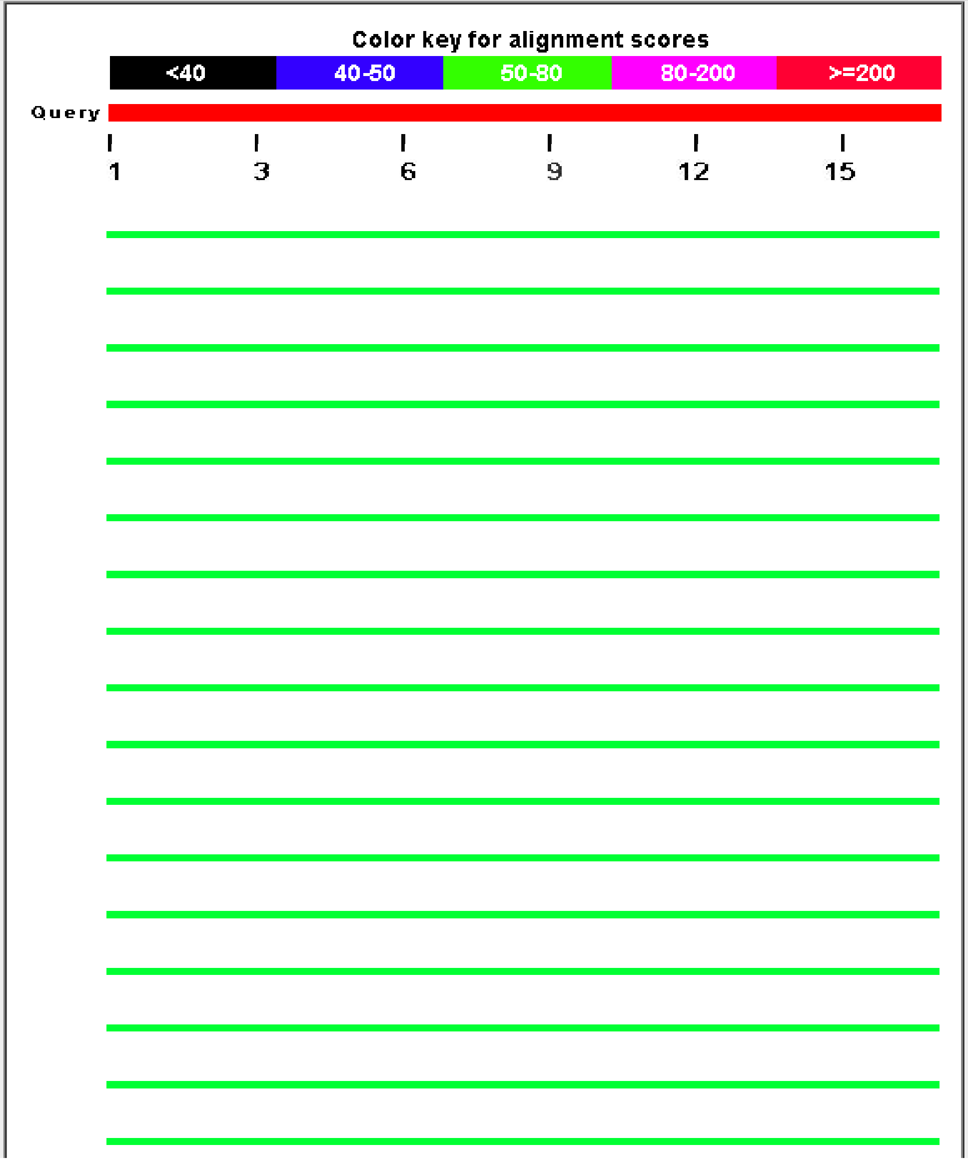
Graphic Summary

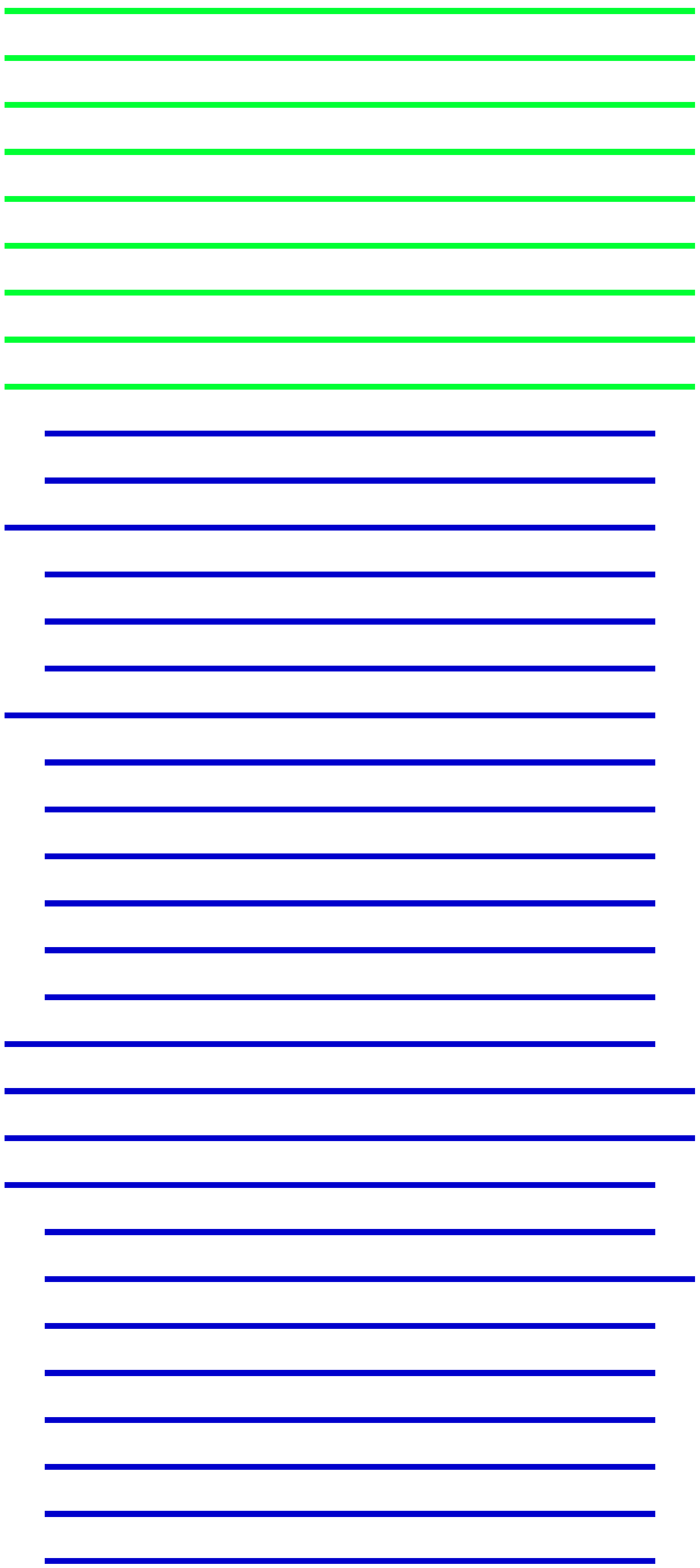
Show Conserved Domains

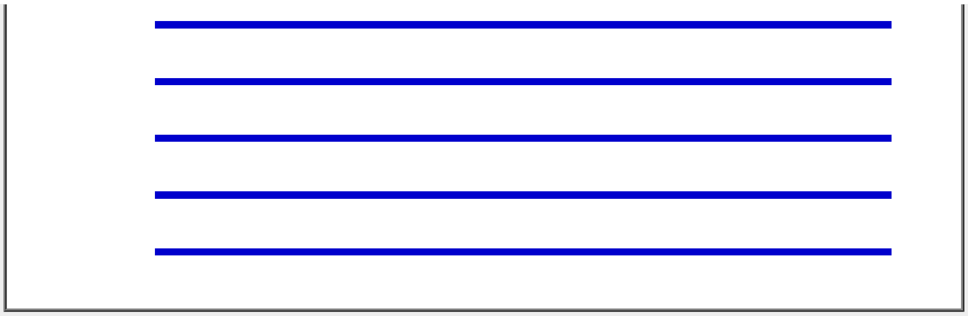
No putative conserved domains have been detected

Distribution of 107 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, L-selectin Lectin And Egf Domains [Homo sapiens]	57.1	57.1	100%	4e-08	94%	3CFW_A
☐	selectin L (lymphocyte adhesion molecule 1), isoform CRA_c [Homo sapiens]	57.1	57.1	100%	5e-08	94%	EAW90857.1
☐	unnamed protein product [Homo sapiens]	57.1	57.1	100%	5e-08	94%	BAG60862.1
☐	Leu-8 antigen short form [Homo sapiens]	57.1	57.1	100%	5e-08	94%	CAB43537.1
☐	lymph node homing receptor precursor [Homo sapiens]	57.1	57.1	100%	5e-08	94%	AAC63053.1
☐	L-selectin precursor [Pan troglodytes]	57.1	57.1	100%	5e-08	94%	NP_001009074.1
☐	unnamed protein product [Homo sapiens]	57.1	57.1	100%	5e-08	94%	CAA34275.1
☐	pln homing receptor [Homo sapiens]	57.1	57.1	100%	5e-08	94%	CAA34203.1
☐	RecName: Full=L-selectin; AltName: Full=CD62 antigen-like family member L;	57.1	57.1	100%	5e-08	94%	P14151.2
☐	selectin L (lymphocyte adhesion molecule 1), isoform CRA_a [Homo sapiens]	57.1	57.1	100%	5e-08	94%	EAW90855.1
☐	SELL [synthetic construct]	57.1	57.1	100%	5e-08	94%	AIC62025.1
☐	SELL protein [Homo sapiens]	57.1	57.1	100%	5e-08	94%	AAH20758.1
☐	PREDICTED: L-selectin [Gorilla gorilla gorilla]	57.1	57.1	100%	5e-08	94%	XP_004027917.1
☐	unnamed protein product [Homo sapiens]	57.1	57.1	100%	5e-08	94%	CAB43536.1
☐	PREDICTED: L-selectin [Pan paniscus]	57.1	57.1	100%	5e-08	94%	XP_003824676.1
☐	L-selectin precursor [Homo sapiens]	57.1	57.1	100%	5e-08	94%	NP_000646.2
☐	PREDICTED: L-selectin isoform X2 [Macaca fascicularis]	54.5	54.5	100%	3e-07	88%	XP_005539997.1
☐	L-selectin [Papio anubis]	54.5	54.5	100%	3e-07	88%	NP_001106096.1
☐	L-selectin precursor [Macaca mulatta]	54.5	54.5	100%	3e-07	88%	NP_001036228.1
☐	RecName: Full=L-selectin; AltName: Full=CD62 antigen-like family member L;	54.5	54.5	100%	3e-07	88%	Q95235.1
☐	Lymph node homing receptor [Macaca mulatta]	54.5	54.5	100%	4e-07	88%	EHH15803.1
☐	PREDICTED: L-selectin [Rhinopithecus roxellana]	54.5	54.5	100%	4e-07	88%	XP_010359291.1
☐	PREDICTED: L-selectin [Chlorocebus sabaeus]	54.5	54.5	100%	4e-07	88%	XP_007987763.1
☐	PREDICTED: L-selectin isoform X1 [Macaca fascicularis]	54.5	54.5	100%	4e-07	88%	XP_005539996.1
☐	PREDICTED: L-selectin [Pongo abelii]	54.5	54.5	100%	4e-07	88%	XP_002809857.2
☐	PREDICTED: L-selectin [Nomascus leucogenys]	54.5	54.5	100%	4e-07	88%	XP_003258894.1
☐	PREDICTED: L-selectin-like [Peromyscus maniculatus bairdii]	48.6	48.6	88%	3e-05	87%	XP_006974839.1
☐	PREDICTED: L-selectin isoform X2 [Bison bison bison]	48.6	48.6	88%	3e-05	87%	XP_010835001.1
☐	PREDICTED: L-selectin isoform X2 [Canis lupus familiaris]	48.6	48.6	94%	4e-05	81%	XP_005622604.1

☐	L-selectin [Bos mutus]	48.6	48.6	88%	4e-05	87%	ELR51562.1
☐	L-selectin precursor [Bos taurus]	48.6	48.6	88%	4e-05	87%	NP_776607.1
☐	TPA: L-selectin [Bos taurus]	48.6	48.6	88%	4e-05	87%	DAA21340.1
☐	PREDICTED: L-selectin isoformX1 [Canis lupus familiaris]	48.6	48.6	94%	4e-05	81%	XP_537201.2
☐	PREDICTED: L-selectin-like isoform X2 [Peromyscus maniculatus bairdii]	48.6	48.6	88%	4e-05	87%	XP_006974823.1
☐	PREDICTED: L-selectin isoform X1 [Bison bison bison]	48.6	48.6	88%	4e-05	87%	XP_010835000.1
☐	PREDICTED: L-selectin [Bos mutus]	48.6	48.6	88%	4e-05	87%	XP_005902444.1
☐	PREDICTED: L-selectin isoform X1 [Bos taurus]	48.6	48.6	88%	4e-05	87%	XP_005216937.1
☐	L-selectin precursor [Oryctolagus cuniculus]	48.6	48.6	88%	4e-05	87%	NP_001075821.1
☐	PREDICTED: L-selectin-like isoform X1 [Peromyscus maniculatus bairdii]	48.6	48.6	88%	4e-05	87%	XP_006974822.1
☐	PREDICTED: L-selectin [Galeopterus variegatus]	47.7	47.7	94%	7e-05	81%	XP_008589968.1
☐	PREDICTED: L-selectin [Callithrix jacchus]	47.7	47.7	100%	7e-05	82%	XP_002760427.1
☐	PREDICTED: L-selectin [Saimiri boliviensis boliviensis]	47.7	47.7	100%	7e-05	82%	XP_003925442.1
☐	PREDICTED: L-selectin-like [Leptonychotes weddellii]	47.3	47.3	94%	8e-05	81%	XP_006739818.1
☐	PREDICTED: L-selectin isoform X2 [Ursus maritimus]	46.9	46.9	88%	1e-04	87%	XP_008694116.1
☐	PREDICTED: L-selectin [Ceratotherium simum simum]	46.9	46.9	94%	1e-04	81%	XP_004425116.1
☐	PREDICTED: L-selectin isoform X1 [Ursus maritimus]	46.9	46.9	88%	1e-04	87%	XP_008694111.1
☐	PREDICTED: L-selectin [Panthera tigris altaica]	46.9	46.9	88%	1e-04	87%	XP_007077079.1
☐	PREDICTED: L-selectin isoform X4 [Bubalus bubalis]	46.4	46.4	88%	2e-04	87%	XP_006073161.1
☐	PREDICTED: L-selectin isoform X3 [Bubalus bubalis]	46.4	46.4	88%	2e-04	87%	XP_006073160.1
☐	PREDICTED: L-selectin isoform X2 [Bubalus bubalis]	46.4	46.4	88%	2e-04	87%	XP_006073159.1
☐	PREDICTED: L-selectin isoform X1 [Bubalus bubalis]	46.4	46.4	88%	2e-04	87%	XP_006073158.1
☐	PREDICTED: L-selectin isoform X2 [Balaenoptera acutorostrata scammoni]	46.0	46.0	88%	2e-04	87%	XP_007172554.1
☐	PREDICTED: L-selectin [Camelus dromedarius]	46.0	46.0	88%	2e-04	87%	XP_010982785.1
☐	PREDICTED: L-selectin [Camelus bactrianus]	46.0	46.0	88%	2e-04	87%	XP_010952144.1
☐	PREDICTED: L-selectin isoform X2 [Vicugna pacos]	46.0	46.0	88%	2e-04	87%	XP_006211162.1
☐	PREDICTED: L-selectin isoform X1 [Vicugna pacos]	46.0	46.0	88%	2e-04	87%	XP_006211161.1
☐	PREDICTED: L-selectin [Pteropus alecto]	46.0	46.0	94%	2e-04	81%	XP_006907882.1
☐	PREDICTED: L-selectin [Camelus ferus]	46.0	46.0	88%	3e-04	87%	XP_006173301.1
☐	PREDICTED: L-selectin [Lipotes vexillifer]	46.0	46.0	88%	3e-04	87%	XP_007458185.1
☐	PREDICTED: L-selectin isoform X1 [Balaenoptera acutorostrata scammoni]	46.0	46.0	88%	3e-04	87%	XP_007172553.1
☐	PREDICTED: L-selectin [Physeter catodon]	46.0	46.0	88%	3e-04	87%	XP_007102109.1
☐	PREDICTED: L-selectin [Tursiops truncatus]	46.0	46.0	88%	3e-04	87%	XP_004319819.1
☐	PREDICTED: L-selectin [Orcinus orca]	46.0	46.0	88%	3e-04	87%	XP_004269787.1
☐	PREDICTED: E-selectin [Eptesicus fuscus]	46.0	75.1	94%	3e-04	81%	XP_008151404.1
☐	E-selectin [Pteropus alecto]	46.0	107	94%	3e-04	81%	ELK16299.1
☐	hypothetical protein CB1_000094012 [Camelus ferus]	46.0	105	94%	3e-04	87%	EPY89559.1
☐	PREDICTED: L-selectin [Trichechus manatus latirostris]	45.6	45.6	94%	3e-04	75%	XP_004384151.1
☐	PREDICTED: L-selectin isoform X2 [Cricetulus griseus]	45.2	45.2	88%	5e-04	80%	XP_007628167.1
☐	LECAM-1 [Sigmodon hispidus]	45.2	45.2	88%	5e-04	80%	AAN87893.1
☐	PREDICTED: L-selectin isoform X1 [Cricetulus griseus]	45.2	45.2	88%	5e-04	80%	XP_007647090.1
☐	PREDICTED: L-selectin [Microtus ochrogaster]	45.2	45.2	88%	5e-04	80%	XP_005364074.1
☐	PREDICTED: L-selectin [Mesocricetus auratus]	45.2	45.2	88%	5e-04	80%	XP_005071531.1
☐	PREDICTED: L-selectin [Octodon degus]	45.2	45.2	94%	5e-04	81%	XP_004648568.1
☐	P-selectin-like protein [Cricetulus griseus]	45.2	81.0	88%	5e-04	80%	ERE72501.1

☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Mustela putorius furo]	44.8	44.8	94%	7e-04	75%	XP_004756722.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Mustela putorius furo]	44.8	44.8	94%	7e-04	75%	XP_004799211.1
☐	PREDICTED: L-selectin isoform X3 [Fukomys damarensis]	44.3	44.3	88%	0.001	80%	XP_010632293.1
☐	PREDICTED: L-selectin [Elephantulus edwardii]	44.3	44.3	88%	0.001	80%	XP_006887476.1
☐	hypothetical protein PANDA_007106 [Ailuropoda melanoleuca]	44.3	44.3	88%	0.001	80%	EFB23838.1
☐	PREDICTED: L-selectin isoform X2 [Fukomys damarensis]	44.3	44.3	88%	0.001	80%	XP_010632292.1
☐	PREDICTED: L-selectin isoform 4 [Dasypus novemcinctus]	44.3	44.3	88%	0.001	80%	XP_004464223.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Tarsius syrichta]	44.3	44.3	88%	0.001	80%	XP_008059542.1
☐	PREDICTED: L-selectin isoform 5 [Dasypus novemcinctus]	44.3	44.3	88%	0.001	80%	XP_004464224.1
☐	PREDICTED: L-selectin isoform 3 [Dasypus novemcinctus]	44.3	44.3	88%	0.001	80%	XP_004464222.1
☐	PREDICTED: L-selectin [Nannospalax galili]	44.3	44.3	88%	0.001	80%	XP_008823120.1
☐	PREDICTED: L-selectin isoform X1 [Fukomys damarensis]	44.3	44.3	88%	0.001	80%	XP_010632291.1
☐	PREDICTED: L-selectin isoform 2 [Dasypus novemcinctus]	44.3	44.3	88%	0.001	80%	XP_004464221.1
☐	L-selectin precursor [Sus scrofa]	44.3	44.3	88%	0.001	80%	NP_001106148.1
☐	L-selectin [Felis catus]	44.3	44.3	88%	0.001	80%	NP_001082779.1
☐	PREDICTED: L-selectin isoform 1 [Dasypus novemcinctus]	44.3	44.3	88%	0.001	80%	XP_004464220.1
☐	PREDICTED: L-selectin [Jaculus jaculus]	44.3	44.3	88%	0.001	80%	XP_004658951.1
☐	PREDICTED: l-selectin-like [Ailuropoda melanoleuca]	44.3	44.3	88%	0.001	80%	XP_002918625.1
☐	PREDICTED: L-selectin [Ochotona princeps]	44.3	44.3	88%	0.001	80%	XP_004589372.1
☐	PREDICTED: L-selectin isoform X3 [Equus przewalskii]	44.3	44.3	88%	0.001	80%	XP_008523771.1
☐	PREDICTED: L-selectin isoform X3 [Equus caballus]	44.3	44.3	88%	0.001	80%	XP_005609701.1
☐	PREDICTED: L-selectin isoform X2 [Equus przewalskii]	44.3	44.3	88%	0.001	80%	XP_008523770.1
☐	PREDICTED: L-selectin isoform X2 [Equus caballus]	44.3	44.3	88%	0.001	80%	XP_005609700.1
☐	PREDICTED: L-selectin isoform X1 [Equus przewalskii]	44.3	44.3	88%	0.001	80%	XP_008523769.1
☐	PREDICTED: L-selectin isoform X1 [Equus caballus]	44.3	44.3	88%	0.001	80%	XP_005609699.1
☐	E-selectin [Fukomys damarensis]	44.3	76.4	88%	0.001	80%	KFO29135.1

⊖ Alignments

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Chain A, L-selectin Lectin And Egf Domains

Sequence ID: pdb|3CFW|A **Length:** 164 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 17 to 33 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.1 bits(127)	4e-08	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   RFCRDDYTDLVAIQNKA  17
           RFCRD+YTDLVAIQNKA
Sbjct  17  RFCRDNYTDLVAIQNKA  33
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

selectin L (lymphocyte adhesion molecule 1), isoform CRA_c [Homo sapiens]

Sequence ID: gb|EAW90857.1| **Length:** 320 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 68 to 84 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.1 bits(127)	5e-08	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   RFCRDDYTDLVAIQNKA  17
           RFCRD+YTDLVAIQNKA
Sbjct  68  RFCRDNYTDLVAIQNKA  84
```

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unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG60862.1| **Length:** 325 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 24 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.1 bits(127)	5e-08	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   RFCRDDYTDLVAIQNKA  17
           RFCRD+YTDLVAIQNKA
Sbjct  8   RFCRDNYTDLVAIQNKA  24
```

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Leu-8 antigen short form [Homo sapiens]

Sequence ID: emb|CAB43537.1| **Length:** 363 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 68 to 84 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.1 bits(127)	5e-08	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   RFCRDDYTDLVAIQNKA  17
           RFCRD+YTDLVAIQNKA
Sbjct  68  RFCRDNYTDLVAIQNKA  84
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

lymph node homing receptor precursor [Homo sapiens]

Sequence ID: gb|AAC63053.1| **Length:** 372 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 55 to 71 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
57.1 bits(127)	5e-08	16/17(94%)	17/17(100%)	0/17(0%)

```
Query  1   RFCRDDYTDLVAIQNKA  17
           RFCRD+YTDLVAIQNKA
Sbjct  55  RFCRDNYTDLVAIQNKA  71
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - BE841U92014

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download

How to read this page | Blast report description

SELL_RFCRDNYTDLVAIQNKA_NonMod

RID BE841U92014 (Expires on 01-16 09:05 am)

Query ID lcl|77738
Description None
Molecule type amino acid
Query Length 17

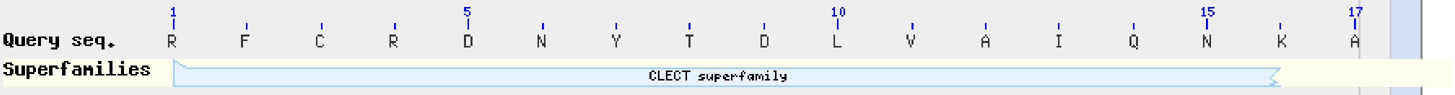
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

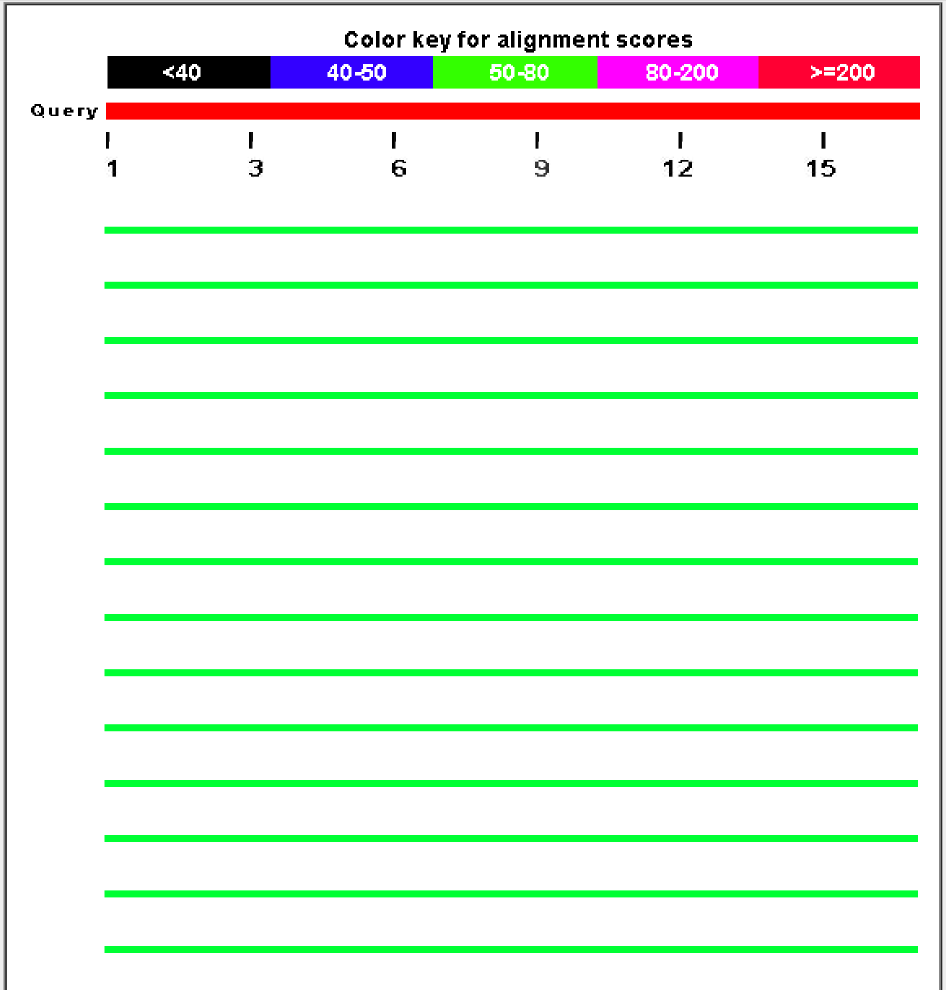
Show Conserved Domains

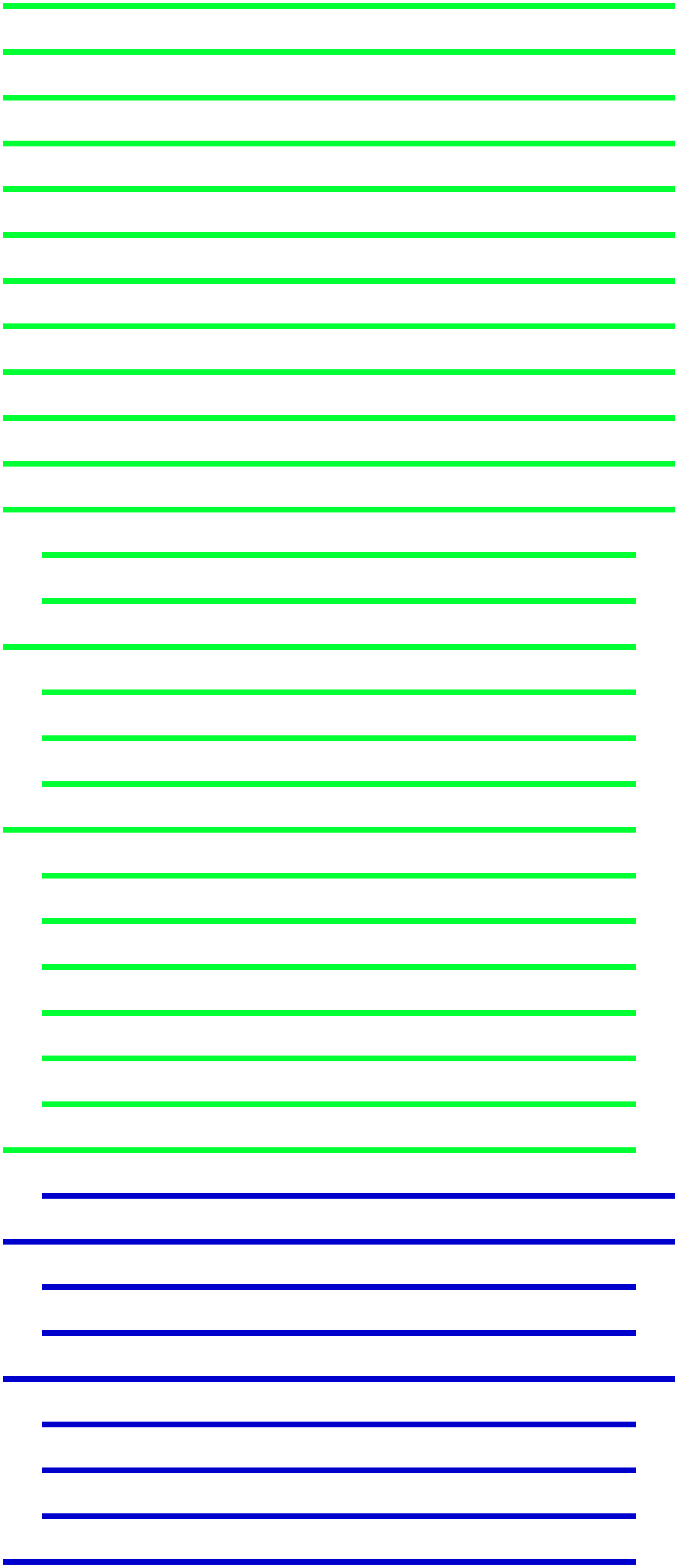
Putative conserved domains have been detected, click on the image below for detailed results.

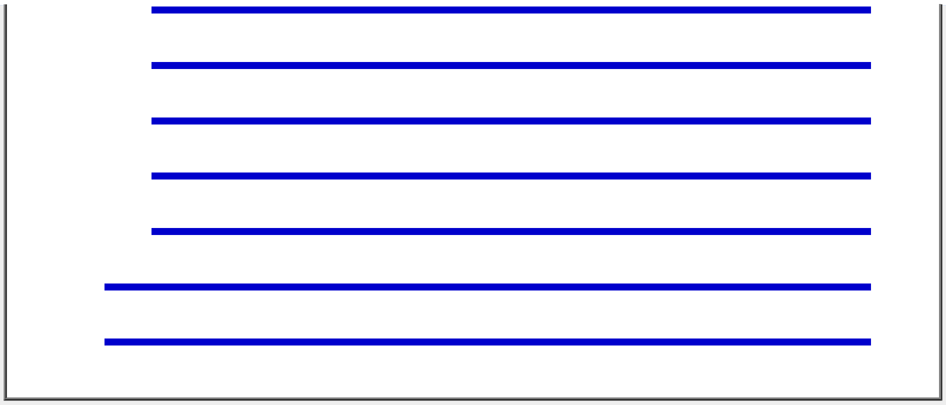


Distribution of 106 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, L-selectin Lectin And Egf Domains [Homo sapiens]	59.6	59.6	100%	5e-09	100%	gi|170292544|3CFW_A
☐	selectin L (lymphocyte adhesion molecule 1), isoform CRA_c [Hom	59.6	59.6	100%	6e-09	100%	gi|119611263|EAW90857.1
☐	unnamed protein product [Homo sapiens]	59.6	59.6	100%	6e-09	100%	gi|194384912|BAG60862.1
☐	Leu-8 antigen short form [Homo sapiens]	59.6	59.6	100%	6e-09	100%	gi|4902830|CAB43537.1
☐	lymph node homing receptor precursor [Homo sapiens]	59.6	59.6	100%	6e-09	100%	gi|307134|AAC63053.1
☐	L-selectin precursor [Pan troglodytes]	59.6	59.6	100%	6e-09	100%	gi|57114019|NP_001009074.1
☐	unnamed protein product [Homo sapiens]	59.6	59.6	100%	6e-09	100%	gi|34429|CAA34275.1
☐	pln homing receptor [Homo sapiens]	59.6	59.6	100%	6e-09	100%	gi|38093|CAA34203.1
☐	RecName: Full=L-selectin; AltName: Full=CD62 antigen-like family	59.6	59.6	100%	6e-09	100%	gi|126178|P14151.2
☐	selectin L (lymphocyte adhesion molecule 1), isoform CRA_a [Hom	59.6	59.6	100%	6e-09	100%	gi|119611261|EAW90855.1
☐	SELL [synthetic construct]	59.6	59.6	100%	6e-09	100%	gi|649149084|AIC62025.1
☐	SELL protein [Homo sapiens]	59.6	59.6	100%	6e-09	100%	gi|18088808|AAH20758.1
☐	PREDICTED: L-selectin [Gorilla gorilla gorilla]	59.6	59.6	100%	6e-09	100%	gi|426332662|XP_004027917.1
☐	unnamed protein product [Homo sapiens]	59.6	59.6	100%	6e-09	100%	gi|4902829|CAB43536.1
☐	PREDICTED: L-selectin [Pan paniscus]	59.6	59.6	100%	6e-09	100%	gi|397508469|XP_003824676.1
☐	L-selectin precursor [Homo sapiens]	59.6	59.6	100%	6e-09	100%	gi|262206315|NP_000646.2
☐	PREDICTED: L-selectin isoform X2 [Macaca fascicularis]	57.1	57.1	100%	5e-08	94%	gi|544398261|XP_005539997.1
☐	L-selectin [Papio anubis]	57.1	57.1	100%	5e-08	94%	gi|162951976|NP_001106096.1
☐	L-selectin precursor [Macaca mulatta]	57.1	57.1	100%	5e-08	94%	gi|112363117|NP_001036228.1
☐	RecName: Full=L-selectin; AltName: Full=CD62 antigen-like family	57.1	57.1	100%	5e-08	94%	gi|2497646|Q95235.1
☐	Lymph node homing receptor [Macaca mulatta]	57.1	57.1	100%	5e-08	94%	gi|355559023|EHH15803.1
☐	PREDICTED: L-selectin [Rhinopithecus roxellana]	57.1	57.1	100%	5e-08	94%	gi|724796904|XP_010359291.1
☐	PREDICTED: L-selectin [Chlorocebus sabaeus]	57.1	57.1	100%	5e-08	94%	gi|635132726|XP_007987763.1
☐	PREDICTED: L-selectin isoform X1 [Macaca fascicularis]	57.1	57.1	100%	5e-08	94%	gi|544398259|XP_005539996.1
☐	PREDICTED: L-selectin [Pongo abelii]	57.1	57.1	100%	5e-08	94%	gi|395729434|XP_002809857.2
☐	PREDICTED: L-selectin [Nomascus leucogenys]	57.1	57.1	100%	5e-08	94%	gi|332219505|XP_003258894.1
☐	PREDICTED: L-selectin-like [Peromyscus maniculatus bairdii]	51.1	51.1	88%	4e-06	93%	gi|589923917|XP_006974839.1
☐	PREDICTED: L-selectin isoform X2 [Bison bison bison]	51.1	51.1	88%	5e-06	93%	gi|742104371|XP_010835001.1

☐	PREDICTED: L-selectin isoform X2 [Canis lupus familiaris]	51.1	51.1	94%	5e-06	88%	gi|545504917|XP_005622604.1
☐	L-selectin [Bos mutus]	51.1	51.1	88%	5e-06	93%	gi|440900418|ELR51562.1
☐	L-selectin precursor [Bos taurus]	51.1	51.1	88%	5e-06	93%	gi|27901801|NP_776607.1
☐	TPA: L-selectin [Bos taurus]	51.1	51.1	88%	5e-06	93%	gi|296479225|DAA21340.1
☐	PREDICTED: L-selectin isoformX1 [Canis lupus familiaris]	51.1	51.1	94%	5e-06	88%	gi|73960664|XP_537201.2
☐	PREDICTED: L-selectin-like isoform X2 [Peromyscus maniculatus b	51.1	51.1	88%	5e-06	93%	gi|589923885|XP_006974823.1
☐	PREDICTED: L-selectin isoform X1 [Bison bison bison]	51.1	51.1	88%	5e-06	93%	gi|742104367|XP_010835000.1
☐	PREDICTED: L-selectin [Bos mutus]	51.1	51.1	88%	5e-06	93%	gi|555981044|XP_005902444.1
☐	PREDICTED: L-selectin isoform X1 [Bos taurus]	51.1	51.1	88%	5e-06	93%	gi|528979726|XP_005216937.1
☐	L-selectin precursor [Oryctolagus cuniculus]	51.1	51.1	88%	5e-06	93%	gi|126723231|NP_001075821.1
☐	PREDICTED: L-selectin-like isoform X1 [Peromyscus maniculatus b	51.1	51.1	88%	5e-06	93%	gi|589923883|XP_006974822.1
☐	PREDICTED: L-selectin [Galeopterus variegatus]	50.3	50.3	94%	9e-06	88%	gi|667326711|XP_008589968.1
☐	PREDICTED: L-selectin [Ceratotherium simum simum]	49.4	49.4	94%	2e-05	88%	gi|478501608|XP_004425116.1
☐	PREDICTED: L-selectin [Callithrix jacchus]	49.4	49.4	100%	2e-05	82%	gi|296229840|XP_002760427.1
☐	PREDICTED: L-selectin isoform X4 [Bubalus bubalis]	49.0	49.0	88%	2e-05	93%	gi|594100108|XP_006073161.1
☐	PREDICTED: L-selectin isoform X3 [Bubalus bubalis]	49.0	49.0	88%	3e-05	93%	gi|594100106|XP_006073160.1
☐	PREDICTED: L-selectin [Saimiri boliviensis boliviensis]	49.0	49.0	100%	3e-05	82%	gi|403266555|XP_003925442.1
☐	PREDICTED: L-selectin isoform X2 [Bubalus bubalis]	49.0	49.0	88%	3e-05	93%	gi|594100104|XP_006073159.1
☐	PREDICTED: L-selectin isoform X1 [Bubalus bubalis]	49.0	49.0	88%	3e-05	93%	gi|594100102|XP_006073158.1
☐	PREDICTED: L-selectin isoform X2 [Balaenoptera acutorostrata sca	48.6	48.6	88%	3e-05	93%	gi|594638526|XP_007172554.1
☐	PREDICTED: L-selectin [Pteropus alecto]	48.6	48.6	94%	4e-05	88%	gi|586545543|XP_006907882.1
☐	PREDICTED: L-selectin [Lipotes vexillifer]	48.6	48.6	88%	4e-05	93%	gi|602692142|XP_007458185.1
☐	PREDICTED: L-selectin isoform X1 [Balaenoptera acutorostrata sca	48.6	48.6	88%	4e-05	93%	gi|594638524|XP_007172553.1
☐	PREDICTED: L-selectin [Physeter catodon]	48.6	48.6	88%	4e-05	93%	gi|593711089|XP_007102109.1
☐	PREDICTED: L-selectin [Tursiops truncatus]	48.6	48.6	88%	4e-05	93%	gi|470624768|XP_004319819.1
☐	PREDICTED: L-selectin [Orcinus orca]	48.6	48.6	88%	4e-05	93%	gi|466008816|XP_004269787.1
☐	PREDICTED: E-selectin [Eptesicus fuscus]	48.6	79.3	94%	4e-05	88%	gi|641723183|XP_008151404.1
☐	E-selectin [Pteropus alecto]	48.6	114	94%	4e-05	88%	gi|431916045|ELK16299.1
☐	PREDICTED: L-selectin [Trichechus manatus latirostris]	48.1	48.1	94%	5e-05	81%	gi|471403937|XP_004384151.1
☐	PREDICTED: L-selectin [Camelus dromedarius]	47.7	47.7	88%	7e-05	87%	gi|744577738|XP_010982785.1
☐	PREDICTED: L-selectin [Camelus bactrianus]	47.7	47.7	88%	7e-05	87%	gi|743716948|XP_010952144.1
☐	PREDICTED: L-selectin isoform X2 [Vicugna pacos]	47.7	47.7	88%	7e-05	87%	gi|560977773|XP_006211162.1
☐	PREDICTED: L-selectin isoform X1 [Vicugna pacos]	47.7	47.7	88%	7e-05	87%	gi|560977771|XP_006211161.1
☐	PREDICTED: L-selectin [Camelus ferus]	47.7	47.7	88%	7e-05	87%	gi|560893596|XP_006173301.1
☐	PREDICTED: L-selectin isoform X2 [Cricetulus griseus]	47.7	47.7	88%	7e-05	87%	gi|625273173|XP_007628167.1
☐	LECAM-1 [Sigmodon hispidus]	47.7	47.7	88%	7e-05	87%	gi|27372091|AAN87893.1
☐	PREDICTED: L-selectin isoform X1 [Cricetulus griseus]	47.7	47.7	88%	7e-05	87%	gi|625212795|XP_007647090.1
☐	PREDICTED: L-selectin [Microtus ochrogaster]	47.7	47.7	88%	7e-05	87%	gi|532042485|XP_005364074.1
☐	PREDICTED: L-selectin [Mesocricetus auratus]	47.7	47.7	88%	7e-05	87%	gi|524937978|XP_005071531.1
☐	PREDICTED: L-selectin [Octodon degus]	47.7	47.7	94%	7e-05	88%	gi|507715087|XP_004648568.1
☐	P-selectin-like protein [Cricetulus griseus]	47.7	85.3	88%	7e-05	87%	gi|537153471|ERE72501.1
☐	hypothetical protein CB1_000094012 [Camelus ferus]	47.7	107	88%	7e-05	87%	gi|528769900|EPY89559.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Mustela putoriu	47.3	47.3	94%	9e-05	81%	gi|511872755|XP_004756722.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Mustela putoriu	47.3	47.3	94%	9e-05	81%	gi|511962048|XP_004799211.1
☐	PREDICTED: L-selectin isoform X3 [Fukomys damarensis]	46.9	46.9	88%	1e-04	87%	gi|731237513|XP_010632293.1
☐	PREDICTED: L-selectin [Elephantulus edwardii]	46.9	46.9	88%	1e-04	87%	gi|585664723|XP_006887476.1

☐ hypothetical protein PANDA_007106 [Ailuropoda melanoleuca]	46.9	46.9	88%	1e-04	87%	gi|281348254|EFB23838.1
☐ PREDICTED: L-selectin isoform X2 [Fukomys damarensis]	46.9	46.9	88%	1e-04	87%	gi|731237511|XP_010632292.1
☐ PREDICTED: L-selectin isoform 4 [Dasypus novemcinctus]	46.9	46.9	88%	1e-04	87%	gi|488545385|XP_004464223.1
☐ PREDICTED: LOW QUALITY PROTEIN: L-selectin [Tarsius syrichta	46.9	46.9	88%	1e-04	87%	gi|640806175|XP_008059542.1
☐ PREDICTED: L-selectin isoform 5 [Dasypus novemcinctus]	46.9	46.9	88%	1e-04	87%	gi|488545387|XP_004464224.1
☐ PREDICTED: L-selectin isoform 3 [Dasypus novemcinctus]	46.9	46.9	88%	1e-04	87%	gi|488545383|XP_004464222.1
☐ PREDICTED: L-selectin [Nannospalax galili]	46.9	46.9	88%	1e-04	87%	gi|674099452|XP_008823120.1
☐ PREDICTED: L-selectin isoform X1 [Fukomys damarensis]	46.9	46.9	88%	1e-04	87%	gi|731237509|XP_010632291.1
☐ PREDICTED: L-selectin isoform 2 [Dasypus novemcinctus]	46.9	46.9	88%	1e-04	87%	gi|488545381|XP_004464221.1
☐ L-selectin precursor [Sus scrofa]	46.9	46.9	88%	1e-04	87%	gi|162952046|NP_001106148.1
☐ L-selectin [Felis catus]	46.9	46.9	88%	1e-04	87%	gi|148234680|NP_001082779.1
☐ PREDICTED: L-selectin isoform X2 [Ornithorhynchus anatinus]	46.9	46.9	94%	1e-04	88%	gi|620963547|XP_007667058.1
☐ PREDICTED: L-selectin isoform 1 [Dasypus novemcinctus]	46.9	46.9	88%	1e-04	87%	gi|488545379|XP_004464220.1
☐ PREDICTED: L-selectin [Jaculus jaculus]	46.9	46.9	88%	1e-04	87%	gi|507550287|XP_004658951.1
☐ PREDICTED: l-selectin-like [Ailuropoda melanoleuca]	46.9	46.9	88%	1e-04	87%	gi|301766396|XP_002918625.1
☐ PREDICTED: L-selectin isoform X1 [Ornithorhynchus anatinus]	46.9	46.9	94%	1e-04	88%	gi|620963545|XP_007667057.1
☐ PREDICTED: L-selectin [Ochotona princeps]	46.9	46.9	88%	1e-04	87%	gi|504154850|XP_004589372.1
☐ PREDICTED: L-selectin isoform X3 [Equus przewalskii]	46.9	46.9	88%	1e-04	87%	gi|664733114|XP_008523771.1
☐ PREDICTED: L-selectin isoform X3 [Equus caballus]	46.9	46.9	88%	1e-04	87%	gi|545215476|XP_005609701.1
☐ PREDICTED: L-selectin isoform X2 [Equus przewalskii]	46.9	46.9	88%	1e-04	87%	gi|664733112|XP_008523770.1
☐ PREDICTED: L-selectin isoform X2 [Equus caballus]	46.9	46.9	88%	1e-04	87%	gi|545215474|XP_005609700.1
☐ PREDICTED: L-selectin isoform X1 [Equus przewalskii]	46.9	46.9	88%	1e-04	87%	gi|664733110|XP_008523769.1
☐ PREDICTED: L-selectin isoform X1 [Equus caballus]	46.9	46.9	88%	1e-04	87%	gi|545215472|XP_005609699.1
☐ E-selectin [Fukomys damarensis]	46.9	80.2	88%	1e-04	87%	gi|676274615|KFO29135.1
☐ PREDICTED: L-selectin isoform X3 [Capra hircus]	46.0	46.0	88%	2e-04	93%	gi|548498158|XP_005690682.1

⊟ Alignments

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Chain A, L-selectin Lectin And Egf Domains

Sequence ID: gi|170292544|pdb|3CFW|A **Length:** 164 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 17 to 33 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
59.6 bits(133)	5e-09	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RFCRDNYTDLVAIQNKA  17
            RFCRDNYTDLVAIQNKA
Sbjct  17   RFCRDNYTDLVAIQNKA  33
```

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selectin L (lymphocyte adhesion molecule 1), isoform CRA_c [Homo sapiens]

Sequence ID: gi|119611263|gb|EAW90857.1| **Length:** 320 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 68 to 84 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
59.6 bits(133)	6e-09	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RFCRDNYTDLVAIQNKA  17
            RFCRDNYTDLVAIQNKA
Sbjct  68   RFCRDNYTDLVAIQNKA  84
```

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194384912|dbj|BAG60862.1| **Length:** 325 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 8 to 24 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
59.6 bits(133)	6e-09	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RFCRDNYTDLVAIQNKA  17
            RFCRDNYTDLVAIQNKA
Sbjct  8    RFCRDNYTDLVAIQNKA  24
```

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Leu-8 antigen short form [Homo sapiens]

Sequence ID: gi|4902830|emb|CAB43537.1| **Length:** 363 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 68 to 84 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
59.6 bits(133)	6e-09	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RFCRDNYTDLVAIQNKA  17
            RFCRDNYTDLVAIQNKA
Sbjct  68   RFCRDNYTDLVAIQNKA  84
```

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lymph node homing receptor precursor [Homo sapiens]

Sequence ID: gi|307134|gb|AAC63053.1| **Length:** 372 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 55 to 71 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
59.6 bits(133)	6e-09	17/17(100%)	17/17(100%)	0/17(0%)

```
Query  1    RFCRDNYTDLVAIQNKA  17
            RFCRDNYTDLVAIQNKA
Sbjct  55   RFCRDNYTDLVAIQNKA  71
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVKG2GA501R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies ▷Formatting options ▷Download YouTube How to read this page Blast report description

SELL_RRFCRDDYTDLVAIQNKA_Mod

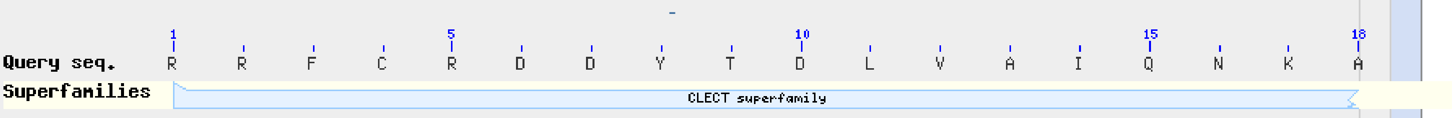
RID	BVKG2GA501R (Expires on 01-21 10:39 am)		
Query ID	lcl|383567	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	18	**Program**	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

⊟Graphic Summary

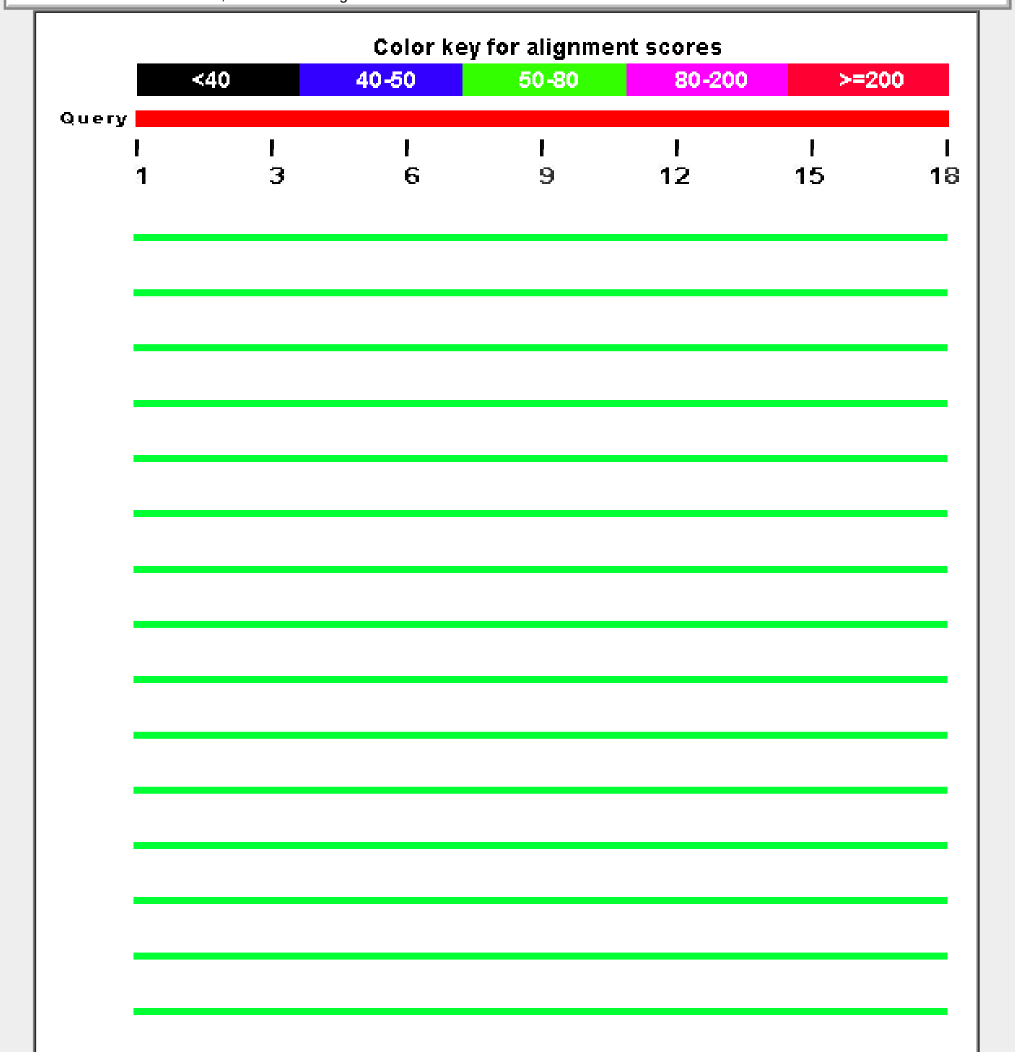
⊟Show Conserved Domains

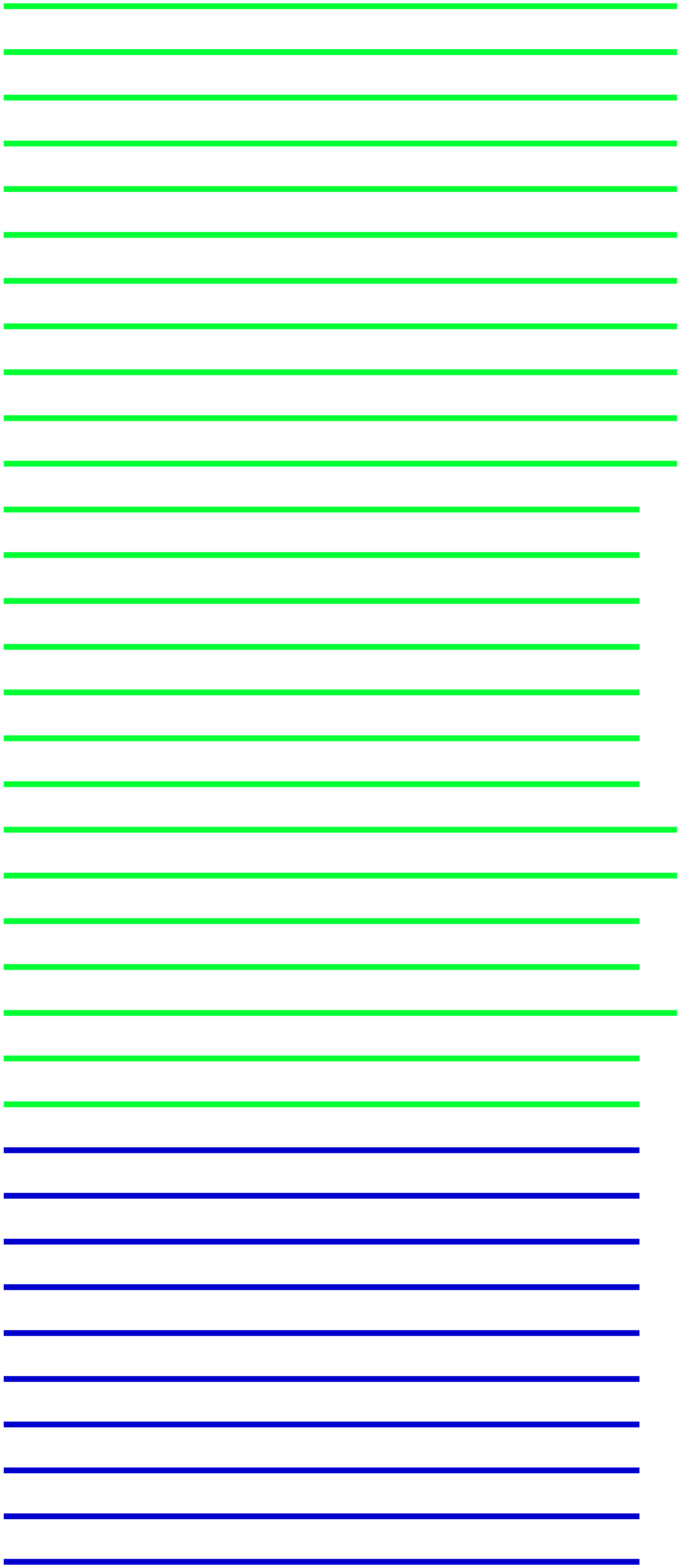
Putative conserved domains have been detected, click on the image below for detailed results.

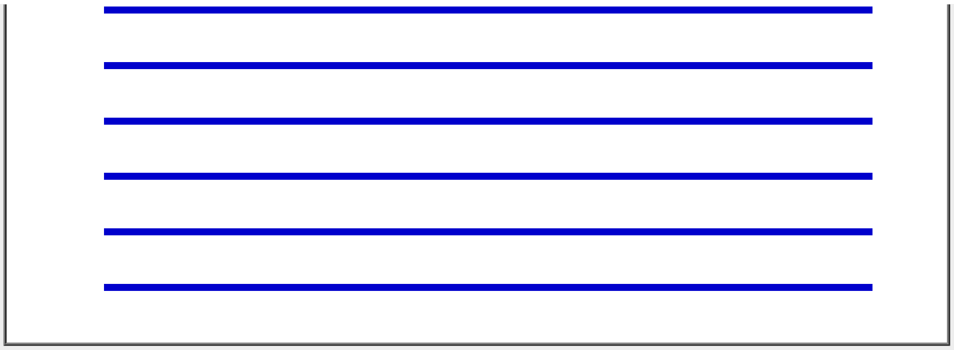


Distribution of 105 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, L-selectin Lectin And Egf Domains [Homo sapiens]	60.4	60.4	100%	3e-09	94%	3CFW_A
☐	selectin L (lymphocyte adhesion molecule 1), isoform CRA_c [Homo sapiens]	60.4	60.4	100%	4e-09	94%	EAW90857.1
☐	unnamed protein product [Homo sapiens]	60.4	60.4	100%	4e-09	94%	BAG60862.1
☐	Leu-8 antigen short form [Homo sapiens]	60.4	60.4	100%	4e-09	94%	CAB43537.1
☐	lymph node homing receptor precursor [Homo sapiens]	60.4	60.4	100%	4e-09	94%	AAC63053.1
☐	L-selectin precursor [Pan troglodytes]	60.4	60.4	100%	4e-09	94%	NP_001009074.1
☐	unnamed protein product [Homo sapiens]	60.4	60.4	100%	4e-09	94%	CAA34275.1
☐	pln homing receptor [Homo sapiens]	60.4	60.4	100%	4e-09	94%	CAA34203.1
☐	RecName: Full=L-selectin; AltName: Full=CD62 antigen-like family member L	60.4	60.4	100%	4e-09	94%	P14151.2
☐	selectin L (lymphocyte adhesion molecule 1), isoform CRA_a [Homo sapiens]	60.4	60.4	100%	4e-09	94%	EAW90855.1
☐	SELL [synthetic construct]	60.4	60.4	100%	4e-09	94%	AIC62025.1
☐	SELL protein [Homo sapiens]	60.4	60.4	100%	4e-09	94%	AAH20758.1
☐	PREDICTED: L-selectin [Gorilla gorilla gorilla]	60.4	60.4	100%	4e-09	94%	XP_004027917.1
☐	unnamed protein product [Homo sapiens]	60.4	60.4	100%	4e-09	94%	CAB43536.1
☐	PREDICTED: L-selectin [Pan paniscus]	60.4	60.4	100%	4e-09	94%	XP_003824676.1
☐	L-selectin precursor [Homo sapiens]	60.4	60.4	100%	4e-09	94%	NP_000646.2
☐	PREDICTED: L-selectin isoform X2 [Macaca fascicularis]	57.9	57.9	100%	3e-08	89%	XP_005539997.1
☐	L-selectin [Papio anubis]	57.9	57.9	100%	3e-08	89%	NP_001106096.1
☐	L-selectin precursor [Macaca mulatta]	57.9	57.9	100%	3e-08	89%	NP_001036228.1
☐	RecName: Full=L-selectin; AltName: Full=CD62 antigen-like family member L	57.9	57.9	100%	3e-08	89%	Q95235.1
☐	Lymph node homing receptor [Macaca mulatta]	57.9	57.9	100%	3e-08	89%	EHH15803.1
☐	PREDICTED: L-selectin [Rhinopithecus roxellana]	57.9	57.9	100%	3e-08	89%	XP_010359291.1
☐	PREDICTED: L-selectin [Chlorocebus sabaeus]	57.9	57.9	100%	3e-08	89%	XP_007987763.1
☐	PREDICTED: L-selectin isoform X1 [Macaca fascicularis]	57.9	57.9	100%	3e-08	89%	XP_005539996.1
☐	PREDICTED: L-selectin [Pongo abelii]	57.9	57.9	100%	3e-08	89%	XP_002809857.2
☐	PREDICTED: L-selectin [Nomascus leucogenys]	57.9	57.9	100%	3e-08	89%	XP_003258894.1
☐	PREDICTED: L-selectin-like [Peromyscus maniculatus bairdii]	52.0	52.0	94%	3e-06	82%	XP_006974839.1
☐	PREDICTED: L-selectin isoform X2 [Canis lupus familiaris]	52.0	52.0	94%	3e-06	82%	XP_005622604.1
☐	PREDICTED: L-selectin isoformX1 [Canis lupus familiaris]	52.0	52.0	94%	3e-06	82%	XP_537201.2

☐	PREDICTED: L-selectin-like isoform X2 [Peromyscus maniculatus bairdii]	52.0	52.0	94%	3e-06	82%	XP_006974823.1
☐	L-selectin precursor [Oryctolagus cuniculus]	52.0	52.0	94%	3e-06	82%	NP_001075821.1
☐	PREDICTED: L-selectin-like isoform X1 [Peromyscus maniculatus bairdii]	52.0	52.0	94%	3e-06	82%	XP_006974822.1
☐	PREDICTED: L-selectin [Galeopterus variegatus]	51.1	51.1	94%	6e-06	82%	XP_008589968.1
☐	PREDICTED: L-selectin [Callithrix jacchus]	51.1	51.1	100%	6e-06	83%	XP_002760427.1
☐	PREDICTED: L-selectin [Saimiri boliviensis boliviensis]	51.1	51.1	100%	6e-06	83%	XP_003925442.1
☐	PREDICTED: L-selectin-like [Leptonychotes weddellii]	50.7	50.7	94%	6e-06	82%	XP_006739818.1
☐	PREDICTED: L-selectin isoform X2 [Ursus maritimus]	50.3	50.3	94%	1e-05	82%	XP_008694116.1
☐	PREDICTED: L-selectin [Ceratotherium simum simum]	50.3	50.3	100%	1e-05	78%	XP_004425116.1
☐	PREDICTED: L-selectin isoform X1 [Ursus maritimus]	50.3	50.3	94%	1e-05	82%	XP_008694111.1
☐	PREDICTED: L-selectin [Panthera tigris altaica]	50.3	50.3	94%	1e-05	82%	XP_007077079.1
☐	PREDICTED: L-selectin [Pteropus alecto]	49.4	49.4	94%	2e-05	82%	XP_006907882.1
☐	PREDICTED: E-selectin [Eptesicus fuscus]	49.4	78.5	94%	2e-05	82%	XP_008151404.1
☐	E-selectin [Pteropus alecto]	49.4	111	94%	2e-05	82%	ELK16299.1
☐	PREDICTED: L-selectin isoform X2 [Bison bison bison]	49.0	49.0	94%	3e-05	82%	XP_010835001.1
☐	L-selectin [Bos mutus]	49.0	49.0	94%	3e-05	82%	ELR51562.1
☐	L-selectin precursor [Bos taurus]	49.0	49.0	94%	3e-05	82%	NP_776607.1
☐	TPA: L-selectin [Bos taurus]	49.0	49.0	94%	3e-05	82%	DAA21340.1
☐	PREDICTED: L-selectin [Trichechus manatus latirostris]	49.0	49.0	94%	3e-05	76%	XP_004384151.1
☐	PREDICTED: L-selectin isoform X1 [Bison bison bison]	49.0	49.0	94%	3e-05	82%	XP_010835000.1
☐	PREDICTED: L-selectin [Bos mutus]	49.0	49.0	94%	3e-05	82%	XP_005902444.1
☐	PREDICTED: L-selectin isoform X1 [Bos taurus]	49.0	49.0	94%	3e-05	82%	XP_005216937.1
☐	PREDICTED: L-selectin isoform X2 [Cricetulus griseus]	48.6	48.6	94%	4e-05	76%	XP_007628167.1
☐	LECAM-1 [Sigmodon hispidus]	48.6	48.6	94%	4e-05	76%	AAN87893.1
☐	PREDICTED: L-selectin isoform X1 [Cricetulus griseus]	48.6	48.6	94%	4e-05	76%	XP_007647090.1
☐	PREDICTED: L-selectin [Microtus ochrogaster]	48.6	48.6	94%	4e-05	76%	XP_005364074.1
☐	PREDICTED: L-selectin [Mesocricetus auratus]	48.6	48.6	94%	4e-05	76%	XP_005071531.1
☐	PREDICTED: L-selectin [Octodon degus]	48.6	48.6	94%	4e-05	82%	XP_004648568.1
☐	P-selectin-like protein [Cricetulus griseus]	48.6	84.8	94%	4e-05	76%	ERE72501.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Mustela putorius furo]	48.1	48.1	94%	5e-05	76%	XP_004756722.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Mustela putorius furo]	48.1	48.1	94%	6e-05	76%	XP_004799211.1
☐	PREDICTED: L-selectin isoform X2 [Balaenoptera acutorostrata scammoni]	47.7	47.7	94%	7e-05	82%	XP_007172554.1
☐	PREDICTED: L-selectin isoform X3 [Fukomys damarensis]	47.7	47.7	94%	7e-05	76%	XP_010632293.1
☐	PREDICTED: L-selectin [Elephantulus edwardii]	47.7	47.7	94%	7e-05	76%	XP_006887476.1
☐	hypothetical protein PANDA_007106 [Ailuropoda melanoleuca]	47.7	47.7	94%	7e-05	76%	EFB23838.1
☐	PREDICTED: L-selectin isoform X2 [Fukomys damarensis]	47.7	47.7	94%	8e-05	76%	XP_010632292.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Tarsius syrichta]	47.7	47.7	94%	8e-05	76%	XP_008059542.1
☐	PREDICTED: L-selectin [Nannospalax galili]	47.7	47.7	94%	8e-05	76%	XP_008823120.1
☐	PREDICTED: L-selectin isoform X1 [Fukomys damarensis]	47.7	47.7	94%	8e-05	76%	XP_010632291.1
☐	PREDICTED: L-selectin [Lipotes vexillifer]	47.7	47.7	94%	8e-05	82%	XP_007458185.1
☐	PREDICTED: L-selectin isoform X1 [Balaenoptera acutorostrata scammoni]	47.7	47.7	94%	8e-05	82%	XP_007172553.1
☐	PREDICTED: L-selectin [Physeter catodon]	47.7	47.7	94%	8e-05	82%	XP_007102109.1
☐	PREDICTED: L-selectin [Tursiops truncatus]	47.7	47.7	94%	8e-05	82%	XP_004319819.1
☐	PREDICTED: L-selectin [Orcinus orca]	47.7	47.7	94%	8e-05	82%	XP_004269787.1
☐	L-selectin precursor [Sus scrofa]	47.7	47.7	94%	8e-05	76%	NP_001106148.1
☐	L-selectin [Felis catus]	47.7	47.7	94%	8e-05	76%	NP_001082779.1

☐	PREDICTED: L-selectin [Jaculus jaculus]	47.7	47.7	94%	8e-05	76%	XP_004658951.1
☐	PREDICTED: l-selectin-like [Ailuropoda melanoleuca]	47.7	47.7	94%	8e-05	76%	XP_002918625.1
☐	PREDICTED: L-selectin [Ochotona princeps]	47.7	47.7	94%	8e-05	76%	XP_004589372.1
☐	PREDICTED: L-selectin isoform X3 [Equus przewalskii]	47.7	47.7	94%	8e-05	76%	XP_008523771.1
☐	PREDICTED: L-selectin isoform X3 [Equus caballus]	47.7	47.7	94%	8e-05	76%	XP_005609701.1
☐	PREDICTED: L-selectin isoform X2 [Equus przewalskii]	47.7	47.7	94%	8e-05	76%	XP_008523770.1
☐	PREDICTED: L-selectin isoform X2 [Equus caballus]	47.7	47.7	94%	8e-05	76%	XP_005609700.1
☐	PREDICTED: L-selectin isoform X1 [Equus przewalskii]	47.7	47.7	94%	8e-05	76%	XP_008523769.1
☐	PREDICTED: L-selectin isoform X1 [Equus caballus]	47.7	47.7	94%	8e-05	76%	XP_005609699.1
☐	E-selectin [Fukomys damarensis]	47.7	80.2	94%	8e-05	76%	KFO29135.1
☐	PREDICTED: L-selectin isoform X2 [Ornithorhynchus anatinus]	47.3	47.3	94%	1e-04	88%	XP_007667058.1
☐	PREDICTED: L-selectin isoform X1 [Ornithorhynchus anatinus]	47.3	47.3	94%	1e-04	88%	XP_007667057.1
☐	PREDICTED: L-selectin isoform X3 [Mus musculus]	46.9	46.9	94%	1e-04	76%	XP_006496781.1
☐	PREDICTED: L-selectin isoform X4 [Bubalus bubalis]	46.9	46.9	94%	1e-04	82%	XP_006073161.1
☐	L-selectin isoform 2 precursor [Mus musculus]	46.9	46.9	94%	1e-04	76%	NP_001157531.1
☐	lymphocyte homing receptor [Mus musculus]	46.9	46.9	94%	1e-04	76%	AAA75651.1
☐	PREDICTED: L-selectin isoform X3 [Bubalus bubalis]	46.9	46.9	94%	1e-04	82%	XP_006073160.1
☐	L-selectin isoform 1 precursor [Mus musculus]	46.9	46.9	94%	1e-04	76%	NP_035476.1
☐	unnamed protein product [Mus musculus]	46.9	46.9	94%	1e-04	76%	BAE36559.1
☐	unnamed protein product [Mus musculus]	46.9	46.9	94%	1e-04	76%	BAE42834.1
☐	PREDICTED: L-selectin isoform X2 [Mus musculus]	46.9	46.9	94%	1e-04	76%	XP_006496780.1
☐	PREDICTED: L-selectin isoform X1 [Mus musculus]	46.9	46.9	94%	1e-04	76%	XP_006496779.1
☐	PREDICTED: L-selectin isoform X2 [Bubalus bubalis]	46.9	46.9	94%	1e-04	82%	XP_006073159.1
☐	PREDICTED: L-selectin isoform X1 [Bubalus bubalis]	46.9	46.9	94%	1e-04	82%	XP_006073158.1
☐	PREDICTED: L-selectin [Myotis brandtii]	46.4	46.4	94%	2e-04	76%	XP_005861291.1

⊟ Alignments

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Chain A, L-selectin Lectin And Egf Domains

Sequence ID: pdb|3CFW|A **Length:** 164 **Number of Matches:** 1

Related Information

Structure - 3D structure displays

Range 1: 16 to 33 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	3e-09	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1   RRFCRDDYTDLVAIQNKA  18
           RRFCRD+YTDLVAIQNKA
Sbjct  16  RRFCRDNYTDLVAIQNKA  33
```

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selectin L (lymphocyte adhesion molecule 1), isoform CRA_c [Homo sapiens]

Sequence ID: gb|EAW90857.1| **Length:** 320 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 67 to 84 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	4e-09	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1   RRFCRDDYTDLVAIQNKA  18
           RRFCRD+YTDLVAIQNKA
Sbjct  67  RRFCRDNYTDLVAIQNKA  84
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Homo sapiens]

Sequence ID: dbj|BAG60862.1| **Length:** 325 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 7 to 24 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	4e-09	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    RRFCRDDYTDLVAIQNKA  18
            RRFCRD+YTDLVAIQNKA
Sbjct  7    RRFCRDNYTDLVAIQNKA  24
```

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Leu-8 antigen short form [Homo sapiens]

Sequence ID: emb|CAB43537.1| **Length:** 363 **Number of Matches:** 1

See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 67 to 84 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	4e-09	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    RRFCRDDYTDLVAIQNKA  18
            RRFCRD+YTDLVAIQNKA
Sbjct  67   RRFCRDNYTDLVAIQNKA  84
```

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lymph node homing receptor precursor [Homo sapiens]

Sequence ID: gb|AAC63053.1| **Length:** 372 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 54 to 71 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.4 bits(135)	4e-09	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    RRFCRDDYTDLVAIQNKA  18
            RRFCRD+YTDLVAIQNKA
Sbjct  54   RRFCRDNYTDLVAIQNKA  71
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

SELL_RRFCRDNYTDLVAIQNKA_NonMod

RID BE84AXZD014 (Expires on 01-16 09:06 am)

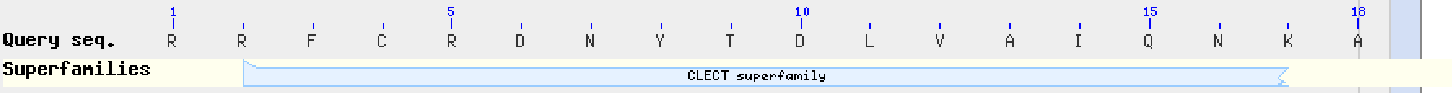
Query ID	lcl|10478	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	18		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

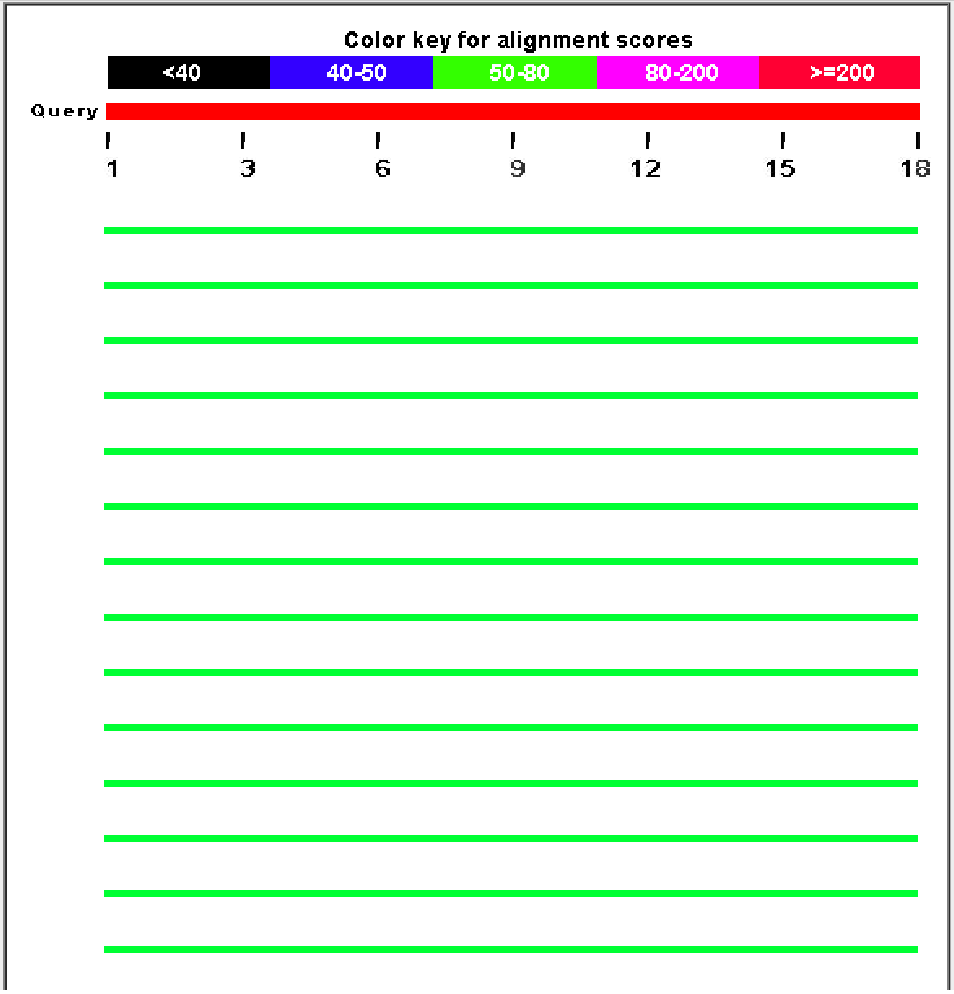
Show Conserved Domains

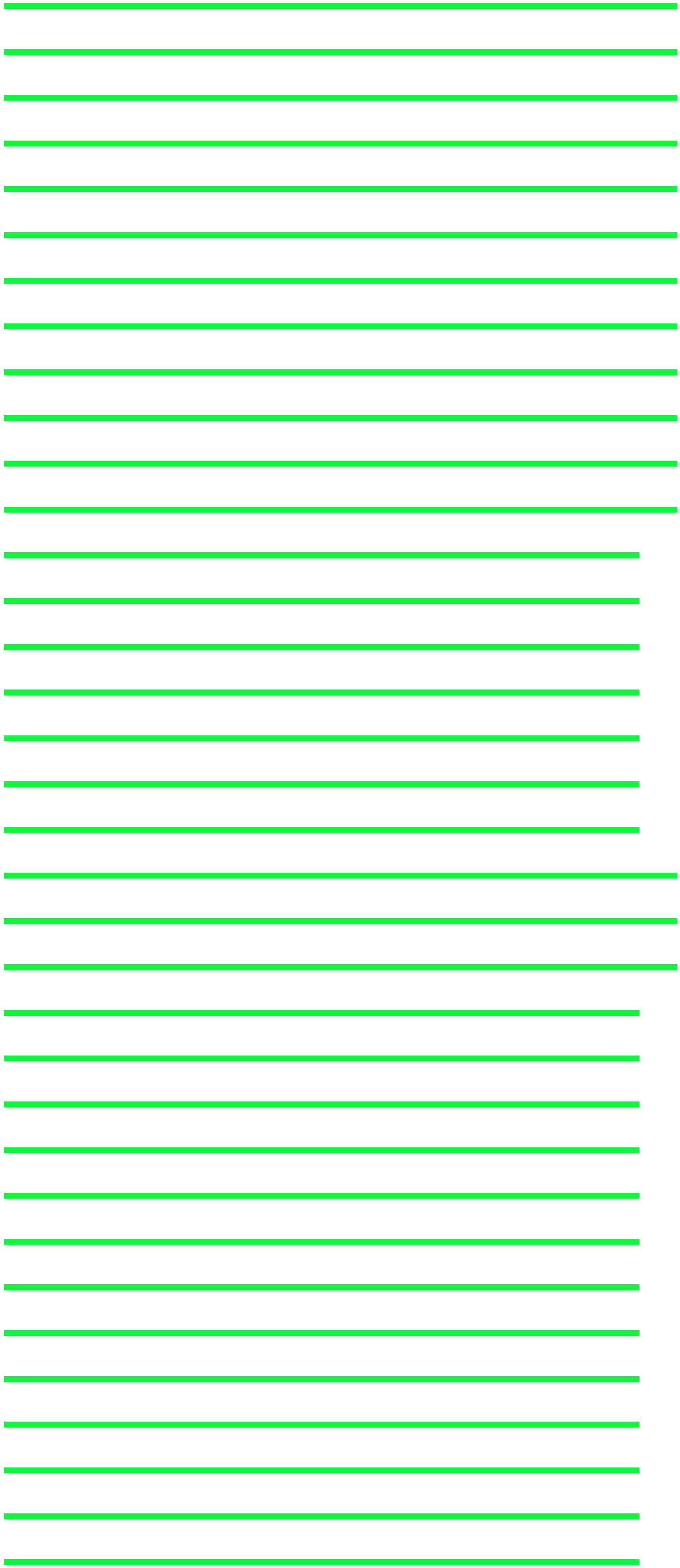
Putative conserved domains have been detected, click on the image below for detailed results.

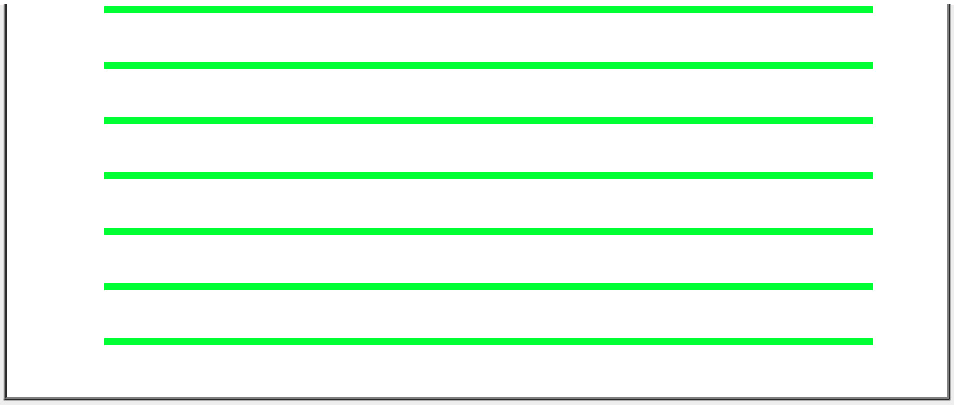


Distribution of 105 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊖Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Chain A, L-selectin Lectin And Egf Domains [Homo sapiens]	63.0	63.0	100%	4e-10	100%	gi|170292544|3CFW_A
☐	selectin L (lymphocyte adhesion molecule 1), isoform CRA_c [Homo	63.0	63.0	100%	5e-10	100%	gi|119611263|EAW90857.1
☐	unnamed protein product [Homo sapiens]	63.0	63.0	100%	5e-10	100%	gi|194384912|BAG60862.1
☐	Leu-8 antigen short form [Homo sapiens]	63.0	63.0	100%	5e-10	100%	gi|4902830|CAB43537.1
☐	lymph node homing receptor precursor [Homo sapiens]	63.0	63.0	100%	5e-10	100%	gi|307134|AAC63053.1
☐	L-selectin precursor [Pan troglodytes]	63.0	63.0	100%	5e-10	100%	gi|57114019|NP_001009074.1
☐	unnamed protein product [Homo sapiens]	63.0	63.0	100%	5e-10	100%	gi|34429|CAA34275.1
☐	pln homing receptor [Homo sapiens]	63.0	63.0	100%	5e-10	100%	gi|38093|CAA34203.1
☐	RecName: Full=L-selectin; AltName: Full=CD62 antigen-like family	63.0	63.0	100%	5e-10	100%	gi|126178|P14151.2
☐	selectin L (lymphocyte adhesion molecule 1), isoform CRA_a [Homo	63.0	63.0	100%	5e-10	100%	gi|119611261|EAW90855.1
☐	SELL [synthetic construct]	63.0	63.0	100%	5e-10	100%	gi|649149084|AIC62025.1
☐	SELL protein [Homo sapiens]	63.0	63.0	100%	5e-10	100%	gi|18088808|AAH20758.1
☐	PREDICTED: L-selectin [Gorilla gorilla gorilla]	63.0	63.0	100%	5e-10	100%	gi|426332662|XP_004027917.1
☐	unnamed protein product [Homo sapiens]	63.0	63.0	100%	5e-10	100%	gi|4902829|CAB43536.1
☐	PREDICTED: L-selectin [Pan paniscus]	63.0	63.0	100%	5e-10	100%	gi|397508469|XP_003824676.1
☐	L-selectin precursor [Homo sapiens]	63.0	63.0	100%	5e-10	100%	gi|262206315|NP_000646.2
☐	PREDICTED: L-selectin isoform X2 [Macaca fascicularis]	60.4	60.4	100%	4e-09	94%	gi|544398261|XP_005539997.1
☐	L-selectin [Papio anubis]	60.4	60.4	100%	4e-09	94%	gi|162951976|NP_001106096.1
☐	L-selectin precursor [Macaca mulatta]	60.4	60.4	100%	4e-09	94%	gi|112363117|NP_001036228.1
☐	RecName: Full=L-selectin; AltName: Full=CD62 antigen-like family	60.4	60.4	100%	4e-09	94%	gi|2497646|Q95235.1
☐	Lymph node homing receptor [Macaca mulatta]	60.4	60.4	100%	4e-09	94%	gi|355559023|EHH15803.1
☐	PREDICTED: L-selectin [Rhinopithecus roxellana]	60.4	60.4	100%	4e-09	94%	gi|724796904|XP_010359291.1
☐	PREDICTED: L-selectin [Chlorocebus sabaeus]	60.4	60.4	100%	4e-09	94%	gi|635132726|XP_007987763.1
☐	PREDICTED: L-selectin isoform X1 [Macaca fascicularis]	60.4	60.4	100%	4e-09	94%	gi|544398259|XP_005539996.1
☐	PREDICTED: L-selectin [Pongo abelii]	60.4	60.4	100%	4e-09	94%	gi|395729434|XP_002809857.2
☐	PREDICTED: L-selectin [Nomascus leucogenys]	60.4	60.4	100%	4e-09	94%	gi|332219505|XP_003258894.1
☐	PREDICTED: L-selectin-like [Peromyscus maniculatus bairdii]	54.5	54.5	94%	3e-07	88%	gi|589923917|XP_006974839.1
☐	PREDICTED: L-selectin isoform X2 [Canis lupus familiaris]	54.5	54.5	94%	4e-07	88%	gi|545504917|XP_005622604.1

☐	PREDICTED: L-selectin isoformX1 [Canis lupus familiaris]	54.5	54.5	94%	4e-07	88%	gi|73960664|XP_537201.2
☐	PREDICTED: L-selectin-like isoform X2 [Peromyscus maniculatus b	54.5	54.5	94%	4e-07	88%	gi|589923885|XP_006974823.1
☐	L-selectin precursor [Oryctolagus cuniculus]	54.5	54.5	94%	4e-07	88%	gi|126723231|NP_001075821.1
☐	PREDICTED: L-selectin-like isoform X1 [Peromyscus maniculatus b	54.5	54.5	94%	4e-07	88%	gi|589923883|XP_006974822.1
☐	PREDICTED: L-selectin [Galeopterus variegatus]	53.7	53.7	94%	8e-07	88%	gi|667326711|XP_008589968.1
☐	PREDICTED: L-selectin [Ceratotherium simum simum]	52.8	52.8	100%	1e-06	83%	gi|478501608|XP_004425116.1
☐	PREDICTED: L-selectin [Callithrix jacchus]	52.8	52.8	100%	1e-06	83%	gi|296229840|XP_002760427.1
☐	PREDICTED: L-selectin [Saimiri boliviensis boliviensis]	52.4	52.4	100%	2e-06	83%	gi|403266555|XP_003925442.1
☐	PREDICTED: L-selectin [Pteropus alecto]	52.0	52.0	94%	3e-06	88%	gi|586545543|XP_006907882.1
☐	PREDICTED: E-selectin [Eptesicus fuscus]	52.0	82.7	94%	3e-06	88%	gi|641723183|XP_008151404.1
☐	E-selectin [Pteropus alecto]	52.0	118	94%	3e-06	88%	gi|431916045|ELK16299.1
☐	PREDICTED: L-selectin isoform X2 [Bison bison bison]	51.5	51.5	94%	4e-06	88%	gi|742104371|XP_010835001.1
☐	L-selectin [Bos mutus]	51.5	51.5	94%	4e-06	88%	gi|440900418|ELR51562.1
☐	L-selectin precursor [Bos taurus]	51.5	51.5	94%	4e-06	88%	gi|27901801|NP_776607.1
☐	TPA: L-selectin [Bos taurus]	51.5	51.5	94%	4e-06	88%	gi|296479225|DAA21340.1
☐	PREDICTED: L-selectin [Trichechus manatus latirostris]	51.5	51.5	94%	4e-06	82%	gi|471403937|XP_004384151.1
☐	PREDICTED: L-selectin isoform X1 [Bison bison bison]	51.5	51.5	94%	4e-06	88%	gi|742104367|XP_010835000.1
☐	PREDICTED: L-selectin [Bos mutus]	51.5	51.5	94%	4e-06	88%	gi|555981044|XP_005902444.1
☐	PREDICTED: L-selectin isoform X1 [Bos taurus]	51.5	51.5	94%	4e-06	88%	gi|528979726|XP_005216937.1
☐	PREDICTED: L-selectin isoform X2 [Cricetulus griseus]	51.1	51.1	94%	6e-06	82%	gi|625273173|XP_007628167.1
☐	LECAM-1 [Sigmodon hispidus]	51.1	51.1	94%	6e-06	82%	gi|27372091|AAN87893.1
☐	PREDICTED: L-selectin isoform X1 [Cricetulus griseus]	51.1	51.1	94%	6e-06	82%	gi|625212795|XP_007647090.1
☐	PREDICTED: L-selectin [Microtus ochrogaster]	51.1	51.1	94%	6e-06	82%	gi|532042485|XP_005364074.1
☐	PREDICTED: L-selectin [Mesocricetus auratus]	51.1	51.1	94%	6e-06	82%	gi|524937978|XP_005071531.1
☐	PREDICTED: L-selectin [Octodon degus]	51.1	51.1	94%	6e-06	88%	gi|507715087|XP_004648568.1
☐	P-selectin-like protein [Cricetulus griseus]	51.1	89.1	94%	6e-06	82%	gi|537153471|ERE72501.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Mustela putoriu	50.7	50.7	94%	8e-06	82%	gi|511872755|XP_004756722.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Mustela putoriu	50.7	50.7	94%	8e-06	82%	gi|511962048|XP_004799211.1
☐	PREDICTED: L-selectin isoform X2 [Balaenoptera acutorostrata sca	50.3	50.3	94%	1e-05	88%	gi|594638526|XP_007172554.1
☐	PREDICTED: L-selectin isoform X3 [Fukomys damarensis]	50.3	50.3	94%	1e-05	82%	gi|731237513|XP_010632293.1
☐	PREDICTED: L-selectin [Elephantulus edwardii]	50.3	50.3	94%	1e-05	82%	gi|585664723|XP_006887476.1
☐	hypothetical protein PANDA_007106 [Ailuropoda melanoleuca]	50.3	50.3	94%	1e-05	82%	gi|281348254|EFB23838.1
☐	PREDICTED: L-selectin isoform X2 [Fukomys damarensis]	50.3	50.3	94%	1e-05	82%	gi|731237511|XP_010632292.1
☐	PREDICTED: LOW QUALITY PROTEIN: L-selectin [Tarsius syricht	50.3	50.3	94%	1e-05	82%	gi|640806175|XP_008059542.1
☐	PREDICTED: L-selectin [Nannospalax galili]	50.3	50.3	94%	1e-05	82%	gi|674099452|XP_008823120.1
☐	PREDICTED: L-selectin isoform X1 [Fukomys damarensis]	50.3	50.3	94%	1e-05	82%	gi|731237509|XP_010632291.1
☐	PREDICTED: L-selectin [Lipotes vexillifer]	50.3	50.3	94%	1e-05	88%	gi|602692142|XP_007458185.1
☐	PREDICTED: L-selectin isoform X1 [Balaenoptera acutorostrata sca	50.3	50.3	94%	1e-05	88%	gi|594638524|XP_007172553.1
☐	PREDICTED: L-selectin [Physeter catodon]	50.3	50.3	94%	1e-05	88%	gi|593711089|XP_007102109.1
☐	PREDICTED: L-selectin [Tursiops truncatus]	50.3	50.3	94%	1e-05	88%	gi|470624768|XP_004319819.1
☐	PREDICTED: L-selectin [Orcinus orca]	50.3	50.3	94%	1e-05	88%	gi|466008816|XP_004269787.1
☐	L-selectin precursor [Sus scrofa]	50.3	50.3	94%	1e-05	82%	gi|162952046|NP_001106148.1
☐	L-selectin [Felis catus]	50.3	50.3	94%	1e-05	82%	gi|148234680|NP_001082779.1
☐	PREDICTED: L-selectin isoform X2 [Ornithorhynchus anatinus]	50.3	50.3	94%	1e-05	88%	gi|620963547|XP_007667058.1
☐	PREDICTED: L-selectin [Jaculus jaculus]	50.3	50.3	94%	1e-05	82%	gi|507550287|XP_004658951.1
☐	PREDICTED: l-selectin-like [Ailuropoda melanoleuca]	50.3	50.3	94%	1e-05	82%	gi|301766396|XP_002918625.1

☐	PREDICTED: L-selectin isoform X1 [Ornithorhynchus anatinus]	50.3	50.3	94%	1e-05	88%	gi|620963545|XP_007667057.1
☐	PREDICTED: L-selectin [Ochotona princeps]	50.3	50.3	94%	1e-05	82%	gi|504154850|XP_004589372.1
☐	PREDICTED: L-selectin isoform X3 [Equus przewalskii]	50.3	50.3	94%	1e-05	82%	gi|664733114|XP_008523771.1
☐	PREDICTED: L-selectin isoform X3 [Equus caballus]	50.3	50.3	94%	1e-05	82%	gi|545215476|XP_005609701.1
☐	PREDICTED: L-selectin isoform X2 [Equus przewalskii]	50.3	50.3	94%	1e-05	82%	gi|664733112|XP_008523770.1
☐	PREDICTED: L-selectin isoform X2 [Equus caballus]	50.3	50.3	94%	1e-05	82%	gi|545215474|XP_005609700.1
☐	PREDICTED: L-selectin isoform X1 [Equus przewalskii]	50.3	50.3	94%	1e-05	82%	gi|664733110|XP_008523769.1
☐	PREDICTED: L-selectin isoform X1 [Equus caballus]	50.3	50.3	94%	1e-05	82%	gi|545215472|XP_005609699.1
☐	E-selectin [Fukomys damarensis]	50.3	84.0	94%	1e-05	82%	gi|676274615|KFO29135.1
☐	PREDICTED: L-selectin isoform X3 [Mus musculus]	49.4	49.4	94%	2e-05	82%	gi|568910596|XP_006496781.1
☐	PREDICTED: L-selectin isoform X4 [Bubalus bubalis]	49.4	49.4	94%	2e-05	88%	gi|594100108|XP_006073161.1
☐	L-selectin isoform 2 precursor [Mus musculus]	49.4	49.4	94%	2e-05	82%	gi|255708471|NP_001157531.1
☐	lymphocyte homing receptor [Mus musculus]	49.4	49.4	94%	2e-05	82%	gi|554190|AAA75651.1
☐	PREDICTED: L-selectin isoform X3 [Bubalus bubalis]	49.4	49.4	94%	2e-05	88%	gi|594100106|XP_006073160.1
☐	L-selectin isoform 1 precursor [Mus musculus]	49.4	49.4	94%	2e-05	82%	gi|6755454|NP_035476.1
☐	unnamed protein product [Mus musculus]	49.4	49.4	94%	2e-05	82%	gi|74180049|BAE36559.1
☐	unnamed protein product [Mus musculus]	49.4	49.4	94%	2e-05	82%	gi|74182394|BAE42834.1
☐	PREDICTED: L-selectin isoform X2 [Mus musculus]	49.4	49.4	94%	2e-05	82%	gi|568910594|XP_006496780.1
☐	PREDICTED: L-selectin isoform X1 [Mus musculus]	49.4	49.4	94%	2e-05	82%	gi|568910592|XP_006496779.1
☐	PREDICTED: L-selectin isoform X2 [Bubalus bubalis]	49.4	49.4	94%	2e-05	88%	gi|594100104|XP_006073159.1
☐	PREDICTED: L-selectin isoform X1 [Bubalus bubalis]	49.4	49.4	94%	2e-05	88%	gi|594100102|XP_006073158.1
☐	PREDICTED: L-selectin [Myotis brandtii]	49.0	49.0	94%	3e-05	82%	gi|554533070|XP_005861291.1
☐	PREDICTED: L-selectin [Myotis davidii]	49.0	49.0	94%	3e-05	82%	gi|584089194|XP_006764234.1
☐	L-selectin [Myotis davidii]	49.0	49.0	94%	3e-05	82%	gi|432102050|ELK29869.1
☐	E-selectin [Myotis brandtii]	49.0	79.7	94%	3e-05	82%	gi|521022803|EPQ04591.1

Alignments

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Chain A, L-selectin Lectin And Egf Domains

Sequence ID: gi|170292544|pdb|3CFW|A **Length:** 164 **Number of Matches:** 1

Range 1: 16 to 33 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	4e-10	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    RRFCRDNYTDLVAIQNKA  18
            RRFCRDNYTDLVAIQNKA
Sbjct  16   RRFCRDNYTDLVAIQNKA  33
```

Related Information

Structure - 3D structure displays

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selectin L (lymphocyte adhesion molecule 1), isoform CRA_c [Homo sapiens]

Sequence ID: gi|119611263|gb|EAW90857.1| **Length:** 320 **Number of Matches:** 1

Range 1: 67 to 84 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	5e-10	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    RRFCRDNYTDLVAIQNKA  18
            RRFCRDNYTDLVAIQNKA
Sbjct  67   RRFCRDNYTDLVAIQNKA  84
```

Related Information

Gene - associated gene details

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unnamed protein product [Homo sapiens]

Sequence ID: gi|194384912|dbj|BAG60862.1| **Length:** 325 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 7 to 24 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	5e-10	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    RRFCRDNYTDLVAIQNKA  18
           RRFCRDNYTDLVAIQNKA
Sbjct  7    RRFCRDNYTDLVAIQNKA  24
```

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Leu-8 antigen short form [Homo sapiens]

Sequence ID: gi|4902830|emb|CAB43537.1| **Length:** 363 **Number of Matches:** 1

▷ See 1 more title(s)

Related Information

Gene - associated gene details

Identical Proteins - Proteins identical to the subject

Range 1: 67 to 84 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	5e-10	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    RRFCRDNYTDLVAIQNKA  18
           RRFCRDNYTDLVAIQNKA
Sbjct  67   RRFCRDNYTDLVAIQNKA  84
```

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lymph node homing receptor precursor [Homo sapiens]

Sequence ID: gi|307134|gb|AAC63053.1| **Length:** 372 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 54 to 71 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	5e-10	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    RRFCRDNYTDLVAIQNKA  18
           RRFCRDNYTDLVAIQNKA
Sbjct  54   RRFCRDNYTDLVAIQNKA  71
```

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVKGDS9Z01R

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   Formatting options   Download   How to read this page   Blast report description

SEPP1_KCGDCSLTTLKDEDFCKR_Mod

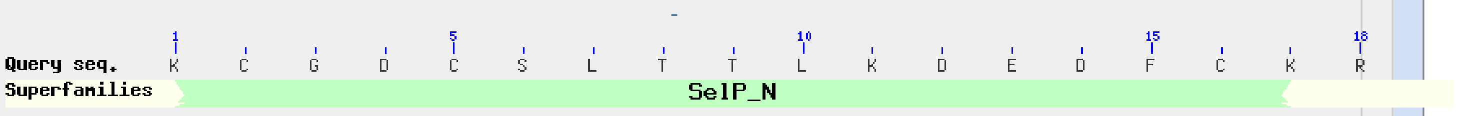
RID	BVKGDS9Z01R (Expires on 01-21 10:39 am)
Query ID	lcl|387095
Description	None
Molecule type	amino acid
Query Length	18
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

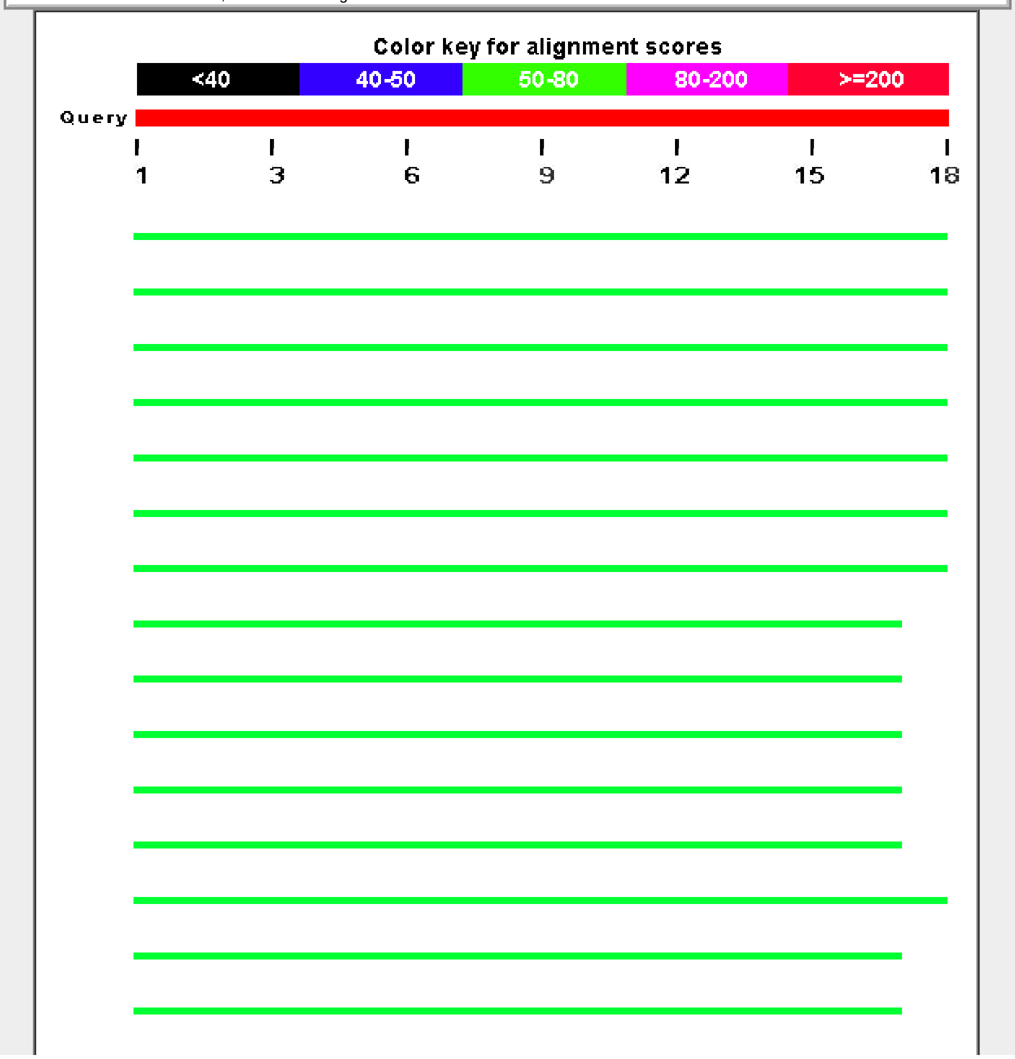
Show Conserved Domains

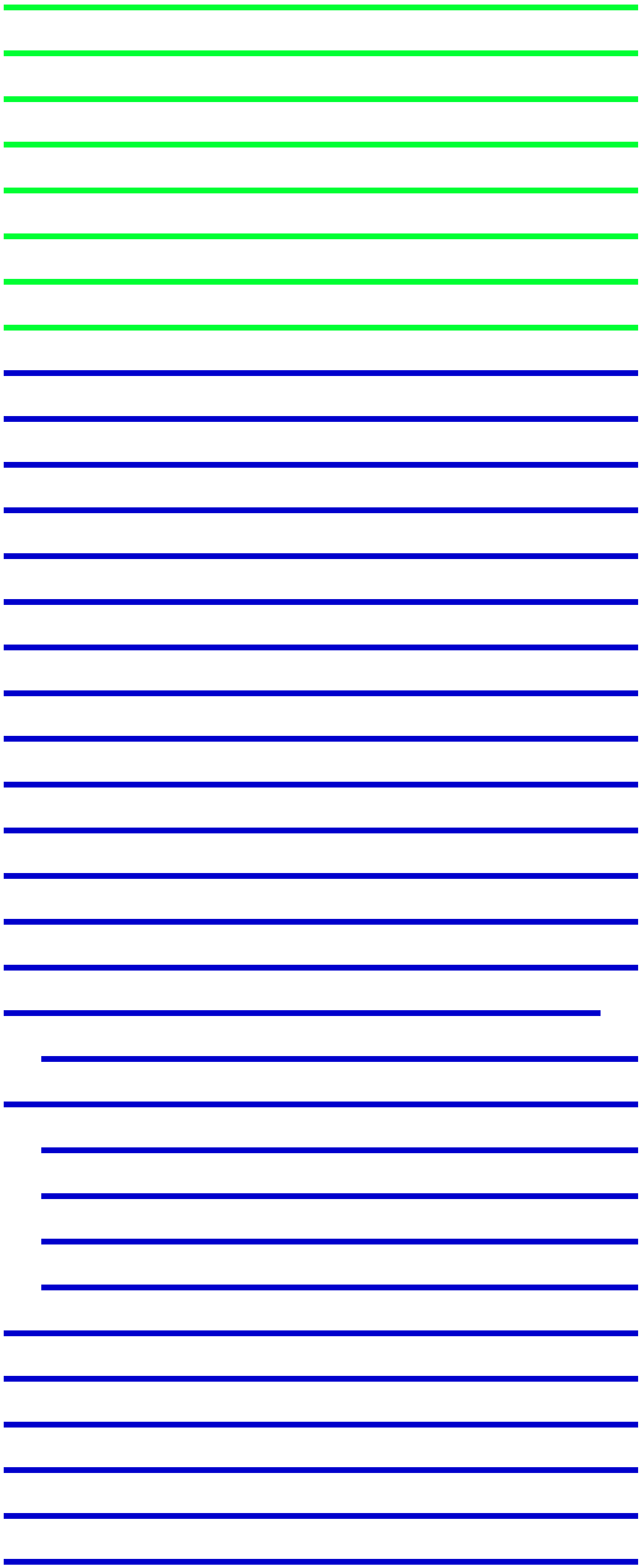
Putative conserved domains have been detected, click on the image below for detailed results.

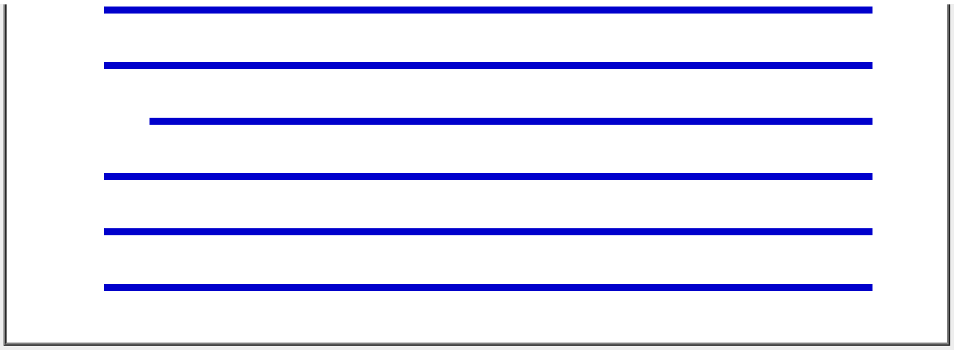


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]	60.0	60.0	100%	5e-09	94%	XP_008961588.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	60.0	60.0	100%	5e-09	94%	AAH46152.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	60.0	60.0	100%	5e-09	94%	NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	60.0	60.0	100%	5e-09	94%	AAH58919.1
☐	selenoprotein P [Homo sapiens]	60.0	60.0	100%	5e-09	94%	CAA77836.2
☐	selenoprotein P precursor [Pan troglodytes]	60.0	60.0	100%	5e-09	94%	NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	60.0	60.0	100%	5e-09	94%	NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri boliviensis	56.6	56.6	94%	8e-08	94%	XP_003925940.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxe	56.6	56.6	94%	8e-08	94%	XP_010372696.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]	56.6	56.6	94%	8e-08	94%	XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocebus sabae	56.6	56.6	94%	8e-08	94%	XP_007959679.1
☐	selenoprotein P precursor [Macaca mulatta]	56.6	56.6	94%	8e-08	94%	NP_001152962.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	55.4	55.4	100%	2e-07	89%	AAH15875.1
☐	selenoprotein P precursor [Sus scrofa]	52.4	52.4	94%	2e-06	88%	NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis davidii]	52.0	52.0	94%	3e-06	88%	XP_006774623.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lucifugus]	52.0	52.0	94%	3e-06	88%	XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicus fuscus]	52.0	52.0	94%	3e-06	88%	XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichechus manatu	52.0	52.0	94%	3e-06	88%	XP_004388500.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis brandtii]	52.0	52.0	94%	3e-06	88%	XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia chinensis]	51.5	51.5	94%	4e-06	88%	XP_006167023.1
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	51.1	51.1	94%	5e-06	88%	XP_003793045.1
☐	selenoprotein P precursor [Pongo abelii]	51.1	51.1	94%	6e-06	94%	NP_001127462.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomascus leucoge	50.7	50.7	94%	8e-06	88%	XP_003274442.1
☐	selenoprotein P precursor [Callithrix jacchus]	49.8	49.8	94%	1e-05	82%	NP_001186857.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius syrichta]	49.4	49.4	94%	2e-05	82%	XP_008050904.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratotherium simu	49.4	49.4	94%	2e-05	88%	XP_004422836.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex araneus]	49.0	49.0	94%	3e-05	82%	XP_004605590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromyscus manic	49.0	49.0	94%	3e-05	82%	XP_006997157.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchilla lanigera]	47.7	47.7	94%	8e-05	82%	XP_005386312.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus przewalskii]	47.3	47.3	94%	1e-04	82%	XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	47.3	47.3	94%	1e-04	82%	NP_001129077.1
☐	Selenoprotein P [Heterocephalus glaber]	46.4	46.4	94%	2e-04	82%	EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys damarens	46.4	46.4	94%	2e-04	82%	XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus ochrogast	46.4	46.4	94%	2e-04	76%	XP_005369861.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gla	46.4	46.4	94%	2e-04	82%	XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gla	46.4	46.4	94%	2e-04	82%	XP_004878213.1
☐	selenoprotein P precursor [Cricetulus griseus]	44.8	44.8	94%	7e-04	76%	ERE84145.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannospalax galili]	43.9	43.9	88%	0.001	88%	XP_008840327.1
☐	selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	43.5	43.5	88%	0.002	75%	EDL03405.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Octodon degus]	43.5	43.5	94%	0.002	76%	XP_004641866.1
☐	Selenoprotein P, plasma, 1 [Mus musculus]	43.5	43.5	88%	0.002	75%	AAH01991.2
☐	plasma selenoprotein P [Mus musculus]	43.5	43.5	88%	0.002	75%	AAD01684.1
☐	unnamed protein product [Mus musculus]	43.5	43.5	88%	0.002	75%	BAE34948.1
☐	selenoprotein P precursor [Mus musculus]	43.5	43.5	88%	0.002	75%	NP_033181.3
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaenoptera acutc	43.1	43.1	94%	0.003	76%	XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes vexillifer]	43.1	43.1	94%	0.003	76%	XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physeter catodon]	43.1	43.1	94%	0.003	76%	XP_007119423.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus bubalis]	43.1	43.1	94%	0.003	76%	XP_006067130.1
☐	membrane selenoprotein P [Capra hircus]	42.6	42.6	94%	0.003	76%	AAF67201.1
☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	42.6	42.6	94%	0.004	76%	NP_001272511.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis aries]	42.6	42.6	94%	0.004	76%	XP_004017062.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopterus varieg	41.8	41.8	94%	0.007	76%	XP_008564915.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenus rosmaru	41.8	41.8	88%	0.007	81%	XP_004409206.1
☐	selenoprotein P precursor [Cavia porcellus]	41.4	41.4	94%	0.010	71%	NP_001244936.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodonta africana	41.4	41.4	94%	0.010	76%	XP_010586424.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera tigris alta	41.4	41.4	94%	0.010	76%	XP_007095490.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus jaculus]	39.7	39.7	94%	0.034	76%	XP_004652550.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus orca]	39.7	39.7	94%	0.034	76%	XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops truncatus]	39.7	39.7	94%	0.034	76%	XP_004320390.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela putorius fu	39.2	39.2	88%	0.047	75%	XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Monodelphis dome	38.4	38.4	88%	0.087	75%	XP_003340675.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephantulus edwa	38.4	38.4	88%	0.088	75%	XP_006889619.1
☐	selenoprotein P precursor [Cricetulus griseus]	38.4	38.4	94%	0.088	71%	NP_001243807.1
☐	selenoprotein P precursor [Canis lupus familiaris]	38.0	38.0	94%	0.12	71%	NP_001108590.1
☐	PREDICTED: selenoprotein P-like [Ailuropoda melanoleuca]	37.5	37.5	94%	0.15	71%	XP_002921760.1
☐	unnamed protein product [Mus musculus]	37.5	37.5	88%	0.16	69%	BAE39664.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus dromedar	37.5	37.5	94%	0.16	71%	XP_010999134.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus ferus]	37.5	37.5	94%	0.16	71%	XP_006191986.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna pacos]	37.5	37.5	94%	0.16	71%	XP_006207756.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus maritimus]	37.5	37.5	94%	0.17	71%	XP_008690806.1
☐	selenoprotein P precursor [Rattus norvegicus]	37.1	37.1	88%	0.22	69%	NP_062065.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bison bison]	37.1	37.1	94%	0.22	71%	XP_010831114.1
☐	selenoprotein P [Bos taurus]	37.1	37.1	94%	0.22	71%	BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mutus]	37.1	37.1	94%	0.22	71%	XP_005894930.1
☐	selenoprotein P precursor [Bos taurus]	37.1	37.1	94%	0.22	71%	NP_776884.2

☐	selenoprotein P [Bubalus bubalis]	37.1	37.1	94%	0.22	71%	AFM77782.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Gorilla gorilla gorilla	36.7	36.7	55%	0.29	100%	XP_004065356.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orycteropus afer af	36.3	36.3	94%	0.41	71%	XP_007952213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceus europae	36.3	36.3	88%	0.42	69%	XP_007517681.1
☐	unnamed protein product [Mus musculus]	35.4	35.4	88%	0.78	69%	BAC55264.3
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Dasypus novemcin	35.0	35.0	94%	1.1	71%	XP_004448278.1
☐	PREDICTED: selenoprotein P [Sarcophilus harrisii]	34.6	34.6	88%	1.4	69%	XP_003759960.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Condylura cristata]	34.6	34.6	94%	1.4	71%	XP_004678402.1
☐	selenoprotein P precursor [Oryctolagus cuniculus]	33.3	33.3	88%	3.7	69%	NP_001186775.1
☐	RNA-binding protein (NOP10, NOLA3) [uncultured marine thaumarchaeote KM	32.5	32.5	94%	4.6	65%	AIF05018.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ochotona princeps	32.9	32.9	88%	5.0	69%	XP_004583736.1
☐	predicted protein [Phaeodactylum tricornutum CCAP 1055/1]	32.0	32.0	61%	9.6	82%	XP_002178290.1
☐	hypothetical protein [Coraliomargarita akajimensis]	31.6	31.6	72%	11	71%	WP_013044828.1
☐	hypothetical protein [Sorangium cellulosum]	31.6	31.6	88%	12	61%	WP_012240780.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops telfairi]	31.6	31.6	94%	13	65%	XP_004716992.1
☐	dihydroxy-acid dehydratase [Campylobacter sp. FOBRC14]	31.2	31.2	66%	17	73%	WP_009649466.1
☐	putative ATP-dependent RNA helicase DDX60-like protein [Cricetulus griseus	31.2	31.2	83%	18	75%	ERE91786.1
☐	PREDICTED: probable ATP-dependent RNA helicase DDX60 [Cricetulus gris	31.2	31.2	83%	18	75%	XP_003498842.2
☐	selenoprotein P-like protein [Bos taurus]	30.8	30.8	94%	22	65%	BAB39395.1
☐	selenoprotein P-like protein [Bos taurus]	30.8	30.8	94%	22	65%	BAB39394.1
☐	selenoprotein P-like protein [Bos taurus]	30.8	30.8	94%	22	65%	BAB39393.1
☐	selenoprotein P-like protein [Bos taurus]	30.8	30.8	94%	22	65%	BAB39392.1
☐	2-oxoglutarate ferredoxin oxidoreductase beta subunit [Legionella fallonii LLAI	30.8	30.8	50%	23	89%	CEG56463.1
☐	hypothetical protein ACD_69C00091G0003 [uncultured bacterium]	30.8	30.8	88%	23	63%	EKD45887.1
☐	selenoprotein P like protein [Bos taurus]	30.8	30.8	94%	24	65%	BAA04949.2

⊟ Alignments

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]

Sequence ID: ref|XP_008961588.1| **Length:** 381 **Number of Matches:** 1

Range 1: 171 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	5e-09	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KCGDCSLTTLKDEDFCKR  18
            KCG+CSLTTLKDEDFCKR
Sbjct  171  KCGNCSLTTLKDEDFCKR  188
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gb|AAH46152.1| **Length:** 381 **Number of Matches:** 1

Range 1: 171 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	5e-09	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KCGDCSLTTLKDEDFCKR  18
            KCG+CSLTTLKDEDFCKR
Sbjct  171  KCGNCSLTTLKDEDFCKR  188
```

Related Information

Gene - associated gene details

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selenoprotein P isoform 1 precursor [Homo sapiens]

Sequence ID: ref|NP_005401.3| **Length:** 381 **Number of Matches:** 1

▷ See 4 more title(s)

Related Information

- Gene - associated gene details
- UniGene - clustered expressed sequence tags
- Map Viewer - aligned genomic context
- Identical Proteins - Proteins identical to the subject

Range 1: 171 to 188 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	5e-09	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KCGDCSLTTLKDEDFCKR  18
            KCG+CSLTTLKDEDFCKR
Sbjct  171  KCGNCSLTTLKDEDFCKR  188
```

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gb|AAH58919.1| **Length:** 381 **Number of Matches:** 1

Related Information

- Gene - associated gene details

Range 1: 171 to 188 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	5e-09	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KCGDCSLTTLKDEDFCKR  18
            KCG+CSLTTLKDEDFCKR
Sbjct  171  KCGNCSLTTLKDEDFCKR  188
```

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selenoprotein P [Homo sapiens]

Sequence ID: emb|CAA77836.2| **Length:** 381 **Number of Matches:** 1

Related Information

- Gene - associated gene details

Range 1: 171 to 188 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
60.0 bits(134)	5e-09	17/18(94%)	18/18(100%)	0/18(0%)

```
Query  1    KCGDCSLTTLKDEDFCKR  18
            KCG+CSLTTLKDEDFCKR
Sbjct  171  KCGNCSLTTLKDEDFCKR  188
```

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Your search parameters were adjusted to search for a short input sequence.

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SEPP1_KCGDCSLTTLKDEDFCKRV_Mod

RID BVKGR72V01R (Expires on 01-21 10:40 am)

Query ID lcl|391100
Description None
Molecule type amino acid
Query Length 19

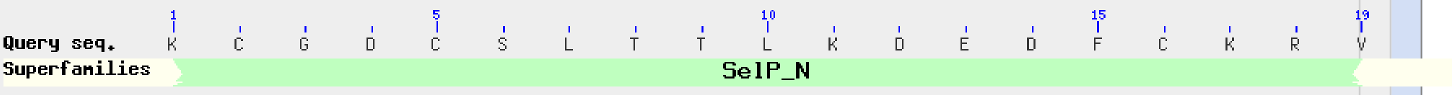
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

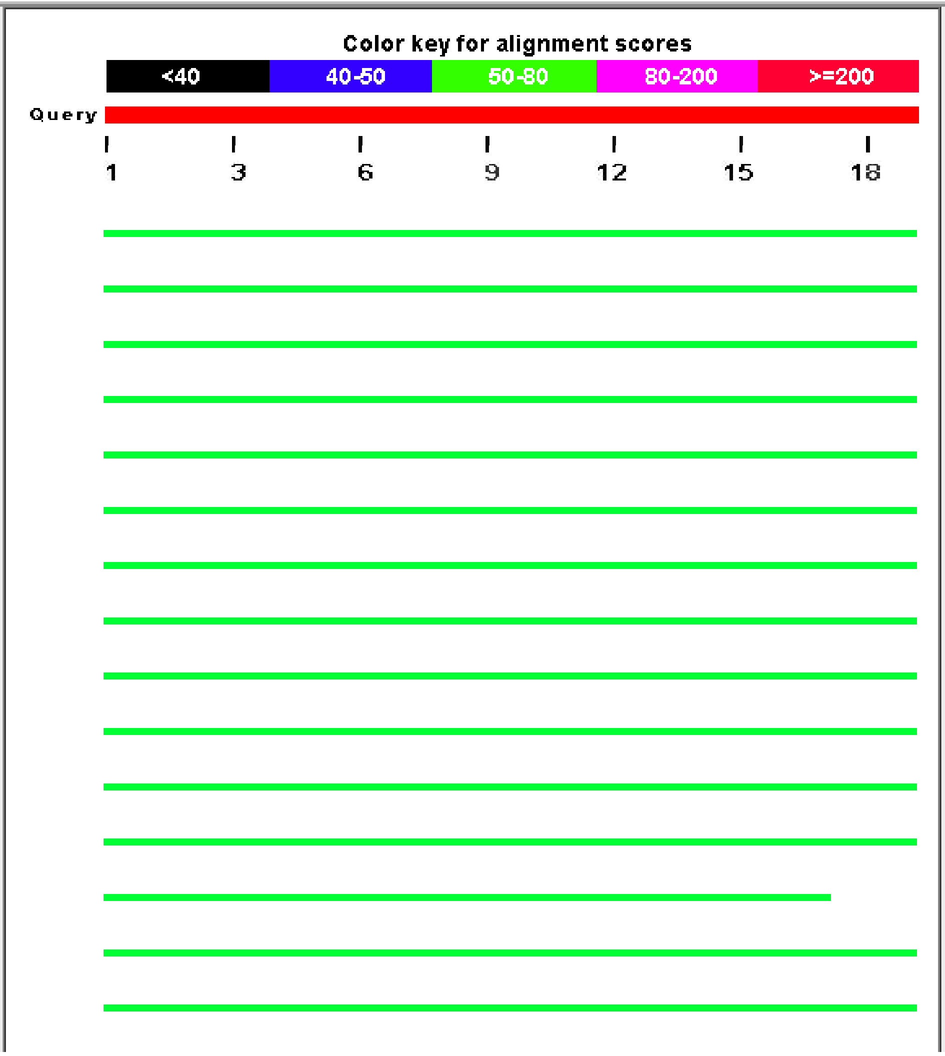
Show Conserved Domains

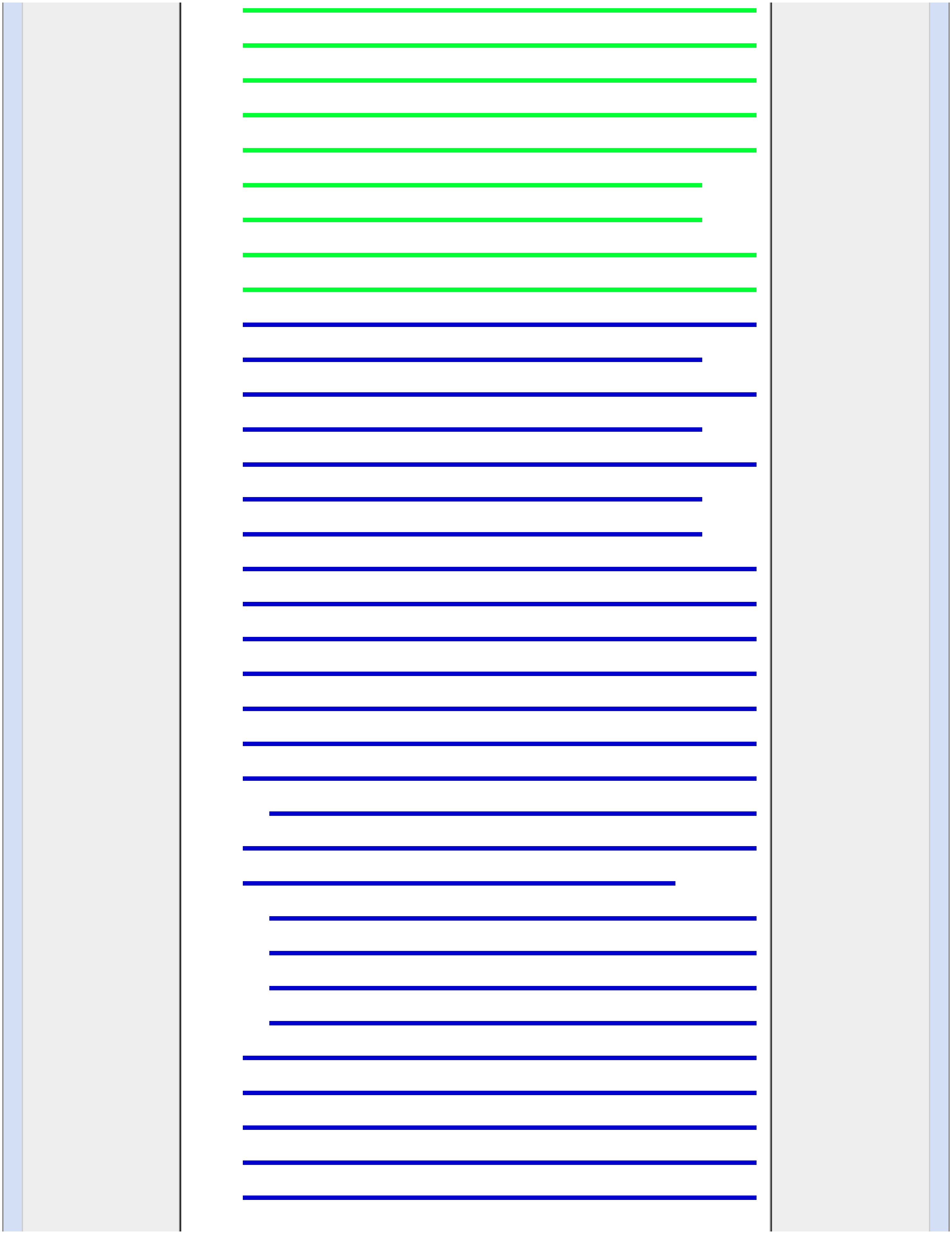
Putative conserved domains have been detected, click on the image below for detailed results.

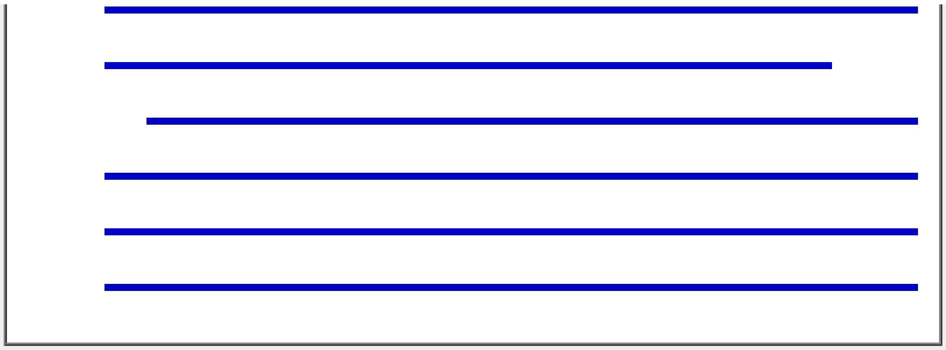


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]	63.0	63.0	100%	6e-10	95%	XP_008961588.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	63.0	63.0	100%	6e-10	95%	AAH46152.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	63.0	63.0	100%	6e-10	95%	NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	63.0	63.0	100%	6e-10	95%	AAH58919.1
☐	selenoprotein P [Homo sapiens]	63.0	63.0	100%	6e-10	95%	CAA77836.2
☐	selenoprotein P precursor [Pan troglodytes]	63.0	63.0	100%	6e-10	95%	NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	63.0	63.0	100%	6e-10	95%	NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]	58.3	58.3	100%	2e-08	89%	XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocebus sabae	58.3	58.3	100%	2e-08	89%	XP_007959679.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	58.3	58.3	100%	2e-08	89%	AAH15875.1
☐	selenoprotein P precursor [Macaca mulatta]	58.3	58.3	100%	2e-08	89%	NP_001152962.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri boliviensis I	57.1	57.1	100%	6e-08	89%	XP_003925940.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxe	56.6	56.6	89%	9e-08	94%	XP_010372696.1
☐	selenoprotein P precursor [Pongo abelii]	52.8	52.8	100%	2e-06	89%	NP_001127462.1
☐	selenoprotein P precursor [Sus scrofa]	52.8	52.8	100%	2e-06	84%	NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis davidii]	52.4	52.4	100%	2e-06	84%	XP_006774623.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicus fuscus]	52.4	52.4	100%	2e-06	84%	XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis brandtii]	52.4	52.4	100%	2e-06	84%	XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomascus leucoge	52.4	52.4	100%	2e-06	84%	XP_003274442.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia chinensis]	52.0	52.0	100%	3e-06	84%	XP_006167023.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lucifugus]	52.0	52.0	89%	3e-06	88%	XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichechus manatu	52.0	52.0	89%	3e-06	88%	XP_004388500.1
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	51.5	51.5	100%	4e-06	84%	XP_003793045.1
☐	selenoprotein P precursor [Callithrix jacchus]	50.3	50.3	100%	1e-05	79%	NP_001186857.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius syrichta]	49.8	49.8	100%	2e-05	79%	XP_008050904.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratotherium simu	49.4	49.4	89%	2e-05	88%	XP_004422836.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromyscus manic	49.4	49.4	100%	2e-05	79%	XP_006997157.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex araneus]	49.0	49.0	89%	3e-05	82%	XP_004605590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchilla lanigera]	48.1	48.1	100%	6e-05	79%	XP_005386312.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus przewalskii]	47.3	47.3	89%	1e-04	82%	XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	47.3	47.3	89%	1e-04	82%	NP_001129077.1
☐	Selenoprotein P [Heterocephalus glaber]	46.9	46.9	100%	2e-04	79%	EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys damaren	46.9	46.9	100%	2e-04	79%	XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus ochrogast	46.9	46.9	100%	2e-04	74%	XP_005369861.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gl	46.9	46.9	100%	2e-04	79%	XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gl	46.9	46.9	100%	2e-04	79%	XP_004878213.1
☐	selenoprotein P precursor [Cricetulus griseus]	45.2	45.2	100%	6e-04	74%	ERE84145.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodonta africana	44.3	44.3	100%	0.001	74%	XP_010586424.1
☐	selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	43.9	43.9	94%	0.001	72%	EDL03405.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Octodon degus]	43.9	43.9	100%	0.002	74%	XP_004641866.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannospalax galili]	43.9	43.9	84%	0.002	88%	XP_008840327.1
☐	Selenoprotein P, plasma, 1 [Mus musculus]	43.9	43.9	94%	0.002	72%	AAH01991.2
☐	plasma selenoprotein P [Mus musculus]	43.9	43.9	94%	0.002	72%	AAD01684.1
☐	unnamed protein product [Mus musculus]	43.9	43.9	94%	0.002	72%	BAE34948.1
☐	selenoprotein P precursor [Mus musculus]	43.9	43.9	94%	0.002	72%	NP_033181.3
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaenoptera acut	43.5	43.5	100%	0.002	74%	XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physeter catodon]	43.5	43.5	100%	0.002	74%	XP_007119423.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus bubalis]	43.5	43.5	100%	0.002	74%	XP_006067130.1
☐	membrane selenoprotein P [Capra hircus]	43.1	43.1	100%	0.003	74%	AAF67201.1
☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	43.1	43.1	100%	0.003	74%	NP_001272511.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis aries]	43.1	43.1	100%	0.003	74%	XP_004017062.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes vexillifer]	43.1	43.1	89%	0.003	76%	XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenus rosmar	43.1	43.1	94%	0.003	78%	XP_004409206.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopterus varieg	42.2	42.2	100%	0.006	74%	XP_008564915.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera tigris alta	42.2	42.2	100%	0.006	74%	XP_007095490.1
☐	selenoprotein P precursor [Cavia porcellus]	41.8	41.8	100%	0.008	68%	NP_001244936.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus orca]	40.1	40.1	100%	0.027	74%	XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops truncatus]	40.1	40.1	100%	0.027	74%	XP_004320390.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Gorilla gorilla gorill	39.7	39.7	57%	0.035	100%	XP_004065356.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus jaculus]	39.7	39.7	89%	0.037	76%	XP_004652550.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela putorius fu	39.2	39.2	84%	0.050	75%	XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus dromeda	39.2	39.2	100%	0.050	68%	XP_010999134.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus ferus]	39.2	39.2	100%	0.050	68%	XP_006191986.1
☐	selenoprotein P precursor [Canis lupus familiaris]	39.2	39.2	100%	0.050	68%	NP_001108590.1
☐	PREDICTED: selenoprotein P-like [Ailuropoda melanoleuca]	38.8	38.8	100%	0.061	68%	XP_002921760.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Monodelphis dome	38.8	38.8	94%	0.069	72%	XP_003340675.2
☐	selenoprotein P precursor [Cricetulus griseus]	38.8	38.8	100%	0.069	68%	NP_001243807.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus maritimus]	38.8	38.8	100%	0.069	68%	XP_008690806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephantulus edwa	38.4	38.4	84%	0.094	75%	XP_006889619.1
☐	unnamed protein product [Mus musculus]	38.0	38.0	94%	0.13	67%	BAE39664.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna pacos]	38.0	38.0	100%	0.13	68%	XP_006207756.1
☐	selenoprotein P precursor [Rattus norvegicus]	37.5	37.5	94%	0.18	67%	NP_062065.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bison bison]	37.5	37.5	100%	0.18	68%	XP_010831114.1
☐	selenoprotein P [Bos taurus]	37.5	37.5	100%	0.18	68%	BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mutus]	37.5	37.5	100%	0.18	68%	XP_005894930.1

☐	selenoprotein P precursor [Bos taurus]	37.5	37.5	100%	0.18	68%	NP_776884.2
☐	selenoprotein P [Bubalus bubalis]	37.5	37.5	100%	0.18	68%	AFM77782.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orycteropus afer af	36.3	36.3	89%	0.44	71%	XP_007952213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceus europae	36.3	36.3	84%	0.44	69%	XP_007517681.1
☐	unnamed protein product [Mus musculus]	35.8	35.8	94%	0.61	67%	BAC55264.3
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Dasypus novemcin	35.0	35.0	89%	1.1	71%	XP_004448278.1
☐	PREDICTED: selenoprotein P [Sarcophilus harrisii]	34.6	34.6	84%	1.5	69%	XP_003759960.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Condylura cristata]	34.6	34.6	89%	1.5	71%	XP_004678402.1
☐	selenoprotein P precursor [Oryctolagus cuniculus]	33.7	33.7	94%	2.9	67%	NP_001186775.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ochotona princeps	33.3	33.3	94%	3.9	67%	XP_004583736.1
☐	RNA-binding protein (NOP10, NOLA3) [uncultured marine thaumarchaeote KM	32.5	32.5	89%	5.1	65%	AIF05018.1
☐	predicted protein [Phaeodactylum tricornutum CCAP 1055/1]	32.0	32.0	57%	10	82%	XP_002178290.1
☐	hypothetical protein [Coraliomargarita akajimensis]	31.6	31.6	68%	12	71%	WP_013044828.1
☐	hypothetical protein [Sorangium cellulosum]	31.6	31.6	84%	13	61%	WP_012240780.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops telfairi]	31.6	31.6	89%	13	65%	XP_004716992.1
☐	selenoprotein P-like protein [Bos taurus]	31.2	31.2	100%	17	63%	BAB39395.1
☐	selenoprotein P-like protein [Bos taurus]	31.2	31.2	100%	17	63%	BAB39394.1
☐	selenoprotein P-like protein [Bos taurus]	31.2	31.2	100%	17	63%	BAB39393.1
☐	selenoprotein P-like protein [Bos taurus]	31.2	31.2	100%	17	63%	BAB39392.1
☐	selenoprotein P-like protein [Bos taurus]	31.2	31.2	100%	18	63%	2117379A
☐	selenoprotein P like protein [Bos taurus]	31.2	31.2	100%	18	63%	BAA04949.2
☐	radical SAM protein [Blautia producta]	31.2	31.2	84%	19	58%	WP_018593457.1
☐	dihydroxy-acid dehydratase [Campylobacter sp. FOBRC14]	31.2	31.2	63%	19	73%	WP_009649466.1
☐	rhUL97 [Macacine herpesvirus 3]	31.2	31.2	47%	19	89%	AAZ80638.1
☐	tegument protein UL97 [Cynomolgus macaque cytomegalovirus strain Ottawa	31.2	31.2	47%	19	89%	YP_004933873.1

⊟ Alignments

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]

Sequence ID: ref|XP_008961588.1| **Length:** 381 **Number of Matches:** 1

Range 1: 171 to 189 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	6e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KCGDCSLTTLKDEDFCKRV  19
            KCG+CSLTTLKDEDFCKRV
Sbjct  171  KCGNCSLTTLKDEDFCKRV  189
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gb|AAH46152.1| **Length:** 381 **Number of Matches:** 1

Range 1: 171 to 189 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	6e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KCGDCSLTTLKDEDFCKRV  19
            KCG+CSLTTLKDEDFCKRV
Sbjct  171  KCGNCSLTTLKDEDFCKRV  189
```

Related Information

Gene - associated gene details

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selenoprotein P isoform 1 precursor [Homo sapiens]

Sequence ID: ref|NP_005401.3| **Length:** 381 **Number of Matches:** 1

▷ See 4 more title(s)

Range 1: 171 to 189 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	6e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KCGDCSLTTLKDEDFCKRV  19
            KCG+CSLTTLKDEDFCKRV
Sbjct  171  KCGNCSLTTLKDEDFCKRV  189
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gb|AAH58919.1| **Length:** 381 **Number of Matches:** 1

Range 1: 171 to 189 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	6e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KCGDCSLTTLKDEDFCKRV  19
            KCG+CSLTTLKDEDFCKRV
Sbjct  171  KCGNCSLTTLKDEDFCKRV  189
```

Related Information

Gene - associated gene details

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selenoprotein P [Homo sapiens]

Sequence ID: emb|CAA77836.2| **Length:** 381 **Number of Matches:** 1

Range 1: 171 to 189 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
63.0 bits(141)	6e-10	18/19(95%)	19/19(100%)	0/19(0%)

```
Query  1    KCGDCSLTTLKDEDFCKRV  19
            KCG+CSLTTLKDEDFCKRV
Sbjct  171  KCGNCSLTTLKDEDFCKRV  189
```

Related Information

Gene - associated gene details

NCBI/ BLAST/ blastp suite/ Formatting Results - BE84P2KH015

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

SEPP1_KCGNCSLTTLKDEDFCKR_NonMod

RID BE84P2KH015 (Expires on 01-16 09:06 am)

Query ID lcl|18695
Description None
Molecule type amino acid
Query Length 18

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

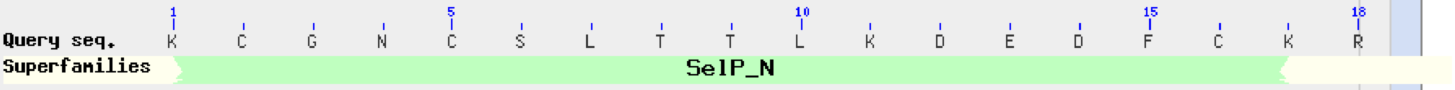
Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

New DELTA-BLAST a more sensitive protein-protein search Go

Graphic Summary

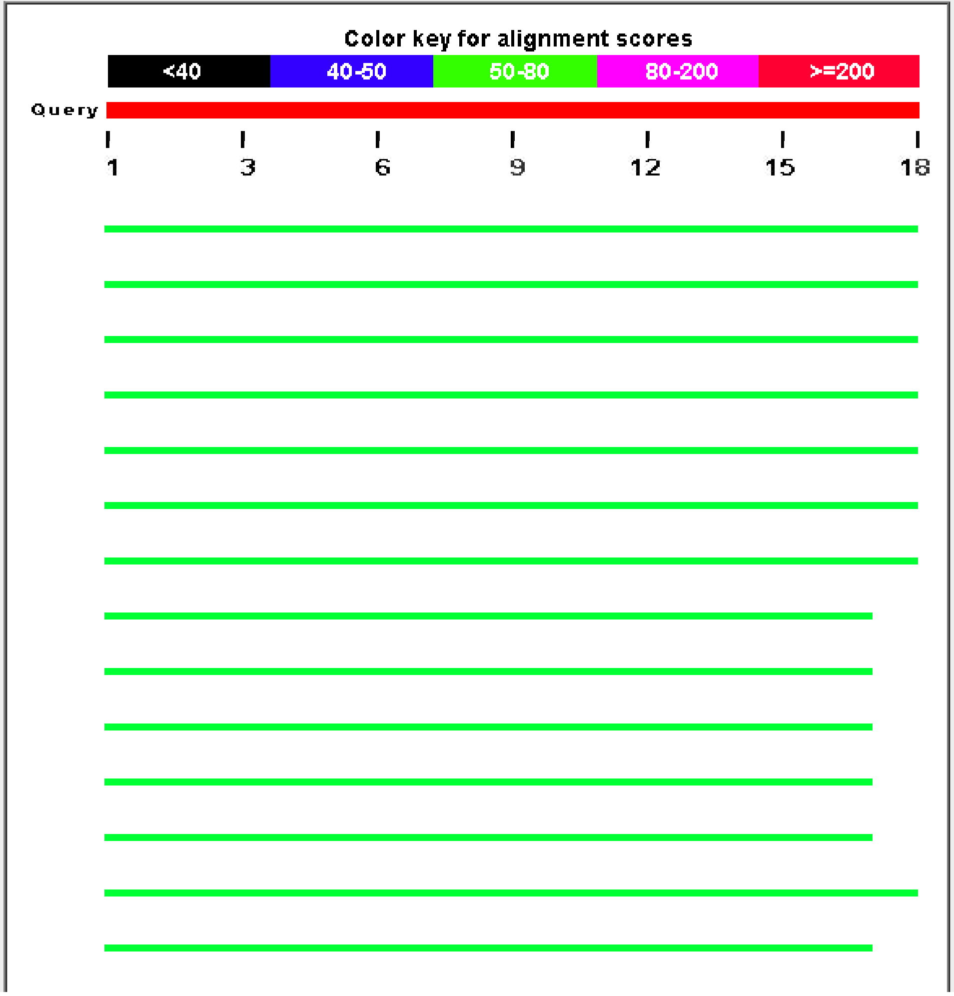
Show Conserved Domains

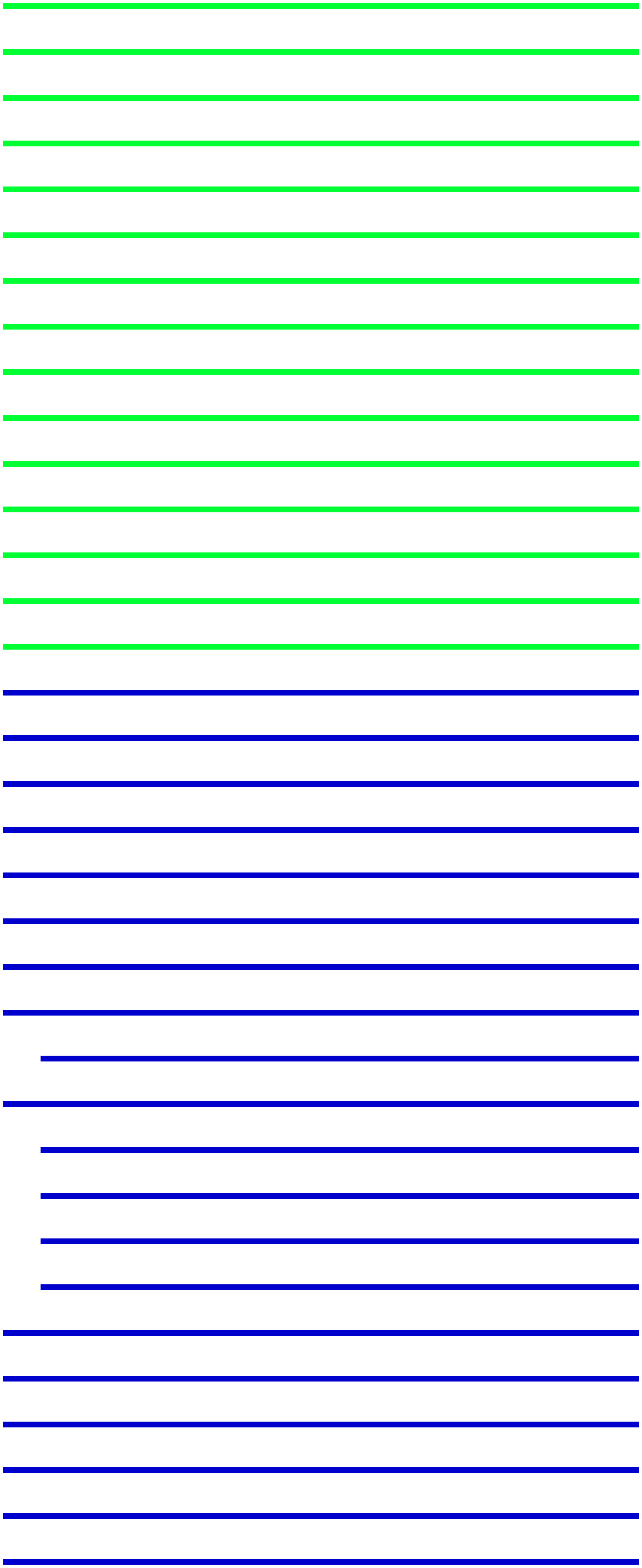
Putative conserved domains have been detected, click on the image below for detailed results.

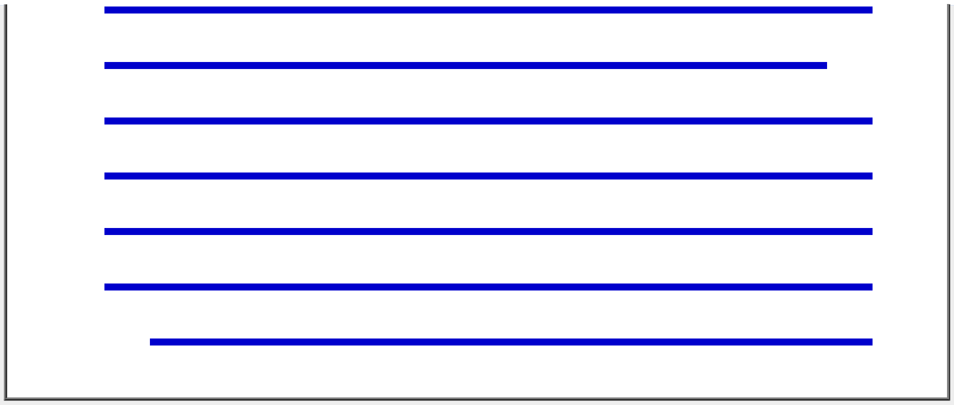


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊖Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan pani	62.6	62.6	100%	7e-10	100%	gi|675710689|XP_008961588.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	62.6	62.6	100%	7e-10	100%	gi|34783648|AAH46152.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	62.6	62.6	100%	7e-10	100%	gi|62530391|NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	62.6	62.6	100%	7e-10	100%	gi|37596694|AAH58919.1
☐	selenoprotein P [Homo sapiens]	62.6	62.6	100%	7e-10	100%	gi|312004116|CAA77836.2
☐	selenoprotein P precursor [Pan troglodytes]	62.6	62.6	100%	7e-10	100%	gi|169403955|NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	62.6	62.6	100%	7e-10	100%	gi|148277022|NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri b	59.2	59.2	94%	1e-08	100%	gi|725563213|XP_003925940.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopitl	59.2	59.2	94%	1e-08	100%	gi|724878613|XP_010372696.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio ar	59.2	59.2	94%	1e-08	100%	gi|685545348|XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chloroce	59.2	59.2	94%	1e-08	100%	gi|635028004|XP_007959679.1
☐	selenoprotein P precursor [Macaca mulatta]	59.2	59.2	94%	1e-08	100%	gi|226958322|NP_001152962.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	57.9	57.9	100%	3e-08	94%	gi|34783164|AAH15875.1
☐	selenoprotein P precursor [Sus scrofa]	54.9	54.9	94%	3e-07	94%	gi|198282079|NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis d	54.5	54.5	94%	4e-07	94%	gi|584060316|XP_006774623.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lu	54.5	54.5	94%	4e-07	94%	gi|558205011|XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicu	54.5	54.5	94%	4e-07	94%	gi|641727491|XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichech	54.5	54.5	94%	4e-07	94%	gi|471413922|XP_004388500.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis b	54.5	54.5	94%	4e-07	94%	gi|554563465|XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia c	54.1	54.1	94%	6e-07	94%	gi|562878609|XP_006167023.1
☐	selenoprotein P precursor [Pongo abelii]	54.1	54.1	94%	6e-07	94%	gi|197101233|NP_001127462.1
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	53.7	53.7	94%	7e-07	94%	gi|395840394|XP_003793045.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomascı	53.2	53.2	94%	1e-06	94%	gi|332250603|XP_003274442.1
☐	selenoprotein P precursor [Callithrix jacchus]	52.4	52.4	94%	2e-06	88%	gi|315630400|NP_001186857.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius s	52.0	52.0	94%	3e-06	88%	gi|640790108|XP_008050904.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex ar	51.5	51.5	94%	4e-06	88%	gi|505790024|XP_004605590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromys	51.5	51.5	94%	4e-06	88%	gi|589969345|XP_006997157.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratoth	50.7	50.7	94%	8e-06	88%	gi|478496995|XP_004422836.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchill	50.3	50.3	94%	1e-05	88%	gi|533143496|XP_005386312.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus p	49.8	49.8	94%	1e-05	88%	gi|664731166|XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	49.8	49.8	94%	1e-05	88%	gi|208022673|NP_001129077.1
☐	Selenoprotein P [Heterocephalus glaber]	49.0	49.0	94%	3e-05	88%	gi|351695949|EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys	49.0	49.0	94%	3e-05	88%	gi|731237262|XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus	49.0	49.0	94%	3e-05	82%	gi|532054271|XP_005369861.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	49.0	49.0	94%	3e-05	88%	gi|512973043|XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	49.0	49.0	94%	3e-05	88%	gi|512816050|XP_004878213.1
☐	selenoprotein P precursor [Cricetulus griseus]	47.3	47.3	94%	1e-04	82%	gi|537231220|ERE84145.1
☐	selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	46.0	46.0	88%	2e-04	81%	gi|148671458|EDL03405.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Octodon	46.0	46.0	94%	3e-04	82%	gi|507690845|XP_004641866.1
☐	Selenoprotein P, plasma, 1 [Mus musculus]	46.0	46.0	88%	3e-04	81%	gi|34809553|AAH01991.2
☐	plasma selenoprotein P [Mus musculus]	46.0	46.0	88%	3e-04	81%	gi|4103142|AAD01684.1
☐	unnamed protein product [Mus musculus]	46.0	46.0	88%	3e-04	81%	gi|74192879|BAE34948.1
☐	selenoprotein P precursor [Mus musculus]	46.0	46.0	88%	3e-04	81%	gi|74271806|NP_033181.3
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaeno	45.6	45.6	94%	4e-04	82%	gi|594696840|XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes	45.6	45.6	94%	4e-04	82%	gi|602724444|XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physete	45.6	45.6	94%	4e-04	82%	gi|593761497|XP_007119423.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus	45.6	45.6	94%	4e-04	82%	gi|594087306|XP_006067130.1
☐	membrane selenoprotein P [Capra hircus]	45.2	45.2	94%	5e-04	82%	gi|7677620|AAF67201.1
☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	45.2	45.2	94%	5e-04	82%	gi|550822255|NP_001272511.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis arie	45.2	45.2	94%	5e-04	82%	gi|426246564|XP_004017062.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannosp	44.8	44.8	88%	7e-04	88%	gi|674066756|XP_008840327.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopte	44.3	44.3	94%	0.001	82%	gi|667253652|XP_008564915.1
☐	selenoprotein P precursor [Cavia porcellus]	43.9	43.9	94%	0.001	76%	gi|384367995|NP_001244936.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodon	43.9	43.9	94%	0.001	82%	gi|731464182|XP_010586424.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera	43.9	43.9	94%	0.001	82%	gi|591339998|XP_007095490.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenu	43.5	43.5	88%	0.002	81%	gi|472379594|XP_004409206.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus	42.2	42.2	94%	0.005	82%	gi|507537041|XP_004652550.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus	42.2	42.2	94%	0.005	82%	gi|465986750|XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops	42.2	42.2	94%	0.005	82%	gi|470626535|XP_004320390.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela	41.8	41.8	88%	0.007	81%	gi|511826454|XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Monodel	40.9	40.9	88%	0.013	81%	gi|612006645|XP_003340675.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephant	40.9	40.9	88%	0.013	81%	gi|585672710|XP_006889619.1
☐	selenoprotein P precursor [Cricetulus griseus]	40.9	40.9	94%	0.013	76%	gi|379056379|NP_001243807.1
☐	selenoprotein P precursor [Canis lupus familiaris]	40.5	40.5	94%	0.018	76%	gi|169403968|NP_001108590.1
☐	PREDICTED: selenoprotein P-like [Ailuropoda melanoleuca]	40.1	40.1	94%	0.022	76%	gi|301772662|XP_002921760.1
☐	unnamed protein product [Mus musculus]	40.1	40.1	88%	0.025	75%	gi|74198358|BAE39664.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	40.1	40.1	94%	0.025	76%	gi|744538058|XP_010999134.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	40.1	40.1	94%	0.025	76%	gi|560931717|XP_006191986.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna	40.1	40.1	94%	0.025	76%	gi|560970802|XP_006207756.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus m	40.1	40.1	94%	0.025	76%	gi|670999853|XP_008690806.1
☐	selenoprotein P precursor [Rattus norvegicus]	39.7	39.7	88%	0.034	75%	gi|15011857|NP_062065.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bis	39.7	39.7	94%	0.034	76%	gi|742088280|XP_010831114.1
☐	selenoprotein P [Bos taurus]	39.7	39.7	94%	0.034	76%	gi|6006351|BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mut	39.7	39.7	94%	0.034	76%	gi|555965745|XP_005894930.1

☐	selenoprotein P precursor [Bos taurus]	39.7	39.7	94%	0.034	76%	gi|156631001|NP_776884.2
☐	selenoprotein P [Bubalus bubalis]	39.7	39.7	94%	0.034	76%	gi|430001945|AFM77782.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Oryctero	38.8	38.8	94%	0.063	76%	gi|634885032|XP_007952213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceu	38.8	38.8	88%	0.063	75%	gi|617575753|XP_007517681.1
☐	unnamed protein product [Mus musculus]	38.0	38.0	88%	0.12	75%	gi|74213751|BAC55264.3
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Dasypus	37.5	37.5	94%	0.16	76%	gi|488512454|XP_004448278.1
☐	PREDICTED: selenoprotein P [Sarcophilus harrisii]	37.1	37.1	88%	0.21	75%	gi|395511426|XP_003759960.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Gorilla g	36.7	36.7	55%	0.29	100%	gi|426384833|XP_004065356.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Condylu	36.3	36.3	94%	0.42	71%	gi|507934338|XP_004678402.1
☐	selenoprotein P precursor [Oryctolagus cuniculus]	35.8	35.8	88%	0.57	75%	gi|315434200|NP_001186775.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ochoton	35.4	35.4	88%	0.77	75%	gi|504142600|XP_004583736.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops	34.1	34.1	94%	2.0	71%	gi|507708621|XP_004716992.1
☐	putative ATP-dependent RNA helicase DDX60-like protein [Cricetul	33.7	33.7	83%	2.8	81%	gi|537270315|ERE91786.1
☐	PREDICTED: probable ATP-dependent RNA helicase DDX60 [Cric	33.7	33.7	83%	2.8	81%	gi|625189695|XP_003498842.2
☐	selenoprotein P-like protein [Bos taurus]	33.3	33.3	94%	3.2	71%	gi|13366148|BAB39395.1
☐	selenoprotein P-like protein [Bos taurus]	33.3	33.3	94%	3.2	71%	gi|13366146|BAB39394.1
☐	selenoprotein P-like protein [Bos taurus]	33.3	33.3	94%	3.3	71%	gi|13366144|BAB39393.1
☐	selenoprotein P-like protein [Bos taurus]	33.3	33.3	94%	3.3	71%	gi|13366142|BAB39392.1
☐	selenoprotein P-like protein [Bos taurus]	33.3	33.3	94%	3.6	71%	gi|1582026|2117379A
☐	selenoprotein P like protein [Bos taurus]	33.3	33.3	94%	3.6	71%	gi|14970947|BAA04949.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ictidomy	31.2	31.2	83%	17	67%	gi|532079811|XP_005325668.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Leptonyc	31.2	31.2	94%	17	65%	gi|585192742|XP_006747601.1
☐	dihydroxy-acid dehydratase [Campylobacter sp. FOBRC14]	31.2	31.2	66%	17	73%	gi|497335253|WP_009649466.1
☐	unnamed protein product [Mus musculus]	31.2	31.2	77%	17	80%	gi|26331444|BAC29452.1
☐	Ddx60 protein [Mus musculus]	31.2	31.2	77%	17	80%	gi|27696190|AAH43663.1
☐	RNA-binding protein (NOP10, NOLA3) [uncultured marine thaumarc	30.8	30.8	94%	18	65%	gi|663514510|AIF05018.1

⊟ Alignments

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]

Sequence ID: gi|675710689|ref|XP_008961588.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 171 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	7e-10	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    KCGNCSLTTLKDEDFCKR  18
            KCGNCSLTTLKDEDFCKR
Sbjct  171  KCGNCSLTTLKDEDFCKR  188
```

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gi|34783648|gb|AAH46152.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 171 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	7e-10	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    KCGNCSLTTLKDEDFCKR  18
            KCGNCSLTTLKDEDFCKR
Sbjct  171  KCGNCSLTTLKDEDFCKR  188
```

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selenoprotein P isoform 1 precursor [Homo sapiens]

Sequence ID: gi|62530391|ref|NP_005401.3| **Length:** 381 **Number of Matches:** 1

▷ See 4 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 171 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	7e-10	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    KCGNCSLTTLKDEDFCKR  18
            KCGNCSLTTLKDEDFCKR
Sbjct  171  KCGNCSLTTLKDEDFCKR  188
```

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gi|37596694|gb|AAH58919.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 171 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	7e-10	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    KCGNCSLTTLKDEDFCKR  18
            KCGNCSLTTLKDEDFCKR
Sbjct  171  KCGNCSLTTLKDEDFCKR  188
```

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selenoprotein P [Homo sapiens]

Sequence ID: gi|312004116|emb|CAA77836.2| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 171 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
62.6 bits(140)	7e-10	18/18(100%)	18/18(100%)	0/18(0%)

```
Query  1    KCGNCSLTTLKDEDFCKR  18
            KCGNCSLTTLKDEDFCKR
Sbjct  171  KCGNCSLTTLKDEDFCKR  188
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

SEPP1_KCGNCSLTTLKDEDFCKRV_NonMod

RID BE84ZGUS014 (Expires on 01-16 09:06 am)

Query ID lcl|87215
Description None
Molecule type amino acid
Query Length 19

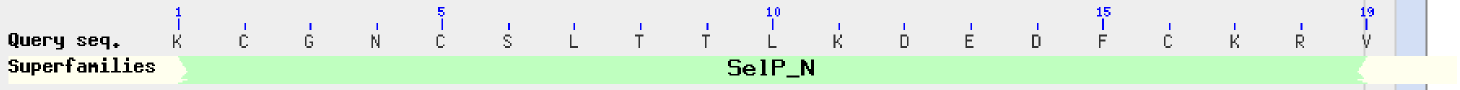
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

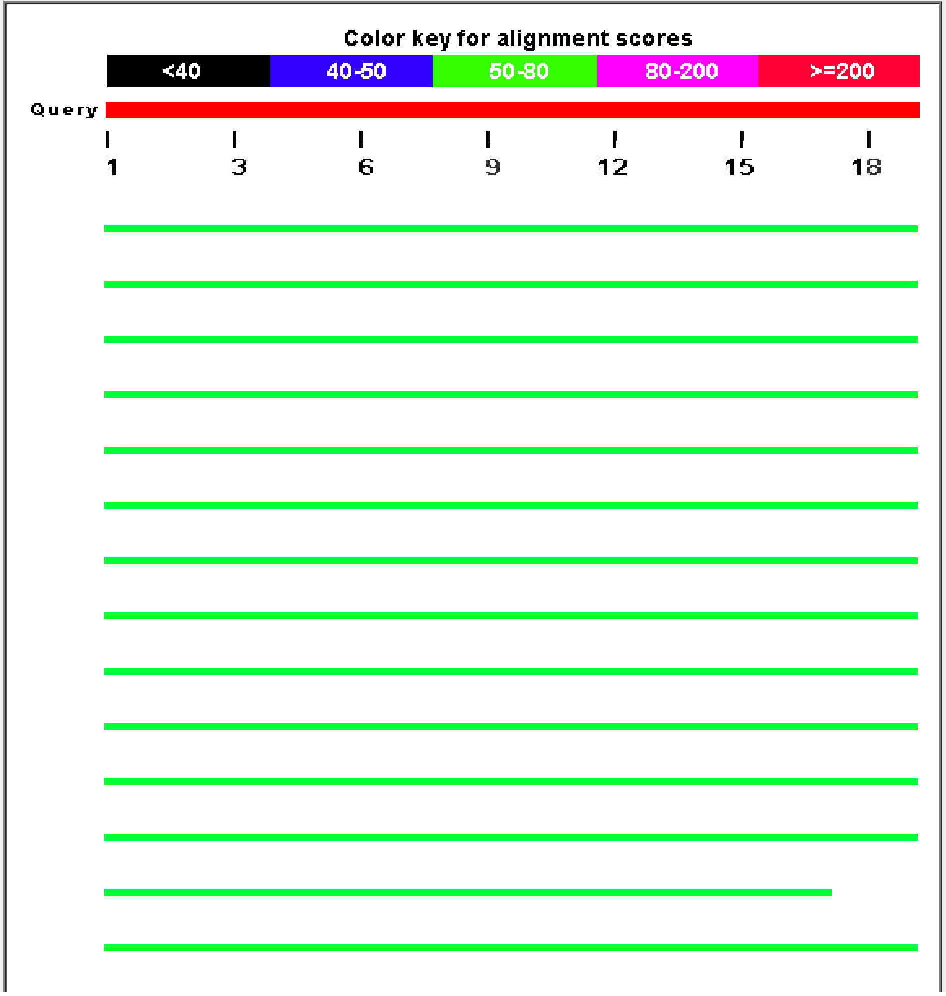
Show Conserved Domains

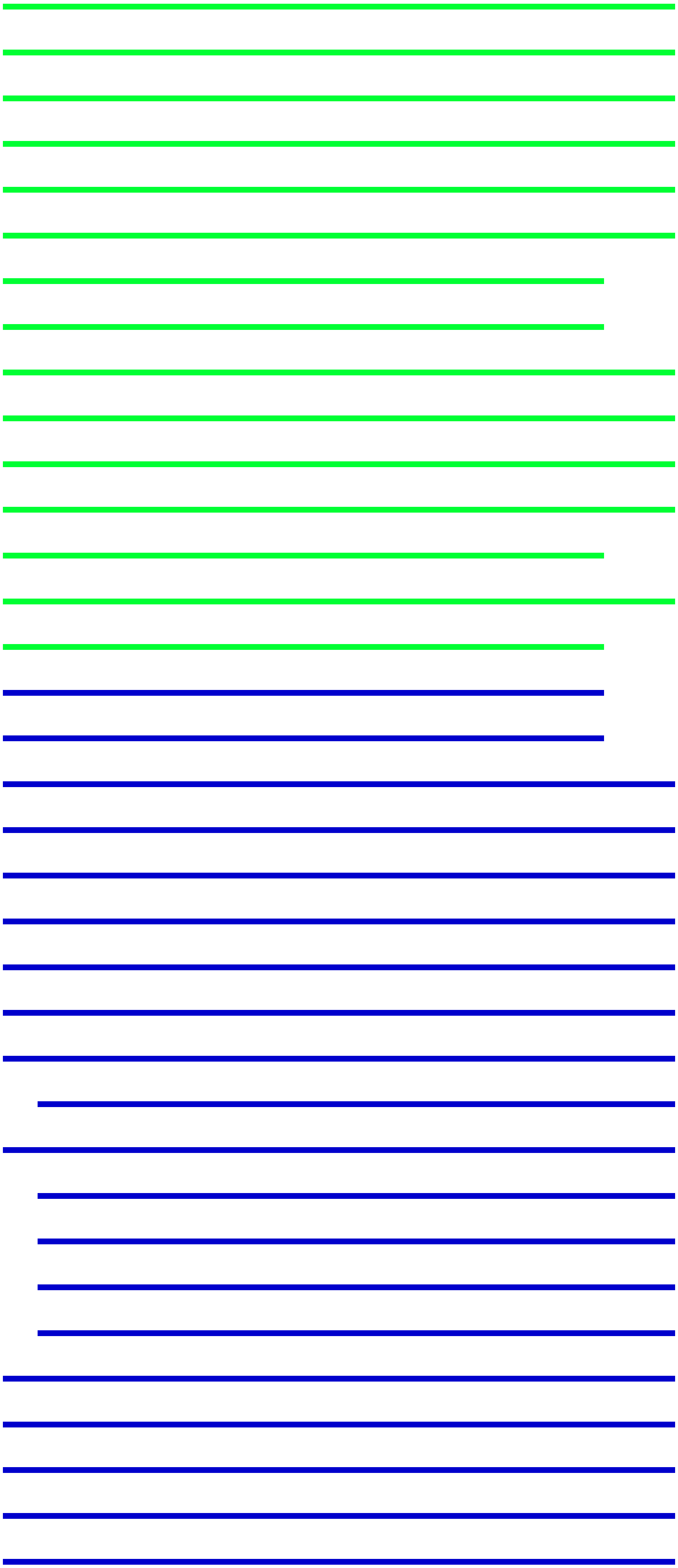
Putative conserved domains have been detected, click on the image below for detailed results.

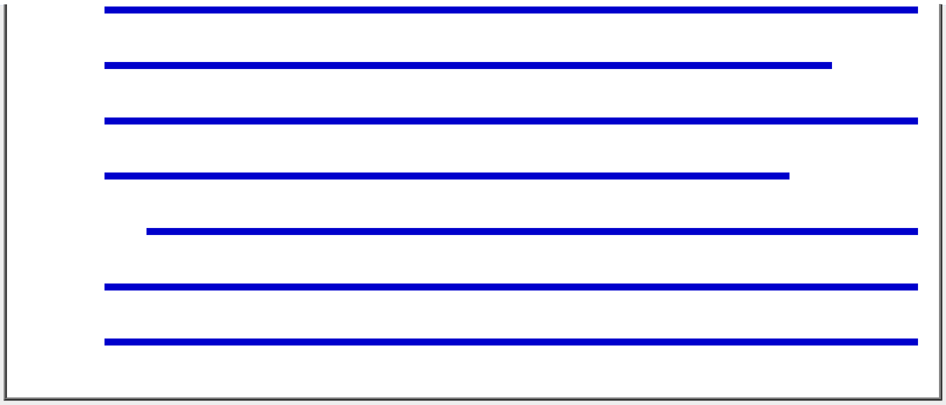


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan pani	65.5	65.5	100%	8e-11	100%	gi|675710689|XP_008961588.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	65.5	65.5	100%	8e-11	100%	gi|34783648|AAH46152.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	65.5	65.5	100%	8e-11	100%	gi|62530391|NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	65.5	65.5	100%	8e-11	100%	gi|37596694|AAH58919.1
☐	selenoprotein P [Homo sapiens]	65.5	65.5	100%	8e-11	100%	gi|312004116|CAA77836.2
☐	selenoprotein P precursor [Pan troglodytes]	65.5	65.5	100%	8e-11	100%	gi|169403955|NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	65.5	65.5	100%	8e-11	100%	gi|148277022|NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio ar	60.9	60.9	100%	3e-09	95%	gi|685545348|XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chloroce	60.9	60.9	100%	3e-09	95%	gi|635028004|XP_007959679.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	60.9	60.9	100%	3e-09	95%	gi|34783164|AAH15875.1
☐	selenoprotein P precursor [Macaca mulatta]	60.9	60.9	100%	3e-09	95%	gi|226958322|NP_001152962.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri b	59.6	59.6	100%	8e-09	95%	gi|725563213|XP_003925940.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopitl	59.2	59.2	89%	1e-08	100%	gi|724878613|XP_010372696.1
☐	selenoprotein P precursor [Pongo abelii]	55.8	55.8	100%	2e-07	89%	gi|197101233|NP_001127462.1
☐	selenoprotein P precursor [Sus scrofa]	55.4	55.4	100%	2e-07	89%	gi|198282079|NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis d	54.9	54.9	100%	3e-07	89%	gi|584060316|XP_006774623.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicu	54.9	54.9	100%	3e-07	89%	gi|641727491|XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis b	54.9	54.9	100%	3e-07	89%	gi|554563465|XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomascı	54.9	54.9	100%	3e-07	89%	gi|332250603|XP_003274442.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia c	54.5	54.5	100%	4e-07	89%	gi|562878609|XP_006167023.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lu	54.5	54.5	89%	4e-07	94%	gi|558205011|XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichech	54.5	54.5	89%	4e-07	94%	gi|471413922|XP_004388500.1
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	54.1	54.1	100%	6e-07	89%	gi|395840394|XP_003793045.1
☐	selenoprotein P precursor [Callithrix jacchus]	52.8	52.8	100%	2e-06	84%	gi|315630400|NP_001186857.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius s	52.4	52.4	100%	2e-06	84%	gi|640790108|XP_008050904.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromys	52.0	52.0	100%	3e-06	84%	gi|589969345|XP_006997157.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex ar	51.5	51.5	89%	4e-06	88%	gi|505790024|XP_004605590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchill	50.7	50.7	100%	9e-06	84%	gi|533143496|XP_005386312.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratoth	50.7	50.7	89%	9e-06	88%	gi|478496995|XP_004422836.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus pr	49.8	49.8	89%	2e-05	88%	gi|664731166|XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	49.8	49.8	89%	2e-05	88%	gi|208022673|NP_001129077.1
☐	Selenoprotein P [Heterocephalus glaber]	49.4	49.4	100%	2e-05	84%	gi|351695949|EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys	49.4	49.4	100%	2e-05	84%	gi|731237262|XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus	49.4	49.4	100%	2e-05	79%	gi|532054271|XP_005369861.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	49.4	49.4	100%	2e-05	84%	gi|512973043|XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	49.4	49.4	100%	2e-05	84%	gi|512816050|XP_004878213.1
☐	selenoprotein P precursor [Cricetulus griseus]	47.7	47.7	100%	8e-05	79%	gi|537231220|ERE84145.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodon	46.9	46.9	100%	2e-04	79%	gi|731464182|XP_010586424.1
☐	selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	46.4	46.4	94%	2e-04	78%	gi|148671458|EDL03405.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Octodon	46.4	46.4	100%	2e-04	79%	gi|507690845|XP_004641866.1
☐	Selenoprotein P, plasma, 1 [Mus musculus]	46.4	46.4	94%	2e-04	78%	gi|34809553|AAH01991.2
☐	plasma selenoprotein P [Mus musculus]	46.4	46.4	94%	2e-04	78%	gi|4103142|AAD01684.1
☐	unnamed protein product [Mus musculus]	46.4	46.4	94%	2e-04	78%	gi|74192879|BAE34948.1
☐	selenoprotein P precursor [Mus musculus]	46.4	46.4	94%	2e-04	78%	gi|74271806|NP_033181.3
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaeno	46.0	46.0	100%	3e-04	79%	gi|594696840|XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physete	46.0	46.0	100%	3e-04	79%	gi|593761497|XP_007119423.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus	46.0	46.0	100%	3e-04	79%	gi|594087306|XP_006067130.1
☐	membrane selenoprotein P [Capra hircus]	45.6	45.6	100%	4e-04	79%	gi|7677620|AAF67201.1
☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	45.6	45.6	100%	4e-04	79%	gi|550822255|NP_001272511.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis arie	45.6	45.6	100%	4e-04	79%	gi|426246564|XP_004017062.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes v	45.6	45.6	89%	4e-04	82%	gi|602724444|XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopte	44.8	44.8	100%	8e-04	79%	gi|667253652|XP_008564915.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannosp	44.8	44.8	84%	8e-04	88%	gi|674066756|XP_008840327.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenu	44.8	44.8	94%	8e-04	78%	gi|472379594|XP_004409206.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera	44.8	44.8	100%	8e-04	79%	gi|591339998|XP_007095490.1
☐	selenoprotein P precursor [Cavia porcellus]	44.3	44.3	100%	0.001	74%	gi|384367995|NP_001244936.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus	42.6	42.6	100%	0.004	79%	gi|465986750|XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops	42.6	42.6	100%	0.004	79%	gi|470626535|XP_004320390.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus	42.2	42.2	89%	0.005	82%	gi|507537041|XP_004652550.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela	41.8	41.8	84%	0.008	81%	gi|511826454|XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	41.8	41.8	100%	0.008	74%	gi|744538058|XP_010999134.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	41.8	41.8	100%	0.008	74%	gi|560931717|XP_006191986.1
☐	selenoprotein P precursor [Canis lupus familiaris]	41.8	41.8	100%	0.008	74%	gi|169403968|NP_001108590.1
☐	PREDICTED: selenoprotein P-like [Ailuropoda melanoleuca]	41.4	41.4	100%	0.009	74%	gi|301772662|XP_002921760.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Monodel	41.4	41.4	94%	0.010	78%	gi|612006645|XP_003340675.2
☐	selenoprotein P precursor [Cricetulus griseus]	41.4	41.4	100%	0.010	74%	gi|379056379|NP_001243807.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus m	41.4	41.4	100%	0.010	74%	gi|670999853|XP_008690806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephant	40.9	40.9	84%	0.014	81%	gi|585672710|XP_006889619.1
☐	unnamed protein product [Mus musculus]	40.5	40.5	94%	0.019	72%	gi|74198358|BAE39664.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna	40.5	40.5	100%	0.019	74%	gi|560970802|XP_006207756.1
☐	selenoprotein P precursor [Rattus norvegicus]	40.1	40.1	94%	0.027	72%	gi|15011857|NP_062065.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bis	40.1	40.1	100%	0.027	74%	gi|742088280|XP_010831114.1
☐	selenoprotein P [Bos taurus]	40.1	40.1	100%	0.027	74%	gi|6006351|BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mut	40.1	40.1	100%	0.027	74%	gi|555965745|XP_005894930.1

☐	selenoprotein P precursor [Bos taurus]	40.1	40.1	100%	0.027	74%	gi|156631001|NP_776884.2
☐	selenoprotein P [Bubalus bubalis]	40.1	40.1	100%	0.027	74%	gi|430001945|AFM77782.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Gorilla g	39.7	39.7	57%	0.034	100%	gi|426384833|XP_004065356.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Oryctero	38.8	38.8	89%	0.067	76%	gi|634885032|XP_007952213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceu	38.8	38.8	84%	0.068	75%	gi|617575753|XP_007517681.1
☐	unnamed protein product [Mus musculus]	38.4	38.4	94%	0.093	72%	gi|74213751|BAC55264.3
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Dasypus	37.5	37.5	89%	0.17	76%	gi|488512454|XP_004448278.1
☐	PREDICTED: selenoprotein P [Sarcophilus harrisii]	37.1	37.1	84%	0.23	75%	gi|395511426|XP_003759960.1
☐	selenoprotein P precursor [Oryctolagus cuniculus]	36.3	36.3	94%	0.44	72%	gi|315434200|NP_001186775.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Condylu	36.3	36.3	89%	0.44	71%	gi|507934338|XP_004678402.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ochoton	35.8	35.8	94%	0.60	72%	gi|504142600|XP_004583736.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops	34.1	34.1	89%	2.1	71%	gi|507708621|XP_004716992.1
☐	selenoprotein P-like protein [Bos taurus]	33.7	33.7	100%	2.5	68%	gi|13366148|BAB39395.1
☐	selenoprotein P-like protein [Bos taurus]	33.7	33.7	100%	2.5	68%	gi|13366146|BAB39394.1
☐	selenoprotein P-like protein [Bos taurus]	33.7	33.7	100%	2.6	68%	gi|13366144|BAB39393.1
☐	selenoprotein P-like protein [Bos taurus]	33.7	33.7	100%	2.6	68%	gi|13366142|BAB39392.1
☐	selenoprotein P-like protein [Bos taurus]	33.7	33.7	100%	2.8	68%	gi|1582026|2117379A
☐	selenoprotein P like protein [Bos taurus]	33.7	33.7	100%	2.8	68%	gi|14970947|BAA04949.2
☐	putative ATP-dependent RNA helicase DDX60-like protein [Cricetul	33.7	33.7	78%	3.0	81%	gi|537270315|ERE91786.1
☐	PREDICTED: probable ATP-dependent RNA helicase DDX60 [Cric	33.7	33.7	78%	3.0	81%	gi|625189695|XP_003498842.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Leptonyc	32.5	32.5	100%	7.2	63%	gi|585192742|XP_006747601.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ictidomy	31.6	31.6	94%	13	61%	gi|532079811|XP_005325668.1
☐	dihydroxy-acid dehydratase [Campylobacter sp. FOBRC14]	31.2	31.2	63%	19	73%	gi|497335253|WP_009649466.1
☐	unnamed protein product [Mus musculus]	31.2	31.2	73%	19	80%	gi|26331444|BAC29452.1
☐	Ddx60 protein [Mus musculus]	31.2	31.2	73%	19	80%	gi|27696190|AAH43663.1
☐	probable ATP-dependent RNA helicase DDX60 [Mus musculus]	31.2	31.2	73%	19	80%	gi|657940862|NP_001280712.1

⊟ Alignments

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]

Sequence ID: gi|675710689|ref|XP_008961588.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 171 to 189 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	8e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KCGNCSLTTLKDEDFCKRV  19
            KCGNCSLTTLKDEDFCKRV
Sbjct  171  KCGNCSLTTLKDEDFCKRV  189
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gi|34783648|gb|AAH46152.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 171 to 189 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	8e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KCGNCSLTTLKDEDFCKRV  19
            KCGNCSLTTLKDEDFCKRV
Sbjct  171  KCGNCSLTTLKDEDFCKRV  189
```

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selenoprotein P isoform 1 precursor [Homo sapiens]

Sequence ID: gi|62530391|ref|NP_005401.3| **Length:** 381 **Number of Matches:** 1

▷ See 4 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 171 to 189 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	8e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KCGNCSLTTLKDEDFCKRV  19
            KCGNCSLTTLKDEDFCKRV
Sbjct  171  KCGNCSLTTLKDEDFCKRV  189
```

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gi|37596694|gb|AAH58919.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 171 to 189 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	8e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KCGNCSLTTLKDEDFCKRV  19
            KCGNCSLTTLKDEDFCKRV
Sbjct  171  KCGNCSLTTLKDEDFCKRV  189
```

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selenoprotein P [Homo sapiens]

Sequence ID: gi|312004116|emb|CAA77836.2| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 171 to 189 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	8e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KCGNCSLTTLKDEDFCKRV  19
            KCGNCSLTTLKDEDFCKRV
Sbjct  171  KCGNCSLTTLKDEDFCKRV  189
```

BLAST ® *Basic Local Alignment Search Tool*

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SEPP1_KEGYSDISYIVVNHQGISSRL_Mod

RID BVKRP2S601R (Expires on 01-21 10:43 am)

Query ID lcl|379850
Description None
Molecule type amino acid
Query Length 21

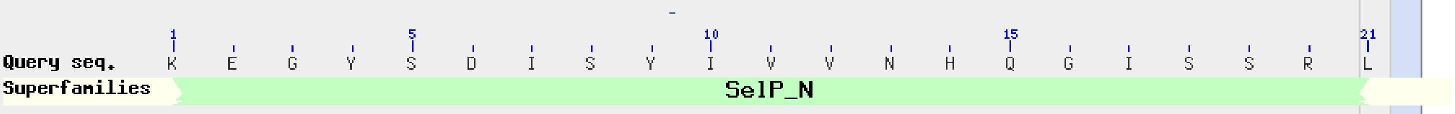
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

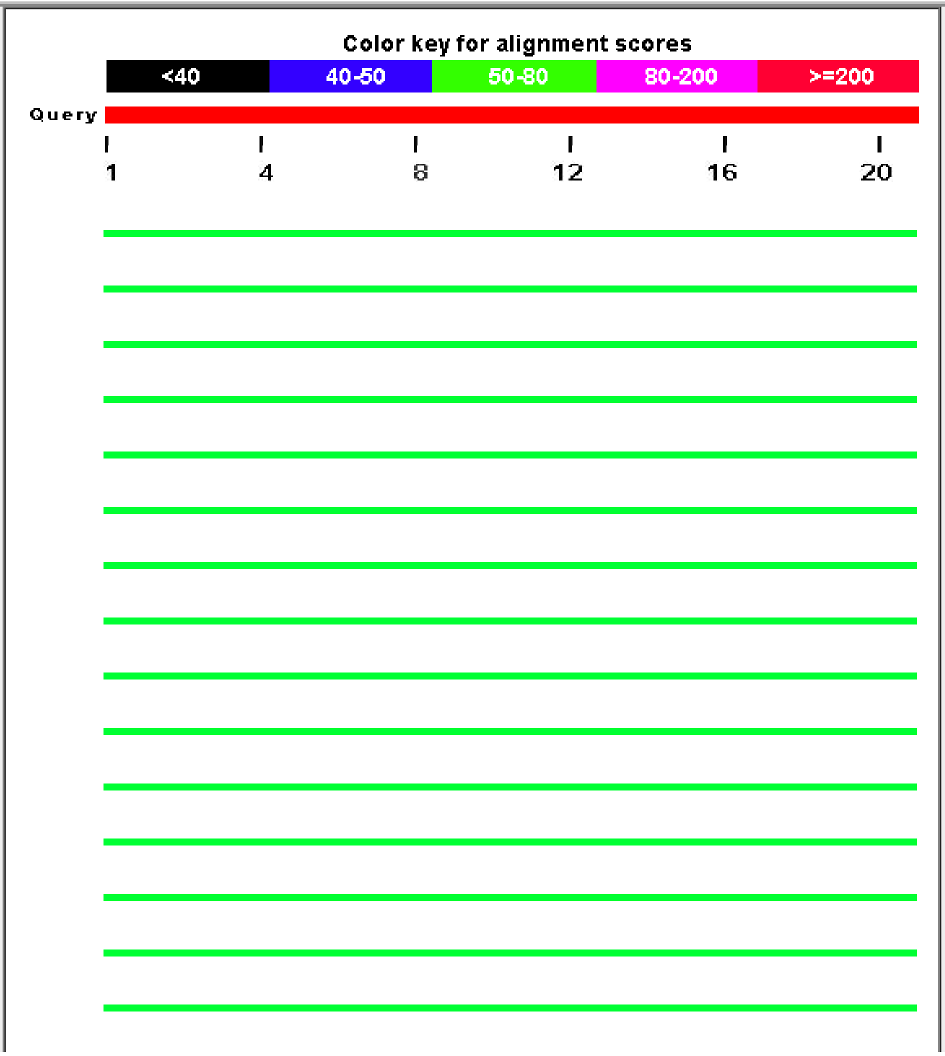
Show Conserved Domains

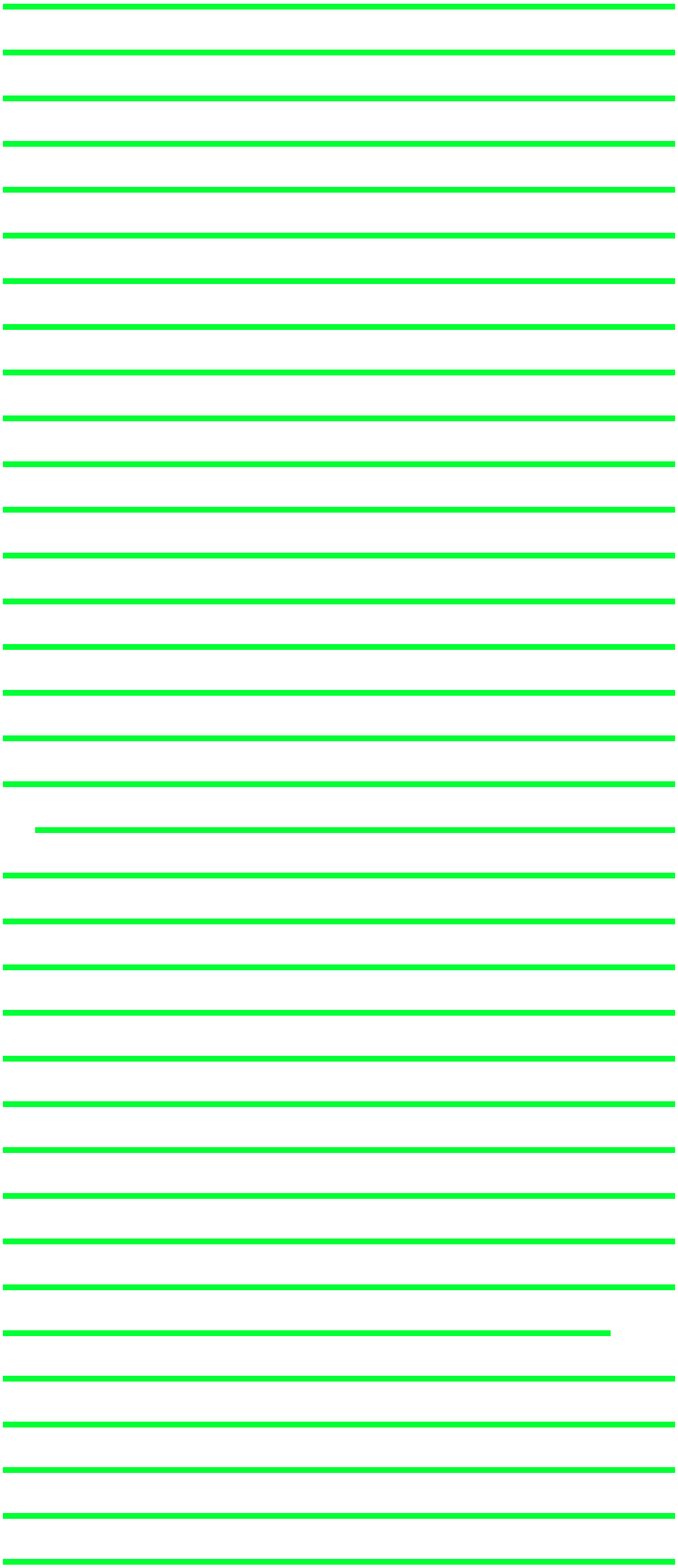
Putative conserved domains have been detected, click on the image below for detailed results.

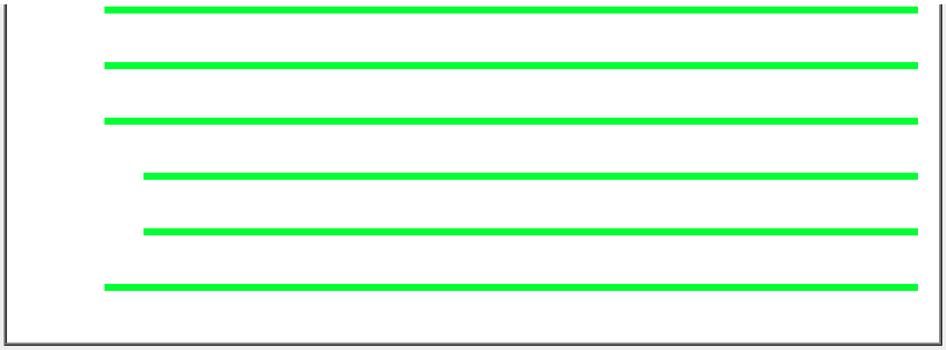


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxe	67.2	67.2	100%	3e-11	95%	XP_010372696.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]	67.2	67.2	100%	3e-11	95%	XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]	67.2	67.2	100%	3e-11	95%	XP_008961588.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocebus sabae	67.2	67.2	100%	3e-11	95%	XP_007959679.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	67.2	67.2	100%	3e-11	95%	AAH46152.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	67.2	67.2	100%	3e-11	95%	AAH15875.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	67.2	67.2	100%	3e-11	95%	NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	67.2	67.2	100%	3e-11	95%	AAH58919.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomascus leucoge	67.2	67.2	100%	3e-11	95%	XP_003274442.1
☐	selenoprotein P [Homo sapiens]	67.2	67.2	100%	3e-11	95%	CAA77836.2
☐	selenoprotein P precursor [Macaca mulatta]	67.2	67.2	100%	3e-11	95%	NP_001152962.1
☐	selenoprotein P precursor [Pan troglodytes]	67.2	67.2	100%	3e-11	95%	NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	67.2	67.2	100%	3e-11	95%	NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaenoptera acuto	64.7	64.7	100%	2e-10	90%	XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes vexillifer]	64.7	64.7	100%	2e-10	90%	XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus orca]	64.7	64.7	100%	2e-10	90%	XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physeter catodon]	64.7	64.7	100%	2e-10	90%	XP_007119423.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops truncatus]	64.7	64.7	100%	2e-10	90%	XP_004320390.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bison bison]	64.7	64.7	100%	2e-10	90%	XP_010831114.1
☐	selenoprotein P [Bos taurus]	64.7	64.7	100%	2e-10	90%	BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mutus]	64.7	64.7	100%	2e-10	90%	XP_005894930.1
☐	selenoprotein P-like protein [Bos taurus]	64.7	64.7	100%	2e-10	90%	2117379A
☐	selenoprotein P like protein [Bos taurus]	64.7	64.7	100%	2e-10	90%	BAA04949.2
☐	selenoprotein P precursor [Bos taurus]	64.7	64.7	100%	2e-10	90%	NP_776884.2
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	63.0	63.0	100%	7e-10	90%	XP_003793045.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ictidomys tridecem	63.0	63.0	100%	8e-10	90%	XP_005325668.1
☐	selenoprotein P precursor [Pongo abelii]	61.7	61.7	100%	2e-09	90%	NP_001127462.1
☐	membrane selenoprotein P [Capra hircus]	60.4	60.4	100%	5e-09	86%	AAF67201.1
☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	60.4	60.4	100%	6e-09	86%	NP_001272511.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis aries]	60.4	60.4	100%	6e-09	86%	XP_004017062.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannospalax galili]	60.4	60.4	100%	6e-09	86%	XP_008840327.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratotherium simu	60.4	60.4	100%	6e-09	86%	XP_004422836.1
☐	selenoprotein P precursor [Sus scrofa]	60.4	60.4	100%	6e-09	86%	NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus jaculus]	60.0	60.0	95%	8e-09	90%	XP_004652550.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus bubalis]	59.6	59.6	100%	1e-08	81%	XP_006067130.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus przewalskii]	57.9	57.9	100%	4e-08	81%	XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	57.9	57.9	100%	4e-08	81%	NP_001129077.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri boliviensis l	57.1	57.1	100%	8e-08	81%	XP_003925940.2
☐	selenoprotein P precursor [Callithrix jacchus]	57.1	57.1	100%	8e-08	81%	NP_001186857.1
☐	selenoprotein P [Bubalus bubalis]	57.1	57.1	100%	8e-08	81%	AFM77782.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ochotona princeps	56.2	56.2	100%	2e-07	81%	XP_004583736.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius syrichta]	55.8	55.8	100%	2e-07	76%	XP_008050904.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia chinensis]	55.4	55.4	100%	3e-07	81%	XP_006167023.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna pacos]	54.9	54.9	100%	4e-07	76%	XP_006207756.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Octodon degus]	54.5	54.5	90%	6e-07	84%	XP_004641866.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orycteropus afer af	54.1	54.1	100%	8e-07	76%	XP_007952213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis brandtii]	54.1	54.1	100%	8e-07	76%	XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchilla lanigera]	54.1	54.1	100%	8e-07	76%	XP_005386312.1
☐	selenoprotein P precursor [Oryctolagus cuniculus]	54.1	54.1	100%	8e-07	76%	NP_001186775.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephantulus edwa	53.7	53.7	100%	1e-06	76%	XP_006889619.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Dasypus novemcin	52.8	52.8	100%	2e-06	76%	XP_004448278.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus dromedar	52.4	52.4	100%	3e-06	76%	XP_010999134.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus ferus]	52.4	52.4	100%	3e-06	76%	XP_006191986.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromyscus manic	51.1	51.1	95%	8e-06	80%	XP_006997157.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ornithorhynchus ar	50.7	50.7	95%	1e-05	75%	XP_007654576.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys damarens	50.7	50.7	100%	1e-05	76%	XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lucifugus]	50.7	50.7	100%	1e-05	76%	XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela putorius fu	50.7	50.7	100%	1e-05	76%	XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Leptonychotes wec	50.7	50.7	100%	1e-05	76%	XP_006747601.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenus rosmaru	50.7	50.7	100%	1e-05	76%	XP_004409206.1
☐	Selenoprotein P [Heterocephalus glaber]	50.3	50.3	100%	1e-05	71%	EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopterus varieg	50.3	50.3	100%	1e-05	76%	XP_008564915.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicus fuscus]	50.3	50.3	100%	1e-05	71%	XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichechus manatu	50.3	50.3	100%	1e-05	76%	XP_004388500.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Monodelphis dome	50.3	50.3	95%	1e-05	75%	XP_003340675.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gla	50.3	50.3	100%	1e-05	71%	XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gla	50.3	50.3	100%	1e-05	71%	XP_004878213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodonta africana	49.8	49.8	100%	2e-05	67%	XP_010586424.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis davidii]	49.0	49.0	100%	4e-05	71%	XP_006774623.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Felis catus]	48.6	48.6	90%	5e-05	79%	XP_006928143.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera tigris alta	48.6	48.6	90%	5e-05	79%	XP_007095490.1
☐	PREDICTED: selenoprotein P [Sarcophilus harrisii]	47.7	47.7	95%	1e-04	75%	XP_003759960.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Condylura cristata]	47.7	47.7	76%	1e-04	81%	XP_004678402.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus ochrogast	47.3	47.3	95%	1e-04	75%	XP_005369861.1
☐	selenoprotein P precursor [Canis lupus familiaris]	47.3	47.3	100%	1e-04	71%	NP_001108590.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus maritimus]	47.3	47.3	100%	1e-04	71%	XP_008690806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceus europae	46.9	46.9	100%	2e-04	71%	XP_007517681.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex araneus]	46.0	46.0	95%	4e-04	70%	XP_004605590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops telfairi]	46.0	46.0	100%	4e-04	67%	XP_004716992.1
☐	Selenoprotein P [Cricetulus griseus]	45.2	45.2	95%	6e-04	70%	EGW04040.1
☐	selenoprotein P precursor [Cricetulus griseus]	45.2	45.2	95%	7e-04	70%	ERE84145.1
☐	selenoprotein P precursor [Cricetulus griseus]	45.2	45.2	95%	7e-04	70%	NP_001243807.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P, plasma, 1 [Mesocri	44.3	44.3	95%	0.001	75%	XP_005139283.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chrysochloris asiat	43.9	43.9	100%	0.002	67%	XP_006877364.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pelodiscus sinensis	43.1	43.1	85%	0.003	78%	XP_006139560.1
☐	selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	42.2	42.2	95%	0.006	70%	EDL03405.1
☐	Selenoprotein P, plasma, 1 [Mus musculus]	42.2	42.2	95%	0.006	70%	AAH01991.2
☐	plasma selenoprotein P [Mus musculus]	42.2	42.2	95%	0.006	70%	AAD01684.1
☐	unnamed protein product [Mus musculus]	42.2	42.2	95%	0.006	70%	BAE39664.1
☐	unnamed protein product [Mus musculus]	42.2	42.2	95%	0.006	70%	BAE34948.1
☐	selenoprotein P precursor [Mus musculus]	42.2	42.2	95%	0.006	70%	NP_033181.3
☐	unnamed protein product [Mus musculus]	42.2	42.2	95%	0.006	70%	BAC55264.3
☐	selenoprotein P precursor [Rattus norvegicus]	42.2	42.2	95%	0.006	70%	NP_062065.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Opisthocomus hoa	39.7	39.7	90%	0.042	74%	XP_009941970.1
☐	selenoprotein P precursor [Taeniopygia guttata]	39.2	39.2	90%	0.058	68%	NP_001257806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Alligator sinensis]	38.8	38.8	66%	0.078	79%	XP_006026767.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Phalacrocorax carb	38.8	38.8	85%	0.078	72%	XP_009511852.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Phaethon lepturus]	38.8	38.8	85%	0.078	72%	XP_010284851.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Gavia stellata]	38.8	38.8	85%	0.078	72%	XP_009818154.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Caprimulgus caroli	38.8	38.8	85%	0.079	72%	XP_010164847.1

Alignments

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxellana]

Sequence ID: ref|XP_010372696.1| **Length:** 381 **Number of Matches:** 1

Range 1: 78 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.2 bits(151)	3e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1   KEGYSDISYIVVNHQGISSRL  21
           KEGYS+ISYIVVNHQGISSRL
Sbjct  78  KEGYSNISYIVVNHQGISSRL  98
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]

Sequence ID: ref|XP_009206607.1| **Length:** 381 **Number of Matches:** 1

Range 1: 78 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.2 bits(151)	3e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1   KEGYSDISYIVVNHQGISSRL  21
           KEGYS+ISYIVVNHQGISSRL
Sbjct  78  KEGYSNISYIVVNHQGISSRL  98
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]

Sequence ID: ref|XP_008961588.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 78 to 98 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.2 bits(151)	3e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1   KEGYSDISYIVVNHQGISSRL  21
           KEGYS+ISYIVVNHQGISSRL
Sbjct  78  KEGYSNISYIVVNHQGISSRL  98
```

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocebus sabaeus]

Sequence ID: ref|XP_007959679.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 78 to 98 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.2 bits(151)	3e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1   KEGYSDISYIVVNHQGISSRL  21
           KEGYS+ISYIVVNHQGISSRL
Sbjct  78  KEGYSNISYIVVNHQGISSRL  98
```

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gb|AAH46152.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 78 to 98 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
67.2 bits(151)	3e-11	20/21(95%)	21/21(100%)	0/21(0%)

```
Query  1   KEGYSDISYIVVNHQGISSRL  21
           KEGYS+ISYIVVNHQGISSRL
Sbjct  78  KEGYSNISYIVVNHQGISSRL  98
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

SEPP1_KEGYSNISYIVVNHQGISSRL_NonMod

RID	BE8859NX015 (Expires on 01-16 09:08 am)
Query ID	lcl|50687
Description	None
Molecule type	amino acid
Query Length	21

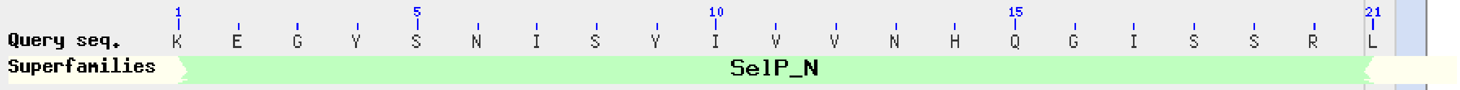
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

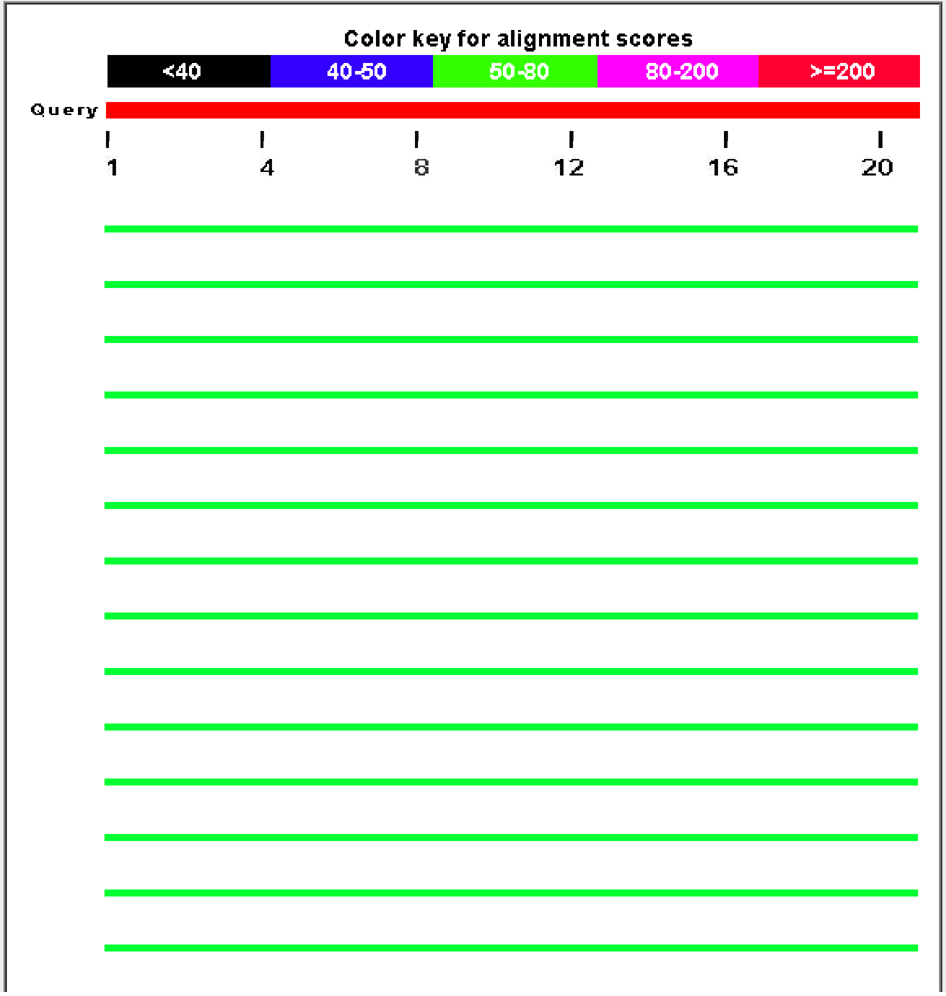
Show Conserved Domains

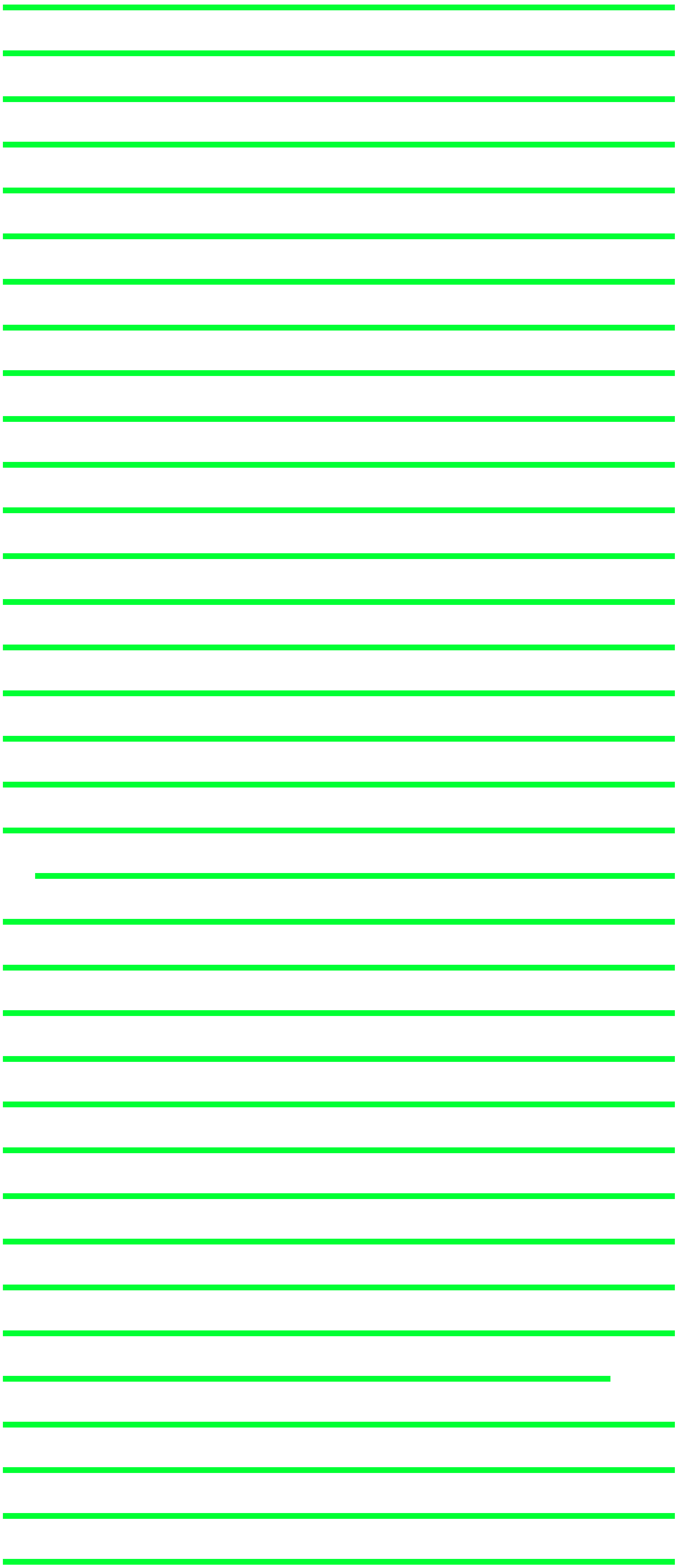
Putative conserved domains have been detected, click on the image below for detailed results.

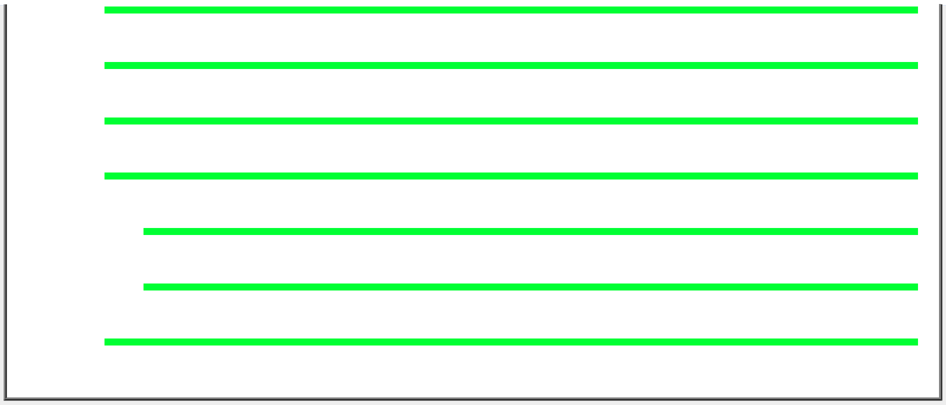


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopitl	69.8	69.8	100%	4e-12	100%	gi|724878613|XP_010372696.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio ar	69.8	69.8	100%	4e-12	100%	gi|685545348|XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan pani	69.8	69.8	100%	4e-12	100%	gi|675710689|XP_008961588.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chloroce	69.8	69.8	100%	4e-12	100%	gi|635028004|XP_007959679.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	69.8	69.8	100%	4e-12	100%	gi|34783648|AAH46152.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	69.8	69.8	100%	4e-12	100%	gi|34783164|AAH15875.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	69.8	69.8	100%	4e-12	100%	gi|62530391|NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	69.8	69.8	100%	4e-12	100%	gi|37596694|AAH58919.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomascu	69.8	69.8	100%	4e-12	100%	gi|332250603|XP_003274442.1
☐	selenoprotein P [Homo sapiens]	69.8	69.8	100%	4e-12	100%	gi|312004116|CAA77836.2
☐	selenoprotein P precursor [Macaca mulatta]	69.8	69.8	100%	4e-12	100%	gi|226958322|NP_001152962.1
☐	selenoprotein P precursor [Pan troglodytes]	69.8	69.8	100%	4e-12	100%	gi|169403955|NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	69.8	69.8	100%	4e-12	100%	gi|148277022|NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaeno	67.2	67.2	100%	3e-11	95%	gi|594696840|XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes	67.2	67.2	100%	3e-11	95%	gi|602724444|XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus	67.2	67.2	100%	3e-11	95%	gi|465986750|XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physeter	67.2	67.2	100%	3e-11	95%	gi|593761497|XP_007119423.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops	67.2	67.2	100%	3e-11	95%	gi|470626535|XP_004320390.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bis	67.2	67.2	100%	3e-11	95%	gi|742088280|XP_010831114.1
☐	selenoprotein P [Bos taurus]	67.2	67.2	100%	3e-11	95%	gi|6006351|BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mut	67.2	67.2	100%	3e-11	95%	gi|555965745|XP_005894930.1
☐	selenoprotein P-like protein [Bos taurus]	67.2	67.2	100%	3e-11	95%	gi|1582026|2117379A
☐	selenoprotein P like protein [Bos taurus]	67.2	67.2	100%	3e-11	95%	gi|14970947|BAA04949.2
☐	selenoprotein P precursor [Bos taurus]	67.2	67.2	100%	3e-11	95%	gi|156631001|NP_776884.2
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	65.5	65.5	100%	9e-11	95%	gi|395840394|XP_003793045.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ictidomy	65.5	65.5	100%	1e-10	95%	gi|532079811|XP_005325668.1
☐	selenoprotein P precursor [Pongo abelii]	64.3	64.3	100%	3e-10	95%	gi|197101233|NP_001127462.1
☐	membrane selenoprotein P [Capra hircus]	63.0	63.0	100%	6e-10	90%	gi|7677620|AAF67201.1

☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	63.0	63.0	100%	8e-10	90%	gi|550822255|NP_001272511.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis arie	63.0	63.0	100%	8e-10	90%	gi|426246564|XP_004017062.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannosp	63.0	63.0	100%	8e-10	90%	gi|674066756|XP_008840327.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratoth	63.0	63.0	100%	8e-10	90%	gi|478496995|XP_004422836.1
☐	selenoprotein P precursor [Sus scrofa]	63.0	63.0	100%	8e-10	90%	gi|198282079|NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus j	62.6	62.6	95%	1e-09	95%	gi|507537041|XP_004652550.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus	62.1	62.1	100%	2e-09	86%	gi|594087306|XP_006067130.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus pr	60.4	60.4	100%	6e-09	86%	gi|664731166|XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	60.4	60.4	100%	6e-09	86%	gi|208022673|NP_001129077.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri b	59.6	59.6	100%	1e-08	86%	gi|725563213|XP_003925940.2
☐	selenoprotein P precursor [Callithrix jacchus]	59.6	59.6	100%	1e-08	86%	gi|315630400|NP_001186857.1
☐	selenoprotein P [Bubalus bubalis]	59.6	59.6	100%	1e-08	86%	gi|430001945|AFM77782.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ochoton	58.7	58.7	100%	2e-08	86%	gi|504142600|XP_004583736.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius s	58.3	58.3	100%	3e-08	81%	gi|640790108|XP_008050904.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia c	57.9	57.9	100%	4e-08	86%	gi|562878609|XP_006167023.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna	57.5	57.5	100%	6e-08	81%	gi|560970802|XP_006207756.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Octodon	57.1	57.1	90%	8e-08	89%	gi|507690845|XP_004641866.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Oryctero	56.6	56.6	100%	1e-07	81%	gi|634885032|XP_007952213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis b	56.6	56.6	100%	1e-07	81%	gi|554563465|XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchill	56.6	56.6	100%	1e-07	81%	gi|533143496|XP_005386312.1
☐	selenoprotein P precursor [Oryctolagus cuniculus]	56.6	56.6	100%	1e-07	81%	gi|315434200|NP_001186775.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephant	56.2	56.2	100%	2e-07	81%	gi|585672710|XP_006889619.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Dasypus	55.4	55.4	100%	3e-07	81%	gi|488512454|XP_004448278.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	54.9	54.9	100%	4e-07	81%	gi|744538058|XP_010999134.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	54.9	54.9	100%	4e-07	81%	gi|560931717|XP_006191986.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromys	53.7	53.7	95%	1e-06	85%	gi|589969345|XP_006997157.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ornithorl	53.2	53.2	95%	1e-06	80%	gi|620968705|XP_007654576.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lu	53.2	53.2	100%	2e-06	81%	gi|558205011|XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela	53.2	53.2	100%	2e-06	81%	gi|511826454|XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Leptonyc	53.2	53.2	100%	2e-06	81%	gi|585192742|XP_006747601.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenu	53.2	53.2	100%	2e-06	81%	gi|472379594|XP_004409206.1
☐	Selenoprotein P [Heterocephalus glaber]	52.8	52.8	100%	2e-06	76%	gi|351695949|EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopte	52.8	52.8	100%	2e-06	81%	gi|667253652|XP_008564915.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicu	52.8	52.8	100%	2e-06	76%	gi|641727491|XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Monodel	52.8	52.8	95%	2e-06	80%	gi|612006645|XP_003340675.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	52.8	52.8	100%	2e-06	76%	gi|512973043|XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	52.8	52.8	100%	2e-06	76%	gi|512816050|XP_004878213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys	52.4	52.4	100%	3e-06	76%	gi|731237262|XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodon	52.4	52.4	100%	3e-06	71%	gi|731464182|XP_010586424.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichech	52.0	52.0	100%	4e-06	76%	gi|471413922|XP_004388500.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Felis cat	51.1	51.1	90%	7e-06	84%	gi|586975923|XP_006928143.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera	51.1	51.1	90%	8e-06	84%	gi|591339998|XP_007095490.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis d	50.7	50.7	100%	1e-05	71%	gi|584060316|XP_006774623.1
☐	PREDICTED: selenoprotein P [Sarcophilus harrisii]	50.3	50.3	95%	1e-05	80%	gi|395511426|XP_003759960.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Condylur	50.3	50.3	76%	1e-05	88%	gi|507934338|XP_004678402.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus	49.8	49.8	95%	2e-05	80%	gi|532054271|XP_005369861.1

☐	selenoprotein P precursor [Canis lupus familiaris]	49.8	49.8	100%	2e-05	76%	gi|169403968|NP_001108590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus ma	49.8	49.8	100%	2e-05	76%	gi|670999853|XP_008690806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex ar	48.6	48.6	95%	5e-05	75%	gi|505790024|XP_004605590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops	48.6	48.6	100%	5e-05	71%	gi|507708621|XP_004716992.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceu	48.1	48.1	100%	7e-05	71%	gi|617575753|XP_007517681.1
☐	Selenoprotein P [Cricetulus griseus]	47.7	47.7	95%	9e-05	75%	gi|344247936|EGW04040.1
☐	selenoprotein P precursor [Cricetulus griseus]	47.7	47.7	95%	1e-04	75%	gi|537231220|ERE84145.1
☐	selenoprotein P precursor [Cricetulus griseus]	47.7	47.7	95%	1e-04	75%	gi|379056379|NP_001243807.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P, plasma,	46.9	46.9	95%	2e-04	80%	gi|524973435|XP_005139283.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chrysocl	46.4	46.4	100%	3e-04	71%	gi|586493836|XP_006877364.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pelodisc	45.6	45.6	85%	5e-04	83%	gi|558231946|XP_006139560.1
☐	selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	44.8	44.8	95%	9e-04	75%	gi|148671458|EDL03405.1
☐	Selenoprotein P, plasma, 1 [Mus musculus]	44.8	44.8	95%	0.001	75%	gi|34809553|AAH01991.2
☐	plasma selenoprotein P [Mus musculus]	44.8	44.8	95%	0.001	75%	gi|4103142|AAD01684.1
☐	unnamed protein product [Mus musculus]	44.8	44.8	95%	0.001	75%	gi|74198358|BAE39664.1
☐	unnamed protein product [Mus musculus]	44.8	44.8	95%	0.001	75%	gi|74192879|BAE34948.1
☐	selenoprotein P precursor [Mus musculus]	44.8	44.8	95%	0.001	75%	gi|74271806|NP_033181.3
☐	unnamed protein product [Mus musculus]	44.8	44.8	95%	0.001	75%	gi|74213751|BAC55264.3
☐	selenoprotein P precursor [Rattus norvegicus]	44.8	44.8	95%	0.001	75%	gi|15011857|NP_062065.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Opisthoc	42.2	42.2	90%	0.006	79%	gi|700402061|XP_009941970.1
☐	selenoprotein P precursor [Taeniopygia guttata]	41.8	41.8	90%	0.009	74%	gi|399567825|NP_001257806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Alligator	41.4	41.4	66%	0.012	86%	gi|557288151|XP_006026767.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Phalacro	41.4	41.4	85%	0.012	78%	gi|695138937|XP_009511852.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Phaetho	41.4	41.4	85%	0.012	78%	gi|723136355|XP_010284851.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Gavia st	41.4	41.4	85%	0.012	78%	gi|698446985|XP_009818154.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Caprimu	41.4	41.4	85%	0.012	78%	gi|704307382|XP_010164847.1

Alignments

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxellana]

Sequence ID: gi|724878613|ref|XP_010372696.1| **Length:** 381 **Number of Matches:** 1

Range 1: 78 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.8 bits(157)	4e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KEGYSNISYIVVNHQGISSRL  21
            KEGYSNISYIVVNHQGISSRL
Sbjct  78   KEGYSNISYIVVNHQGISSRL  98
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]

Sequence ID: gi|685545348|ref|XP_009206607.1| **Length:** 381 **Number of Matches:** 1

Range 1: 78 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.8 bits(157)	4e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KEGYSNISYIVVNHQGISSRL  21
            KEGYSNISYIVVNHQGISSRL
Sbjct  78   KEGYSNISYIVVNHQGISSRL  98
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]

Sequence ID: gi|675710689|ref|XP_008961588.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 78 to 98 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.8 bits(157)	4e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KEGYSNISYIVVNHQGISSRL  21
            KEGYSNISYIVVNHQGISSRL
Sbjct  78   KEGYSNISYIVVNHQGISSRL  98
```

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocebus sabaeus]

Sequence ID: gi|635028004|ref|XP_007959679.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 78 to 98 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.8 bits(157)	4e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KEGYSNISYIVVNHQGISSRL  21
            KEGYSNISYIVVNHQGISSRL
Sbjct  78   KEGYSNISYIVVNHQGISSRL  98
```

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gi|34783648|gb|AAH46152.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 78 to 98 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
69.8 bits(157)	4e-12	21/21(100%)	21/21(100%)	0/21(0%)

```
Query  1    KEGYSNISYIVVNHQGISSRL  21
            KEGYSNISYIVVNHQGISSRL
Sbjct  78   KEGYSNISYIVVNHQGISSRL  98
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVKHEDWT01R

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Edit and Resubmit | Save Search Strategies | Formatting options | Download | How to read this page | Blast report description

SEPP1_KKCGDCSLTTLKD_Mod

RID	BVKHEDWT01R (Expires on 01-21 10:40 am)		
Query ID	lcl|337286	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	13	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

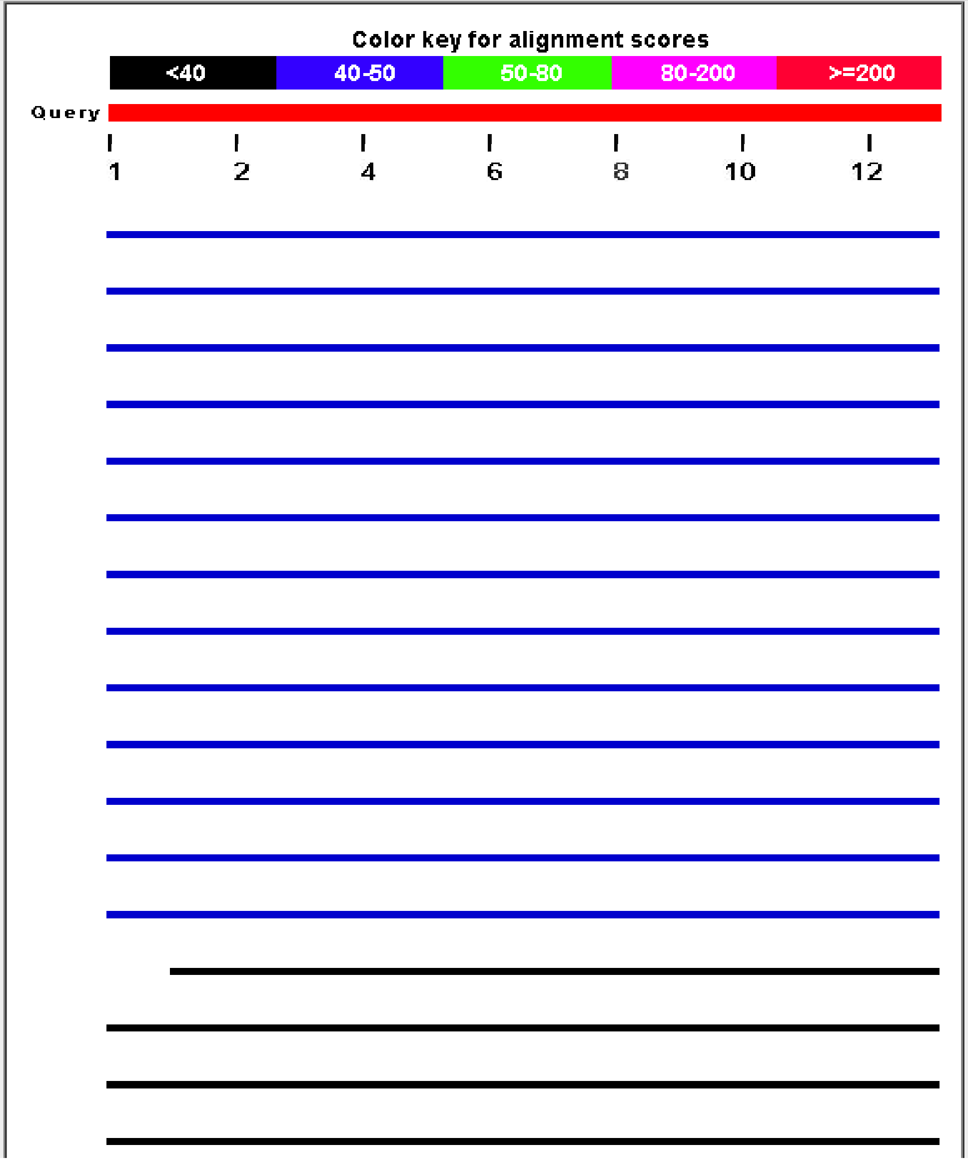
Graphic Summary

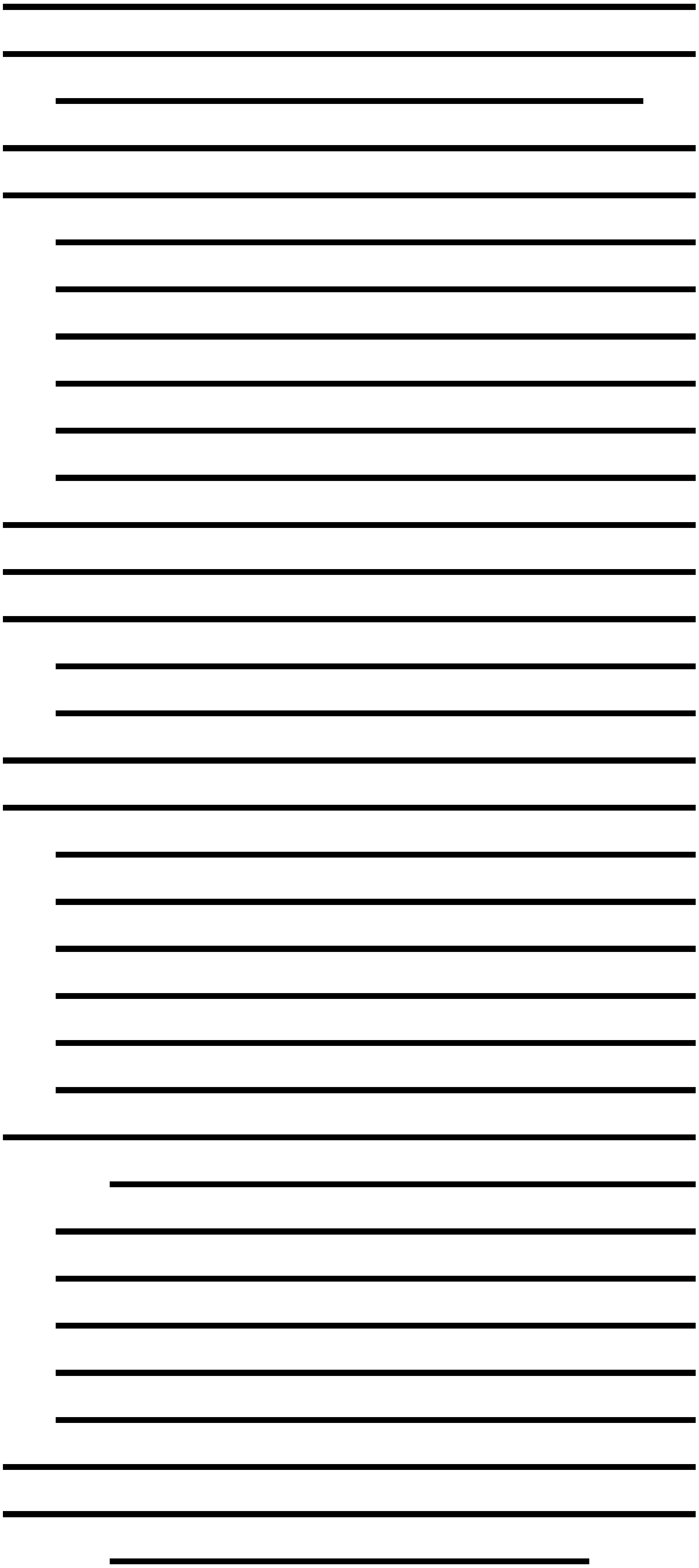
Show Conserved Domains

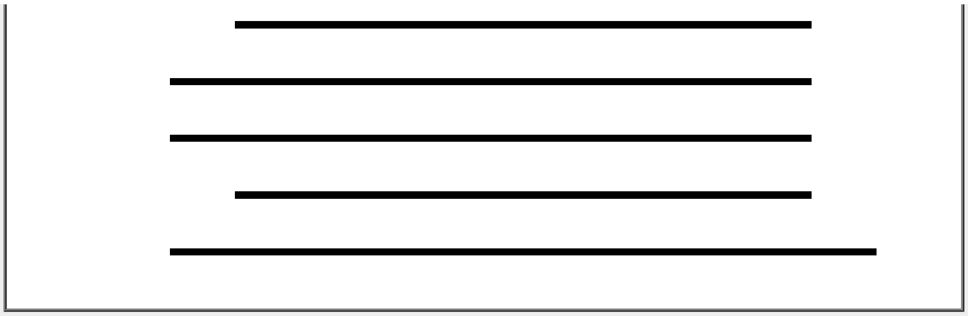
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri boliviensis	41.8	41.8	100%	0.004	92%	XP_003925940.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxe	41.8	41.8	100%	0.004	92%	XP_010372696.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]	41.8	41.8	100%	0.004	92%	XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]	41.8	41.8	100%	0.004	92%	XP_008961588.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocebus sabae	41.8	41.8	100%	0.004	92%	XP_007959679.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	41.8	41.8	100%	0.004	92%	AAH46152.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	41.8	41.8	100%	0.004	92%	AAH15875.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	41.8	41.8	100%	0.004	92%	NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	41.8	41.8	100%	0.004	92%	AAH58919.1
☐	selenoprotein P [Homo sapiens]	41.8	41.8	100%	0.004	92%	CAA77836.2
☐	selenoprotein P precursor [Macaca mulatta]	41.8	41.8	100%	0.004	92%	NP_001152962.1
☐	selenoprotein P precursor [Pan troglodytes]	41.8	41.8	100%	0.004	92%	NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	41.8	41.8	100%	0.004	92%	NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia chinensis]	38.8	38.8	92%	0.040	92%	XP_006167023.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius syrichta]	37.1	37.1	100%	0.14	85%	XP_008050904.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichechus manatu	37.1	37.1	100%	0.14	85%	XP_004388500.1
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	36.3	36.3	100%	0.26	85%	XP_003793045.1
☐	selenoprotein P precursor [Pongo abelii]	36.3	36.3	100%	0.27	92%	NP_001127462.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomascus leucoge	35.8	35.8	100%	0.38	85%	XP_003274442.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex araneus]	35.4	35.4	84%	0.52	91%	XP_004605590.1
☐	selenoprotein P precursor [Callithrix jacchus]	35.0	35.0	100%	0.72	77%	NP_001186857.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratotherium simu	34.6	34.6	100%	0.98	85%	XP_004422836.1
☐	selenoprotein P precursor [Sus scrofa]	34.6	34.6	92%	0.98	83%	NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis davidii]	34.1	34.1	92%	1.3	83%	XP_006774623.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lucifugus]	34.1	34.1	92%	1.3	83%	XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicus fuscus]	34.1	34.1	92%	1.3	83%	XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis brandtii]	34.1	34.1	92%	1.3	83%	XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela putorius fu	34.1	34.1	92%	1.3	79%	XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephantulus edwa	32.9	32.9	100%	3.5	77%	XP_006889619.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus przewalskii]	32.5	32.5	100%	4.8	77%	XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	32.5	32.5	100%	4.8	77%	NP_001129077.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus ochrogast	31.2	31.2	92%	12	75%	XP_005369861.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromyscus manic	31.2	31.2	92%	12	75%	XP_006997157.1
☐	methylthioribose kinase [Blautia sp. CAG:257]	30.3	30.3	100%	23	77%	WP_022068881.1
☐	selenoprotein P precursor [Cricetulus griseus]	29.9	29.9	100%	30	69%	ERE84145.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaenoptera acuto	29.9	29.9	92%	31	75%	XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes vexillifer]	29.9	29.9	92%	31	75%	XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physeter catodon]	29.9	29.9	92%	31	75%	XP_007119423.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchilla lanigera]	29.9	29.9	92%	31	75%	XP_005386312.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus bubalis]	29.9	29.9	92%	31	75%	XP_006067130.1
☐	selenoprotein P precursor [Canis lupus familiaris]	29.9	29.9	92%	31	75%	NP_001108590.1
☐	5-methylthioribose kinase [Blautia wexlerae]	29.9	29.9	100%	31	77%	WP_026649811.1
☐	hypothetical protein [Coraliomargarita akajimensis]	29.1	29.1	84%	49	73%	WP_013044828.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannospalax galili]	29.1	29.1	92%	58	83%	XP_008840327.1
☐	Selenoprotein P [Heterocephalus glaber]	28.6	28.6	92%	77	75%	EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys damarens	28.6	28.6	92%	78	75%	XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gla	28.6	28.6	92%	79	75%	XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gla	28.6	28.6	92%	79	75%	XP_004878213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops telfairi]	28.6	28.6	100%	79	69%	XP_004716992.1
☐	hypothetical protein [Ruminococcus sp. JC304]	28.6	28.6	100%	79	77%	WP_019162697.1
☐	uncharacterized protein [Bacteroides sp. CAG:20]	28.2	28.2	69%	106	89%	WP_021891142.1
☐	hypothetical protein [Barnesiella intestinihominis]	28.2	28.2	69%	106	89%	WP_008862596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus orca]	28.2	28.2	76%	107	80%	XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops truncatus]	28.2	28.2	76%	107	80%	XP_004320390.1
☐	hypothetical protein Esi_0352_0027 [Ectocarpus siliculosus]	28.2	28.2	69%	109	89%	CBJ32646.1
☐	zinc finger protein [Loa loa]	28.2	28.2	84%	109	73%	XP_003137480.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera tigris alta	27.8	27.8	76%	146	80%	XP_007095490.1
☐	hypothetical protein [Butyrivibrio sp. XPD2002]	27.8	27.8	84%	146	75%	WP_026491875.1
☐	dNA internalization-related competence protein ComEC/Rec2 [Firmicutes bac	27.8	27.8	76%	149	80%	WP_022367536.1
☐	hypothetical protein M438DRAFT_345168 [Aureobasidium pullulans EXF-150	27.4	27.4	76%	197	80%	KEQ84957.1
☐	PREDICTED: uncharacterized protein LOC102600716 [Solanum tuberosum]	27.4	27.4	76%	198	80%	XP_006356388.1
☐	PREDICTED: oocyte zinc finger protein XlCOF6-like [Erinaceus europaeus]	27.4	27.4	76%	202	75%	XP_007538022.1
☐	leucyl-tRNA synthetase [Candidatus Portiera aleyrodidarum]	27.4	27.4	84%	202	73%	WP_014943273.1
☐	leucyl-tRNA synthetase [Candidatus Portiera aleyrodidarum]	27.4	27.4	84%	202	73%	WP_014895123.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopterus varieg	26.9	26.9	100%	269	69%	XP_008564915.1
☐	selenoprotein P precursor [Rattus norvegicus]	26.9	26.9	100%	270	62%	NP_062065.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenus rosmaru	26.9	26.9	69%	270	89%	XP_004409206.1
☐	PREDICTED: neurogenic locus notch homolog protein 2 [Callorhinchus milii]	26.9	26.9	76%	278	90%	XP_007901212.1
☐	RNA-binding protein (NOP10, NOLA3) [uncultured marine thaumarchaeote KI	26.5	26.5	92%	287	67%	AIF05018.1
☐	Neuroparsin-A [Zootermopsis nevadensis]	26.5	26.5	76%	335	80%	KDR17790.1
☐	MULTISPECIES: fimbria A protein [Serratia]	26.5	26.5	69%	352	78%	WP_013814891.1
☐	aminobenzoate synthetase [Helicobacter bilis]	26.5	26.5	69%	354	89%	WP_034564808.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Felis catus]	26.5	26.5	61%	355	88%	XP_006928143.1
☐	ferric iron reductase [Saccharothrix syringae]	26.5	26.5	61%	358	88%	WP_033434995.1

☐	Deoxyribonuclease, TatD family [Giardia lamblia ATCC 50803]	26.5	26.5	61%	365	88%	XP_001704151.1
☐	Putative DNase, TatD family protein [Giardia intestinalis]	26.5	26.5	61%	365	88%	ESU35103.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bison bison]	26.5	26.5	92%	367	67%	XP_010831114.1
☐	selenoprotein P [Bos taurus]	26.5	26.5	92%	367	67%	BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mutus]	26.5	26.5	92%	367	67%	XP_005894930.1
☐	selenoprotein P precursor [Bos taurus]	26.5	26.5	92%	368	67%	NP_776884.2
☐	selenoprotein P [Bubalus bubalis]	26.5	26.5	92%	368	67%	AFM77782.2
☐	mur ligase middle domain protein [Clostridium sp. CAG:217]	26.5	26.5	69%	368	90%	WP_022194186.1
☐	hypothetical protein AMTR_s00056p00139340 [Amborella trichopoda]	26.5	26.5	84%	368	64%	XP_006853693.1
☐	ATPase AAA [Methylovorus glucosotrophus]	26.5	26.5	76%	370	80%	WP_015830617.1
☐	cyanophycinase [Pseudoalteromonas sp. BSi20439]	26.5	26.5	84%	371	82%	WP_008468441.1
☐	hypothetical protein WUBG_06014 [Wuchereria bancrofti]	26.5	26.5	76%	371	69%	EJW83076.1
☐	Leucine Rich Repeat family protein [Brugia malayi]	26.5	26.5	76%	373	69%	XP_001896206.1
☐	Protein Bm3117, isoform b [Brugia malayi]	26.5	26.5	76%	373	69%	CDP97463.1
☐	hypothetical protein [Kluyvera ascorbata]	26.5	26.5	76%	374	80%	WP_035895790.1
☐	hypothetical protein [Buttiauxella agrestis]	26.5	26.5	76%	374	80%	WP_034495237.1
☐	coppertranslocating P-type ATPase [Acanthamoeba castellanii str. Neff]	26.5	26.5	76%	375	69%	XP_004339167.1
☐	PREDICTED: A-kinase anchor protein 9 [Larimichthys crocea]	26.5	26.5	69%	378	89%	XP_010740000.1
☐	hypothetical protein [Niastella koreensis]	26.1	26.1	76%	470	70%	WP_014220009.1
☐	Zinc uptake regulation protein ZUR [Legionella pneumophila]	26.1	26.1	84%	474	64%	WP_015444909.1
☐	transcriptional regulator [Legionella pneumophila]	26.1	26.1	84%	475	64%	WP_027227933.1
☐	transcriptional regulator [Legionella pneumophila]	26.1	26.1	84%	475	64%	WP_011212926.1
☐	transcriptional regulator [Legionella pneumophila]	26.1	26.1	84%	475	64%	WP_025862461.1
☐	transcriptional regulator [Legionella pneumophila]	26.1	26.1	84%	482	64%	WP_010945993.1
☐	transcriptional regulator [Legionella pneumophila]	26.1	26.1	84%	482	64%	WP_011945474.1
☐	transcriptional regulator [Legionella pneumophila]	26.1	26.1	84%	482	64%	WP_014326617.1

⊟ Alignments

Download ⌄ GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri boliviensis boliviensis]

Sequence ID: ref|XP_003925940.2| **Length:** 381 **Number of Matches:** 1

Range 1: 170 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.8 bits(91)	0.004	12/13(92%)	13/13(100%)	0/13(0%)

```
Query  1    KKCGDCSLTTLKD  13
            KKCG+CSLTTLKD
Sbjct  170  KKCGNCSLTTLKD  182
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxellana]

Sequence ID: ref|XP_010372696.1| **Length:** 381 **Number of Matches:** 1

Range 1: 170 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.8 bits(91)	0.004	12/13(92%)	13/13(100%)	0/13(0%)

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

```
Query  1    KKCGDCSLTTLKD  13
            KKCG+CSLTTLKD
Sbjct  170  KKCGNCSLTTLKD  182
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]

Sequence ID: ref|XP_009206607.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

Range 1: 170 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.8 bits(91)	0.004	12/13(92%)	13/13(100%)	0/13(0%)

```
Query  1    KKCGDCSLTTLKD  13
            KKCG+CSLTTLKD
Sbjct  170  KKCGNCSLTTLKD  182
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]

Sequence ID: ref|XP_008961588.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

Range 1: 170 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.8 bits(91)	0.004	12/13(92%)	13/13(100%)	0/13(0%)

```
Query  1    KKCGDCSLTTLKD  13
            KKCG+CSLTTLKD
Sbjct  170  KKCGNCSLTTLKD  182
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocebus sabaeus]

Sequence ID: ref|XP_007959679.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details
Map Viewer - aligned genomic context

Range 1: 170 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
41.8 bits(91)	0.004	12/13(92%)	13/13(100%)	0/13(0%)

```
Query  1    KKCGDCSLTTLKD  13
            KKCG+CSLTTLKD
Sbjct  170  KKCGNCSLTTLKD  182
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

SEPP1_KKCGDCSLTTLKDEDFCKR_Mod

RID BVKYZVRR01R (Expires on 01-21 10:47 am)

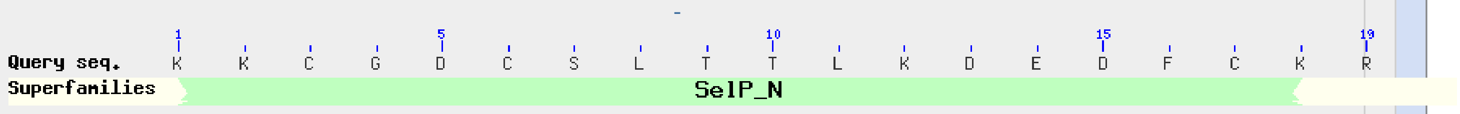
Query ID	lcl|120308	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	19	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

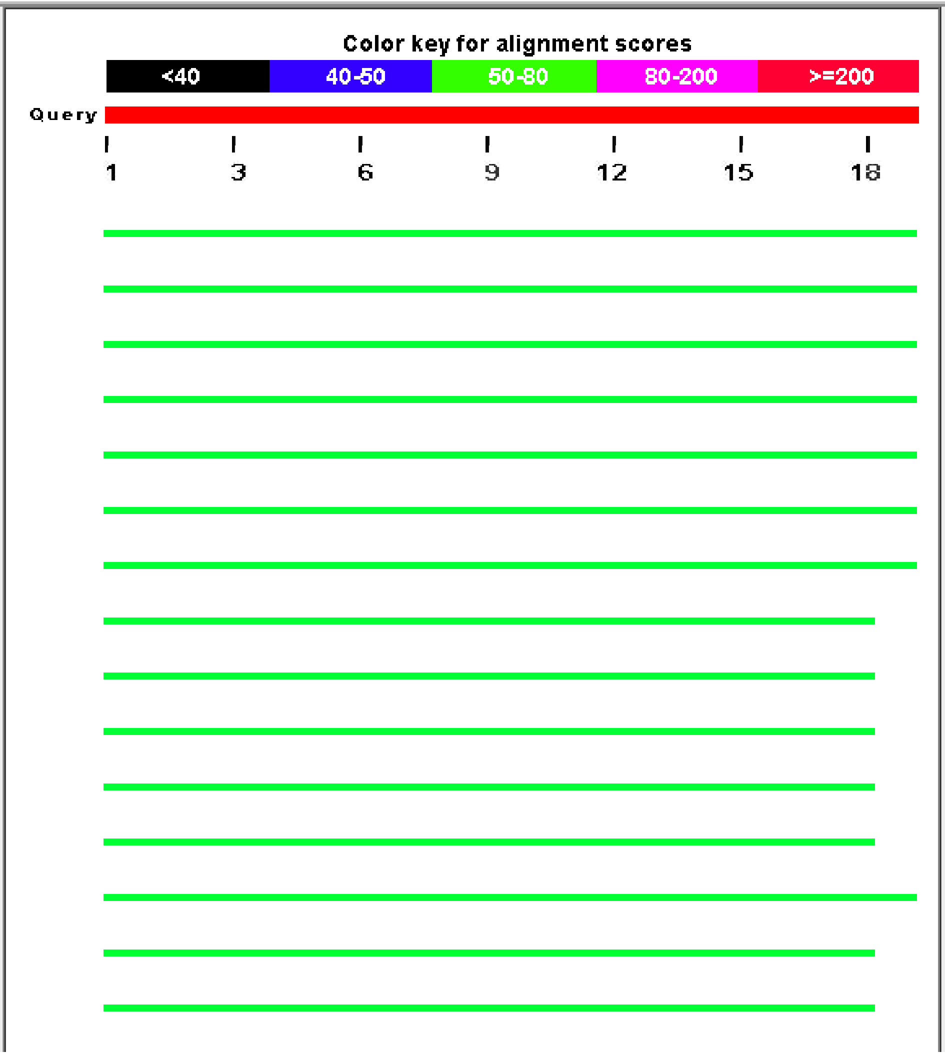
Show Conserved Domains

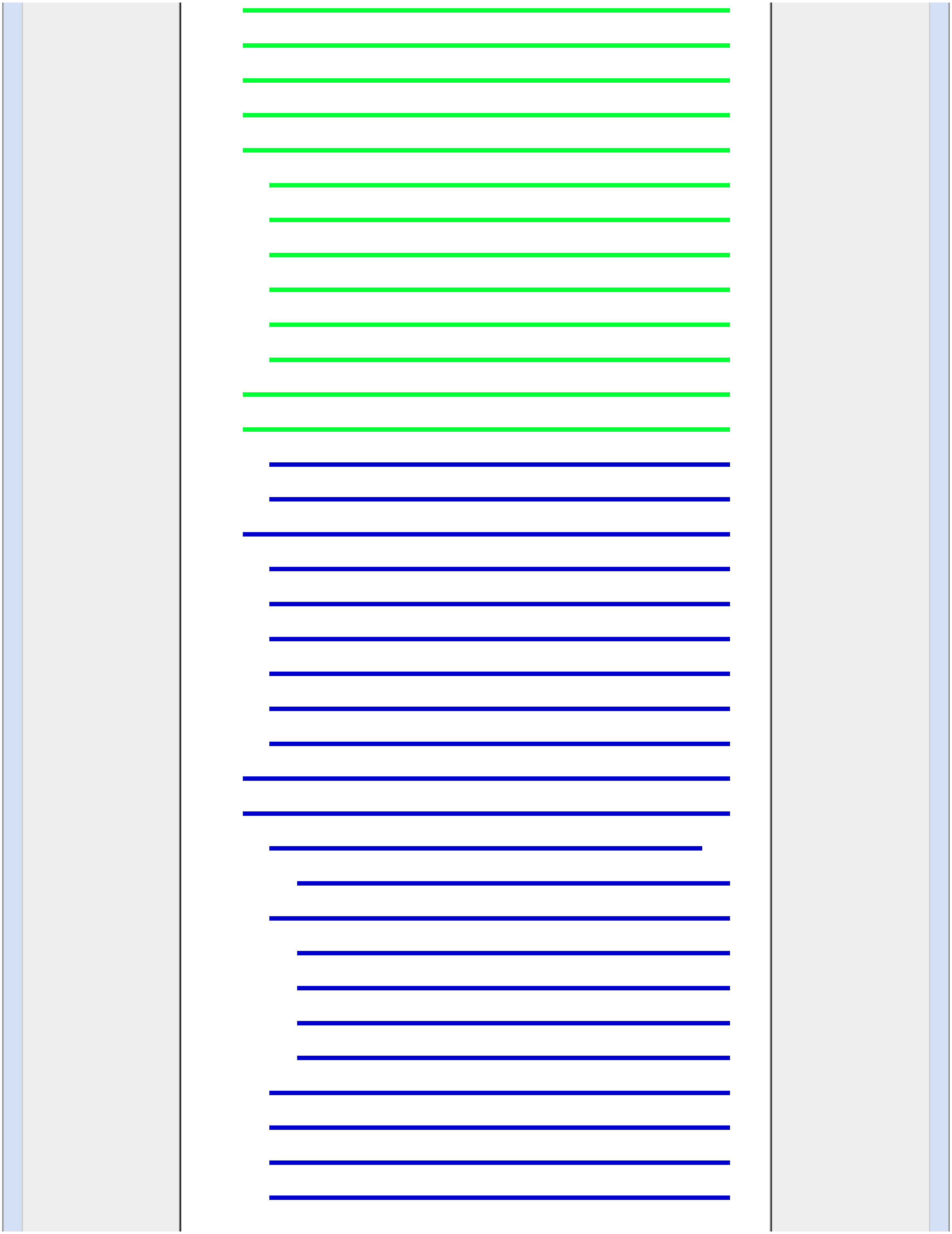
Putative conserved domains have been detected, click on the image below for detailed results.

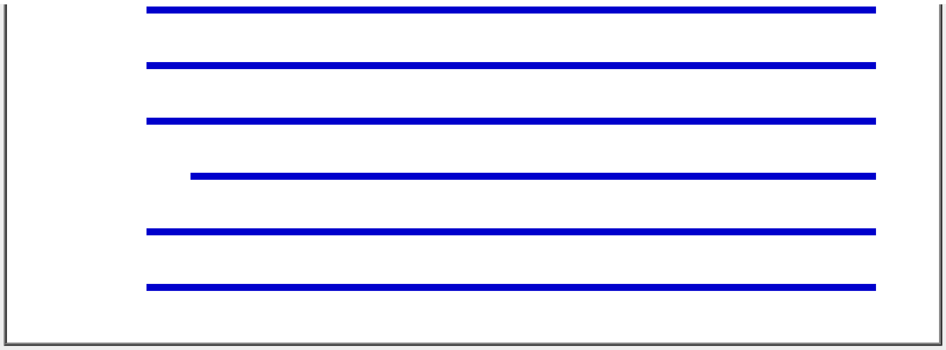


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]	63.0	63.0	100%	6e-10	95%	XP_008961588.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	63.0	63.0	100%	6e-10	95%	AAH46152.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	63.0	63.0	100%	6e-10	95%	NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	63.0	63.0	100%	6e-10	95%	AAH58919.1
☐	selenoprotein P [Homo sapiens]	63.0	63.0	100%	6e-10	95%	CAA77836.2
☐	selenoprotein P precursor [Pan troglodytes]	63.0	63.0	100%	6e-10	95%	NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	63.0	63.0	100%	6e-10	95%	NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri boliviensis	59.6	59.6	94%	9e-09	94%	XP_003925940.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxe	59.6	59.6	94%	9e-09	94%	XP_010372696.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]	59.6	59.6	94%	9e-09	94%	XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocebus sabae	59.6	59.6	94%	9e-09	94%	XP_007959679.1
☐	selenoprotein P precursor [Macaca mulatta]	59.6	59.6	94%	9e-09	94%	NP_001152962.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	58.3	58.3	100%	2e-08	89%	AAH15875.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichechus manatu	54.9	54.9	94%	3e-07	89%	XP_004388500.1
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	54.1	54.1	94%	6e-07	89%	XP_003793045.1
☐	selenoprotein P precursor [Pongo abelii]	54.1	54.1	94%	6e-07	94%	NP_001127462.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomascus leucoge	53.7	53.7	94%	9e-07	89%	XP_003274442.1
☐	selenoprotein P precursor [Callithrix jacchus]	52.8	52.8	94%	2e-06	83%	NP_001186857.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius syrichta]	52.4	52.4	94%	2e-06	83%	XP_008050904.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratotherium simu	52.4	52.4	94%	2e-06	89%	XP_004422836.1
☐	selenoprotein P precursor [Sus scrofa]	52.4	52.4	89%	2e-06	88%	NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis davidii]	52.0	52.0	89%	3e-06	88%	XP_006774623.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lucifugus]	52.0	52.0	89%	3e-06	88%	XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicus fuscus]	52.0	52.0	89%	3e-06	88%	XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis brandtii]	52.0	52.0	89%	3e-06	88%	XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia chinensis]	51.5	51.5	89%	5e-06	88%	XP_006167023.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus przewalskii]	50.3	50.3	94%	1e-05	83%	XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	50.3	50.3	94%	1e-05	83%	NP_001129077.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex araneus]	49.0	49.0	89%	3e-05	82%	XP_004605590.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromyscus manic	49.0	49.0	89%	3e-05	82%	XP_006997157.1
☐	selenoprotein P precursor [Cricetulus griseus]	47.7	47.7	94%	8e-05	78%	ERE84145.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchilla lanigera]	47.7	47.7	89%	8e-05	82%	XP_005386312.1
☐	Selenoprotein P [Heterocephalus glaber]	46.4	46.4	89%	2e-04	82%	EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys damarens	46.4	46.4	89%	2e-04	82%	XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus ochrogast	46.4	46.4	89%	2e-04	76%	XP_005369861.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gla	46.4	46.4	89%	2e-04	82%	XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gla	46.4	46.4	89%	2e-04	82%	XP_004878213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopterus varieg	44.8	44.8	94%	8e-04	78%	XP_008564915.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera tigris alta	44.3	44.3	94%	0.001	78%	XP_007095490.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannospalax galili]	43.9	43.9	84%	0.002	88%	XP_008840327.1
☐	selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	43.5	43.5	84%	0.002	75%	EDL03405.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Octodon degus]	43.5	43.5	89%	0.002	76%	XP_004641866.1
☐	Selenoprotein P, plasma, 1 [Mus musculus]	43.5	43.5	84%	0.002	75%	AAH01991.2
☐	plasma selenoprotein P [Mus musculus]	43.5	43.5	84%	0.002	75%	AAD01684.1
☐	unnamed protein product [Mus musculus]	43.5	43.5	84%	0.002	75%	BAE34948.1
☐	selenoprotein P precursor [Mus musculus]	43.5	43.5	84%	0.002	75%	NP_033181.3
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaenoptera acuto	43.1	43.1	89%	0.003	76%	XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes vexillifer]	43.1	43.1	89%	0.003	76%	XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physeter catodon]	43.1	43.1	89%	0.003	76%	XP_007119423.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus bubalis]	43.1	43.1	89%	0.003	76%	XP_006067130.1
☐	membrane selenoprotein P [Capra hircus]	42.6	42.6	89%	0.004	76%	AAF67201.1
☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	42.6	42.6	89%	0.004	76%	NP_001272511.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis aries]	42.6	42.6	89%	0.004	76%	XP_004017062.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenus rosmaru	41.8	41.8	84%	0.008	81%	XP_004409206.1
☐	selenoprotein P precursor [Cavia porcellus]	41.4	41.4	89%	0.010	71%	NP_001244936.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodonta africana	41.4	41.4	89%	0.010	76%	XP_010586424.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephantulus edwa	41.4	41.4	89%	0.010	76%	XP_006889619.1
☐	selenoprotein P precursor [Cricetulus griseus]	41.4	41.4	94%	0.010	72%	NP_001243807.1
☐	selenoprotein P precursor [Rattus norvegicus]	40.1	40.1	94%	0.027	67%	NP_062065.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus jaculus]	39.7	39.7	89%	0.037	76%	XP_004652550.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus orca]	39.7	39.7	89%	0.037	76%	XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops truncatus]	39.7	39.7	89%	0.037	76%	XP_004320390.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orycteropus afer af	39.2	39.2	94%	0.050	72%	XP_007952213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela putorius fu	39.2	39.2	84%	0.050	75%	XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Monodelphis dome	38.4	38.4	84%	0.094	75%	XP_003340675.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceus europae	38.0	38.0	94%	0.13	67%	XP_007517681.1
☐	selenoprotein P precursor [Canis lupus familiaris]	38.0	38.0	89%	0.13	71%	NP_001108590.1
☐	PREDICTED: selenoprotein P-like [Ailuropoda melanoleuca]	37.5	37.5	89%	0.16	71%	XP_002921760.1
☐	unnamed protein product [Mus musculus]	37.5	37.5	84%	0.18	69%	BAE39664.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus dromedar	37.5	37.5	89%	0.18	71%	XP_010999134.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus ferus]	37.5	37.5	89%	0.18	71%	XP_006191986.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna pacos]	37.5	37.5	89%	0.18	71%	XP_006207756.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Condylura cristata]	37.5	37.5	94%	0.18	72%	XP_004678402.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus maritimus]	37.5	37.5	89%	0.18	71%	XP_008690806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bison bison]	37.1	37.1	89%	0.24	71%	XP_010831114.1

☐	selenoprotein P [Bos taurus]	37.1	37.1	89%	0.24	71%	BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mutus]	37.1	37.1	89%	0.24	71%	XP_005894930.1
☐	selenoprotein P precursor [Bos taurus]	37.1	37.1	89%	0.24	71%	NP_776884.2
☐	selenoprotein P [Bubalus bubalis]	37.1	37.1	89%	0.24	71%	AFM77782.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Gorilla gorilla gorill	36.7	36.7	52%	0.31	100%	XP_004065356.1
☐	PREDICTED: selenoprotein P [Sarcophilus harrisii]	35.8	35.8	94%	0.58	67%	XP_003759960.1
☐	unnamed protein product [Mus musculus]	35.4	35.4	84%	0.83	69%	BAC55264.3
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Dasypus novemcin	35.0	35.0	89%	1.1	71%	XP_004448278.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops telfairi]	34.6	34.6	94%	1.5	67%	XP_004716992.1
☐	selenoprotein P precursor [Oryctolagus cuniculus]	33.3	33.3	84%	3.9	69%	NP_001186775.1
☐	RNA-binding protein (NOP10, NOLA3) [uncultured marine thaumarchaeote K	32.5	32.5	89%	5.1	65%	AIF05018.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ochotona princeps	32.9	32.9	84%	5.3	69%	XP_004583736.1
☐	predicted protein [Phaeodactylum tricornutum CCAP 1055/1]	32.0	32.0	57%	10	82%	XP_002178290.1
☐	hypothetical protein [Coraliomargarita akajimensis]	31.6	31.6	68%	12	71%	WP_013044828.1
☐	hypothetical protein [Sorangium cellulosum]	31.6	31.6	84%	13	61%	WP_012240780.1
☐	dihydroxy-acid dehydratase [Campylobacter sp. FOBRC14]	31.2	31.2	63%	19	73%	WP_009649466.1
☐	putative ATP-dependent RNA helicase DDX60-like protein [Cricetulus griseus	31.2	31.2	78%	19	75%	ERE91786.1
☐	PREDICTED: probable ATP-dependent RNA helicase DDX60 [Cricetulus gris	31.2	31.2	78%	19	75%	XP_003498842.2
☐	selenoprotein P-like protein [Bos taurus]	30.8	30.8	89%	23	65%	BAB39395.1
☐	selenoprotein P-like protein [Bos taurus]	30.8	30.8	89%	23	65%	BAB39394.1
☐	selenoprotein P-like protein [Bos taurus]	30.8	30.8	89%	24	65%	BAB39393.1
☐	selenoprotein P-like protein [Bos taurus]	30.8	30.8	89%	24	65%	BAB39392.1
☐	2-oxoglutarate ferredoxin oxidoreductase beta subunit [Legionella fallonii LLA	30.8	30.8	47%	25	89%	CEG56463.1
☐	hypothetical protein ACD_69C00091G0003 [uncultured bacterium]	30.8	30.8	84%	25	63%	EKD45887.1
☐	selenoprotein P like protein [Bos taurus]	30.8	30.8	89%	25	65%	BAA04949.2

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SEPP1_KKCGNCSLTTLKD_NonMod

RID BE88JH4F015 (Expires on 01-16 09:08 am)

Query ID lcl|59387
Description None
Molecule type amino acid
Query Length 13

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

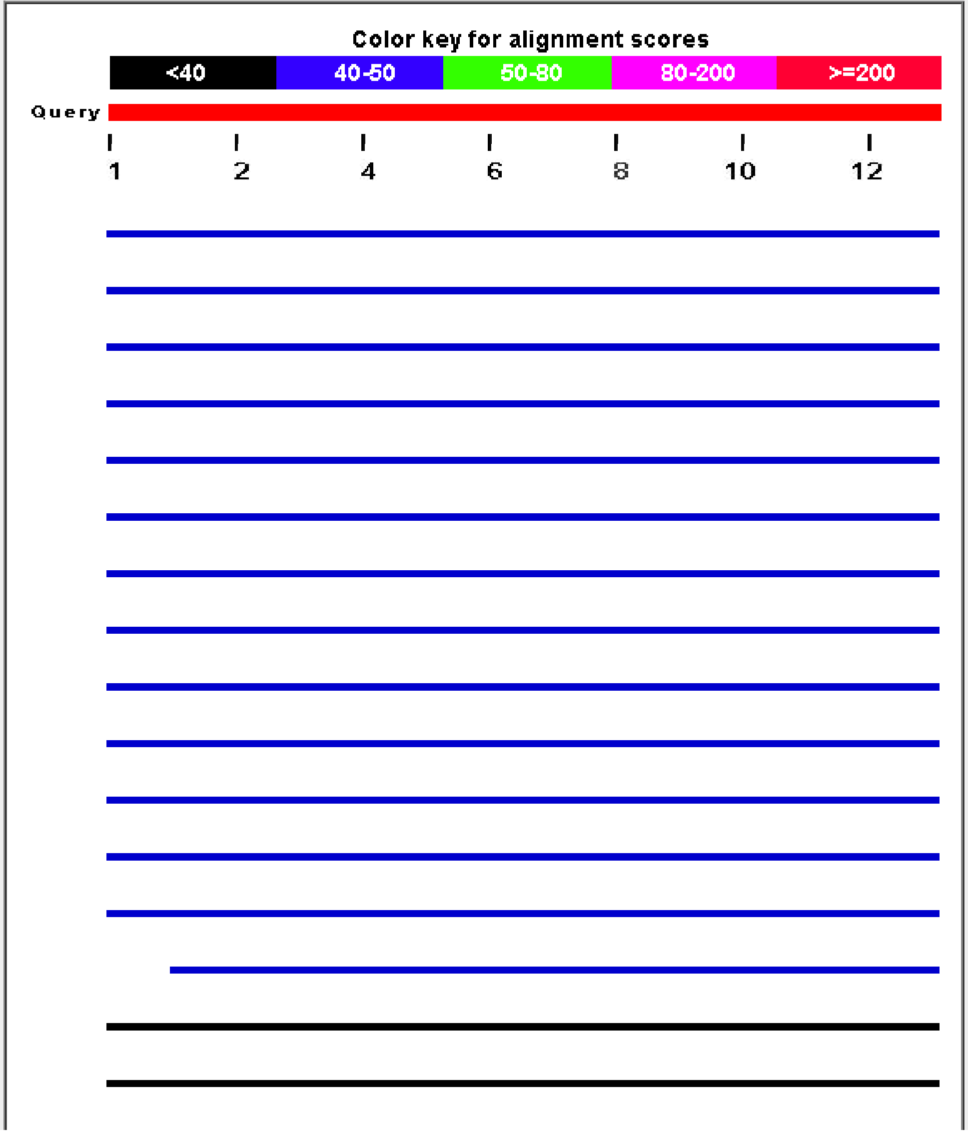
Graphic Summary

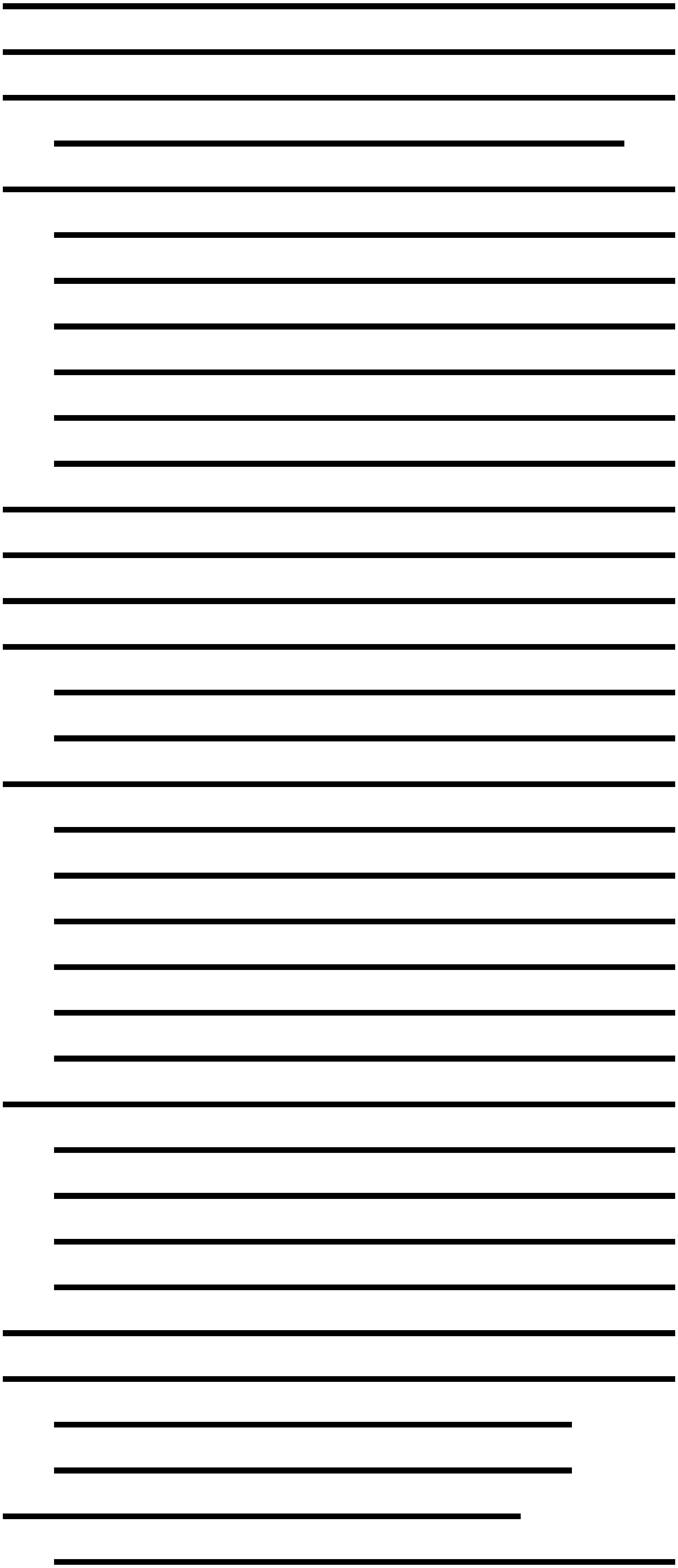
Show Conserved Domains

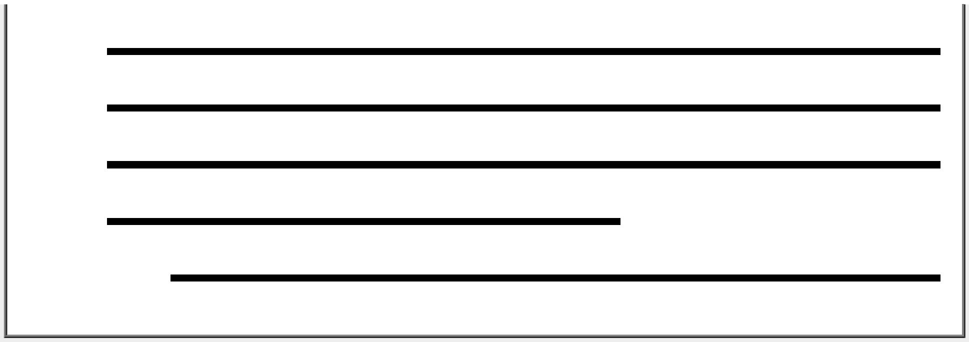
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri b	44.3	44.3	100%	6e-04	100%	gi|725563213|XP_003925940.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopitl	44.3	44.3	100%	6e-04	100%	gi|724878613|XP_010372696.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio ar	44.3	44.3	100%	6e-04	100%	gi|685545348|XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan pani	44.3	44.3	100%	6e-04	100%	gi|675710689|XP_008961588.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chloroce	44.3	44.3	100%	6e-04	100%	gi|635028004|XP_007959679.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	44.3	44.3	100%	6e-04	100%	gi|34783648|AAH46152.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	44.3	44.3	100%	6e-04	100%	gi|34783164|AAH15875.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	44.3	44.3	100%	6e-04	100%	gi|62530391|NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	44.3	44.3	100%	6e-04	100%	gi|37596694|AAH58919.1
☐	selenoprotein P [Homo sapiens]	44.3	44.3	100%	6e-04	100%	gi|312004116|CAA77836.2
☐	selenoprotein P precursor [Macaca mulatta]	44.3	44.3	100%	6e-04	100%	gi|226958322|NP_001152962.1
☐	selenoprotein P precursor [Pan troglodytes]	44.3	44.3	100%	6e-04	100%	gi|169403955|NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	44.3	44.3	100%	6e-04	100%	gi|148277022|NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia c	41.4	41.4	92%	0.006	100%	gi|562878609|XP_006167023.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius s	39.7	39.7	100%	0.021	92%	gi|640790108|XP_008050904.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichech	39.7	39.7	100%	0.021	92%	gi|471413922|XP_004388500.1
☐	selenoprotein P precursor [Pongo abelii]	39.2	39.2	100%	0.029	92%	gi|197101233|NP_001127462.1
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	38.8	38.8	100%	0.037	92%	gi|395840394|XP_003793045.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomascı	38.4	38.4	100%	0.055	92%	gi|332250603|XP_003274442.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex ar	38.0	38.0	84%	0.075	100%	gi|505790024|XP_004605590.1
☐	selenoprotein P precursor [Callithrix jacchus]	37.5	37.5	100%	0.10	85%	gi|315630400|NP_001186857.1
☐	selenoprotein P precursor [Sus scrofa]	37.1	37.1	92%	0.14	92%	gi|198282079|NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis d	36.7	36.7	92%	0.20	92%	gi|584060316|XP_006774623.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lu	36.7	36.7	92%	0.20	92%	gi|558205011|XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicu	36.7	36.7	92%	0.20	92%	gi|641727491|XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis b	36.7	36.7	92%	0.20	92%	gi|554563465|XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela	36.7	36.7	92%	0.20	86%	gi|511826454|XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratoth	35.8	35.8	100%	0.38	85%	gi|478496995|XP_004422836.1
☐							

	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephant	35.4	35.4	100%	0.52	85%	gi|585672710|XP_006889619.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus pr	35.0	35.0	100%	0.71	85%	gi|664731166|XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	35.0	35.0	100%	0.71	85%	gi|208022673|NP_001129077.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus	33.7	33.7	92%	1.8	83%	gi|532054271|XP_005369861.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromys	33.7	33.7	92%	1.8	83%	gi|589969345|XP_006997157.1
☐	selenoprotein P precursor [Cricetulus griseus]	32.5	32.5	100%	4.6	77%	gi|537231220|ERE84145.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaenop	32.5	32.5	92%	4.7	83%	gi|594696840|XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes v	32.5	32.5	92%	4.7	83%	gi|602724444|XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physeter	32.5	32.5	92%	4.7	83%	gi|593761497|XP_007119423.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchill	32.5	32.5	92%	4.7	83%	gi|533143496|XP_005386312.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus	32.5	32.5	92%	4.7	83%	gi|594087306|XP_006067130.1
☐	selenoprotein P precursor [Canis lupus familiaris]	32.5	32.5	92%	4.7	83%	gi|169403968|NP_001108590.1
☐	methylthioribose kinase [Blautia sp. CAG:257]	31.6	31.6	100%	8.9	77%	gi|547449133|WP_022068881.1
☐	Selenoprotein P [Heterocephalus glaber]	31.2	31.2	92%	12	83%	gi|351695949|EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys	31.2	31.2	92%	12	83%	gi|731237262|XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	31.2	31.2	92%	12	83%	gi|512973043|XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	31.2	31.2	92%	12	83%	gi|512816050|XP_004878213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops	31.2	31.2	100%	12	77%	gi|507708621|XP_004716992.1
☐	5-methylthioribose kinase [Blautia wexlerae]	31.2	31.2	100%	12	77%	gi|651890337|WP_026649811.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus	30.8	30.8	76%	17	90%	gi|465986750|XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops	30.8	30.8	76%	17	90%	gi|470626535|XP_004320390.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera	30.3	30.3	76%	23	90%	gi|591339998|XP_007095490.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannosp	29.9	29.9	92%	31	83%	gi|674066756|XP_008840327.1
☐	hypothetical protein [Ruminococcus sp. JC304]	29.9	29.9	100%	31	77%	gi|517992489|WP_019162697.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopte	29.5	29.5	100%	42	77%	gi|667253652|XP_008564915.1
☐	selenoprotein P precursor [Rattus norvegicus]	29.5	29.5	100%	42	69%	gi|15011857|NP_062065.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Felis catu	29.1	29.1	61%	55	100%	gi|586975923|XP_006928143.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bis	29.1	29.1	92%	57	75%	gi|742088280|XP_010831114.1
☐	selenoprotein P [Bos taurus]	29.1	29.1	92%	57	75%	gi|6006351|BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mutu	29.1	29.1	92%	57	75%	gi|555965745|XP_005894930.1
☐	selenoprotein P precursor [Bos taurus]	29.1	29.1	92%	57	75%	gi|156631001|NP_776884.2
☐	selenoprotein P [Bubalus bubalis]	29.1	29.1	92%	57	75%	gi|430001945|AFM77782.2
☐	selenoprotein P precursor [Cavia porcellus]	28.6	28.6	92%	78	75%	gi|384367995|NP_001244936.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenu	28.6	28.6	69%	78	89%	gi|472379594|XP_004409206.1
☐	leucyl-tRNA synthetase [Candidatus Portiera aleyrodidarum]	28.6	28.6	84%	80	73%	gi|504756171|WP_014943273.1
☐	leucyl-tRNA synthetase [Candidatus Portiera aleyrodidarum]	28.6	28.6	84%	80	73%	gi|504708021|WP_014895123.1
☐	selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	28.2	28.2	84%	102	73%	gi|148671458|EDL03405.1
☐	SJCHGC06731 protein [Schistosoma japonicum]	28.2	28.2	61%	103	100%	gi|56759152|AAW27716.1
☐	PREDICTED: uncharacterized protein LOC102703395 [Oryza brach	28.2	28.2	61%	105	100%	gi|573942981|XP_006653873.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Octodon	28.2	28.2	92%	106	75%	gi|507690845|XP_004641866.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceu	28.2	28.2	84%	106	82%	gi|617575753|XP_007517681.1
☐	probable bacteriophage tail fiber protein [Fusobacterium sp. CAG:4	28.2	28.2	61%	106	100%	gi|548239104|WP_022457330.1
☐	Selenoprotein P, plasma, 1 [Mus musculus]	28.2	28.2	84%	106	73%	gi|34809553|AAH01991.2
☐	plasma selenoprotein P [Mus musculus]	28.2	28.2	84%	106	73%	gi|4103142|AAD01684.1
☐	unnamed protein product [Mus musculus]	28.2	28.2	84%	106	73%	gi|74192879|BAE34948.1

☐	selenoprotein P precursor [Mus musculus]	28.2	28.2	84%	106	73%	gi|74271806|NP_033181.3
☐	unnamed protein product [Mus musculus]	28.2	28.2	84%	106	73%	gi|74213751|BAC55264.3
☐	ATPase AAA [Methylovorus glucosotrophus]	28.2	28.2	76%	107	80%	gi|506310842|WP_015830617.1
☐	membrane selenoprotein P [Capra hircus]	27.8	27.8	69%	139	89%	gi|7677620|AAF67201.1
☐	hypothetical protein [Bifidobacterium longum]	27.8	27.8	84%	141	75%	gi|695759205|WP_032682416.1
☐	hypothetical protein [Anaerostipes hadrus]	27.8	27.8	84%	141	75%	gi|496495012|WP_009203548.1
☐	MULTISPECIES: hypothetical protein [Clostridiales]	27.8	27.8	84%	141	75%	gi|489600928|WP_003505369.1
☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	27.8	27.8	69%	144	89%	gi|550822255|NP_001272511.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus j	27.8	27.8	69%	144	89%	gi|507537041|XP_004652550.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis arie	27.8	27.8	69%	144	89%	gi|426246564|XP_004017062.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Monodel	27.8	27.8	84%	144	82%	gi|612006645|XP_003340675.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	27.8	27.8	69%	144	89%	gi|744538058|XP_010999134.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	27.8	27.8	69%	145	89%	gi|560931717|XP_006191986.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna	27.8	27.8	69%	145	89%	gi|560970802|XP_006207756.1
☐	hypothetical protein [Dyadobacter crusticola]	27.8	27.8	69%	145	89%	gi|737351556|WP_035333761.1
☐	hypothetical protein [Corallococcus coralloides]	27.8	27.8	84%	148	75%	gi|504210603|WP_014397705.1
☐	hypothetical protein [Coraliomargarita akajimensis]	27.4	27.4	84%	174	73%	gi|502809852|WP_013044828.1
☐	PREDICTED: selenoprotein P-like [Ailuropoda melanoleuca]	27.4	27.4	69%	187	89%	gi|301772662|XP_002921760.1
☐	hypothetical protein [Leptospirillum ferrooxidans]	27.4	27.4	69%	188	82%	gi|504262968|WP_014450070.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodon	27.4	27.4	69%	197	89%	gi|731464182|XP_010586424.1
☐	glycosyl transferase family 1 [Ilyobacter polytropus]	27.4	27.4	100%	197	71%	gi|503154435|WP_013389096.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus m	27.4	27.4	69%	198	89%	gi|670999853|XP_008690806.1
☐	PREDICTED: chloride channel protein ClC-Ka isoform X2 [Peromys	27.4	27.4	69%	200	90%	gi|589925330|XP_006975530.1
☐	PREDICTED: chloride channel protein ClC-Ka isoform X1 [Peromys	27.4	27.4	69%	200	90%	gi|589925328|XP_006975529.1
☐	PREDICTED: macoilin-1-like [Apis florea]	26.9	26.9	84%	261	82%	gi|380022212|XP_003694946.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Leptony	26.9	26.9	76%	268	80%	gi|585192742|XP_006747601.1
☐	PREDICTED: ribonuclease inhibitor-like [Pundamilia nyererei]	26.9	26.9	69%	268	82%	gi|548543470|XP_005753681.1

⊟ Alignments

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri boliviensis boliviensis]

Sequence ID: gi|725563213|ref|XP_003925940.2| **Length:** 381 **Number of Matches:** 1

Range 1: 170 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	6e-04	13/13(100%)	13/13(100%)	0/13(0%)

```
Query  1    KKCGNCSLTTLKD  13
            KKCGNCSLTTLKD
Sbjct  170  KKCGNCSLTTLKD  182
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxellana]

Sequence ID: gi|724878613|ref|XP_010372696.1| **Length:** 381 **Number of Matches:** 1

Range 1: 170 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	6e-04	13/13(100%)	13/13(100%)	0/13(0%)

```
Query  1    KKCGNCSLTTLKD  13
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

```
               KKCGNCSLTTLKD
Sbjct  170  KKCGNCSLTTLKD  182
```

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]

Sequence ID: gi|685545348|ref|XP_009206607.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 170 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	6e-04	13/13(100%)	13/13(100%)	0/13(0%)

```
Query  1    KKCGNCSLTTLKD  13
            KKCGNCSLTTLKD
Sbjct  170  KKCGNCSLTTLKD  182
```

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]

Sequence ID: gi|675710689|ref|XP_008961588.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 170 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	6e-04	13/13(100%)	13/13(100%)	0/13(0%)

```
Query  1    KKCGNCSLTTLKD  13
            KKCGNCSLTTLKD
Sbjct  170  KKCGNCSLTTLKD  182
```

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocebus sabaeus]

Sequence ID: gi|635028004|ref|XP_007959679.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 170 to 182 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
44.3 bits(97)	6e-04	13/13(100%)	13/13(100%)	0/13(0%)

```
Query  1    KKCGNCSLTTLKD  13
            KKCGNCSLTTLKD
Sbjct  170  KKCGNCSLTTLKD  182
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download

How to read this page   Blast report description

SEPP1_KKCGNCSLTTLKDEDFCKR_NonMod

RID BE88U4J0015 (Expires on 01-16 09:08 am)

Query ID lcl|65177
Description None
Molecule type amino acid
Query Length 19

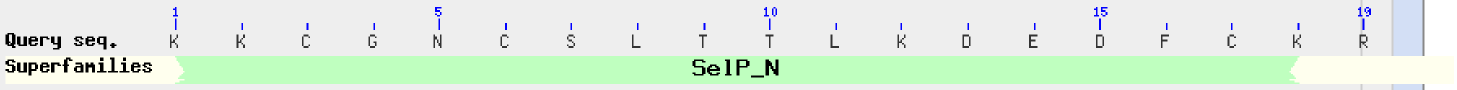
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

Graphic Summary

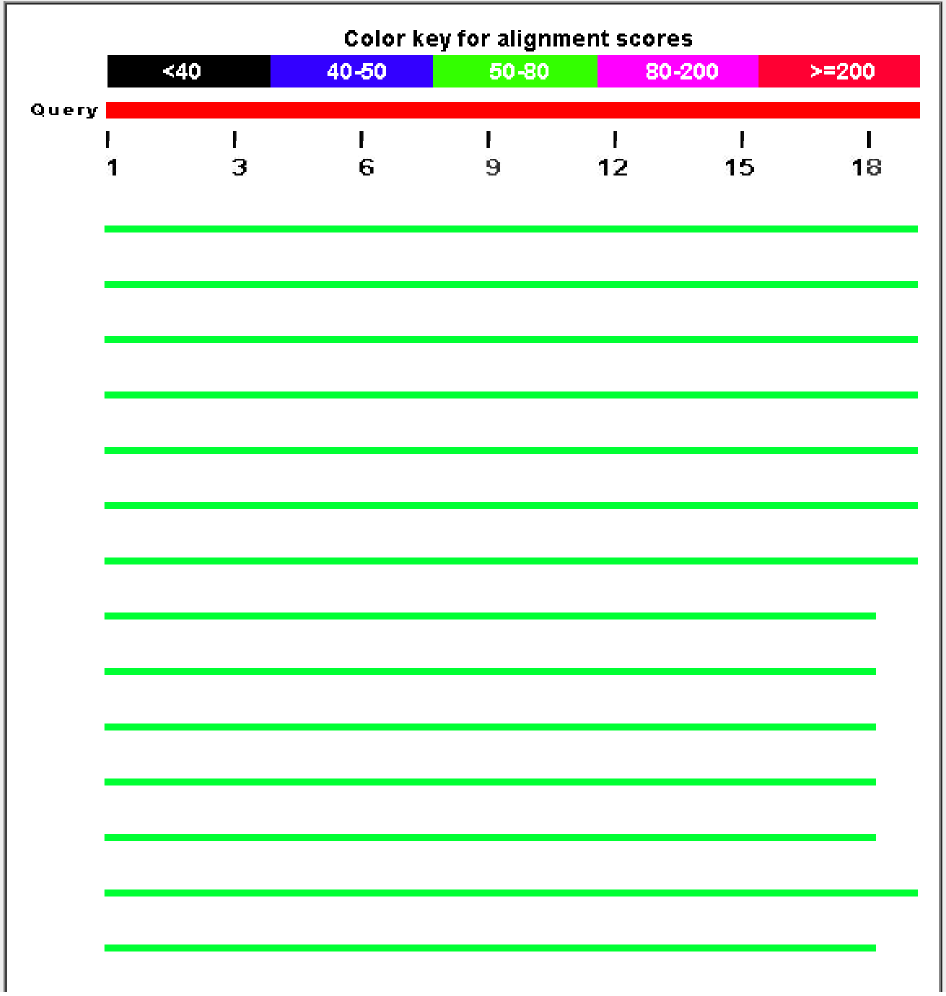
Show Conserved Domains

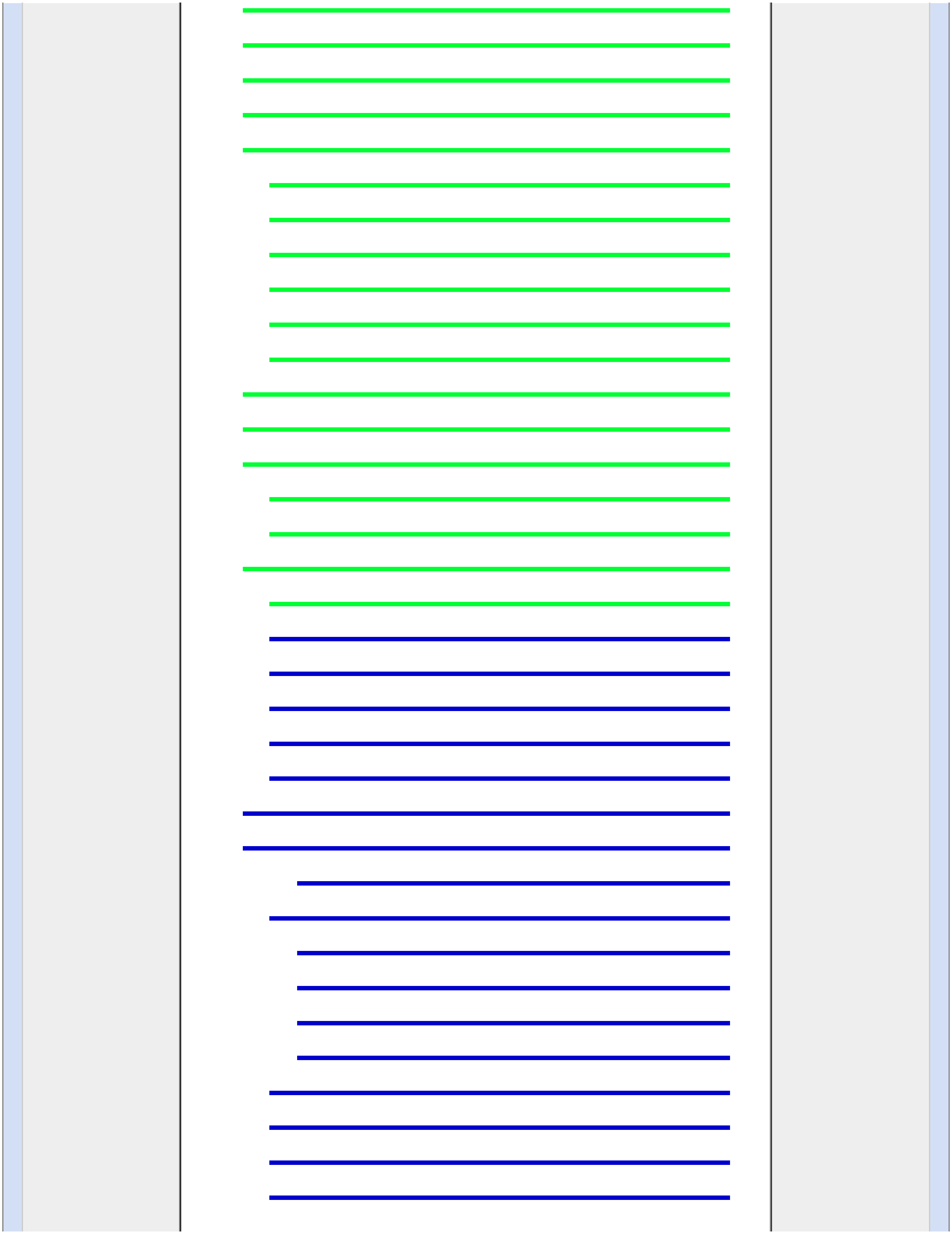
Putative conserved domains have been detected, click on the image below for detailed results.

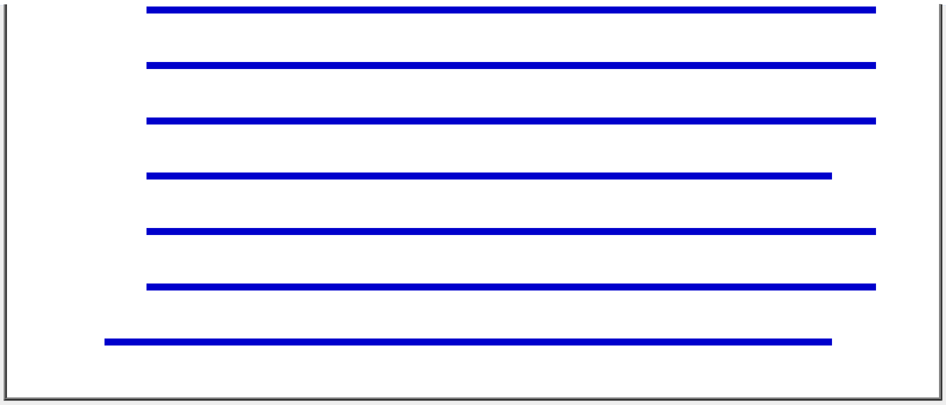


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan pani	65.5	65.5	100%	8e-11	100%	gi|675710689|XP_008961588.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	65.5	65.5	100%	8e-11	100%	gi|34783648|AAH46152.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	65.5	65.5	100%	8e-11	100%	gi|62530391|NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	65.5	65.5	100%	8e-11	100%	gi|37596694|AAH58919.1
☐	selenoprotein P [Homo sapiens]	65.5	65.5	100%	8e-11	100%	gi|312004116|CAA77836.2
☐	selenoprotein P precursor [Pan troglodytes]	65.5	65.5	100%	8e-11	100%	gi|169403955|NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	65.5	65.5	100%	8e-11	100%	gi|148277022|NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri b	62.1	62.1	94%	1e-09	100%	gi|725563213|XP_003925940.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopitl	62.1	62.1	94%	1e-09	100%	gi|724878613|XP_010372696.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio ar	62.1	62.1	94%	1e-09	100%	gi|685545348|XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocε	62.1	62.1	94%	1e-09	100%	gi|635028004|XP_007959679.1
☐	selenoprotein P precursor [Macaca mulatta]	62.1	62.1	94%	1e-09	100%	gi|226958322|NP_001152962.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	60.9	60.9	100%	3e-09	95%	gi|34783164|AAH15875.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichech	57.5	57.5	94%	4e-08	94%	gi|471413922|XP_004388500.1
☐	selenoprotein P precursor [Pongo abelii]	57.1	57.1	94%	6e-08	94%	gi|197101233|NP_001127462.1
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	56.6	56.6	94%	8e-08	94%	gi|395840394|XP_003793045.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomascı	56.2	56.2	94%	1e-07	94%	gi|332250603|XP_003274442.1
☐	selenoprotein P precursor [Callithrix jacchus]	55.4	55.4	94%	2e-07	89%	gi|315630400|NP_001186857.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius s	54.9	54.9	94%	3e-07	89%	gi|640790108|XP_008050904.1
☐	selenoprotein P precursor [Sus scrofa]	54.9	54.9	89%	3e-07	94%	gi|198282079|NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis d	54.5	54.5	89%	4e-07	94%	gi|584060316|XP_006774623.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lı	54.5	54.5	89%	4e-07	94%	gi|558205011|XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicu	54.5	54.5	89%	4e-07	94%	gi|641727491|XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis b	54.5	54.5	89%	4e-07	94%	gi|554563465|XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia c	54.1	54.1	89%	6e-07	94%	gi|562878609|XP_006167023.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratoth	53.7	53.7	94%	9e-07	89%	gi|478496995|XP_004422836.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus pı	52.8	52.8	94%	2e-06	89%	gi|664731166|XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	52.8	52.8	94%	2e-06	89%	gi|208022673|NP_001129077.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex ar	51.5	51.5	89%	4e-06	88%	gi|505790024|XP_004605590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromys	51.5	51.5	89%	5e-06	88%	gi|589969345|XP_006997157.1
☐	selenoprotein P precursor [Cricetulus griseus]	50.3	50.3	94%	1e-05	83%	gi|537231220|ERE84145.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchill	50.3	50.3	89%	1e-05	88%	gi|533143496|XP_005386312.1
☐	Selenoprotein P [Heterocephalus glaber]	49.0	49.0	89%	3e-05	88%	gi|351695949|EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys	49.0	49.0	89%	3e-05	88%	gi|731237262|XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus	49.0	49.0	89%	3e-05	82%	gi|532054271|XP_005369861.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	49.0	49.0	89%	3e-05	88%	gi|512973043|XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	49.0	49.0	89%	3e-05	88%	gi|512816050|XP_004878213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopte	47.3	47.3	94%	1e-04	83%	gi|667253652|XP_008564915.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera	46.9	46.9	94%	2e-04	83%	gi|591339998|XP_007095490.1
☐	selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	46.0	46.0	84%	3e-04	81%	gi|148671458|EDL03405.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Octodon	46.0	46.0	89%	3e-04	82%	gi|507690845|XP_004641866.1
☐	Selenoprotein P, plasma, 1 [Mus musculus]	46.0	46.0	84%	3e-04	81%	gi|34809553|AAH01991.2
☐	plasma selenoprotein P [Mus musculus]	46.0	46.0	84%	3e-04	81%	gi|4103142|AAD01684.1
☐	unnamed protein product [Mus musculus]	46.0	46.0	84%	3e-04	81%	gi|74192879|BAE34948.1
☐	selenoprotein P precursor [Mus musculus]	46.0	46.0	84%	3e-04	81%	gi|74271806|NP_033181.3
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaeno	45.6	45.6	89%	4e-04	82%	gi|594696840|XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes	45.6	45.6	89%	4e-04	82%	gi|602724444|XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physeter	45.6	45.6	89%	4e-04	82%	gi|593761497|XP_007119423.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus	45.6	45.6	89%	4e-04	82%	gi|594087306|XP_006067130.1
☐	membrane selenoprotein P [Capra hircus]	45.2	45.2	89%	5e-04	82%	gi|7677620|AAF67201.1
☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	45.2	45.2	89%	6e-04	82%	gi|550822255|NP_001272511.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis arie	45.2	45.2	89%	6e-04	82%	gi|426246564|XP_004017062.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannosp	44.8	44.8	84%	8e-04	88%	gi|674066756|XP_008840327.1
☐	selenoprotein P precursor [Cavia porcellus]	43.9	43.9	89%	0.002	76%	gi|384367995|NP_001244936.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodon	43.9	43.9	89%	0.002	82%	gi|731464182|XP_010586424.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephant	43.9	43.9	89%	0.002	82%	gi|585672710|XP_006889619.1
☐	selenoprotein P precursor [Cricetulus griseus]	43.9	43.9	94%	0.002	78%	gi|379056379|NP_001243807.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenu	43.5	43.5	84%	0.002	81%	gi|472379594|XP_004409206.1
☐	selenoprotein P precursor [Rattus norvegicus]	42.6	42.6	94%	0.004	72%	gi|15011857|NP_062065.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus	42.2	42.2	89%	0.005	82%	gi|507537041|XP_004652550.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus	42.2	42.2	89%	0.005	82%	gi|465986750|XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops	42.2	42.2	89%	0.005	82%	gi|470626535|XP_004320390.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Oryctero	41.8	41.8	94%	0.007	78%	gi|634885032|XP_007952213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela	41.8	41.8	84%	0.008	81%	gi|511826454|XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Monodel	40.9	40.9	84%	0.014	81%	gi|612006645|XP_003340675.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceu	40.5	40.5	94%	0.019	72%	gi|617575753|XP_007517681.1
☐	selenoprotein P precursor [Canis lupus familiaris]	40.5	40.5	89%	0.019	76%	gi|169403968|NP_001108590.1
☐	PREDICTED: selenoprotein P-like [Ailuropoda melanoleuca]	40.1	40.1	89%	0.023	76%	gi|301772662|XP_002921760.1
☐	unnamed protein product [Mus musculus]	40.1	40.1	84%	0.027	75%	gi|74198358|BAE39664.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	40.1	40.1	89%	0.027	76%	gi|744538058|XP_010999134.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	40.1	40.1	89%	0.027	76%	gi|560931717|XP_006191986.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna	40.1	40.1	89%	0.027	76%	gi|560970802|XP_006207756.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus m	40.1	40.1	89%	0.027	76%	gi|670999853|XP_008690806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bis	39.7	39.7	89%	0.037	76%	gi|742088280|XP_010831114.1

☐	selenoprotein P [Bos taurus]	39.7	39.7	89%	0.037	76%	gi|6006351|BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mut	39.7	39.7	89%	0.037	76%	gi|555965745|XP_005894930.1
☐	selenoprotein P precursor [Bos taurus]	39.7	39.7	89%	0.037	76%	gi|156631001|NP_776884.2
☐	selenoprotein P [Bubalus bubalis]	39.7	39.7	89%	0.037	76%	gi|430001945|AFM77782.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Condylu	39.2	39.2	94%	0.050	72%	gi|507934338|XP_004678402.1
☐	PREDICTED: selenoprotein P [Sarcophilus harrisii]	38.4	38.4	94%	0.089	72%	gi|395511426|XP_003759960.1
☐	unnamed protein product [Mus musculus]	38.0	38.0	84%	0.13	75%	gi|74213751|BAC55264.3
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Dasypus	37.5	37.5	89%	0.17	76%	gi|488512454|XP_004448278.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops	37.1	37.1	94%	0.24	72%	gi|507708621|XP_004716992.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Gorilla g	36.7	36.7	52%	0.31	100%	gi|426384833|XP_004065356.1
☐	selenoprotein P precursor [Oryctolagus cuniculus]	35.8	35.8	84%	0.60	75%	gi|315434200|NP_001186775.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ochoton	35.4	35.4	84%	0.82	75%	gi|504142600|XP_004583736.1
☐	putative ATP-dependent RNA helicase DDX60-like protein [Cricetul	33.7	33.7	78%	3.0	81%	gi|537270315|ERE91786.1
☐	PREDICTED: probable ATP-dependent RNA helicase DDX60 [Cric	33.7	33.7	78%	3.0	81%	gi|625189695|XP_003498842.2
☐	selenoprotein P-like protein [Bos taurus]	33.3	33.3	89%	3.5	71%	gi|13366148|BAB39395.1
☐	selenoprotein P-like protein [Bos taurus]	33.3	33.3	89%	3.5	71%	gi|13366146|BAB39394.1
☐	selenoprotein P-like protein [Bos taurus]	33.3	33.3	89%	3.5	71%	gi|13366144|BAB39393.1
☐	selenoprotein P-like protein [Bos taurus]	33.3	33.3	89%	3.5	71%	gi|13366142|BAB39392.1
☐	selenoprotein P-like protein [Bos taurus]	33.3	33.3	89%	3.9	71%	gi|1582026|2117379A
☐	selenoprotein P like protein [Bos taurus]	33.3	33.3	89%	3.9	71%	gi|14970947|BAA04949.2
☐	methylthioribose kinase [Blautia sp. CAG:257]	31.6	31.6	68%	13	77%	gi|547449133|WP_022068881.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ictidomy	31.2	31.2	78%	18	67%	gi|532079811|XP_005325668.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Leptonyc	31.2	31.2	89%	18	65%	gi|585192742|XP_006747601.1
☐	5-methylthioribose kinase [Blautia wexlerae]	31.2	31.2	68%	18	77%	gi|651890337|WP_026649811.1
☐	dihydroxy-acid dehydratase [Campylobacter sp. FOBRC14]	31.2	31.2	63%	19	73%	gi|497335253|WP_009649466.1
☐	unnamed protein product [Mus musculus]	31.2	31.2	73%	19	80%	gi|26331444|BAC29452.1

⊖ Alignments

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]

Sequence ID: gi|675710689|ref|XP_008961588.1| **Length:** 381 **Number of Matches:** 1

Range 1: 170 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	8e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KKCGNCSLTTLKDEDFCKR  19
            KKCGNCSLTTLKDEDFCKR
Sbjct  170  KKCGNCSLTTLKDEDFCKR  188
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gi|34783648|gb|AAH46152.1| **Length:** 381 **Number of Matches:** 1

Range 1: 170 to 188 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	8e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KKCGNCSLTTLKDEDFCKR  19
            KKCGNCSLTTLKDEDFCKR
Sbjct  170  KKCGNCSLTTLKDEDFCKR  188
```

Related Information

Gene - associated gene details

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selenoprotein P isoform 1 precursor [Homo sapiens]

Sequence ID: gi|62530391|ref|NP_005401.3| **Length:** 381 **Number of Matches:** 1

▷ See 4 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 170 to 188 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	8e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KKCGNCSLTTLKDEDFCKR  19
            KKCGNCSLTTLKDEDFCKR
Sbjct  170  KKCGNCSLTTLKDEDFCKR  188
```

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gi|37596694|gb|AAH58919.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 170 to 188 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	8e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KKCGNCSLTTLKDEDFCKR  19
            KKCGNCSLTTLKDEDFCKR
Sbjct  170  KKCGNCSLTTLKDEDFCKR  188
```

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selenoprotein P [Homo sapiens]

Sequence ID: gi|312004116|emb|CAA77836.2| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 170 to 188 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
65.5 bits(147)	8e-11	19/19(100%)	19/19(100%)	0/19(0%)

```
Query  1    KKCGNCSLTTLKDEDFCKR  19
            KKCGNCSLTTLKDEDFCKR
Sbjct  170  KKCGNCSLTTLKDEDFCKR  188
```

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SEPP1_KLKKEGYSDISYIVVNHQGISSRL_Mod

RID BVM8196401R (Expires on 01-21 10:52 am)

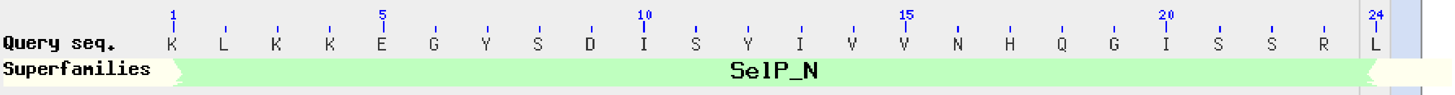
Query ID	lcl|220784	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	24		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

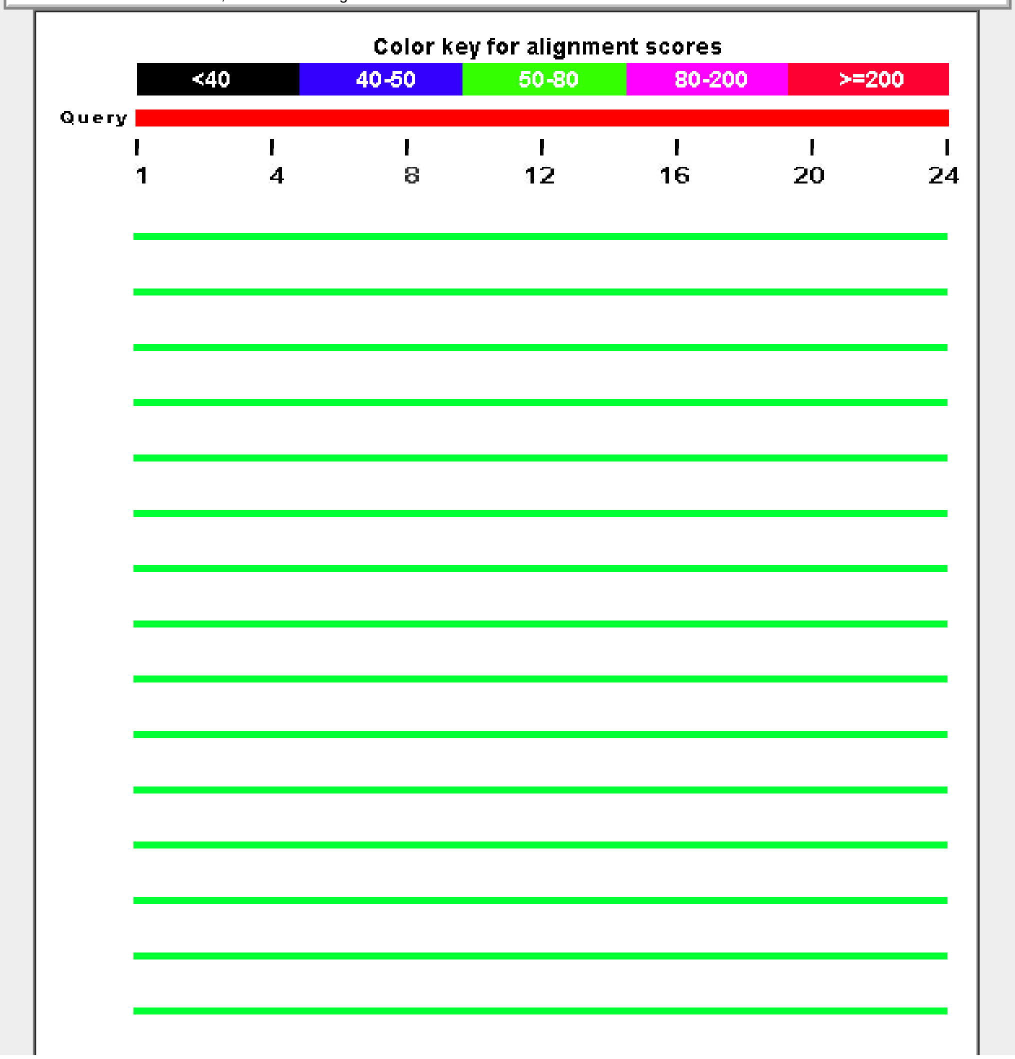
Show Conserved Domains

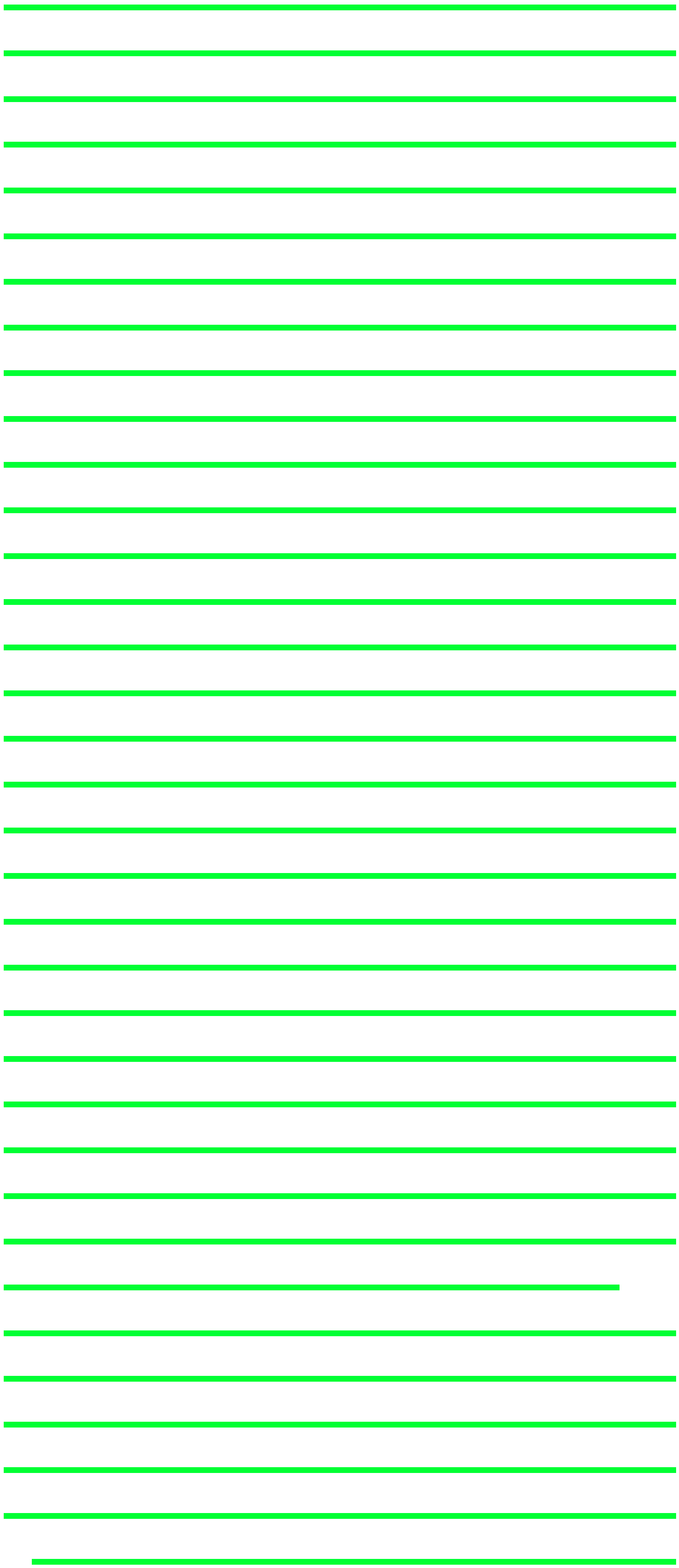
Putative conserved domains have been detected, click on the image below for detailed results.

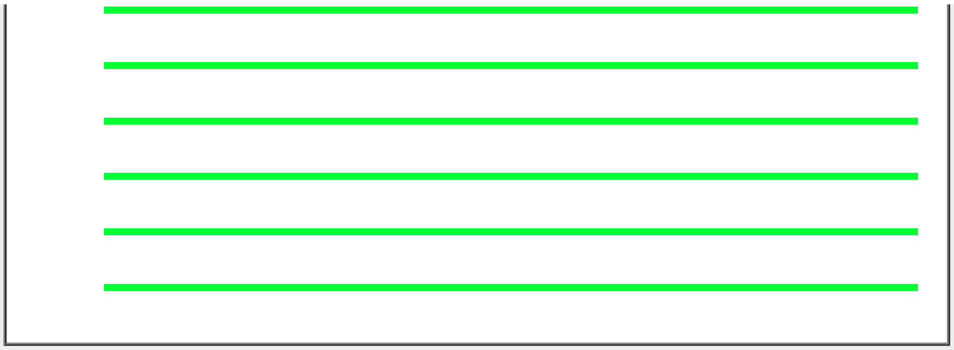


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊖ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]	76.1	76.1	100%	4e-14	96%	XP_008961588.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	76.1	76.1	100%	4e-14	96%	AAH46152.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	76.1	76.1	100%	4e-14	96%	AAH15875.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	76.1	76.1	100%	4e-14	96%	NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	76.1	76.1	100%	4e-14	96%	AAH58919.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomascus leucoge	76.1	76.1	100%	4e-14	96%	XP_003274442.1
☐	selenoprotein P [Homo sapiens]	76.1	76.1	100%	4e-14	96%	CAA77836.2
☐	selenoprotein P precursor [Pan troglodytes]	76.1	76.1	100%	4e-14	96%	NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	76.1	76.1	100%	4e-14	96%	NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxe	71.5	71.5	100%	1e-12	92%	XP_010372696.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]	71.5	71.5	100%	1e-12	92%	XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocebus sabae	71.5	71.5	100%	1e-12	92%	XP_007959679.1
☐	selenoprotein P precursor [Macaca mulatta]	71.5	71.5	100%	1e-12	92%	NP_001152962.1
☐	selenoprotein P precursor [Pongo abelii]	70.6	70.6	100%	3e-12	92%	NP_001127462.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaenoptera acuto	68.9	68.9	100%	1e-11	88%	XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes vexillifer]	68.9	68.9	100%	1e-11	88%	XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus orca]	68.9	68.9	100%	1e-11	88%	XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physeter catodon]	68.9	68.9	100%	1e-11	88%	XP_007119423.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops truncatus]	68.9	68.9	100%	1e-11	88%	XP_004320390.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bison bison]	68.9	68.9	100%	1e-11	88%	XP_010831114.1
☐	selenoprotein P [Bos taurus]	68.9	68.9	100%	1e-11	88%	BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mutus]	68.9	68.9	100%	1e-11	88%	XP_005894930.1
☐	selenoprotein P-like protein [Bos taurus]	68.9	68.9	100%	1e-11	88%	2117379A
☐	selenoprotein P like protein [Bos taurus]	68.9	68.9	100%	1e-11	88%	BAA04949.2
☐	selenoprotein P precursor [Bos taurus]	68.9	68.9	100%	1e-11	88%	NP_776884.2
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	67.2	67.2	100%	4e-11	88%	XP_003793045.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ictidomys tridecem	67.2	67.2	100%	4e-11	88%	XP_005325668.1
☐	membrane selenoprotein P [Capra hircus]	64.7	64.7	100%	3e-10	83%	AAF67201.1
☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	64.7	64.7	100%	3e-10	83%	NP_001272511.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis aries]	64.7	64.7	100%	3e-10	83%	XP_004017062.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannospalax galili]	64.7	64.7	100%	3e-10	83%	XP_008840327.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratotherium simu	64.7	64.7	100%	3e-10	83%	XP_004422836.1
☐	selenoprotein P precursor [Sus scrofa]	64.7	64.7	100%	3e-10	83%	NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus jaculus]	63.8	63.8	100%	6e-10	83%	XP_004652550.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus bubalis]	63.8	63.8	100%	6e-10	79%	XP_006067130.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus przewalskii]	62.1	62.1	100%	2e-09	79%	XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	62.1	62.1	100%	2e-09	79%	NP_001129077.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri boliviensis l	61.3	61.3	100%	4e-09	79%	XP_003925940.2
☐	selenoprotein P precursor [Callithrix jacchus]	61.3	61.3	100%	4e-09	79%	NP_001186857.1
☐	selenoprotein P [Bubalus bubalis]	61.3	61.3	100%	4e-09	79%	AFM77782.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ochotona princeps	60.4	60.4	100%	8e-09	79%	XP_004583736.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia chinensis]	59.6	59.6	100%	2e-08	79%	XP_006167023.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna pacos]	59.2	59.2	100%	2e-08	75%	XP_006207756.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Octodon degus]	58.7	58.7	91%	3e-08	82%	XP_004641866.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orycteropus afer af	58.3	58.3	100%	4e-08	75%	XP_007952213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis brandtii]	58.3	58.3	100%	4e-08	75%	XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchilla lanigera]	58.3	58.3	100%	4e-08	75%	XP_005386312.1
☐	selenoprotein P precursor [Oryctolagus cuniculus]	58.3	58.3	100%	4e-08	75%	NP_001186775.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephantulus edwa	57.9	57.9	100%	6e-08	75%	XP_006889619.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius syrichta]	57.1	57.1	95%	1e-07	74%	XP_008050904.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Dasypus novemcin	57.1	57.1	100%	1e-07	75%	XP_004448278.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus dromedar	56.6	56.6	100%	2e-07	75%	XP_010999134.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus ferus]	56.6	56.6	100%	2e-07	75%	XP_006191986.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys damaren	54.9	54.9	100%	6e-07	75%	XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lucifugus]	54.9	54.9	100%	6e-07	75%	XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela putorius fu	54.9	54.9	100%	6e-07	75%	XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Leptonychotes wec	54.9	54.9	100%	6e-07	75%	XP_006747601.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenus rosmaru	54.9	54.9	100%	6e-07	75%	XP_004409206.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromyscus manic	54.9	54.9	100%	6e-07	75%	XP_006997157.1
☐	Selenoprotein P [Heterocephalus glaber]	54.5	54.5	100%	7e-07	71%	EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ornithorhynchus ar	54.5	54.5	100%	7e-07	71%	XP_007654576.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopterus varieg	54.5	54.5	100%	8e-07	75%	XP_008564915.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicus fuscus]	54.5	54.5	100%	8e-07	71%	XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichechus manatu	54.5	54.5	100%	8e-07	75%	XP_004388500.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Monodelphis dome	54.5	54.5	100%	8e-07	71%	XP_003340675.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gla	54.5	54.5	100%	8e-07	71%	XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gla	54.5	54.5	100%	8e-07	71%	XP_004878213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodonta africana	54.1	54.1	100%	1e-06	67%	XP_010586424.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis davidii]	53.2	53.2	100%	2e-06	71%	XP_006774623.1
☐	PREDICTED: selenoprotein P [Sarcophilus harrisii]	52.0	52.0	100%	5e-06	71%	XP_003759960.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Condylura cristata]	52.0	52.0	79%	5e-06	79%	XP_004678402.1
☐	selenoprotein P precursor [Canis lupus familiaris]	51.5	51.5	100%	8e-06	71%	NP_001108590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus maritimus]	51.5	51.5	100%	8e-06	71%	XP_008690806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceus europae	51.1	51.1	100%	1e-05	71%	XP_007517681.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Felis catus]	50.7	50.7	100%	1e-05	71%	XP_006928143.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera tigris alta	50.7	50.7	100%	1e-05	71%	XP_007095490.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops telfairi]	50.3	50.3	100%	2e-05	67%	XP_004716992.1
☐	Selenoprotein P [Cricetulus griseus]	49.0	49.0	100%	4e-05	67%	EGW04040.1
☐	selenoprotein P precursor [Cricetulus griseus]	49.0	49.0	100%	5e-05	67%	ERE84145.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus ochrogast	49.0	49.0	100%	5e-05	71%	XP_005369861.1
☐	selenoprotein P precursor [Cricetulus griseus]	49.0	49.0	100%	5e-05	67%	NP_001243807.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex araneus]	48.6	48.6	100%	7e-05	67%	XP_004605590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P, plasma, 1 [Mesocri	48.1	48.1	100%	8e-05	71%	XP_005139283.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chrysochloris asiat	48.1	48.1	100%	9e-05	67%	XP_006877364.1
☐	selenoprotein P precursor [Rattus norvegicus]	46.0	46.0	100%	5e-04	67%	NP_062065.2
☐	selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	44.8	44.8	100%	0.001	67%	EDL03405.1
☐	Selenoprotein P, plasma, 1 [Mus musculus]	44.8	44.8	100%	0.001	67%	AAH01991.2
☐	plasma selenoprotein P [Mus musculus]	44.8	44.8	100%	0.001	67%	AAD01684.1
☐	unnamed protein product [Mus musculus]	44.8	44.8	100%	0.001	67%	BAE39664.1
☐	unnamed protein product [Mus musculus]	44.8	44.8	100%	0.001	67%	BAE34948.1
☐	selenoprotein P precursor [Mus musculus]	44.8	44.8	100%	0.001	67%	NP_033181.3
☐	unnamed protein product [Mus musculus]	44.8	44.8	100%	0.001	67%	BAC55264.3
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pelodiscus sinensis	44.3	44.3	91%	0.002	73%	XP_006139560.1
☐	selenoprotein P precursor [Cavia porcellus]	43.1	43.1	66%	0.004	81%	NP_001244936.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Phaethon lepturus]	43.1	43.1	91%	0.004	68%	XP_010284851.1
☐	selenoprotein P precursor [Taeniopygia guttata]	43.1	43.1	95%	0.004	65%	NP_001257806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Phalacrocorax carb	42.6	42.6	91%	0.006	68%	XP_009511852.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Gavia stellata]	42.6	42.6	91%	0.006	68%	XP_009818154.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Caprimulgus caroli	42.6	42.6	91%	0.006	68%	XP_010164847.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tauraco erythrolop	42.6	42.6	91%	0.006	68%	XP_009979695.1

⊟ Alignments

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]

Sequence ID: ref|XP_008961588.1| **Length:** 381 **Number of Matches:** 1

Range 1: 75 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.1 bits(172)	4e-14	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1   KLKKEGYSDISYIVVNHQGISSRL  24
           KLKKEGYS+ISYIVVNHQGISSRL
Sbjct  75  KLKKEGYSNISYIVVNHQGISSRL  98
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gb|AAH46152.1| **Length:** 381 **Number of Matches:** 1

Range 1: 75 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.1 bits(172)	4e-14	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1   KLKKEGYSDISYIVVNHQGISSRL  24
           KLKKEGYS+ISYIVVNHQGISSRL
Sbjct  75  KLKKEGYSNISYIVVNHQGISSRL  98
```

Related Information

Gene - associated gene details

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gb|AAH15875.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 75 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.1 bits(172)	4e-14	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1   KLKKEGYSDISYIVVNHQGISSRL  24
           KLKKEGYS+ISYIVVNHQGISSRL
Sbjct  75  KLKKEGYSNISYIVVNHQGISSRL  98
```

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selenoprotein P isoform 1 precursor [Homo sapiens]

Sequence ID: ref|NP_005401.3| **Length:** 381 **Number of Matches:** 1

▷ See 4 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 75 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.1 bits(172)	4e-14	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1   KLKKEGYSDISYIVVNHQGISSRL  24
           KLKKEGYS+ISYIVVNHQGISSRL
Sbjct  75  KLKKEGYSNISYIVVNHQGISSRL  98
```

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gb|AAH58919.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 75 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.1 bits(172)	4e-14	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1   KLKKEGYSDISYIVVNHQGISSRL  24
           KLKKEGYS+ISYIVVNHQGISSRL
Sbjct  75  KLKKEGYSNISYIVVNHQGISSRL  98
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BE892RPB015

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SEPP1_KLKKEGYSNISYIVVNHQGISSRL_NonMod

RID BE892RPB015 (Expires on 01-16 09:08 am)

Query ID	lcl|72485	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	24	**Program**	BLASTP 2.2.30+ Citation

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Graphic Summary

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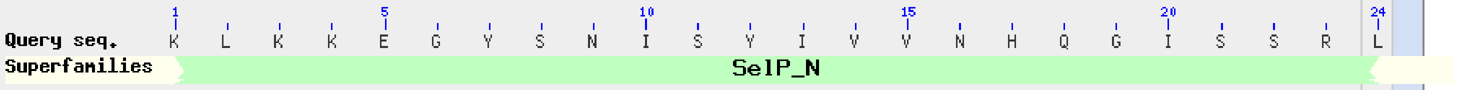
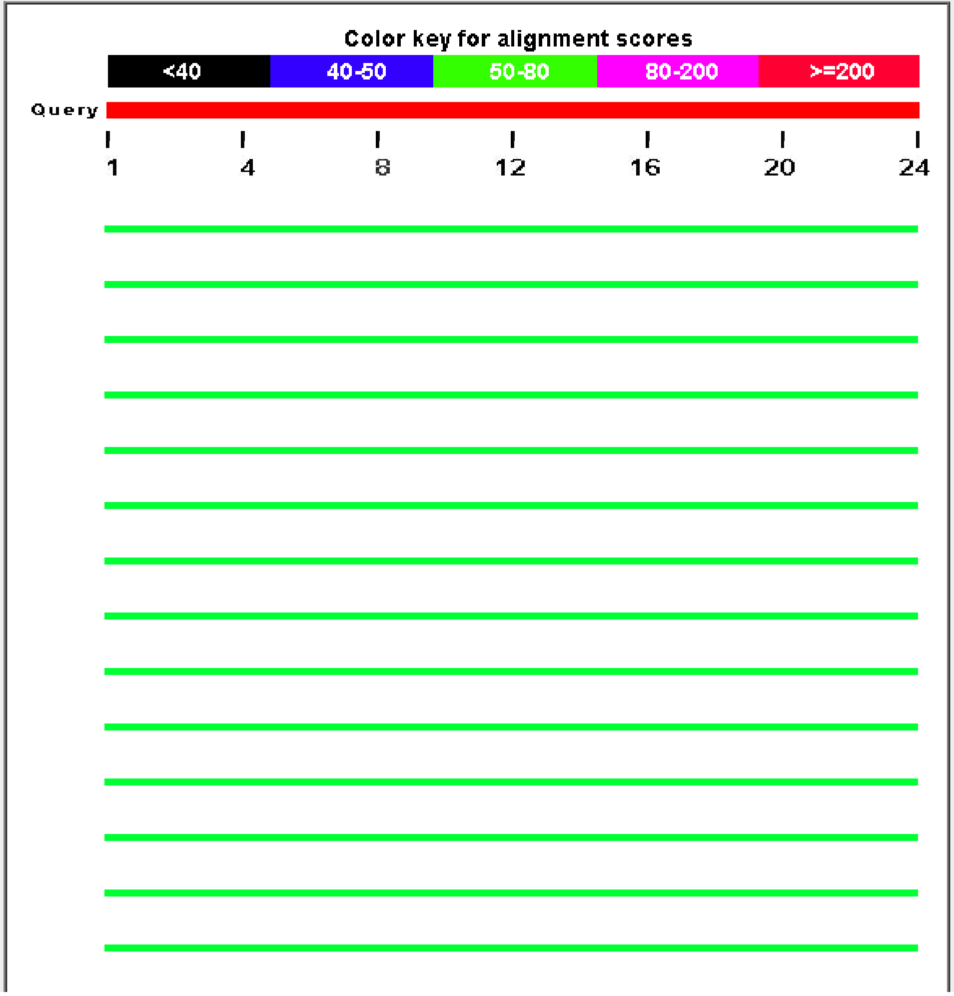
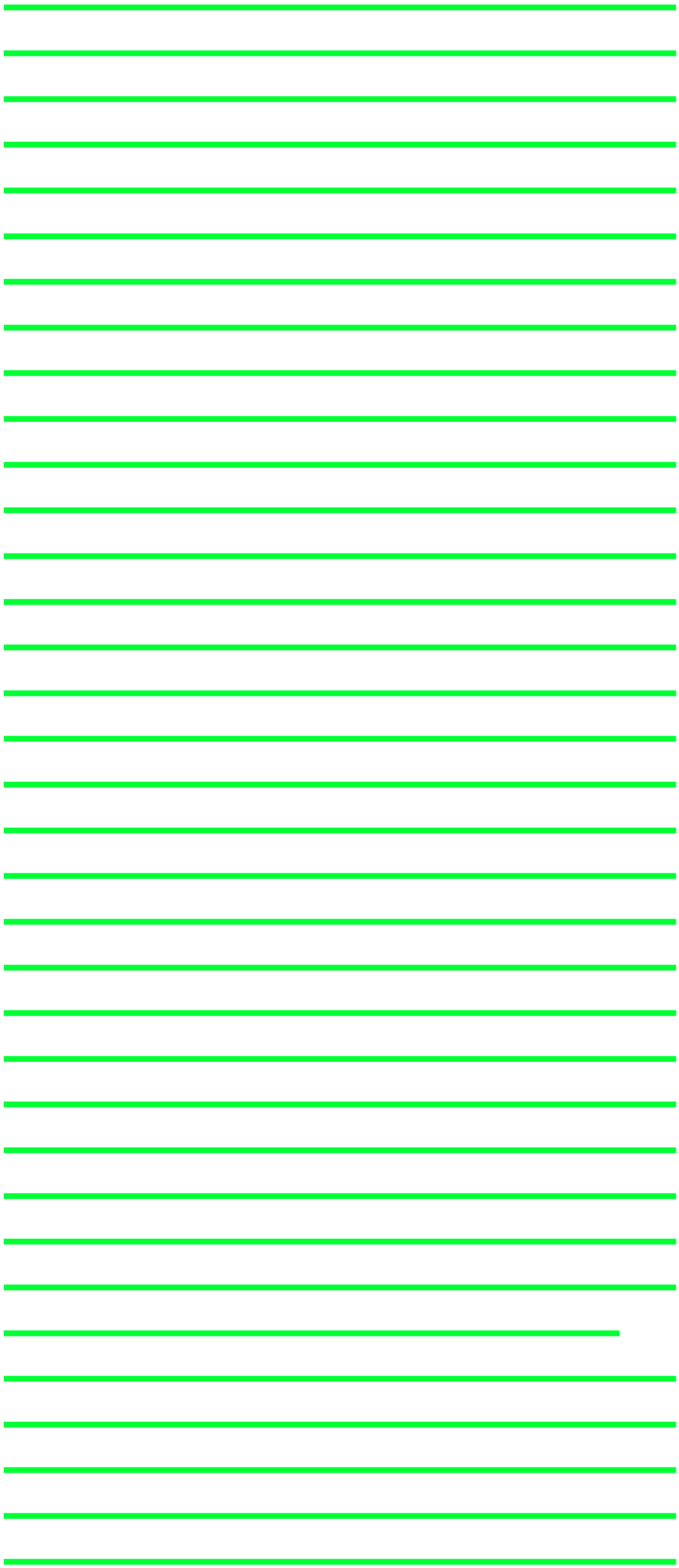
Putative conserved domains have been detected, click on the image below for detailed results.

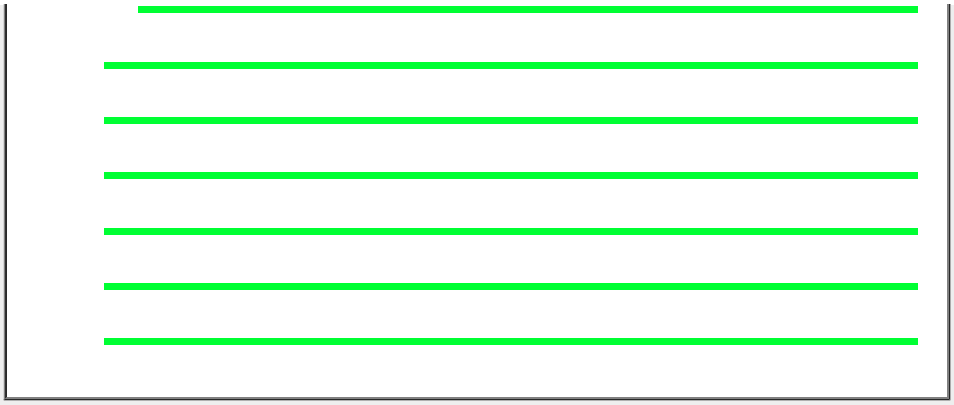


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan pani	78.7	78.7	100%	5e-15	100%	gi|675710689|XP_008961588.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	78.7	78.7	100%	5e-15	100%	gi|34783648|AAH46152.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	78.7	78.7	100%	5e-15	100%	gi|34783164|AAH15875.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	78.7	78.7	100%	5e-15	100%	gi|62530391|NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	78.7	78.7	100%	5e-15	100%	gi|37596694|AAH58919.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomasc	78.7	78.7	100%	5e-15	100%	gi|332250603|XP_003274442.1
☐	selenoprotein P [Homo sapiens]	78.7	78.7	100%	5e-15	100%	gi|312004116|CAA77836.2
☐	selenoprotein P precursor [Pan troglodytes]	78.7	78.7	100%	5e-15	100%	gi|169403955|NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	78.7	78.7	100%	5e-15	100%	gi|148277022|NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopit	74.0	74.0	100%	2e-13	96%	gi|724878613|XP_010372696.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio ar	74.0	74.0	100%	2e-13	96%	gi|685545348|XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chloroce	74.0	74.0	100%	2e-13	96%	gi|635028004|XP_007959679.1
☐	selenoprotein P precursor [Macaca mulatta]	74.0	74.0	100%	2e-13	96%	gi|226958322|NP_001152962.1
☐	selenoprotein P precursor [Pongo abelii]	73.2	73.2	100%	4e-13	96%	gi|197101233|NP_001127462.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaeno	71.5	71.5	100%	1e-12	92%	gi|594696840|XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes	71.5	71.5	100%	1e-12	92%	gi|602724444|XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus	71.5	71.5	100%	1e-12	92%	gi|465986750|XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physete	71.5	71.5	100%	1e-12	92%	gi|593761497|XP_007119423.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops	71.5	71.5	100%	1e-12	92%	gi|470626535|XP_004320390.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bi	71.5	71.5	100%	1e-12	92%	gi|742088280|XP_010831114.1
☐	selenoprotein P [Bos taurus]	71.5	71.5	100%	1e-12	92%	gi|6006351|BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mut	71.5	71.5	100%	1e-12	92%	gi|555965745|XP_005894930.1
☐	selenoprotein P-like protein [Bos taurus]	71.5	71.5	100%	1e-12	92%	gi|1582026|2117379A
☐	selenoprotein P like protein [Bos taurus]	71.5	71.5	100%	1e-12	92%	gi|14970947|BAA04949.2
☐	selenoprotein P precursor [Bos taurus]	71.5	71.5	100%	1e-12	92%	gi|156631001|NP_776884.2
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	69.8	69.8	100%	5e-12	92%	gi|395840394|XP_003793045.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ictidomy	69.8	69.8	100%	6e-12	92%	gi|532079811|XP_005325668.1
☐	membrane selenoprotein P [Capra hircus]	67.2	67.2	100%	3e-11	88%	gi|7677620|AAF67201.1

☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	67.2	67.2	100%	4e-11	88%	gi|550822255|NP_001272511.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis arie	67.2	67.2	100%	4e-11	88%	gi|426246564|XP_004017062.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannosp	67.2	67.2	100%	4e-11	88%	gi|674066756|XP_008840327.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratoth	67.2	67.2	100%	4e-11	88%	gi|478496995|XP_004422836.1
☐	selenoprotein P precursor [Sus scrofa]	67.2	67.2	100%	4e-11	88%	gi|198282079|NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus j	66.4	66.4	100%	8e-11	88%	gi|507537041|XP_004652550.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus	66.4	66.4	100%	8e-11	83%	gi|594087306|XP_006067130.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus pr	64.7	64.7	100%	3e-10	83%	gi|664731166|XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	64.7	64.7	100%	3e-10	83%	gi|208022673|NP_001129077.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri b	63.8	63.8	100%	6e-10	83%	gi|725563213|XP_003925940.2
☐	selenoprotein P precursor [Callithrix jacchus]	63.8	63.8	100%	6e-10	83%	gi|315630400|NP_001186857.1
☐	selenoprotein P [Bubalus bubalis]	63.8	63.8	100%	6e-10	83%	gi|430001945|AFM77782.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ochoton	63.0	63.0	100%	1e-09	83%	gi|504142600|XP_004583736.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia c	62.1	62.1	100%	2e-09	83%	gi|562878609|XP_006167023.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna	61.7	61.7	100%	3e-09	79%	gi|560970802|XP_006207756.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Octodon	61.3	61.3	91%	4e-09	86%	gi|507690845|XP_004641866.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Oryctero	60.9	60.9	100%	6e-09	79%	gi|634885032|XP_007952213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis b	60.9	60.9	100%	6e-09	79%	gi|554563465|XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchill	60.9	60.9	100%	6e-09	79%	gi|533143496|XP_005386312.1
☐	selenoprotein P precursor [Oryctolagus cuniculus]	60.9	60.9	100%	6e-09	79%	gi|315434200|NP_001186775.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephant	60.4	60.4	100%	8e-09	79%	gi|585672710|XP_006889619.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius s	59.6	59.6	95%	2e-08	78%	gi|640790108|XP_008050904.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Dasypus	59.6	59.6	100%	2e-08	79%	gi|488512454|XP_004448278.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	59.2	59.2	100%	2e-08	79%	gi|744538058|XP_010999134.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	59.2	59.2	100%	2e-08	79%	gi|560931717|XP_006191986.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lu	57.5	57.5	100%	8e-08	79%	gi|558205011|XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela	57.5	57.5	100%	8e-08	79%	gi|511826454|XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Leptonyc	57.5	57.5	100%	8e-08	79%	gi|585192742|XP_006747601.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenu	57.5	57.5	100%	8e-08	79%	gi|472379594|XP_004409206.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromys	57.5	57.5	100%	8e-08	79%	gi|589969345|XP_006997157.1
☐	Selenoprotein P [Heterocephalus glaber]	57.1	57.1	100%	1e-07	75%	gi|351695949|EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ornithorh	57.1	57.1	100%	1e-07	75%	gi|620968705|XP_007654576.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopte	57.1	57.1	100%	1e-07	79%	gi|667253652|XP_008564915.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicu	57.1	57.1	100%	1e-07	75%	gi|641727491|XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Monodel	57.1	57.1	100%	1e-07	75%	gi|612006645|XP_003340675.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	57.1	57.1	100%	1e-07	75%	gi|512973043|XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	57.1	57.1	100%	1e-07	75%	gi|512816050|XP_004878213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys	56.6	56.6	100%	2e-07	75%	gi|731237262|XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodon	56.6	56.6	100%	2e-07	71%	gi|731464182|XP_010586424.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichech	56.2	56.2	100%	2e-07	75%	gi|471413922|XP_004388500.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis d	54.9	54.9	100%	6e-07	71%	gi|584060316|XP_006774623.1
☐	PREDICTED: selenoprotein P [Sarcophilus harrisii]	54.5	54.5	100%	7e-07	75%	gi|395511426|XP_003759960.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Condylur	54.5	54.5	79%	8e-07	84%	gi|507934338|XP_004678402.1
☐	selenoprotein P precursor [Canis lupus familiaris]	54.1	54.1	100%	1e-06	75%	gi|169403968|NP_001108590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus ma	54.1	54.1	100%	1e-06	75%	gi|670999853|XP_008690806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Felis cat	53.2	53.2	100%	2e-06	75%	gi|586975923|XP_006928143.1

☐ PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera	53.2	53.2	100%	2e-06	75%	gi|591339998|XP_007095490.1
☐ PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops	52.8	52.8	100%	3e-06	71%	gi|507708621|XP_004716992.1
☐ PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceu	52.4	52.4	100%	4e-06	71%	gi|617575753|XP_007517681.1
☐ Selenoprotein P [Cricetulus griseus]	51.5	51.5	100%	6e-06	71%	gi|344247936|EGW04040.1
☐ selenoprotein P precursor [Cricetulus griseus]	51.5	51.5	100%	7e-06	71%	gi|537231220|ERE84145.1
☐ PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus	51.5	51.5	100%	7e-06	75%	gi|532054271|XP_005369861.1
☐ selenoprotein P precursor [Cricetulus griseus]	51.5	51.5	100%	7e-06	71%	gi|379056379|NP_001243807.1
☐ PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex ar	51.1	51.1	100%	1e-05	71%	gi|505790024|XP_004605590.1
☐ PREDICTED: LOW QUALITY PROTEIN: selenoprotein P, plasma,	50.7	50.7	100%	1e-05	75%	gi|524973435|XP_005139283.1
☐ PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chrysocl	50.7	50.7	100%	1e-05	71%	gi|586493836|XP_006877364.1
☐ selenoprotein P precursor [Rattus norvegicus]	48.6	48.6	100%	7e-05	71%	gi|15011857|NP_062065.2
☐ selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	47.3	47.3	100%	2e-04	71%	gi|148671458|EDL03405.1
☐ Selenoprotein P, plasma, 1 [Mus musculus]	47.3	47.3	100%	2e-04	71%	gi|34809553|AAH01991.2
☐ plasma selenoprotein P [Mus musculus]	47.3	47.3	100%	2e-04	71%	gi|4103142|AAD01684.1
☐ unnamed protein product [Mus musculus]	47.3	47.3	100%	2e-04	71%	gi|74198358|BAE39664.1
☐ unnamed protein product [Mus musculus]	47.3	47.3	100%	2e-04	71%	gi|74192879|BAE34948.1
☐ selenoprotein P precursor [Mus musculus]	47.3	47.3	100%	2e-04	71%	gi|74271806|NP_033181.3
☐ unnamed protein product [Mus musculus]	47.3	47.3	100%	2e-04	71%	gi|74213751|BAC55264.3
☐ PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pelodisc	46.9	46.9	91%	2e-04	77%	gi|558231946|XP_006139560.1
☐ selenoprotein P precursor [Cavia porcellus]	45.6	45.6	66%	6e-04	88%	gi|384367995|NP_001244936.1
☐ PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Phaetho	45.6	45.6	91%	6e-04	73%	gi|723136355|XP_010284851.1
☐ selenoprotein P precursor [Taeniopygia guttata]	45.6	45.6	95%	6e-04	70%	gi|399567825|NP_001257806.1
☐ PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Phalacro	45.2	45.2	91%	9e-04	73%	gi|695138937|XP_009511852.1
☐ PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Gavia st	45.2	45.2	91%	9e-04	73%	gi|698446985|XP_009818154.1
☐ PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Caprimu	45.2	45.2	91%	9e-04	73%	gi|704307382|XP_010164847.1
☐ PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tauraco	45.2	45.2	91%	9e-04	73%	gi|701334103|XP_009979695.1

⊟ Alignments

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]

Sequence ID: gi|675710689|ref|XP_008961588.1| **Length:** 381 **Number of Matches:** 1

Range 1: 75 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
78.7 bits(178)	5e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KLKKEGYSNISYIVVNHQGISSRL  24
            KLKKEGYSNISYIVVNHQGISSRL
Sbjct  75   KLKKEGYSNISYIVVNHQGISSRL  98
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gi|34783648|gb|AAH46152.1| **Length:** 381 **Number of Matches:** 1

Range 1: 75 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
78.7 bits(178)	5e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KLKKEGYSNISYIVVNHQGISSRL  24
            KLKKEGYSNISYIVVNHQGISSRL
Sbjct  75   KLKKEGYSNISYIVVNHQGISSRL  98
```

Related Information

Gene - associated gene details

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gi|34783164|gb|AAH15875.1| **Length:** 381 **Number of Matches:** 1

Range 1: 75 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
78.7 bits(178)	5e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1   KLKKEGYSNISYIVVNHQGISSRL  24
           KLKKEGYSNISYIVVNHQGISSRL
Sbjct  75  KLKKEGYSNISYIVVNHQGISSRL  98
```

Related Information

Gene - associated gene details

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selenoprotein P isoform 1 precursor [Homo sapiens]

Sequence ID: gi|62530391|ref|NP_005401.3| **Length:** 381 **Number of Matches:** 1

See 4 more title(s)

Range 1: 75 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
78.7 bits(178)	5e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1   KLKKEGYSNISYIVVNHQGISSRL  24
           KLKKEGYSNISYIVVNHQGISSRL
Sbjct  75  KLKKEGYSNISYIVVNHQGISSRL  98
```

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

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Selenoprotein P, plasma, 1 [Homo sapiens]

Sequence ID: gi|37596694|gb|AAH58919.1| **Length:** 381 **Number of Matches:** 1

Range 1: 75 to 98 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
78.7 bits(178)	5e-15	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1   KLKKEGYSNISYIVVNHQGISSRL  24
           KLKKEGYSNISYIVVNHQGISSRL
Sbjct  75  KLKKEGYSNISYIVVNHQGISSRL  98
```

Related Information

Gene - associated gene details

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

SEPP1_KVSEHIPVYQQEEDQTDVWTLLNGSKD_Mod

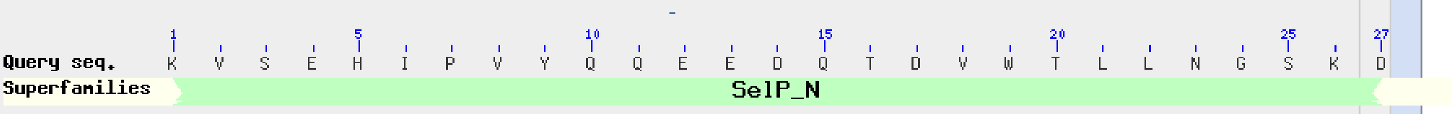
RID	BVKTTZGH01R (Expires on 01-21 10:44 am)		
Query ID	lcl|74909	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	27	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

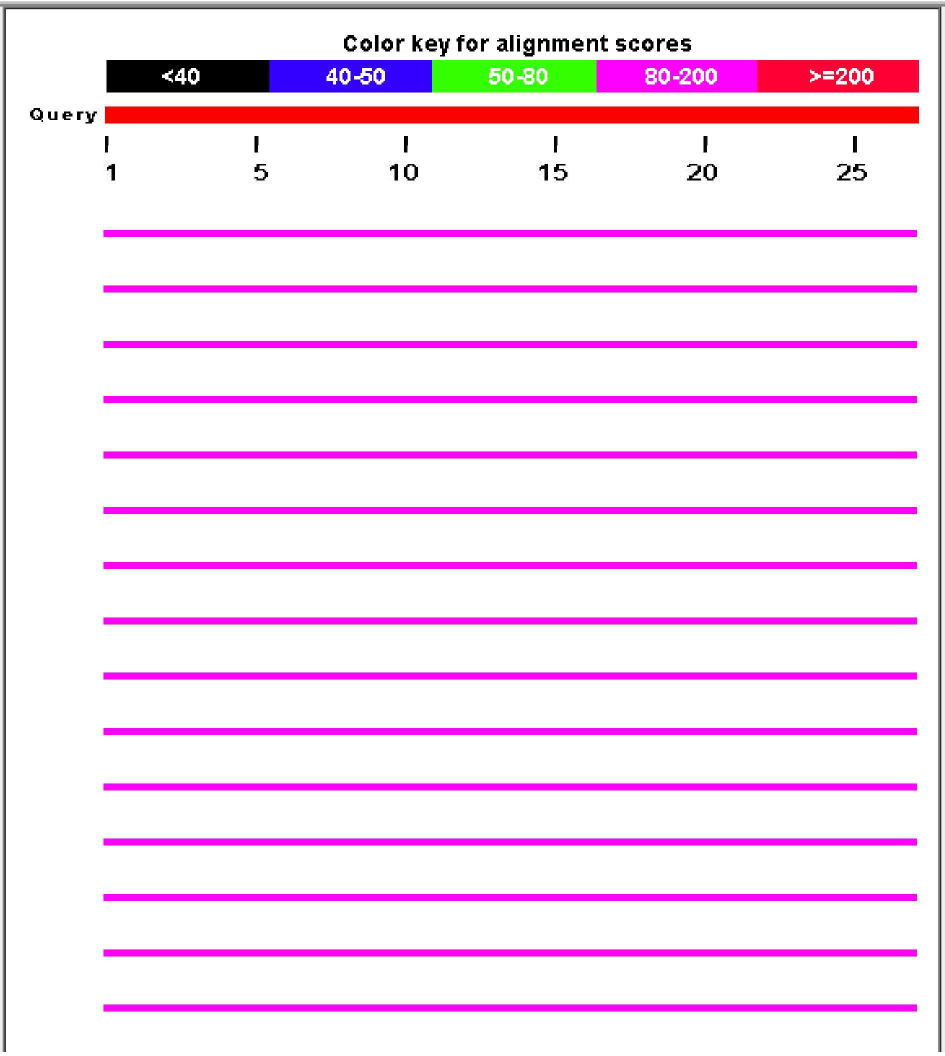
Show Conserved Domains

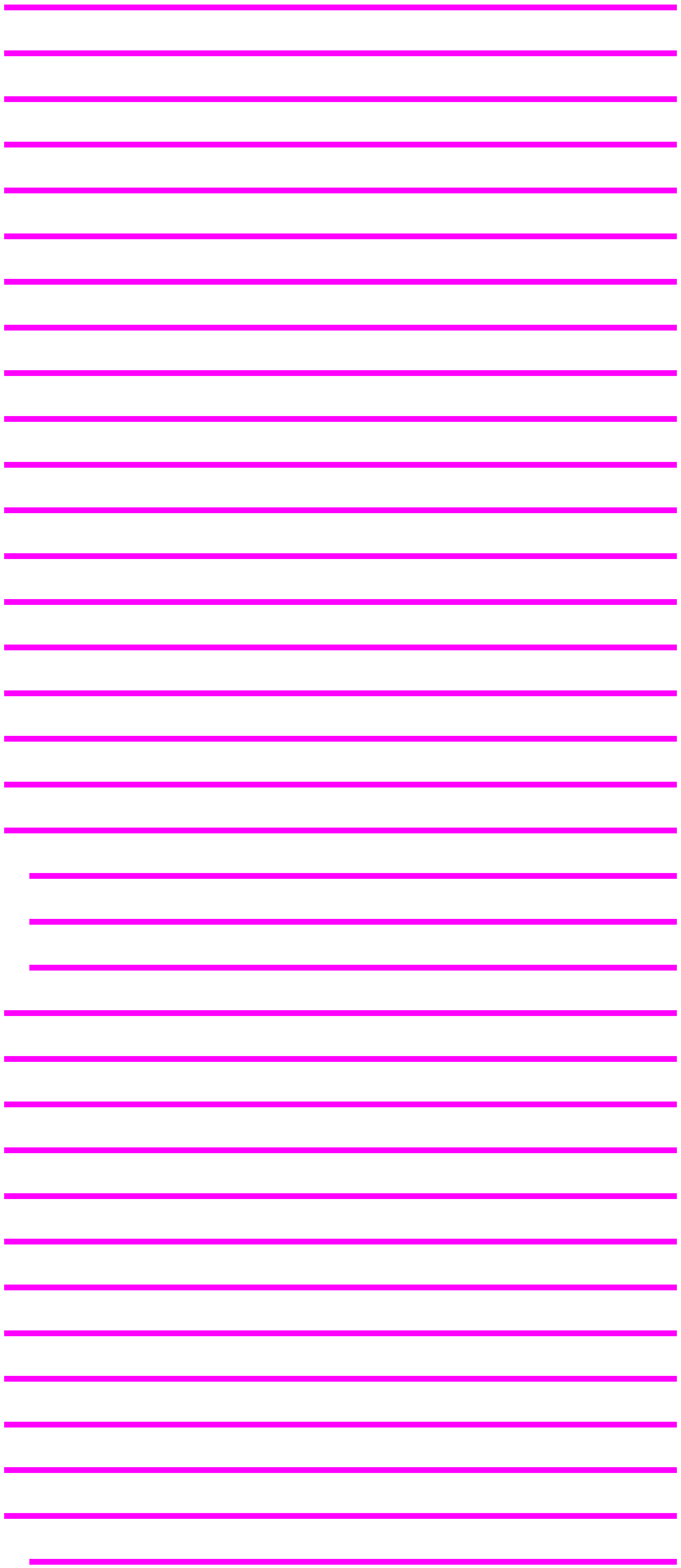
Putative conserved domains have been detected, click on the image below for detailed results.

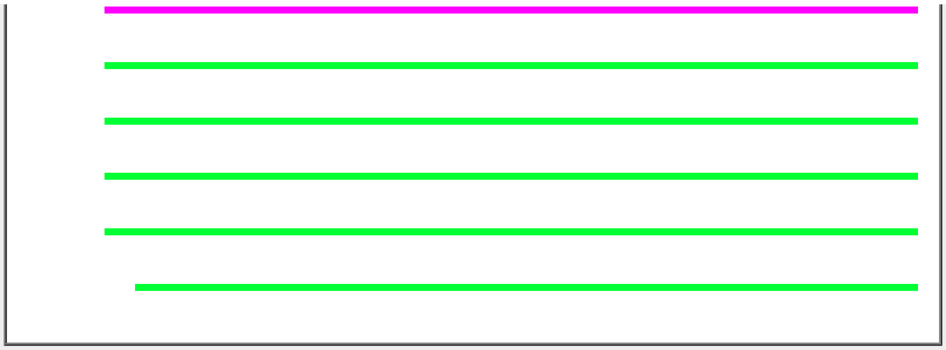


Distribution of 102 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments







⊖Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius syrichta]	89.3	89.3	100%	2e-18	96%	XP_008050904.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxe	89.3	89.3	100%	2e-18	96%	XP_010372696.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]	89.3	89.3	100%	2e-18	96%	XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]	89.3	89.3	100%	2e-18	96%	XP_008961588.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocebus sabae	89.3	89.3	100%	2e-18	96%	XP_007959679.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	89.3	89.3	100%	2e-18	96%	AAH46152.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	89.3	89.3	100%	2e-18	96%	AAH15875.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	89.3	89.3	100%	2e-18	96%	NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	89.3	89.3	100%	2e-18	96%	AAH58919.1
☐	selenoprotein P precursor [Pongo abelii]	89.3	89.3	100%	2e-18	96%	NP_001127462.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomascus leucoge	89.3	89.3	100%	2e-18	96%	XP_003274442.1
☐	selenoprotein P [Homo sapiens]	89.3	89.3	100%	2e-18	96%	CAA77836.2
☐	selenoprotein P precursor [Macaca mulatta]	89.3	89.3	100%	2e-18	96%	NP_001152962.1
☐	selenoprotein P precursor [Pan troglodytes]	89.3	89.3	100%	2e-18	96%	NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	89.3	89.3	100%	2e-18	96%	NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chrysochloris asiat	86.7	86.7	100%	1e-17	93%	XP_006877364.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia chinensis]	86.7	86.7	100%	1e-17	93%	XP_006167023.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaenoptera acuto	86.7	86.7	100%	1e-17	93%	XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lucifugus]	86.7	86.7	100%	1e-17	93%	XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus orca]	86.7	86.7	100%	1e-17	93%	XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus dromedar	86.7	86.7	100%	1e-17	93%	XP_010999134.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodonta africana	86.7	86.7	100%	1e-17	93%	XP_010586424.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephantulus edwa	86.7	86.7	100%	1e-17	93%	XP_006889619.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops truncatus]	86.7	86.7	100%	1e-17	93%	XP_004320390.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus ferus]	86.7	86.7	100%	1e-17	93%	XP_006191986.1
☐	selenoprotein P precursor [Sus scrofa]	86.7	86.7	100%	1e-17	93%	NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna pacos]	86.7	86.7	100%	1e-17	93%	XP_006207756.1
☐	PREDICTED: selenoprotein P-like [Ailuropoda melanoleuca]	85.0	85.0	100%	3e-17	93%	XP_002921760.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes vexillifer]	85.0	85.0	100%	5e-17	93%	XP_007447694.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela putorius fu	85.0	85.0	100%	5e-17	93%	XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physeter catodon]	85.0	85.0	100%	5e-17	93%	XP_007119423.1
☐	selenoprotein P precursor [Canis lupus familiaris]	85.0	85.0	100%	5e-17	93%	NP_001108590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus maritimus]	85.0	85.0	100%	5e-17	93%	XP_008690806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis aries]	84.6	84.6	100%	7e-17	93%	XP_004017062.1
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	83.8	83.8	96%	1e-16	92%	XP_003793045.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicus fuscus]	83.8	83.8	96%	1e-16	92%	XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis brandtii]	83.8	104	96%	1e-16	92%	XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orycteropus afer af	82.9	82.9	100%	3e-16	93%	XP_007952213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Felis catus]	82.1	82.1	100%	4e-16	89%	XP_006928143.1
☐	membrane selenoprotein P [Capra hircus]	82.1	82.1	100%	4e-16	89%	AAF67201.1
☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	82.1	82.1	100%	5e-16	89%	NP_001272511.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus bubalis]	82.1	82.1	100%	5e-16	89%	XP_006067130.1
☐	selenoprotein P [Bos taurus]	82.1	82.1	100%	5e-16	89%	BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera tigris alta	82.1	82.1	100%	5e-16	89%	XP_007095490.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mutus]	82.1	82.1	100%	5e-16	89%	XP_005894930.1
☐	selenoprotein P-like protein [Bos taurus]	82.1	82.1	100%	5e-16	89%	2117379A
☐	selenoprotein P like protein [Bos taurus]	82.1	82.1	100%	5e-16	89%	BAA04949.2
☐	selenoprotein P precursor [Bos taurus]	82.1	82.1	100%	5e-16	89%	NP_776884.2
☐	selenoprotein P [Bubalus bubalis]	82.1	82.1	100%	5e-16	89%	AFM77782.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex araneus]	81.7	81.7	96%	7e-16	88%	XP_004605590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ictidomys tridecem	81.2	81.2	100%	1e-15	89%	XP_005325668.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratotherium simu	80.0	80.0	100%	3e-15	89%	XP_004422836.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopterus varieg	79.5	79.5	100%	4e-15	89%	XP_008564915.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannospalax galili]	79.5	79.5	100%	4e-15	85%	XP_008840327.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bison bison]	79.5	79.5	100%	4e-15	85%	XP_010831114.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Dasypus novemcin	79.5	79.5	96%	4e-15	88%	XP_004448278.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichechus manatu	79.1	79.1	96%	5e-15	88%	XP_004388500.1
☐	selenoprotein P precursor [Callithrix jacchus]	79.1	79.1	96%	5e-15	88%	NP_001186857.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis davidii]	78.7	100	96%	8e-15	88%	XP_006774623.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchilla lanigera]	78.7	78.7	96%	8e-15	88%	XP_005386312.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Condylura cristata]	78.7	78.7	96%	8e-15	88%	XP_004678402.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus przewalskii]	77.8	77.8	100%	1e-14	85%	XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	77.8	77.8	100%	1e-14	85%	NP_001129077.1
☐	Selenoprotein P [Heterocephalus glaber]	75.7	75.7	96%	7e-14	85%	EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri boliviensis l	75.7	75.7	96%	8e-14	85%	XP_003925940.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gla	75.7	75.7	96%	8e-14	85%	XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gla	75.7	75.7	96%	8e-14	85%	XP_004878213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Leptonychotes wec	75.3	75.3	100%	1e-13	85%	XP_006747601.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops telfairi]	74.9	74.9	96%	2e-13	85%	XP_004716992.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys damarens	74.4	74.4	96%	2e-13	85%	XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ochotona princeps	74.4	74.4	100%	2e-13	85%	XP_004583736.1
☐	selenoprotein P precursor [Oryctolagus cuniculus]	73.6	73.6	100%	4e-13	85%	NP_001186775.1
☐	selenoprotein P, plasma, 1 precursor [Xenopus laevis]	73.6	73.6	100%	4e-13	81%	NP_001186825.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenus rosmaru	73.2	73.2	100%	6e-13	81%	XP_004409206.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceus europae	72.3	72.3	96%	1e-12	85%	XP_007517681.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromyscus manic	70.2	70.2	96%	6e-12	81%	XP_006997157.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ornithorhynchus ar	68.9	68.9	100%	1e-11	78%	XP_007654576.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus jaculus]	68.9	68.9	100%	2e-11	81%	XP_004652550.1
☐	selenoprotein P, plasma, 1 precursor [Xenopus (Silurana) tropicalis]	68.1	68.1	100%	3e-11	81%	NP_001186813.1
☐	selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	67.7	67.7	96%	3e-11	81%	EDL03405.1
☐	PREDICTED: selenoprotein P [Chelonia mydas]	67.7	67.7	100%	3e-11	78%	XP_007052890.1
☐	Selenoprotein P, plasma, 1 [Mus musculus]	67.7	67.7	96%	4e-11	81%	AAH01991.2
☐	plasma selenoprotein P [Mus musculus]	67.7	67.7	96%	4e-11	81%	AAD01684.1
☐	unnamed protein product [Mus musculus]	67.7	67.7	96%	4e-11	81%	BAE39664.1
☐	unnamed protein product [Mus musculus]	67.7	67.7	96%	4e-11	81%	BAE34948.1
☐	selenoprotein P precursor [Mus musculus]	67.7	67.7	96%	4e-11	81%	NP_033181.3
☐	unnamed protein product [Mus musculus]	67.7	67.7	96%	4e-11	81%	BAC55264.3
☐	selenoprotein P precursor [Rattus norvegicus]	67.7	67.7	96%	4e-11	77%	NP_062065.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chrysemys picta be	67.7	67.7	100%	4e-11	78%	XP_005282265.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P, plasma, 1 [Mesocri	66.8	66.8	96%	5e-11	77%	XP_005139283.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Falco cherrug]	67.2	67.2	96%	6e-11	81%	XP_005433806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Falco peregrinus]	67.2	67.2	96%	6e-11	81%	XP_005242025.1
☐	Selenoprotein P [Cricetulus griseus]	66.8	66.8	96%	7e-11	77%	EGW04040.1
☐	selenoprotein P precursor [Cricetulus griseus]	66.8	66.8	96%	8e-11	77%	ERE84145.1
☐	selenoprotein P precursor [Cricetulus griseus]	66.8	66.8	96%	8e-11	77%	NP_001243807.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mesitornis unicolor	66.0	66.0	96%	2e-10	81%	XP_010190708.1
☐	PREDICTED: selenoprotein P [Sarcophilus harrisii]	65.5	65.5	100%	2e-10	78%	XP_003759960.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus ochrogast	65.1	65.1	96%	3e-10	77%	XP_005369861.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Alligator mississipp	64.7	64.7	96%	4e-10	77%	XP_006268971.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Alligator sinensis]	64.7	64.7	96%	4e-10	77%	XP_006026767.1

⊟ Alignments

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius syrichta]

Sequence ID: ref|XP_008050904.1| **Length:** 377 **Number of Matches:** 1

Range 1: 106 to 132 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
89.3 bits(203)	2e-18	26/27(96%)	27/27(100%)	0/27(0%)

```
Query  1    KVSEHIPVYQQEEDQTDVWTLLNGSKD  27
            KVSEHIPVYQQEE+QTDVWTLLNGSKD
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKD  132
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxellana]

Sequence ID: ref|XP_010372696.1| **Length:** 381 **Number of Matches:** 1

Range 1: 106 to 132 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
89.3 bits(203)	2e-18	26/27(96%)	27/27(100%)	0/27(0%)

```
Query  1    KVSEHIPVYQQEEDQTDVWTLLNGSKD  27
            KVSEHIPVYQQEE+QTDVWTLLNGSKD
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKD  132
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]

Sequence ID: ref|XP_009206607.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 106 to 132 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
89.3 bits(203)	2e-18	26/27(96%)	27/27(100%)	0/27(0%)

```
Query  1    KVSEHIPVYQQEEDQTDVWTLLNGSKD  27
            KVSEHIPVYQQEE+QTDVWTLLNGSKD
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKD  132
```

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]

Sequence ID: ref|XP_008961588.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 106 to 132 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
89.3 bits(203)	2e-18	26/27(96%)	27/27(100%)	0/27(0%)

```
Query  1    KVSEHIPVYQQEEDQTDVWTLLNGSKD  27
            KVSEHIPVYQQEE+QTDVWTLLNGSKD
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKD  132
```

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocebus sabaeus]

Sequence ID: ref|XP_007959679.1| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 106 to 132 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
89.3 bits(203)	2e-18	26/27(96%)	27/27(100%)	0/27(0%)

```
Query  1    KVSEHIPVYQQEEDQTDVWTLLNGSKD  27
            KVSEHIPVYQQEE+QTDVWTLLNGSKD
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKD  132
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVKYM6E401R

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SEPP1_KVSEHIPVYQQEENQTDVWTLLDGSKDDFLIYDRC_Mod

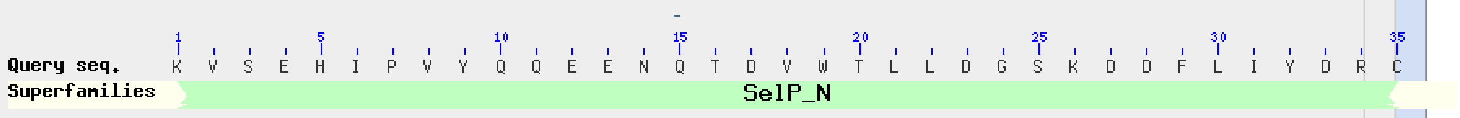
RID	BVKYM6E401R (Expires on 01-21 10:47 am)
Query ID	lcl|49313
Description	None
Molecule type	amino acid
Query Length	35
Database Name	nr
Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

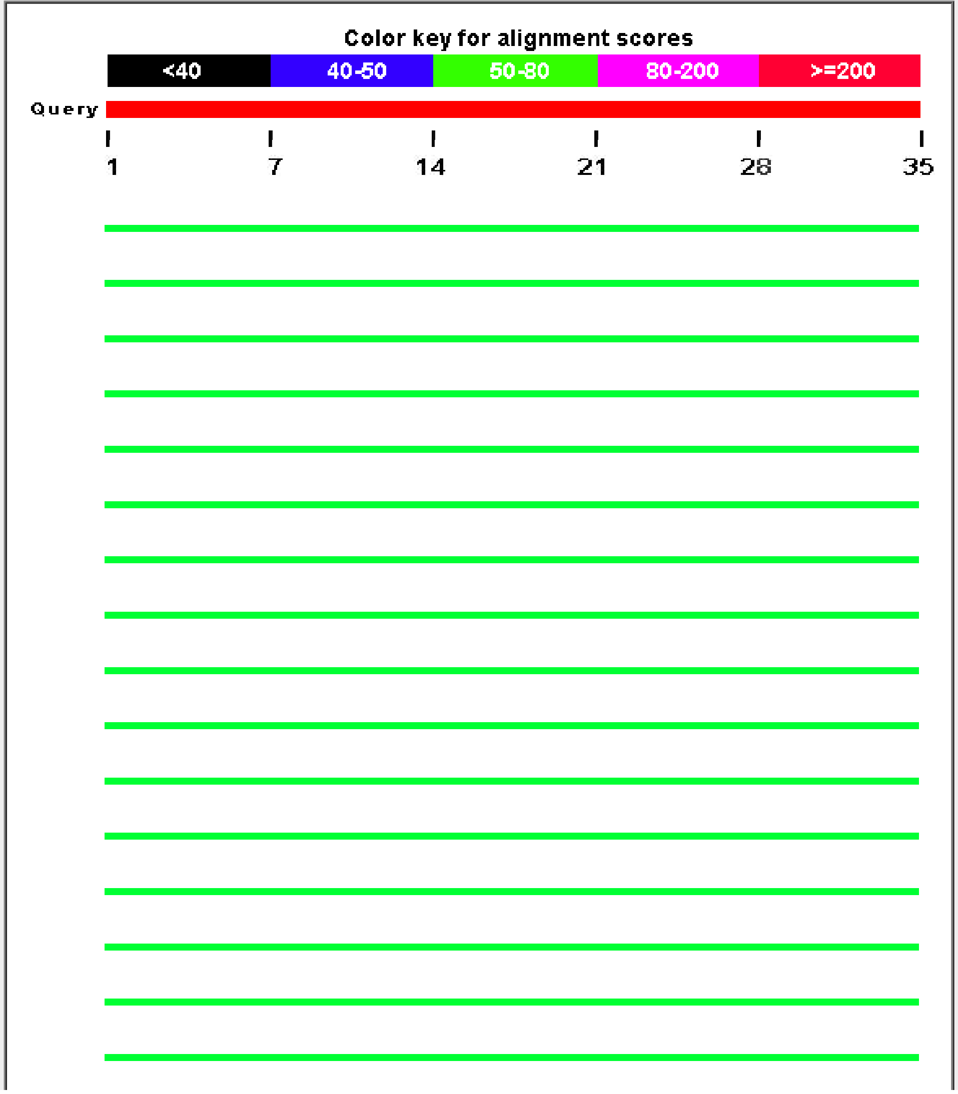
Show Conserved Domains

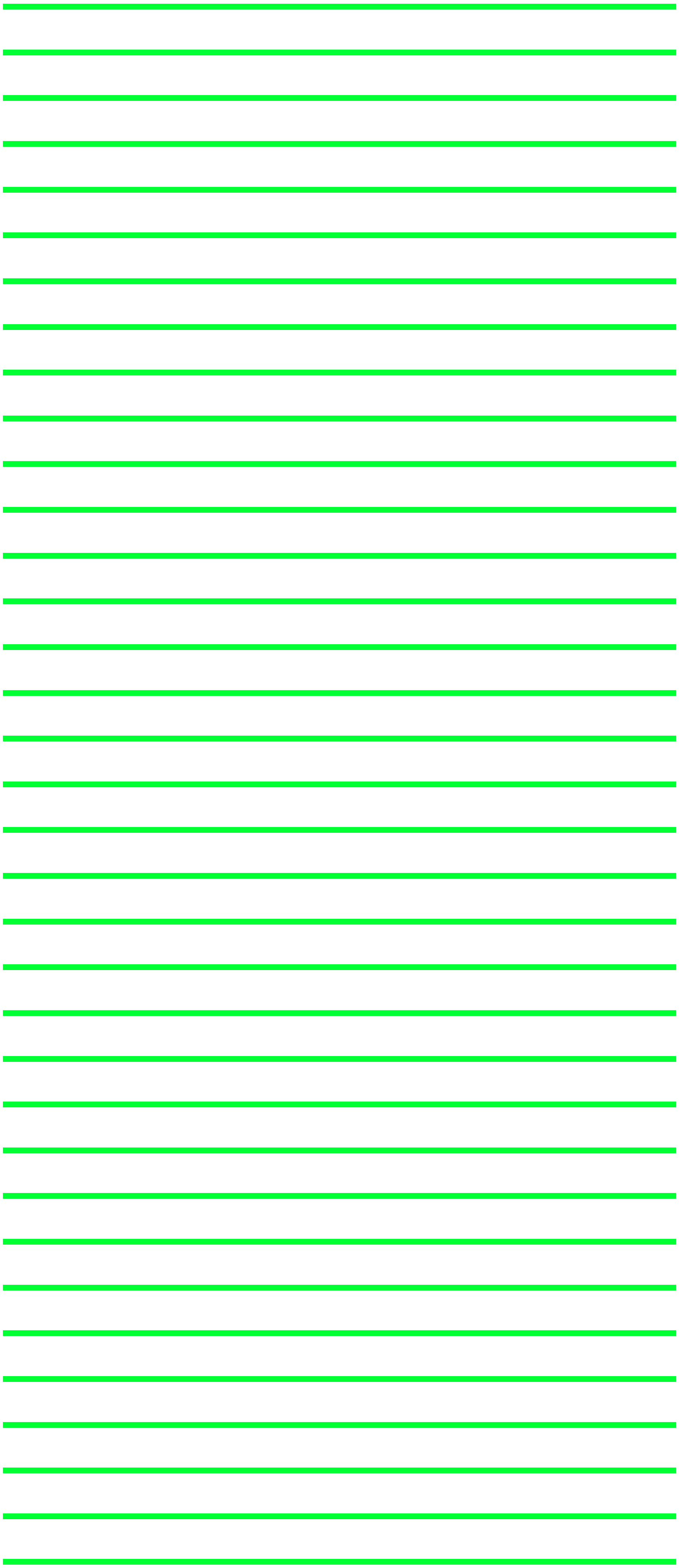
Putative conserved domains have been detected, click on the image below for detailed results.

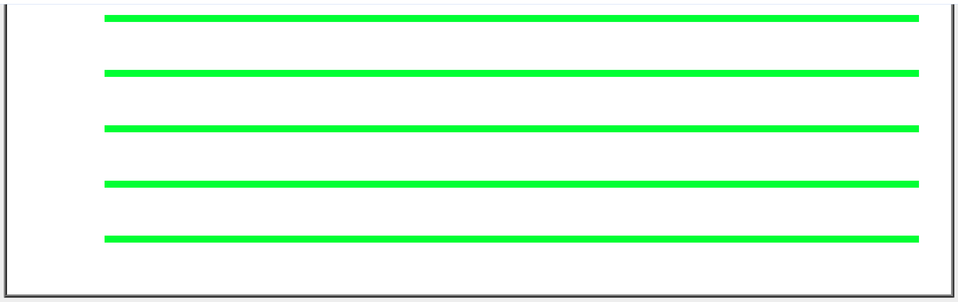


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lucifugus]	78.2	78.2	100%	6e-16	94%	XP_006106371.1
☐	selenoprotein P isoform 2 [Homo sapiens]	78.6	78.6	100%	7e-16	97%	NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius syrichta]	77.8	77.8	100%	8e-16	97%	XP_008050904.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	77.4	77.4	100%	1e-15	97%	NP_005401.3
☐	selenoprotein P [Homo sapiens]	77.4	77.4	100%	1e-15	97%	CAA77836.2
☐	selenoprotein P precursor [Pongo abelii]	77.4	77.4	100%	1e-15	97%	NP_001127462.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	77.4	77.4	100%	1e-15	97%	AAH46152.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	77.4	77.4	100%	1e-15	97%	AAH15875.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	77.4	77.4	100%	1e-15	97%	AAH58919.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomascus leucoge	77.4	77.4	100%	1e-15	97%	XP_003274442.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]	77.0	77.0	100%	2e-15	97%	XP_008961588.1
☐	selenoprotein P precursor [Macaca mulatta]	77.0	77.0	100%	2e-15	97%	NP_001152962.1
☐	selenoprotein P precursor [Pan troglodytes]	77.0	77.0	100%	2e-15	97%	NP_001108587.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela putorius fu	76.6	76.6	100%	2e-15	94%	XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocebus sabae	76.6	76.6	100%	2e-15	97%	XP_007959679.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]	76.6	76.6	100%	2e-15	97%	XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicus fuscus]	76.6	76.6	100%	2e-15	91%	XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxe	76.6	76.6	100%	3e-15	97%	XP_010372696.1
☐	PREDICTED: selenoprotein P-like [Ailuropoda melanoleuca]	74.3	74.3	100%	3e-15	91%	XP_002921760.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus maritimus]	76.6	76.6	100%	3e-15	91%	XP_008690806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis brandtii]	76.3	76.3	100%	3e-15	91%	XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaenoptera acutc	75.9	75.9	100%	4e-15	94%	XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus orca]	75.5	75.5	100%	6e-15	94%	XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephantulus edwa	75.5	75.5	100%	7e-15	94%	XP_006889619.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus dromedar	75.5	75.5	100%	7e-15	94%	XP_010999134.1
☐	selenoprotein P precursor [Sus scrofa]	75.5	75.5	100%	7e-15	94%	NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna pacos]	75.5	75.5	100%	7e-15	94%	XP_006207756.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus ferus]	75.5	75.5	100%	7e-15	94%	XP_006191986.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops truncatus]	75.5	75.5	100%	7e-15	94%	XP_004320390.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodonta africana	75.5	75.5	100%	8e-15	94%	XP_010586424.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes vexillifer]	75.1	75.1	100%	8e-15	94%	XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physeter catodon]	75.1	75.1	100%	8e-15	94%	XP_007119423.1
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	73.6	73.6	100%	9e-15	91%	XP_003793045.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia chinensis]	75.1	75.1	100%	9e-15	94%	XP_006167023.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chrysochloris asiat	74.3	74.3	100%	9e-15	91%	XP_006877364.1
☐	selenoprotein P precursor [Canis lupus familiaris]	74.7	74.7	100%	1e-14	94%	NP_001108590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex araneus]	74.3	74.3	100%	2e-14	86%	XP_004605590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceus europae	73.6	73.6	100%	3e-14	89%	XP_007517681.1
☐	selenoprotein P-like protein [Bos taurus]	73.9	73.9	100%	3e-14	91%	2117379A
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus bubalis]	73.2	73.2	100%	4e-14	91%	XP_006067130.1
☐	selenoprotein P [Bos taurus]	73.2	73.2	100%	4e-14	91%	BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mutus]	73.2	73.2	100%	5e-14	91%	XP_005894930.1
☐	selenoprotein P precursor [Bos taurus]	73.2	73.2	100%	5e-14	91%	NP_776884.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis davidii]	72.8	72.8	100%	5e-14	89%	XP_006774623.1
☐	selenoprotein P like protein [Bos taurus]	73.2	73.2	100%	5e-14	91%	BAA04949.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera tigris alta	73.2	73.2	100%	5e-14	89%	XP_007095490.1
☐	selenoprotein P [Bubalus bubalis]	73.2	73.2	100%	6e-14	91%	AFM77782.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orycteropus afer a	72.0	72.0	100%	7e-14	94%	XP_007952213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Dasypus novemcin	72.8	72.8	100%	8e-14	89%	XP_004448278.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Felis catus]	70.9	70.9	100%	8e-14	86%	XP_006928143.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ictidomys tridecem	72.4	72.4	100%	8e-14	91%	XP_005325668.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Leptonychotes we	72.0	72.0	100%	1e-13	89%	XP_006747601.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopterus varieg	72.0	72.0	100%	1e-13	89%	XP_008564915.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops telfairi]	72.0	72.0	100%	1e-13	91%	XP_004716992.1
☐	selenoprotein P precursor [Callithrix jacchus]	72.0	72.0	100%	1e-13	89%	NP_001186857.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bison bison]	71.6	71.6	100%	2e-13	89%	XP_010831114.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Condylura cristata]	71.6	71.6	100%	2e-13	89%	XP_004678402.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichechus manatu	71.6	71.6	100%	2e-13	89%	XP_004388500.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratotherium sim	71.2	71.2	100%	3e-13	89%	XP_004422836.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannospalax galili]	70.9	70.9	100%	3e-13	86%	XP_008840327.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ochotona princeps	70.9	70.9	100%	3e-13	89%	XP_004583736.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis aries]	70.9	70.9	100%	3e-13	89%	XP_004017062.1
☐	selenoprotein P precursor [Oryctolagus cuniculus]	70.9	70.9	100%	4e-13	91%	NP_001186775.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gla	70.5	70.5	100%	4e-13	83%	XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heterocephalus gla	70.5	70.5	100%	4e-13	83%	XP_004878213.1
☐	selenoprotein P precursor [Equus caballus]	70.5	70.5	100%	5e-13	89%	NP_001129077.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri boliviensis	70.5	70.5	100%	5e-13	86%	XP_003925940.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus przewalskii]	70.5	70.5	100%	5e-13	89%	XP_008522793.1
☐	Selenoprotein P [Heterocephalus glaber]	68.6	68.6	100%	5e-13	83%	EHA98867.1
☐	membrane selenoprotein P [Capra hircus]	68.2	68.2	100%	6e-13	86%	AAF67201.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ornithorhynchus a	68.6	68.6	100%	9e-13	83%	XP_007654576.1
☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	69.3	69.3	100%	1e-12	86%	NP_001272511.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenus rosmaru	68.9	68.9	100%	2e-12	86%	XP_004409206.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys damaren	68.9	68.9	100%	2e-12	83%	XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchilla lanigera]	68.6	68.6	100%	2e-12	83%	XP_005386312.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromyscus manic	68.6	68.6	100%	2e-12	80%	XP_006997157.1

☐	selenoprotein P, plasma, 1 precursor [Xenopus laevis]	68.2	68.2	100%	3e-12	86%	NP_001186825.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus jaculus]	67.8	67.8	100%	4e-12	83%	XP_004652550.1
☐	selenoprotein P precursor [Rattus norvegicus]	66.6	66.6	100%	1e-11	77%	NP_062065.2
☐	PREDICTED: selenoprotein P [Chelonia mydas]	64.3	64.3	100%	2e-11	83%	XP_007052890.1
☐	Selenoprotein P [Cricetulus griseus]	63.5	63.5	97%	3e-11	79%	EGW04040.1
☐	PREDICTED: selenoprotein P [Sarcophilus harrisii]	63.5	63.5	100%	4e-11	83%	XP_003759960.1
☐	selenoprotein P, plasma, 1 precursor [Xenopus (Silurana) tropicalis]	65.1	65.1	100%	5e-11	80%	NP_001186813.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chrysemys picta be	64.7	64.7	100%	6e-11	83%	XP_005282265.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus ochrogast	64.3	64.3	100%	7e-11	77%	XP_005369861.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Alligator sinensis]	64.3	64.3	100%	8e-11	80%	XP_006026767.1
☐	unnamed protein product [Mus musculus]	63.9	63.9	100%	9e-11	77%	BAC55264.3
☐	unnamed protein product [Mus musculus]	63.9	63.9	100%	1e-10	77%	BAE34948.1
☐	selenoprotein P precursor [Mus musculus]	63.9	63.9	100%	1e-10	77%	NP_033181.3
☐	unnamed protein product [Mus musculus]	63.9	63.9	100%	1e-10	77%	BAE39664.1
☐	Selenoprotein P, plasma, 1 [Mus musculus]	63.9	63.9	100%	1e-10	77%	AAH01991.2
☐	selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	62.0	62.0	100%	1e-10	77%	EDL03405.1
☐	plasma selenoprotein P [Mus musculus]	63.9	63.9	100%	1e-10	77%	AAD01684.1
☐	selenoprotein P precursor [Cricetulus griseus]	63.9	63.9	97%	1e-10	79%	NP_001243807.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Alligator mississipp	63.5	63.5	100%	1e-10	80%	XP_006268971.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P-like [Anolis caroline	62.0	62.0	100%	2e-10	74%	XP_003216248.2
☐	selenoprotein P precursor [Cricetulus griseus]	62.0	62.0	97%	2e-10	79%	ERE84145.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Falco cherrug]	62.8	62.8	97%	3e-10	82%	XP_005433806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Falco peregrinus]	62.8	62.8	97%	3e-10	82%	XP_005242025.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mesitornis unicolor	62.8	62.8	97%	3e-10	82%	XP_010190708.1

⊟ Alignments

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lucifugus]

Sequence ID: ref|XP_006106371.1| **Length:** 375 **Number of Matches:** 1

Range 1: 103 to 137 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
78.2 bits(191)	6e-16	Composition-based stats.	33/35(94%)	35/35(100%)	0/35(0%)

```
Query  1    KVSEHIPVYQQEENQTDVWTLLDGSKDDFLIYDRC  35
            KVSEHIPVYQQEENQTDVWTLL+G+KDDFLIYDRC
Sbjct  103  KVSEHIPVYQQEENQTDVWTLLNGNKDDFLIYDRC  137
```

Related Information

Gene - associated gene details

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selenoprotein P isoform 2 [Homo sapiens]

Sequence ID: ref|NP_001087195.1| **Length:** 411 **Number of Matches:** 1

Range 1: 136 to 170 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
78.6 bits(192)	7e-16	Composition-based stats.	34/35(97%)	35/35(100%)	0/35(0%)

```
Query  1    KVSEHIPVYQQEENQTDVWTLLDGSKDDFLIYDRC  35
            KVSEHIPVYQQEENQTDVWTLL+GSKDDFLIYDRC
Sbjct  136  KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC  170
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius syrichta]

Sequence ID: ref|XP_008050904.1| **Length:** 377 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 106 to 140 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
77.8 bits(190)	8e-16	Composition-based stats.	34/35(97%)	35/35(100%)	0/35(0%)

```
Query  1    KVSEHIPVYQQEENQTDVWTLLDGSKDDFLIYDRC  35
            KVSEHIPVYQQEENQTDVWTLL+GSKDDFLIYDRC
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC  140
```

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selenoprotein P isoform 1 precursor [Homo sapiens]

Sequence ID: ref|NP_005401.3| **Length:** 381 **Number of Matches:** 1

▷ See 4 more title(s)

Related Information

Gene - associated gene details

UniGene - clustered expressed sequence tags

Map Viewer - aligned genomic context

Identical Proteins - Proteins identical to the subject

Range 1: 106 to 140 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
77.4 bits(189)	1e-15	Composition-based stats.	34/35(97%)	35/35(100%)	0/35(0%)

```
Query  1    KVSEHIPVYQQEENQTDVWTLLDGSKDDFLIYDRC  35
            KVSEHIPVYQQEENQTDVWTLL+GSKDDFLIYDRC
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC  140
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

selenoprotein P [Homo sapiens]

Sequence ID: emb|CAA77836.2| **Length:** 381 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 106 to 140 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
77.4 bits(189)	1e-15	Composition-based stats.	34/35(97%)	35/35(100%)	0/35(0%)

```
Query  1    KVSEHIPVYQQEENQTDVWTLLDGSKDDFLIYDRC  35
            KVSEHIPVYQQEENQTDVWTLL+GSKDDFLIYDRC
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC  140
```

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SEPP1_KVSEHIPVYQQEENQTDVWTLLNGSKD_NonMod

RID BE8HJVGN015 (Expires on 01-16 09:13 am)

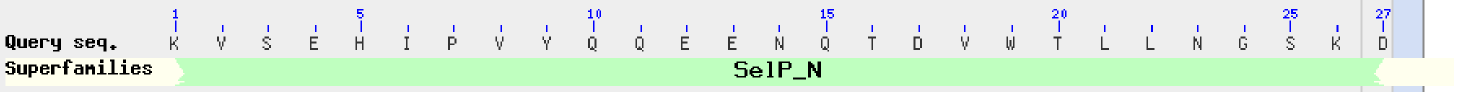
Query ID	lcl|56300	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	27		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

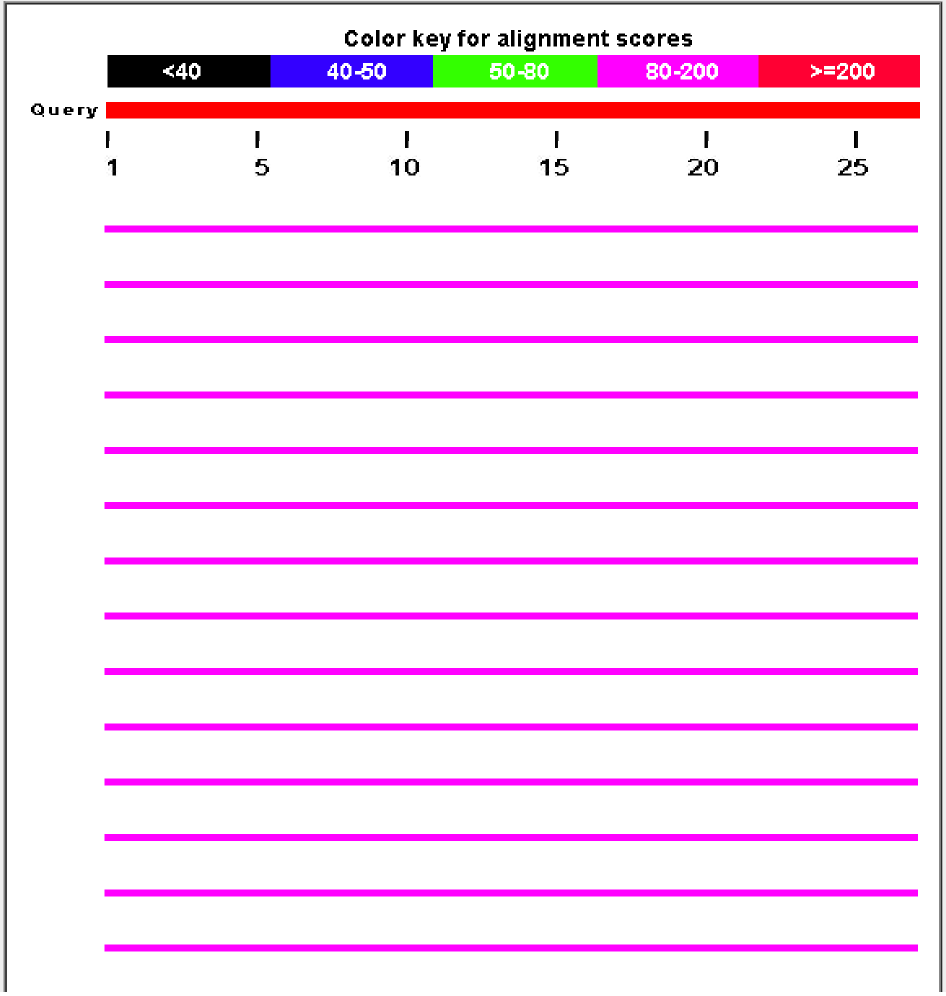
Show Conserved Domains

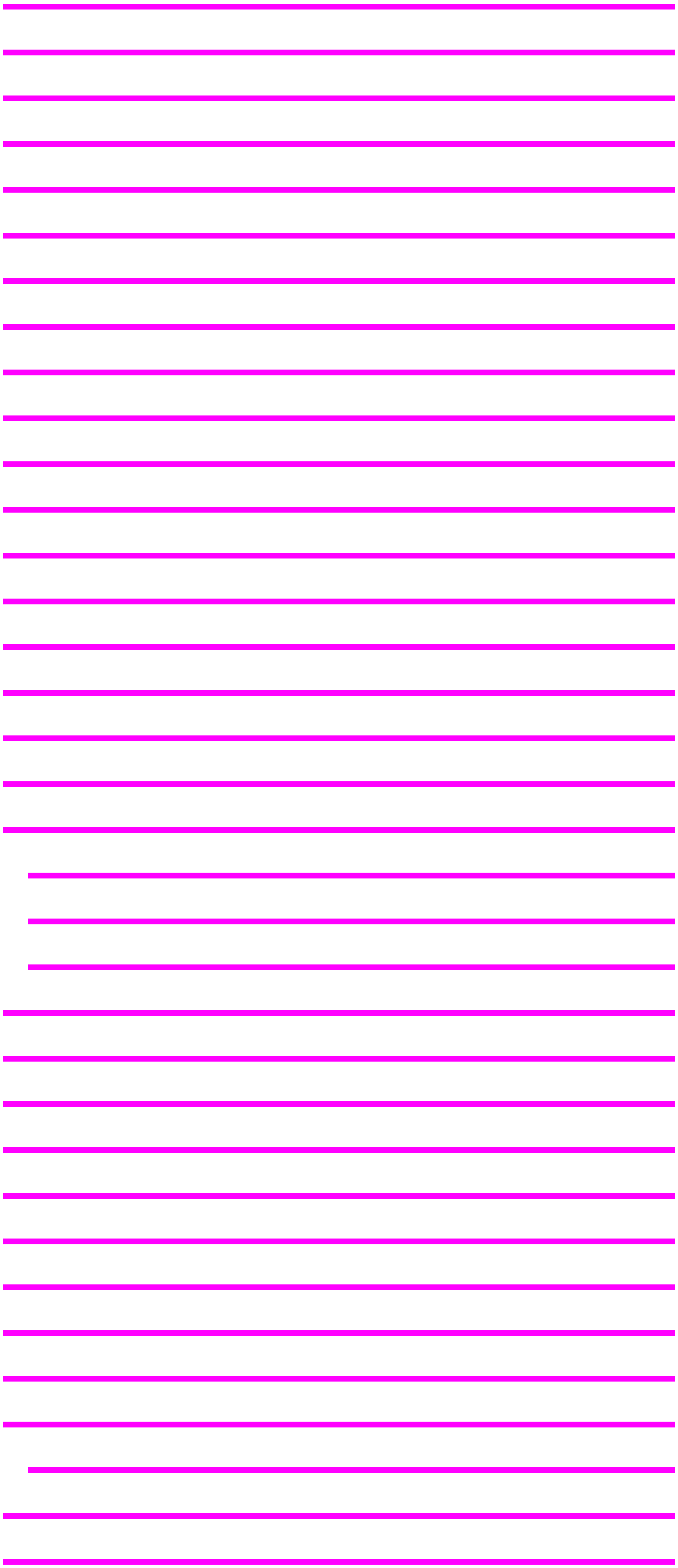
Putative conserved domains have been detected, click on the image below for detailed results.

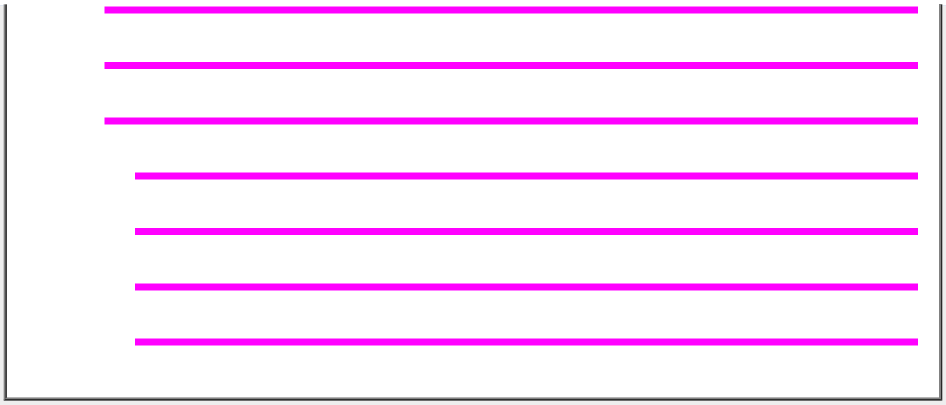


Distribution of 101 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius s	91.8	91.8	100%	2e-19	100%	gi|640790108|XP_008050904.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopitl	91.8	91.8	100%	2e-19	100%	gi|724878613|XP_010372696.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio ar	91.8	91.8	100%	2e-19	100%	gi|685545348|XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan pani	91.8	91.8	100%	2e-19	100%	gi|675710689|XP_008961588.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chloroce	91.8	91.8	100%	2e-19	100%	gi|635028004|XP_007959679.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	91.8	91.8	100%	2e-19	100%	gi|34783648|AAH46152.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	91.8	91.8	100%	2e-19	100%	gi|34783164|AAH15875.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	91.8	91.8	100%	2e-19	100%	gi|62530391|NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	91.8	91.8	100%	2e-19	100%	gi|37596694|AAH58919.1
☐	selenoprotein P precursor [Pongo abelii]	91.8	91.8	100%	2e-19	100%	gi|197101233|NP_001127462.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomascı	91.8	91.8	100%	2e-19	100%	gi|332250603|XP_003274442.1
☐	selenoprotein P [Homo sapiens]	91.8	91.8	100%	2e-19	100%	gi|312004116|CAA77836.2
☐	selenoprotein P precursor [Macaca mulatta]	91.8	91.8	100%	2e-19	100%	gi|226958322|NP_001152962.1
☐	selenoprotein P precursor [Pan troglodytes]	91.8	91.8	100%	2e-19	100%	gi|169403955|NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	91.8	91.8	100%	2e-19	100%	gi|148277022|NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chrysocl	89.3	89.3	100%	2e-18	96%	gi|586493836|XP_006877364.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia c	89.3	89.3	100%	2e-18	96%	gi|562878609|XP_006167023.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaeno	89.3	89.3	100%	2e-18	96%	gi|594696840|XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lı	89.3	89.3	100%	2e-18	96%	gi|558205011|XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus	89.3	89.3	100%	2e-18	96%	gi|465986750|XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	89.3	89.3	100%	2e-18	96%	gi|744538058|XP_010999134.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodon	89.3	89.3	100%	2e-18	96%	gi|731464182|XP_010586424.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephant	89.3	89.3	100%	2e-18	96%	gi|585672710|XP_006889619.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops	89.3	89.3	100%	2e-18	96%	gi|470626535|XP_004320390.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	89.3	89.3	100%	2e-18	96%	gi|560931717|XP_006191986.1
☐	selenoprotein P precursor [Sus scrofa]	89.3	89.3	100%	2e-18	96%	gi|198282079|NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna	89.3	89.3	100%	2e-18	96%	gi|560970802|XP_006207756.1
☐	PREDICTED: selenoprotein P-like [Ailuropoda melanoleuca]	87.6	87.6	100%	4e-18	96%	gi|301772662|XP_002921760.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes v	87.6	87.6	100%	7e-18	96%	gi|602724444|XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela	87.6	87.6	100%	7e-18	96%	gi|511826454|XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physeter	87.6	87.6	100%	7e-18	96%	gi|593761497|XP_007119423.1
☐	selenoprotein P precursor [Canis lupus familiaris]	87.6	87.6	100%	7e-18	96%	gi|169403968|NP_001108590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus ma	87.6	87.6	100%	7e-18	96%	gi|670999853|XP_008690806.1
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	86.3	86.3	96%	1e-17	96%	gi|395840394|XP_003793045.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicu	86.3	107	96%	2e-17	96%	gi|641727491|XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis b	86.3	86.3	96%	2e-17	96%	gi|554563465|XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Oryctero	85.5	85.5	100%	3e-17	96%	gi|634885032|XP_007952213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Felis cat	84.6	84.6	100%	5e-17	93%	gi|586975923|XP_006928143.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus	84.6	84.6	100%	7e-17	93%	gi|594087306|XP_006067130.1
☐	selenoprotein P [Bos taurus]	84.6	84.6	100%	7e-17	93%	gi|6006351|BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera	84.6	84.6	100%	7e-17	93%	gi|591339998|XP_007095490.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mut	84.6	84.6	100%	7e-17	93%	gi|555965745|XP_005894930.1
☐	selenoprotein P-like protein [Bos taurus]	84.6	84.6	100%	7e-17	93%	gi|1582026|2117379A
☐	selenoprotein P like protein [Bos taurus]	84.6	84.6	100%	7e-17	93%	gi|14970947|BAA04949.2
☐	selenoprotein P precursor [Bos taurus]	84.6	84.6	100%	7e-17	93%	gi|156631001|NP_776884.2
☐	selenoprotein P [Bubalus bubalis]	84.6	84.6	100%	7e-17	93%	gi|430001945|AFM77782.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex ar	84.2	84.2	96%	1e-16	92%	gi|505790024|XP_004605590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ictidomys	83.8	83.8	100%	1e-16	93%	gi|532079811|XP_005325668.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratoth	82.5	82.5	100%	4e-16	93%	gi|478496995|XP_004422836.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis arie	82.1	82.1	100%	5e-16	89%	gi|426246564|XP_004017062.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannosp	82.1	82.1	100%	5e-16	89%	gi|674066756|XP_008840327.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bis	82.1	82.1	100%	5e-16	89%	gi|742088280|XP_010831114.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Dasypus	82.1	82.1	96%	5e-16	92%	gi|488512454|XP_004448278.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichech	81.7	81.7	96%	7e-16	92%	gi|471413922|XP_004388500.1
☐	selenoprotein P precursor [Callithrix jacchus]	81.7	81.7	96%	7e-16	92%	gi|315630400|NP_001186857.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis d	81.2	81.2	96%	1e-15	92%	gi|584060316|XP_006774623.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Condylu	81.2	81.2	96%	1e-15	92%	gi|507934338|XP_004678402.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopte	80.8	80.8	100%	1e-15	89%	gi|667253652|XP_008564915.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchill	80.4	80.4	96%	2e-15	88%	gi|533143496|XP_005386312.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus p	80.4	80.4	100%	2e-15	89%	gi|664731166|XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	80.4	80.4	100%	2e-15	89%	gi|208022673|NP_001129077.1
☐	membrane selenoprotein P [Capra hircus]	79.5	79.5	100%	3e-15	85%	gi|7677620|AAF67201.1
☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	79.5	79.5	100%	4e-15	85%	gi|550822255|NP_001272511.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri b	78.3	78.3	96%	1e-14	88%	gi|725563213|XP_003925940.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Leptony	77.8	77.8	100%	1e-14	89%	gi|585192742|XP_006747601.1
☐	Selenoprotein P [Heterocephalus glaber]	77.4	77.4	96%	2e-14	85%	gi|351695949|EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	77.4	77.4	96%	2e-14	85%	gi|512973043|XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	77.4	77.4	96%	2e-14	85%	gi|512816050|XP_004878213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops	77.4	77.4	96%	2e-14	88%	gi|507708621|XP_004716992.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys	76.1	76.1	96%	6e-14	85%	gi|731237262|XP_010632183.1
☐	selenoprotein P precursor [Oryctolagus cuniculus]	76.1	76.1	100%	6e-14	89%	gi|315434200|NP_001186775.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ochoton	76.1	76.1	100%	6e-14	85%	gi|504142600|XP_004583736.1
☐	selenoprotein P, plasma, 1 precursor [Xenopus laevis]	76.1	76.1	100%	6e-14	85%	gi|315570276|NP_001186825.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenu	75.7	75.7	100%	8e-14	85%	gi|472379594|XP_004409206.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceu	74.9	74.9	96%	2e-13	88%	gi|617575753|XP_007517681.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromys	71.9	71.9	96%	2e-12	81%	gi|589969345|XP_006997157.1
☐	selenoprotein P, plasma, 1 precursor [Xenopus (Silurana) tropicalis	71.0	71.0	100%	3e-12	81%	gi|315467861|NP_001186813.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus j	70.6	70.6	100%	4e-12	81%	gi|507537041|XP_004652550.1
☐	PREDICTED: selenoprotein P [Chelonia mydas]	70.2	70.2	100%	5e-12	81%	gi|591359813|XP_007052890.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ornithorh	70.2	70.2	100%	5e-12	78%	gi|620968705|XP_007654576.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chrysem	70.2	70.2	100%	6e-12	81%	gi|530576591|XP_005282265.1
☐	selenoprotein P precursor [Rattus norvegicus]	69.4	69.4	96%	1e-11	77%	gi|15011857|NP_062065.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P, plasma,	68.5	68.5	96%	1e-11	77%	gi|524973435|XP_005139283.1
☐	Selenoprotein P [Cricetulus griseus]	68.5	68.5	96%	2e-11	77%	gi|344247936|EGW04040.1
☐	selenoprotein P precursor [Cricetulus griseus]	68.5	68.5	96%	2e-11	77%	gi|537231220|ERE84145.1
☐	selenoprotein P precursor [Cricetulus griseus]	68.5	68.5	96%	2e-11	77%	gi|379056379|NP_001243807.1
☐	PREDICTED: selenoprotein P [Sarcophilus harrisii]	68.1	68.1	100%	3e-11	81%	gi|395511426|XP_003759960.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Alligator	67.2	67.2	96%	6e-11	81%	gi|564260109|XP_006268971.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Alligator	67.2	67.2	96%	6e-11	81%	gi|557288151|XP_006026767.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Falco ch	67.2	67.2	96%	6e-11	81%	gi|541955801|XP_005433806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Falco pe	67.2	67.2	96%	6e-11	81%	gi|529444627|XP_005242025.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Microtus	66.8	66.8	96%	8e-11	77%	gi|532054271|XP_005369861.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Octodon	65.5	65.5	96%	2e-10	73%	gi|507690845|XP_004641866.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mesitorn	65.5	65.5	96%	2e-10	81%	gi|704588487|XP_010190708.1
☐	selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	65.1	65.1	96%	3e-10	77%	gi|148671458|EDL03405.1
☐	Selenoprotein P, plasma, 1 [Mus musculus]	65.1	65.1	96%	3e-10	77%	gi|34809553|AAH01991.2
☐	unnamed protein product [Mus musculus]	65.1	65.1	96%	3e-10	77%	gi|74198358|BAE39664.1
☐	unnamed protein product [Mus musculus]	65.1	65.1	96%	3e-10	77%	gi|74192879|BAE34948.1
☐	selenoprotein P precursor [Mus musculus]	65.1	65.1	96%	3e-10	77%	gi|74271806|NP_033181.3
☐	unnamed protein product [Mus musculus]	65.1	65.1	96%	3e-10	77%	gi|74213751|BAC55264.3

Alignments

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius syrichta]

Sequence ID: gi|640790108|ref|XP_008050904.1| **Length:** 377 **Number of Matches:** 1

Range 1: 106 to 132 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
91.8 bits(209)	2e-19	27/27(100%)	27/27(100%)	0/27(0%)

```
Query  1    KVSEHIPVYQQEENQTDVWTLLNGSKD  27
            KVSEHIPVYQQEENQTDVWTLLNGSKD
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKD  132
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxellana]

Sequence ID: gi|724878613|ref|XP_010372696.1| **Length:** 381 **Number of Matches:** 1

Range 1: 106 to 132 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
91.8 bits(209)	2e-19	27/27(100%)	27/27(100%)	0/27(0%)

```
Query  1    KVSEHIPVYQQEENQTDVWTLLNGSKD  27
            KVSEHIPVYQQEENQTDVWTLLNGSKD
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKD  132
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]

Sequence ID: gi|685545348|ref|XP_009206607.1| **Length:** 381 **Number of Matches:** 1

Range 1: 106 to 132 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
91.8 bits(209)	2e-19	27/27(100%)	27/27(100%)	0/27(0%)

```
Query  1    KVSEHIPVYQQEENQTDVWTLLNGSKD  27
            KVSEHIPVYQQEENQTDVWTLLNGSKD
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKD  132
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]

Sequence ID: gi|675710689|ref|XP_008961588.1| **Length:** 381 **Number of Matches:** 1

Range 1: 106 to 132 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
91.8 bits(209)	2e-19	27/27(100%)	27/27(100%)	0/27(0%)

```
Query  1    KVSEHIPVYQQEENQTDVWTLLNGSKD  27
            KVSEHIPVYQQEENQTDVWTLLNGSKD
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKD  132
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chlorocebus sabaeus]

Sequence ID: gi|635028004|ref|XP_007959679.1| **Length:** 381 **Number of Matches:** 1

Range 1: 106 to 132 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
91.8 bits(209)	2e-19	27/27(100%)	27/27(100%)	0/27(0%)

```
Query  1    KVSEHIPVYQQEENQTDVWTLLNGSKD  27
            KVSEHIPVYQQEENQTDVWTLLNGSKD
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKD  132
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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SEPP1_KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC_NonMod

RID BEB793EN014 (Expires on 01-16 09:58 am)

Query ID lcl|93014
Description None
Molecule type amino acid
Query Length 35

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ Citation

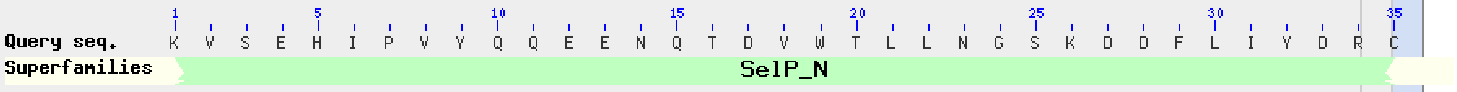
Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

New DELTA-BLAST a more sensitive protein-protein search Go

Graphic Summary

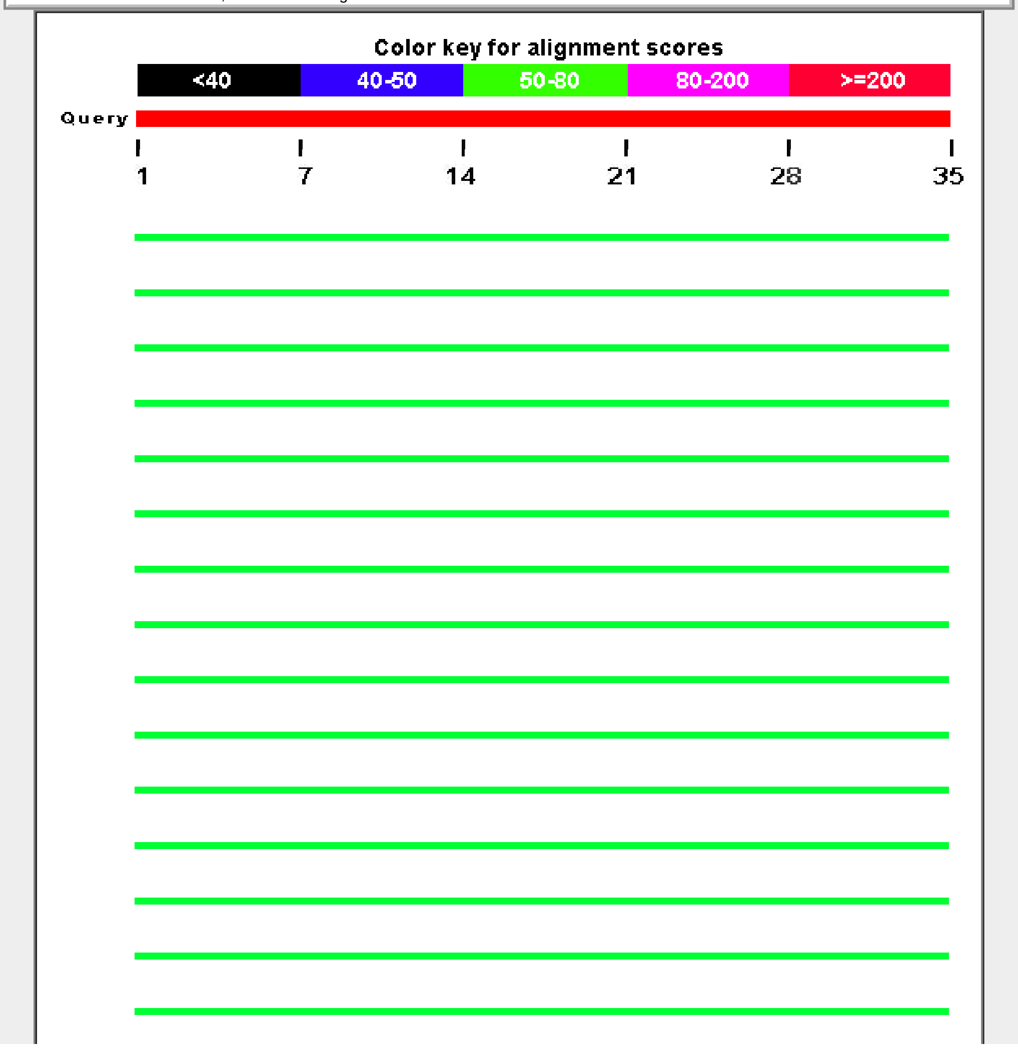
Show Conserved Domains

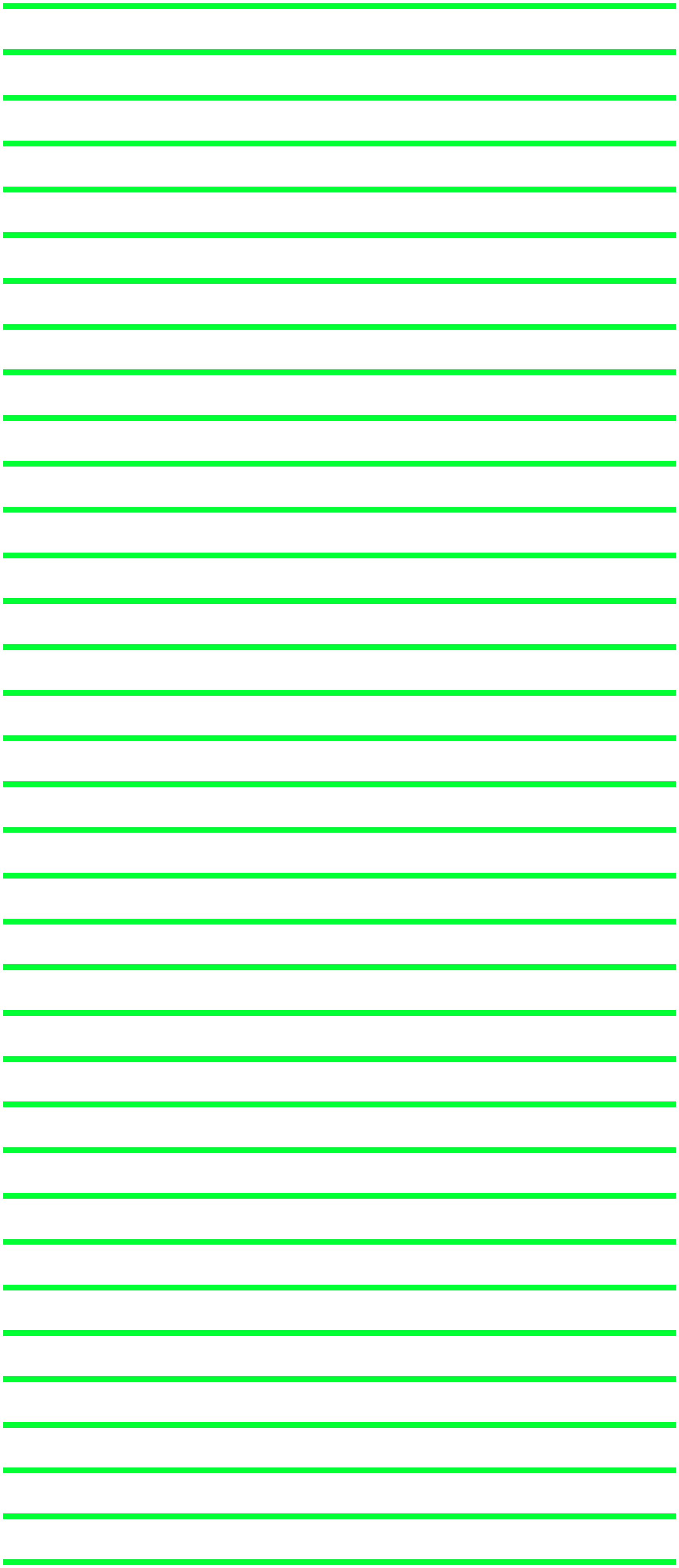
Putative conserved domains have been detected, click on the image below for detailed results.

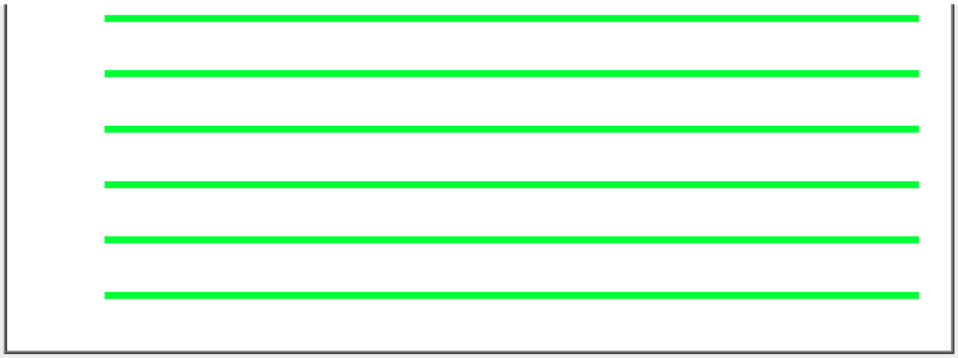


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: selenoprotein P-like [Ailuropoda melanoleuca]	76.6	76.6	100%	4e-16	94%	gi|301772662|XP_002921760.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius s	78.6	78.6	100%	4e-16	100%	gi|640790108|XP_008050904.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopitl	78.6	78.6	100%	5e-16	100%	gi|724878613|XP_010372696.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio ar	78.6	78.6	100%	5e-16	100%	gi|685545348|XP_009206607.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan pani	78.6	78.6	100%	5e-16	100%	gi|675710689|XP_008961588.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chloroce	78.6	78.6	100%	5e-16	100%	gi|635028004|XP_007959679.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	78.6	78.6	100%	5e-16	100%	gi|34783648|AAH46152.1
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	78.6	78.6	100%	5e-16	100%	gi|34783164|AAH15875.1
☐	selenoprotein P isoform 1 precursor [Homo sapiens]	78.6	78.6	100%	5e-16	100%	gi|62530391|NP_005401.3
☐	Selenoprotein P, plasma, 1 [Homo sapiens]	78.6	78.6	100%	5e-16	100%	gi|37596694|AAH58919.1
☐	selenoprotein P precursor [Pongo abelii]	78.6	78.6	100%	5e-16	100%	gi|197101233|NP_001127462.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nomasci	78.6	78.6	100%	5e-16	100%	gi|332250603|XP_003274442.1
☐	selenoprotein P [Homo sapiens]	78.6	78.6	100%	5e-16	100%	gi|312004116|CAA77836.2
☐	selenoprotein P precursor [Macaca mulatta]	78.6	78.6	100%	5e-16	100%	gi|226958322|NP_001152962.1
☐	selenoprotein P precursor [Pan troglodytes]	78.6	78.6	100%	5e-16	100%	gi|169403955|NP_001108587.1
☐	selenoprotein P isoform 2 [Homo sapiens]	78.6	78.6	100%	6e-16	100%	gi|148277022|NP_001087195.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chrysocl	77.0	77.0	100%	8e-16	94%	gi|586493836|XP_006877364.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tupaia c	77.4	77.4	100%	1e-15	97%	gi|562878609|XP_006167023.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Balaeno]	77.4	77.4	100%	1e-15	97%	gi|594696840|XP_007195596.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis lu	77.4	77.4	100%	1e-15	97%	gi|558205011|XP_006106371.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Orcinus	77.4	77.4	100%	1e-15	97%	gi|465986750|XP_004266005.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	77.4	77.4	100%	1e-15	97%	gi|744538058|XP_010999134.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Loxodon	77.4	77.4	100%	1e-15	97%	gi|731464182|XP_010586424.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Elephant	77.4	77.4	100%	1e-15	97%	gi|585672710|XP_006889619.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tursiops	77.4	77.4	100%	1e-15	97%	gi|470626535|XP_004320390.1
☐	PREDICTED: selenoprotein P [Otolemur garnettii]	75.9	75.9	100%	1e-15	94%	gi|395840394|XP_003793045.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Camelus	77.4	77.4	100%	1e-15	97%	gi|560931717|XP_006191986.1
☐	selenoprotein P precursor [Sus scrofa]	77.4	77.4	100%	1e-15	97%	gi|198282079|NP_001128295.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Vicugna	77.4	77.4	100%	1e-15	97%	gi|560970802|XP_006207756.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Lipotes	77.0	77.0	100%	2e-15	97%	gi|602724444|XP_007447694.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mustela	77.0	77.0	100%	2e-15	97%	gi|511826454|XP_004738001.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Physeter	77.0	77.0	100%	2e-15	97%	gi|593761497|XP_007119423.1
☐	selenoprotein P precursor [Canis lupus familiaris]	77.0	77.0	100%	2e-15	97%	gi|169403968|NP_001108590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ursus m	76.6	76.6	100%	4e-15	94%	gi|670999853|XP_008690806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Eptesicu	75.9	75.9	100%	4e-15	94%	gi|641727491|XP_008153843.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis b	75.9	75.9	100%	4e-15	94%	gi|554563465|XP_005876061.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Felis cat	73.9	73.9	100%	5e-15	89%	gi|586975923|XP_006928143.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Sorex ar	75.1	75.1	100%	7e-15	89%	gi|505790024|XP_004605590.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Oryctero	74.7	74.7	100%	8e-15	97%	gi|634885032|XP_007952213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ictidomy	75.1	75.1	100%	8e-15	94%	gi|532079811|XP_005325668.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bubalus	75.1	75.1	100%	9e-15	94%	gi|594087306|XP_006067130.1
☐	selenoprotein P [Bos taurus]	75.1	75.1	100%	9e-15	94%	gi|6006351|BAA84781.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bos mut	75.1	75.1	100%	9e-15	94%	gi|555965745|XP_005894930.1
☐	selenoprotein P-like protein [Bos taurus]	75.1	75.1	100%	1e-14	94%	gi|1582026|2117379A
☐	selenoprotein P like protein [Bos taurus]	75.1	75.1	100%	1e-14	94%	gi|14970947|BAA04949.2
☐	selenoprotein P precursor [Bos taurus]	75.1	75.1	100%	1e-14	94%	gi|156631001|NP_776884.2
☐	selenoprotein P [Bubalus bubalis]	75.1	75.1	100%	1e-14	94%	gi|430001945|AFM77782.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ceratoth	74.3	74.3	100%	2e-14	91%	gi|478496995|XP_004422836.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Panthera	74.3	74.3	100%	2e-14	91%	gi|591339998|XP_007095490.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Condylu	74.3	74.3	100%	2e-14	91%	gi|507934338|XP_004678402.1
☐	membrane selenoprotein P [Capra hircus]	72.0	72.0	100%	3e-14	89%	gi|7677620|AAF67201.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Trichech	73.6	73.6	100%	3e-14	91%	gi|471413922|XP_004388500.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Nannosp	73.6	73.6	100%	3e-14	89%	gi|674066756|XP_008840327.1
☐	selenoprotein P precursor [Callithrix jacchus]	73.6	73.6	100%	3e-14	91%	gi|315630400|NP_001186857.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Bison bis	73.6	73.6	100%	3e-14	91%	gi|742088280|XP_010831114.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ovis arie	73.2	73.2	100%	4e-14	91%	gi|426246564|XP_004017062.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Myotis d	72.8	72.8	100%	6e-14	91%	gi|584060316|XP_006774623.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Galeopte	72.8	72.8	100%	6e-14	91%	gi|667253652|XP_008564915.1
☐	Selenoprotein P [Heterocephalus glaber]	71.2	71.2	100%	6e-14	86%	gi|351695949|EHA98867.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Equus p	72.8	72.8	100%	6e-14	91%	gi|664731166|XP_008522793.1
☐	selenoprotein P precursor [Equus caballus]	72.8	72.8	100%	6e-14	91%	gi|208022673|NP_001129077.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Dasypus	72.8	72.8	100%	7e-14	91%	gi|488512454|XP_004448278.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Leptony	72.4	72.4	100%	9e-14	91%	gi|585192742|XP_006747601.1
☐	selenoprotein P, plasma, 1 precursor [Capra hircus]	72.0	72.0	100%	9e-14	89%	gi|550822255|NP_001272511.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Saimiri b	71.6	71.6	100%	2e-13	89%	gi|725563213|XP_003925940.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Erinaceu	71.2	71.2	100%	2e-13	89%	gi|617575753|XP_007517681.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chinchill	71.2	71.2	100%	2e-13	86%	gi|533143496|XP_005386312.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	71.2	71.2	100%	2e-13	86%	gi|512973043|XP_004848622.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Heteroce	71.2	71.2	100%	2e-13	86%	gi|512816050|XP_004878213.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ochoton	71.2	71.2	100%	2e-13	89%	gi|504142600|XP_004583736.1
☐	selenoprotein P precursor [Oryctolagus cuniculus]	70.5	70.5	100%	4e-13	91%	gi|315434200|NP_001186775.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Fukomys	70.1	70.1	100%	6e-13	86%	gi|731237262|XP_010632183.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Odobenu	70.1	70.1	100%	6e-13	89%	gi|472379594|XP_004409206.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Jaculus	69.7	69.7	100%	8e-13	86%	gi|507537041|XP_004652550.1
☐	PREDICTED: selenoprotein P [Chelonia mydas]	67.8	67.8	100%	9e-13	86%	gi|591359813|XP_007052890.1

☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Ornithorl	68.2	68.2	100%	1e-12	83%	gi|620968705|XP_007654576.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Echinops	69.3	69.3	100%	1e-12	89%	gi|507708621|XP_004716992.1
☐	selenoprotein P, plasma, 1 precursor [Xenopus laevis]	69.3	69.3	100%	1e-12	86%	gi|315570276|NP_001186825.1
☐	PREDICTED: selenoprotein P [Sarcophilus harrisii]	66.6	66.6	100%	3e-12	86%	gi|395511426|XP_003759960.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Peromys	68.2	68.2	100%	3e-12	83%	gi|589969345|XP_006997157.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Chrysem	67.8	67.8	100%	5e-12	86%	gi|530576591|XP_005282265.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Alligator	67.0	67.0	100%	7e-12	83%	gi|564260109|XP_006268971.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Alligator	67.0	67.0	100%	7e-12	83%	gi|557288151|XP_006026767.1
☐	selenoprotein P precursor [Rattus norvegicus]	67.0	67.0	100%	8e-12	80%	gi|15011857|NP_062065.2
☐	Selenoprotein P [Cricetulus griseus]	64.7	64.7	97%	1e-11	82%	gi|344247936|EGW04040.1
☐	selenoprotein P, plasma, 1, isoform CRA_a [Mus musculus]	64.3	64.3	100%	2e-11	80%	gi|148671458|EDL03405.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P-like [Anol	64.7	64.7	100%	2e-11	77%	gi|637259117|XP_003216248.2
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Mesitorn	65.9	65.9	97%	2e-11	85%	gi|704588487|XP_010190708.1
☐	selenoprotein P, plasma, 1 precursor [Xenopus (Silurana) tropicalis	65.9	65.9	100%	2e-11	80%	gi|315467861|NP_001186813.1
☐	selenoprotein P precursor [Cricetulus griseus]	64.7	64.7	97%	2e-11	82%	gi|537231220|ERE84145.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Falco ch	65.5	65.5	97%	3e-11	85%	gi|541955801|XP_005433806.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Falco pe	65.5	65.5	97%	3e-11	85%	gi|529444627|XP_005242025.1
☐	PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Meleagri	63.2	63.2	97%	4e-11	76%	gi|733924998|XP_010723689.1
☐	selenoprotein P precursor [Cricetulus griseus]	64.7	64.7	97%	5e-11	82%	gi|379056379|NP_001243807.1
☐	Selenoprotein P, plasma, 1 [Mus musculus]	64.3	64.3	100%	7e-11	80%	gi|34809553|AAH01991.2
☐	plasma selenoprotein P [Mus musculus]	64.3	64.3	100%	7e-11	80%	gi|4103142|AAD01684.1
☐	unnamed protein product [Mus musculus]	64.3	64.3	100%	7e-11	80%	gi|74198358|BAE39664.1
☐	unnamed protein product [Mus musculus]	64.3	64.3	100%	7e-11	80%	gi|74192879|BAE34948.1
☐	selenoprotein P precursor [Mus musculus]	64.3	64.3	100%	7e-11	80%	gi|74271806|NP_033181.3
☐	unnamed protein product [Mus musculus]	64.3	64.3	100%	7e-11	80%	gi|74213751|BAC55264.3

⊟ Alignments

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PREDICTED: selenoprotein P-like [Ailuropoda melanoleuca]

Sequence ID: gi|301772662|ref|XP_002921760.1| **Length:** 166 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 6 to 40 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
76.6 bits(187)	4e-16	33/35(94%)	34/35(97%)	0/35(0%)

```
Query  1    KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC  35
            KVSEHIPVYQQEENQTDVWTLLNG KDDFL+YDRC
Sbjct  6    KVSEHIPVYQQEENQTDVWTLLNGKKDDFLVYDRC  40
```

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Tarsius syrichta]

Sequence ID: gi|640790108|ref|XP_008050904.1| **Length:** 377 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 106 to 140 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
78.6 bits(192)	4e-16	35/35(100%)	35/35(100%)	0/35(0%)

```
Query  1     KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC  35
             KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC
Sbjct  106   KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC  140
```

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Rhinopithecus roxellana]

Sequence ID: gi|724878613|ref|XP_010372696.1| **Length:** 381 **Number of Matches:** 1

Range 1: 106 to 140 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
78.6 bits(192)	5e-16	35/35(100%)	35/35(100%)	0/35(0%)

```
Query  1    KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC  35
            KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC  140
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Papio anubis]

Sequence ID: gi|685545348|ref|XP_009206607.1| **Length:** 381 **Number of Matches:** 1

Range 1: 106 to 140 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
78.6 bits(192)	5e-16	35/35(100%)	35/35(100%)	0/35(0%)

```
Query  1    KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC  35
            KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC  140
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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PREDICTED: LOW QUALITY PROTEIN: selenoprotein P [Pan paniscus]

Sequence ID: gi|675710689|ref|XP_008961588.1| **Length:** 381 **Number of Matches:** 1

Range 1: 106 to 140 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
78.6 bits(192)	5e-16	35/35(100%)	35/35(100%)	0/35(0%)

```
Query  1    KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC  35
            KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC
Sbjct  106  KVSEHIPVYQQEENQTDVWTLLNGSKDDFLIYDRC  140
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVMAEDJH01R

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SHBG_RLDVDQALDRS_Mod

RID BVMAEDJH01R (Expires on 01-21 10:53 am)

Query ID	lcl|256865	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	11		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

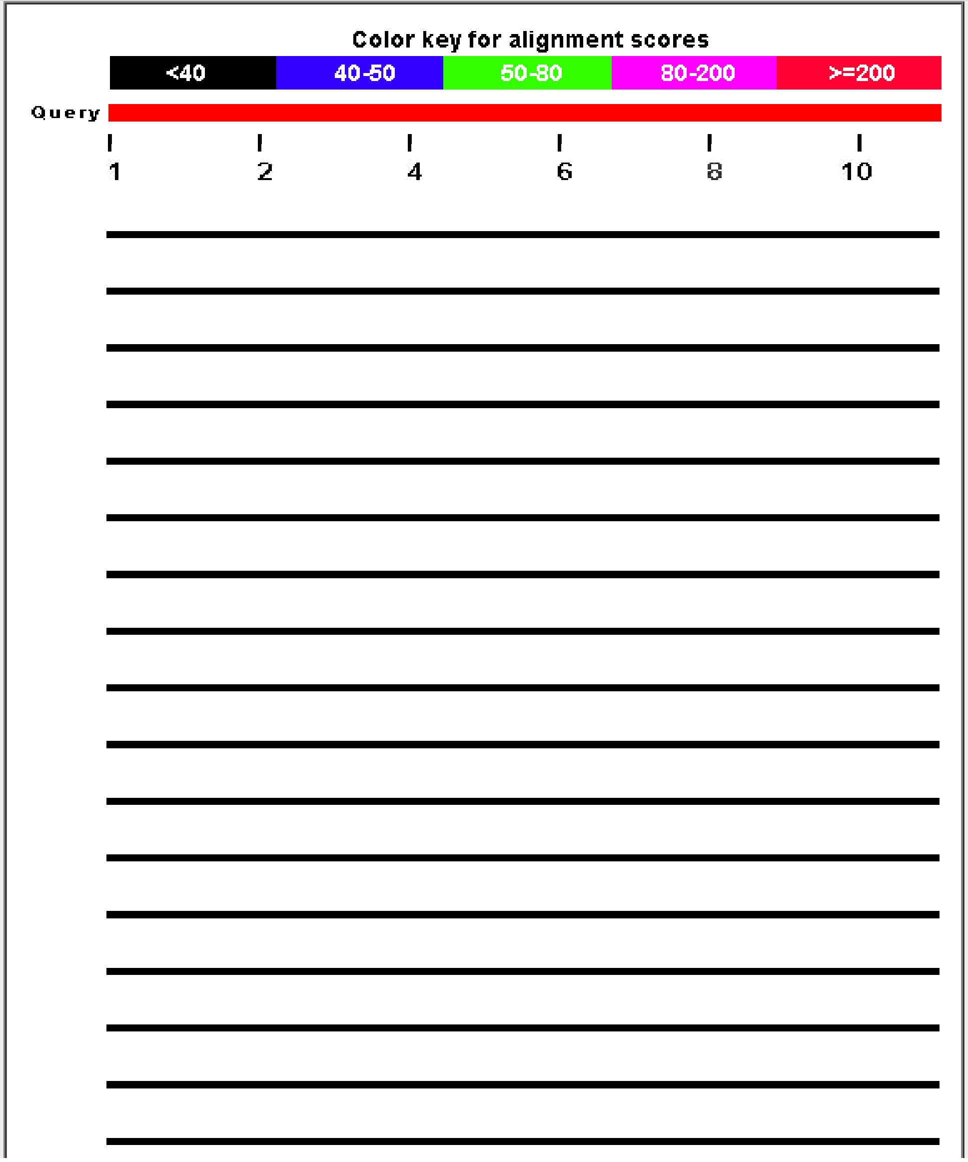
Graphic Summary

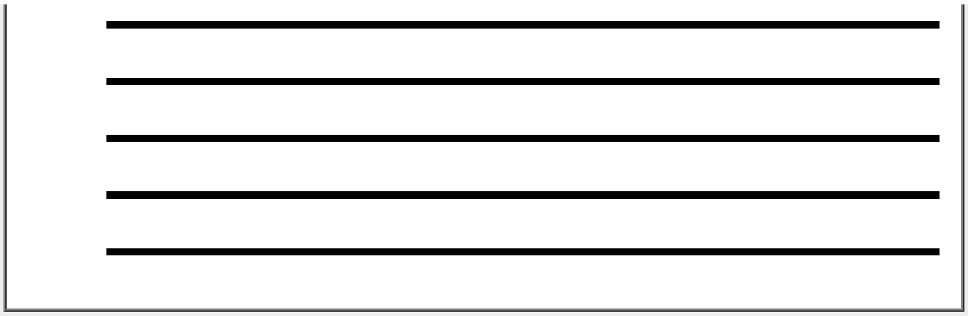
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	sex hormone binding globulin [Homo sapiens]	35.0	35.0	100%	0.54	91%	ABY68001.1
☐	PREDICTED: sex hormone-binding globulin isoform X6 [Homo sapiens]	35.0	35.0	100%	0.55	91%	XP_005256822.1
☐	sex hormone binding globulin [Homo sapiens]	35.0	35.0	100%	0.56	91%	ABY67999.1
☐	sex steroid-binding protein [Homo sapiens]	35.0	35.0	100%	0.56	91%	CAA29234.1
☐	PREDICTED: sex hormone-binding globulin isoform X6 [Pan paniscus]	35.0	35.0	100%	0.56	91%	XP_008960682.1
☐	PREDICTED: sex hormone-binding globulin isoform X6 [Chlorocebus sabaeu	35.0	35.0	100%	0.56	91%	XP_008008379.1
☐	sex hormone-binding globulin isoform 7 [Homo sapiens]	35.0	35.0	100%	0.56	91%	NP_001276045.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Pan paniscus]	35.0	35.0	100%	0.56	91%	XP_003810122.1
☐	sex hormone-binding globulin isoform 4 precursor [Homo sapiens]	35.0	35.0	100%	0.56	91%	NP_001139753.1
☐	PREDICTED: sex hormone-binding globulin isoform 4 [Gorilla gorilla gorilla]	35.0	35.0	100%	0.56	91%	XP_004058549.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Pan paniscus]	35.0	35.0	100%	0.57	91%	XP_008960680.1
☐	sex hormone-binding globulin isoform 5 [Homo sapiens]	35.0	35.0	100%	0.57	91%	NP_001276042.1
☐	PREDICTED: sex hormone-binding globulin isoform X5 [Chlorocebus sabaeu	35.0	35.0	100%	0.57	91%	XP_008008377.1
☐	PREDICTED: sex hormone-binding globulin isoform X7 [Homo sapiens]	35.0	35.0	100%	0.57	91%	XP_006721632.1
☐	unnamed protein product [Homo sapiens]	35.0	35.0	100%	0.58	91%	CAA29309.1
☐	unnamed protein product [Homo sapiens]	35.0	35.0	100%	0.58	91%	CAA28987.1
☐	sex hormone-binding globulin isoform 2 precursor [Homo sapiens]	35.0	35.0	100%	0.58	91%	NP_001139751.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Chlorocebus sabaeu	35.0	35.0	100%	0.58	91%	XP_008008372.1
☐	PREDICTED: sex hormone-binding globulin isoform 3 [Gorilla gorilla gorilla]	35.0	35.0	100%	0.58	91%	XP_004058548.1
☐	SHBG protein [Homo sapiens]	35.0	35.0	100%	0.58	91%	AAH69597.1
☐	sex hormone-binding globulin [Homo sapiens]	35.0	35.0	100%	0.58	91%	AAC18778.1
☐	sex hormone-binding globulin isoform 1 precursor [Homo sapiens]	35.0	35.0	100%	0.58	91%	NP_001031.2
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Pan paniscus]	35.0	35.0	100%	0.58	91%	XP_003810120.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Chlorocebus sabaeu	35.0	35.0	100%	0.58	91%	XP_008008371.1
☐	PREDICTED: sex hormone-binding globulin isoform 1 [Gorilla gorilla gorilla]	35.0	35.0	100%	0.58	91%	XP_004058546.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding globulin [Micr	35.0	35.0	100%	0.58	91%	XP_005350335.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Chlorocebus sabaeu	35.0	35.0	100%	0.59	91%	XP_008008369.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Chlorocebus sabaeu	35.0	35.0	100%	0.59	91%	XP_008008368.1
☐	PREDICTED: sex hormone-binding globulin [Cricetulus griseus]	32.9	32.9	100%	2.9	82%	XP_003497225.1

☐	androgen-binding protein [Phodopus sungorus]	32.9	32.9	100%	2.9	82%	AAB41681.1
☐	RecName: Full=Sex hormone-binding globulin; Short=SHBG; AltName: Full=S	32.9	32.9	100%	2.9	82%	Q62588.1
☐	sex hormone-binding globulin-like protein [Cricetulus griseus]	32.9	32.9	100%	2.9	82%	ERE69391.1
☐	PREDICTED: sex hormone-binding globulin [Trichechus manatus latirostris]	32.5	32.5	100%	3.9	91%	XP_004376080.1
☐	PREDICTED: sex hormone-binding globulin [Orycteropus afer afer]	31.6	31.6	100%	7.3	82%	XP_007950448.1
☐	sex hormone-binding globulin [synthetic construct]	31.6	31.6	100%	7.5	82%	AAX36263.1
☐	lantibiotic dehydratase [Micromonospora aurantiaca]	31.2	31.2	100%	11	82%	WP_013287251.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Saimiri boliviensis bo	30.8	30.8	100%	14	82%	XP_010338103.1
☐	PREDICTED: sex hormone-binding globulin isoform X5 [Rhinopithecus roxella	30.8	30.8	100%	14	82%	XP_010360686.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Papio anubis]	30.8	30.8	100%	14	82%	XP_009187837.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Callithrix jacchus]	30.8	30.8	100%	14	82%	XP_008994833.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Rhinopithecus roxella	30.8	30.8	100%	14	82%	XP_010360685.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Callithrix jacchus]	30.8	30.8	100%	14	82%	XP_008994832.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Rhinopithecus roxella	30.8	30.8	100%	14	82%	XP_010360684.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Callithrix jacchus]	30.8	30.8	100%	14	82%	XP_002747998.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Rhinopithecus roxella	30.8	30.8	100%	14	82%	XP_010360683.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Papio anubis]	30.8	30.8	100%	14	82%	XP_009187836.1
☐	Sex hormone-binding globulin [Macaca mulatta]	30.8	30.8	100%	14	82%	EHH24482.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Rhinopithecus roxella	30.8	30.8	100%	14	82%	XP_010360681.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Papio anubis]	30.8	30.8	100%	14	82%	XP_009187834.1
☐	anibiotic ABC transporter [Burkholderia cepacia]	30.8	30.8	90%	14	90%	WP_034209699.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Saimiri boliviensis bo	30.8	30.8	100%	14	82%	XP_003929225.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding globulin-like [M	30.8	30.8	100%	14	82%	XP_002808160.1
☐	uncharacterized protein LOC101864774 [Macaca fascicularis]	30.8	30.8	100%	14	82%	NP_001270513.1
☐	hypothetical protein [Streptomyces albus]	30.3	30.3	100%	18	82%	WP_037678548.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Jaculus jaculus]	30.3	30.3	100%	19	82%	XP_004669275.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Jaculus jaculus]	30.3	30.3	100%	19	82%	XP_004669274.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Jaculus jaculus]	30.3	30.3	100%	19	82%	XP_004669273.1
☐	sex hormone-binding globulin precursor [Mus musculus]	30.3	30.3	100%	19	82%	NP_035497.1
☐	PREDICTED: sex hormone-binding globulin [Condylura cristata]	29.5	29.5	90%	36	80%	XP_004684701.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding globulin [Pong	29.5	29.5	100%	36	82%	XP_009249533.1
☐	hypothetical protein [Streptomyces carneus]	29.5	29.5	81%	37	89%	WP_033243727.1
☐	hypothetical protein PHYSODRAFT_293694 [Phytophthora sojae]	29.5	29.5	100%	37	82%	XP_009515333.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding globulin [Sarco	29.1	29.1	90%	48	90%	XP_003768811.1
☐	phosphoenolpyruvate phosphomutase [Streptomyces sp. NRRL S-384]	29.1	29.1	81%	48	89%	WP_037876888.1
☐	putative uncharacterized protein [Paraprevotella clara CAG:116]	29.1	29.1	81%	49	89%	WP_021979896.1
☐	hypothetical protein [Paraprevotella clara]	29.1	29.1	81%	49	89%	WP_008617140.1
☐	PREDICTED: sex hormone-binding globulin isoform 3 [Dasypus novemcinctus	29.1	29.1	90%	49	90%	XP_004468805.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding globulin [Cavia	29.1	29.1	90%	49	90%	XP_003466296.1
☐	PREDICTED: sex hormone-binding globulin isoform 1 [Dasypus novemcinctus	29.1	29.1	90%	50	90%	XP_004468803.1
☐	hypothetical protein MGL_0571 [Malassezia globosa CBS 7966]	29.1	29.1	81%	50	89%	XP_001732796.1
☐	hypothetical protein M437DRAFT_51343 [Aureobasidium melanogenum CBS	29.1	29.1	100%	50	50%	KEQ61742.1
☐	unnamed protein product [Malassezia sympodialis ATCC 42132]	29.1	29.1	81%	50	89%	CCV00735.1
☐	hypothetical protein [Marinobacter hydrocarbonoclasticus]	29.1	29.1	81%	50	89%	WP_011786349.1
☐	hypothetical protein [Marinobacter sp. C1S70]	29.1	29.1	81%	50	89%	WP_022991504.1

☐	hypothetical protein [Marinobacter sp. EN3]	29.1	29.1	81%	50	89%	WP_023011180.1
☐	hypothetical protein [Marinobacter hydrocarbonoclasticus]	29.1	29.1	81%	50	89%	WP_014422263.1
☐	hypothetical protein [Streptomyces aureocirculatus]	28.6	28.6	81%	62	89%	WP_030573048.1
☐	nUDIX hydrolase [Eubacterium sp. CAG:251]	28.6	28.6	90%	62	80%	WP_022259296.1
☐	hypothetical protein [Geobacillus thermodenitrificans]	28.6	28.6	90%	63	80%	WP_029760946.1
☐	hypothetical protein [Geobacillus sp. G11MC16]	28.6	28.6	90%	63	80%	WP_008879469.1
☐	hypothetical protein [Geobacillus thermodenitrificans]	28.6	28.6	90%	63	80%	WP_011887232.1
☐	TetR family transcriptional regulator [Anaeromyxobacter sp. Fw109-5]	28.6	28.6	72%	65	100%	WP_012098065.1
☐	hypothetical protein HMPREF1544_07665 [Mucor circinelloides f. circinelloide	28.6	28.6	90%	66	80%	EPB85576.1
☐	hypothetical protein [Thiobacillus prosperus]	28.6	28.6	90%	66	80%	WP_038092651.1
☐	Protein YicC [Thioalkalivibrio nitratireducens]	28.6	28.6	90%	66	80%	WP_015260324.1
☐	putative stress-induced protein [Thiobacillus prosperus]	28.6	28.6	90%	66	80%	KFZ89319.1
☐	hypothetical protein [Thioalkalivibrio sp. ALJ17]	28.6	28.6	90%	66	80%	WP_026289603.1
☐	hypothetical protein [Lamprocystis purpurea]	28.6	28.6	90%	66	80%	WP_026199839.1
☐	hypothetical protein [Thioalkalivibrio sulfidophilus]	28.6	28.6	90%	66	80%	WP_012639494.1
☐	hypothetical protein [Candidatus Contendobacter odensis]	28.6	28.6	90%	66	80%	WP_034434520.1
☐	hypothetical protein [Thioalkalivibrio thiocyanodenitrificans]	28.6	28.6	90%	66	80%	WP_018232780.1
☐	hypothetical protein [Thiothrix nivea]	28.6	28.6	90%	66	80%	WP_002709580.1
☐	hypothetical protein THITH_01470 [Thioalkalivibrio thiocyanoxidans ARh 4]	28.6	28.6	90%	66	80%	AHE97167.1
☐	hypothetical protein [Allochromatium vinosum]	28.6	28.6	90%	66	80%	WP_012972150.1
☐	glutamine amidotransferase [Ahrensia sp. R2A130]	28.6	28.6	90%	66	80%	WP_009758020.1
☐	hydrolase [Clostridiales bacterium VE202-28]	28.6	28.6	81%	66	89%	WP_025485368.1
☐	hydrolase [Clostridiales bacterium 1_7_47FAA]	28.6	28.6	81%	66	89%	WP_008720076.1
☐	hypothetical protein [Janibacter sp. HTCC2649]	28.6	28.6	72%	67	100%	WP_009776442.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Peromyscus manicul	28.6	28.6	100%	67	73%	XP_006973508.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Peromyscus manicul	28.6	28.6	100%	67	73%	XP_006973507.1

⊟ Alignments

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sex hormone binding globulin [Homo sapiens]

Sequence ID: gb|ABY68001.1| **Length:** 206 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 176 to 186 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
35.0 bits(75)	0.54	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    RLDVDQALDRS  11
            RLDVDQAL+RS
Sbjct  176  RLDVDQALNRS  186
```

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PREDICTED: sex hormone-binding globulin isoform X6 [Homo sapiens]

Sequence ID: ref|XP_005256822.1| **Length:** 233 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 203 to 213 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
35.0 bits(75)	0.55	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    RLDVDQALDRS  11
            RLDVDQAL+RS
Sbjct  203  RLDVDQALNRS  213
```

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sex hormone binding globulin [Homo sapiens]

Sequence ID: gb|ABY67999.1| **Length:** 260 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 230 to 240 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
35.0 bits(75)	0.56	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    RLDVDQALDRS  11
            RLDVDQAL+RS
Sbjct  230  RLDVDQALNRS  240
```

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sex steroid-binding protein [Homo sapiens]

Sequence ID: emb|CAA29234.1| **Length:** 282 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 252 to 262 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
35.0 bits(75)	0.56	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    RLDVDQALDRS  11
            RLDVDQAL+RS
Sbjct  252  RLDVDQALNRS  262
```

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PREDICTED: sex hormone-binding globulin isoform X6 [Pan paniscus]

Sequence ID: ref|XP_008960682.1| **Length:** 286 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 256 to 266 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
35.0 bits(75)	0.56	10/11(91%)	11/11(100%)	0/11(0%)

```
Query  1    RLDVDQALDRS  11
            RLDVDQAL+RS
Sbjct  256  RLDVDQALNRS  266
```

BLAST ®

Basic Local Alignment Search Tool

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BE89Y3M7015**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit | Save Search Strategies | Formatting options | Download

How to read this page | Blast report description

SHBG_RLDVDQALNRS_NonMod

RID	BE89Y3M7015 (Expires on 01-16 09:09 am)		
Query ID	lcl|91730	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	11		
		Program	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

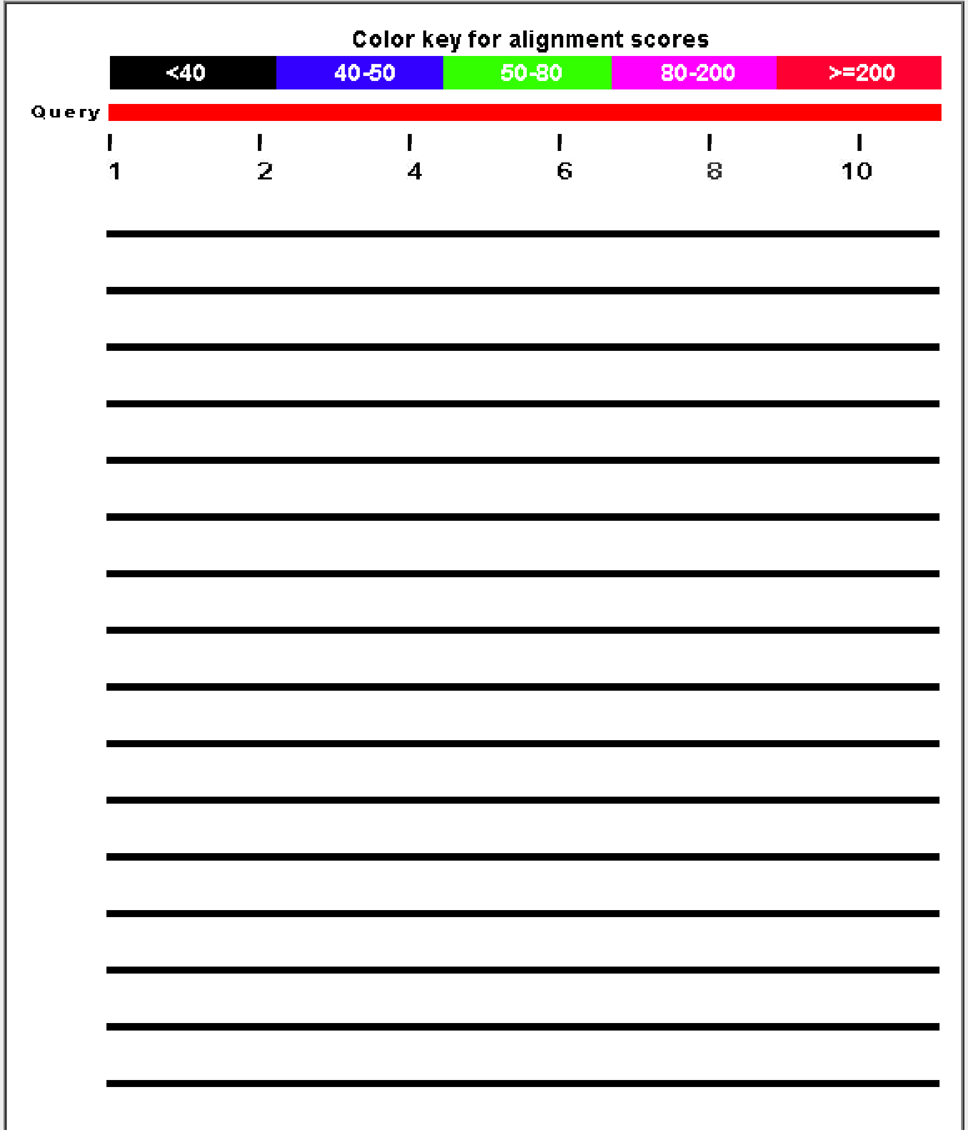
Graphic Summary

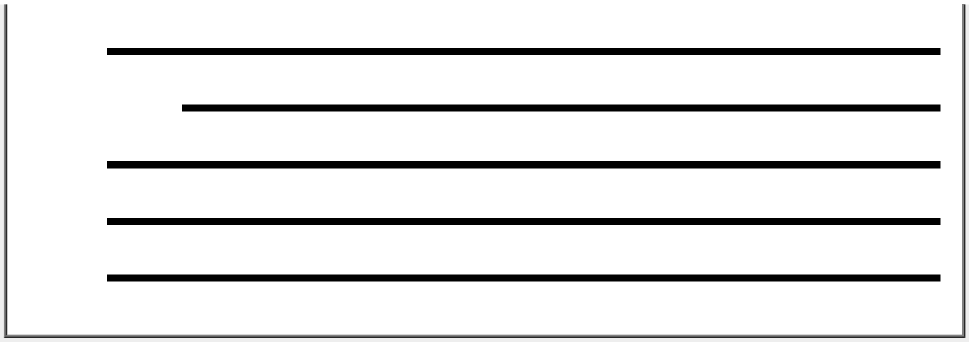
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	sex hormone binding globulin [Homo sapiens]	37.5	37.5	100%	0.076	100%	gi|165873764|ABY68001.1
☐	PREDICTED: sex hormone-binding globulin isoform X6 [Homo sapi	37.5	37.5	100%	0.078	100%	gi|530410575|XP_005256822.1
☐	sex hormone binding globulin [Homo sapiens]	37.5	37.5	100%	0.079	100%	gi|165873760|ABY67999.1
☐	sex steroid-binding protein [Homo sapiens]	37.5	37.5	100%	0.080	100%	gi|825718|CAA29234.1
☐	PREDICTED: sex hormone-binding globulin isoform X6 [Pan panisc	37.5	37.5	100%	0.080	100%	gi|675705950|XP_008960682.1
☐	PREDICTED: sex hormone-binding globulin isoform X6 [Chlorocebu	37.5	37.5	100%	0.080	100%	gi|635087572|XP_008008379.1
☐	sex hormone-binding globulin isoform 7 [Homo sapiens]	37.5	37.5	100%	0.080	100%	gi|574288369|NP_001276045.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Pan panisc	37.5	37.5	100%	0.080	100%	gi|397477529|XP_003810122.1
☐	sex hormone-binding globulin isoform 4 precursor [Homo sapiens]	37.5	37.5	100%	0.080	100%	gi|226371613|NP_001139753.1
☐	PREDICTED: sex hormone-binding globulin isoform 4 [Gorilla gorill	37.5	37.5	100%	0.080	100%	gi|426383969|XP_004058549.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Pan panisc	37.5	37.5	100%	0.082	100%	gi|675705940|XP_008960680.1
☐	sex hormone-binding globulin isoform 5 [Homo sapiens]	37.5	37.5	100%	0.082	100%	gi|574287849|NP_001276042.1
☐	PREDICTED: sex hormone-binding globulin isoform X5 [Chlorocebu	37.5	37.5	100%	0.082	100%	gi|635087568|XP_008008377.1
☐	PREDICTED: sex hormone-binding globulin isoform X7 [Homo sapi	37.5	37.5	100%	0.082	100%	gi|578830017|XP_006721632.1
☐	unnamed protein product [Homo sapiens]	37.5	37.5	100%	0.082	100%	gi|1335306|CAA29309.1
☐	unnamed protein product [Homo sapiens]	37.5	37.5	100%	0.082	100%	gi|36448|CAA28987.1
☐	sex hormone-binding globulin isoform 2 precursor [Homo sapiens]	37.5	37.5	100%	0.082	100%	gi|226371775|NP_001139751.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Chlorocebu	37.5	37.5	100%	0.082	100%	gi|635087558|XP_008008372.1
☐	PREDICTED: sex hormone-binding globulin isoform 3 [Gorilla gorill	37.5	37.5	100%	0.082	100%	gi|426383967|XP_004058548.1
☐	SHBG protein [Homo sapiens]	37.5	37.5	100%	0.083	100%	gi|47479685|AAH69597.1
☐	sex hormone-binding globulin [Homo sapiens]	37.5	37.5	100%	0.083	100%	gi|338075|AAC18778.1
☐	sex hormone-binding globulin isoform 1 precursor [Homo sapiens]	37.5	37.5	100%	0.083	100%	gi|7382460|NP_001031.2
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Pan panisc	37.5	37.5	100%	0.083	100%	gi|397477525|XP_003810120.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Chlorocebu	37.5	37.5	100%	0.083	100%	gi|635087556|XP_008008371.1
☐	PREDICTED: sex hormone-binding globulin isoform 1 [Gorilla gorill	37.5	37.5	100%	0.083	100%	gi|426383963|XP_004058546.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding glob	37.5	37.5	100%	0.083	100%	gi|532013105|XP_005350335.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Chlorocebu	37.5	37.5	100%	0.084	100%	gi|635087554|XP_008008369.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Chlorocebu	37.5	37.5	100%	0.084	100%	gi|635087552|XP_008008368.1
☐							

	PREDICTED: sex hormone-binding globulin [Cricetulus griseus]	35.4	35.4	100%	0.42	91%	gi|354469621|XP_003497225.1
☐	androgen-binding protein [Phodopus sungorus]	35.4	35.4	100%	0.42	91%	gi|1813476|AAB41681.1
☐	RecName: Full=Sex hormone-binding globulin; Short=SHBG; AltNa	35.4	35.4	100%	0.42	91%	gi|6174979|Q62588.1
☐	sex hormone-binding globulin-like protein [Cricetulus griseus]	35.4	35.4	100%	0.42	91%	gi|537145458|ERE69391.1
☐	PREDICTED: sex hormone-binding globulin [Orycteropus afer afer]	34.1	34.1	100%	1.1	91%	gi|634880093|XP_007950448.1
☐	PREDICTED: sex hormone-binding globulin [Trichechus manatus la	34.1	34.1	100%	1.1	91%	gi|471371144|XP_004376080.1
☐	sex hormone-binding globulin [synthetic construct]	34.1	34.1	100%	1.1	91%	gi|60813500|AAX36263.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Saimiri boli	33.3	33.3	100%	2.0	91%	gi|725571085|XP_010338103.1
☐	PREDICTED: sex hormone-binding globulin isoform X5 [Rhinopithe	33.3	33.3	100%	2.0	91%	gi|724818518|XP_010360686.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Papio anub	33.3	33.3	100%	2.0	91%	gi|685595645|XP_009187837.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Callithrix ja	33.3	33.3	100%	2.0	91%	gi|675658295|XP_008994833.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Rhinopithe	33.3	33.3	100%	2.1	91%	gi|724818515|XP_010360685.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Callithrix ja	33.3	33.3	100%	2.1	91%	gi|675658293|XP_008994832.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Rhinopithe	33.3	33.3	100%	2.1	91%	gi|724818512|XP_010360684.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Callithrix ja	33.3	33.3	100%	2.1	91%	gi|296201365|XP_002747998.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Rhinopithe	33.3	33.3	100%	2.1	91%	gi|724818509|XP_010360683.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Papio anub	33.3	33.3	100%	2.1	91%	gi|685595643|XP_009187836.1
☐	Sex hormone-binding globulin [Macaca mulatta]	33.3	33.3	100%	2.1	91%	gi|355568201|EHH24482.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Rhinopithe	33.3	33.3	100%	2.1	91%	gi|724818503|XP_010360681.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Papio anub	33.3	33.3	100%	2.1	91%	gi|685595639|XP_009187834.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Saimiri boli	33.3	33.3	100%	2.1	91%	gi|403274954|XP_003929225.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding glob	33.3	33.3	100%	2.1	91%	gi|297271824|XP_002808160.1
☐	uncharacterized protein LOC101864774 [Macaca fascicularis]	33.3	33.3	100%	2.1	91%	gi|545686862|NP_001270513.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Jaculus jac	32.0	32.0	100%	5.3	82%	gi|507571348|XP_004669275.1
☐	PREDICTED: sex hormone-binding globulin [Condylura cristata]	32.0	32.0	90%	5.4	90%	gi|507953792|XP_004684701.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Jaculus jac	32.0	32.0	100%	5.4	82%	gi|507571346|XP_004669274.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Jaculus jac	32.0	32.0	100%	5.4	82%	gi|507571344|XP_004669273.1
☐	sex hormone-binding globulin precursor [Mus musculus]	32.0	32.0	100%	5.4	82%	gi|6755506|NP_035497.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding glob	32.0	32.0	100%	5.4	91%	gi|686752223|XP_009249533.1
☐	hypothetical protein [Marinobacter hydrocarbonoclasticus]	31.6	31.6	81%	7.6	100%	gi|500110344|WP_011786349.1
☐	hypothetical protein [Marinobacter sp. C1S70]	31.6	31.6	81%	7.6	100%	gi|552452853|WP_022991504.1
☐	hypothetical protein [Marinobacter sp. EN3]	31.6	31.6	81%	7.6	100%	gi|552558269|WP_023011180.1
☐	hypothetical protein [Marinobacter hydrocarbonoclasticus]	31.6	31.6	81%	7.6	100%	gi|504235161|WP_014422263.1
☐	nUDIX hydrolase [Eubacterium sp. CAG:251]	31.2	31.2	90%	9.2	90%	gi|547852293|WP_022259296.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Peromyscu	31.2	31.2	100%	10	82%	gi|589921045|XP_006973508.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Peromyscu	31.2	31.2	100%	10	82%	gi|589921043|XP_006973507.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding glob	30.8	30.8	90%	14	90%	gi|395533530|XP_003768811.1
☐	PREDICTED: sex hormone-binding globulin isoform 3 [Dasypus nov	30.8	30.8	90%	14	90%	gi|488556028|XP_004468805.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding glob	30.8	30.8	90%	14	90%	gi|348560991|XP_003466296.1
☐	PREDICTED: sex hormone-binding globulin isoform 1 [Dasypus nov	30.8	30.8	90%	14	90%	gi|488556022|XP_004468803.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Balaenopte	29.9	29.9	100%	26	82%	gi|594623652|XP_007166454.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Balaenopte	29.9	29.9	100%	26	82%	gi|594623650|XP_007166453.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding glob	29.9	29.9	100%	26	82%	gi|395836756|XP_003791316.1
☐	N-formylglutamate amidohydrolase [Afipia clevelandensis]	29.5	29.5	90%	35	80%	gi|488800992|WP_002713398.1
☐	unknown [Picea sitchensis]	28.6	28.6	81%	60	89%	gi|116781465|ABK22110.1

☐	hypothetical protein [Oceanobacillus iheyensis]	28.6	28.6	72%	61	100%	gi|499378681|WP_011066259.1
☐	formaldehyde:ferredoxin oxidoreductase [Thermofilum sp. 1505]	28.6	28.6	72%	68	100%	gi|742685993|AJB42273.1
☐	lantibiotic dehydratase [Micromonospora aurantiaca]	28.6	28.6	100%	69	73%	gi|503052275|WP_013287251.1
☐	RNA polymerase sigma factor SigM [Intrasporangium chromatiredu	28.2	28.2	90%	86	80%	gi|736717491|WP_034722165.1
☐	phosphate transport system regulatory protein PhoU [Acinetobacter	28.2	28.2	72%	88	100%	gi|491154937|WP_005013328.1
☐	MULTISPECIES: transcriptional regulator [Acinetobacter]	28.2	28.2	72%	88	100%	gi|490407564|WP_004281079.1
☐	transcriptional regulator PhoU [Acinetobacter baumannii]	28.2	28.2	72%	88	100%	gi|736699858|WP_034705351.1
☐	MULTISPECIES: phosphate transport system regulatory protein Ph	28.2	28.2	72%	88	100%	gi|491236189|WP_005094412.1
☐	phosphate transport system regulatory protein PhoU [Acinetobacter	28.2	28.2	72%	88	100%	gi|491243247|WP_005101453.1
☐	MULTISPECIES: phosphate transport system regulatory protein Ph	28.2	28.2	72%	88	100%	gi|490925375|WP_004787240.1
☐	phosphate transport system regulatory protein PhoU [Acinetobacter	28.2	28.2	72%	88	100%	gi|490787882|WP_004650040.1
☐	MULTISPECIES: phosphate transport system regulatory protein Ph	28.2	28.2	72%	88	100%	gi|491250273|WP_005108465.1
☐	transcriptional regulator [Acinetobacter junii]	28.2	28.2	72%	88	100%	gi|491055341|WP_004916988.1
☐	transcriptional regulator [Acinetobacter sp. MDS7A]	28.2	28.2	72%	88	100%	gi|518676428|WP_019838121.1
☐	transcriptional regulator [Acinetobacter tjernbergiae]	28.2	28.2	72%	88	100%	gi|517508950|WP_018679158.1
☐	phosphate transport system regulatory protein PhoU [Acinetobacter	28.2	28.2	72%	88	100%	gi|514971404|WP_016659690.1
☐	phosphate transport system regulatory protein PhoU [Acinetobacter	28.2	28.2	72%	88	100%	gi|507097828|WP_016168465.1
☐	phosphate transport system regulatory protein PhoU [Acinetobacter	28.2	28.2	72%	88	100%	gi|491323653|WP_005181619.1
☐	phosphate transport system regulatory protein PhoU [Acinetobacter	28.2	28.2	72%	88	100%	gi|491192511|WP_005050862.1
☐	phosphate transport system regulatory protein PhoU [Acinetobacter	28.2	28.2	72%	88	100%	gi|491202618|WP_005060960.1
☐	phosphate transport system regulatory protein PhoU [Acinetobacter	28.2	28.2	72%	88	100%	gi|491117281|WP_004975736.1
☐	phosphate transport system regulatory protein PhoU [Acinetobacter	28.2	28.2	72%	88	100%	gi|490938492|WP_004800329.1
☐	phosphate transport system regulatory protein PhoU [Acinetobacter	28.2	28.2	72%	88	100%	gi|490900413|WP_004762350.1
☐	phosphate transport system regulatory protein PhoU [Acinetobacter	28.2	28.2	72%	88	100%	gi|490812193|WP_004674307.1
☐	MULTISPECIES: phosphate transport system regulatory protein Ph	28.2	28.2	72%	88	100%	gi|490806115|WP_004668238.1
☐	MULTISPECIES: transcriptional regulator [Acinetobacter]	28.2	28.2	72%	88	100%	gi|490818655|WP_004680754.1
☐	MULTISPECIES: transcriptional regulator [Acinetobacter]	28.2	28.2	72%	88	100%	gi|491014672|WP_004876380.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

sex hormone binding globulin [Homo sapiens]

Sequence ID: gi|165873764|gb|ABY68001.1| **Length:** 206 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 176 to 186 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
37.5 bits(81)	0.076	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RLDVDQALNRS  11
            RLDVDQALNRS
Sbjct  176  RLDVDQALNRS  186
```

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PREDICTED: sex hormone-binding globulin isoform X6 [Homo sapiens]

Sequence ID: gi|530410575|ref|XP_005256822.1| **Length:** 233 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 203 to 213 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
37.5 bits(81)	0.078	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RLDVDQALNRS  11
```

```
                RLDVDQALNRS
Sbjct  203  RLDVDQALNRS  213
```

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sex hormone binding globulin [Homo sapiens]

Sequence ID: gi|165873760|gb|ABY67999.1| **Length:** 260 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 230 to 240 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
37.5 bits(81)	0.079	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RLDVDQALNRS  11
            RLDVDQALNRS
Sbjct  230  RLDVDQALNRS  240
```

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sex steroid-binding protein [Homo sapiens]

Sequence ID: gi|825718|emb|CAA29234.1| **Length:** 282 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 252 to 262 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
37.5 bits(81)	0.080	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RLDVDQALNRS  11
            RLDVDQALNRS
Sbjct  252  RLDVDQALNRS  262
```

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PREDICTED: sex hormone-binding globulin isoform X6 [Pan paniscus]

Sequence ID: gi|675705950|ref|XP_008960682.1| **Length:** 286 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 256 to 266 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
37.5 bits(81)	0.080	11/11(100%)	11/11(100%)	0/11(0%)

```
Query  1    RLDVDQALNRS  11
            RLDVDQALNRS
Sbjct  256  RLDVDQALNRS  266
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

SHBG_RSHEIWTHSCPQSPGDGTDASH_Mod

RID	BVM4P9BC01R (Expires on 01-21 10:50 am)		
Query ID	lcl|179996	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	22	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

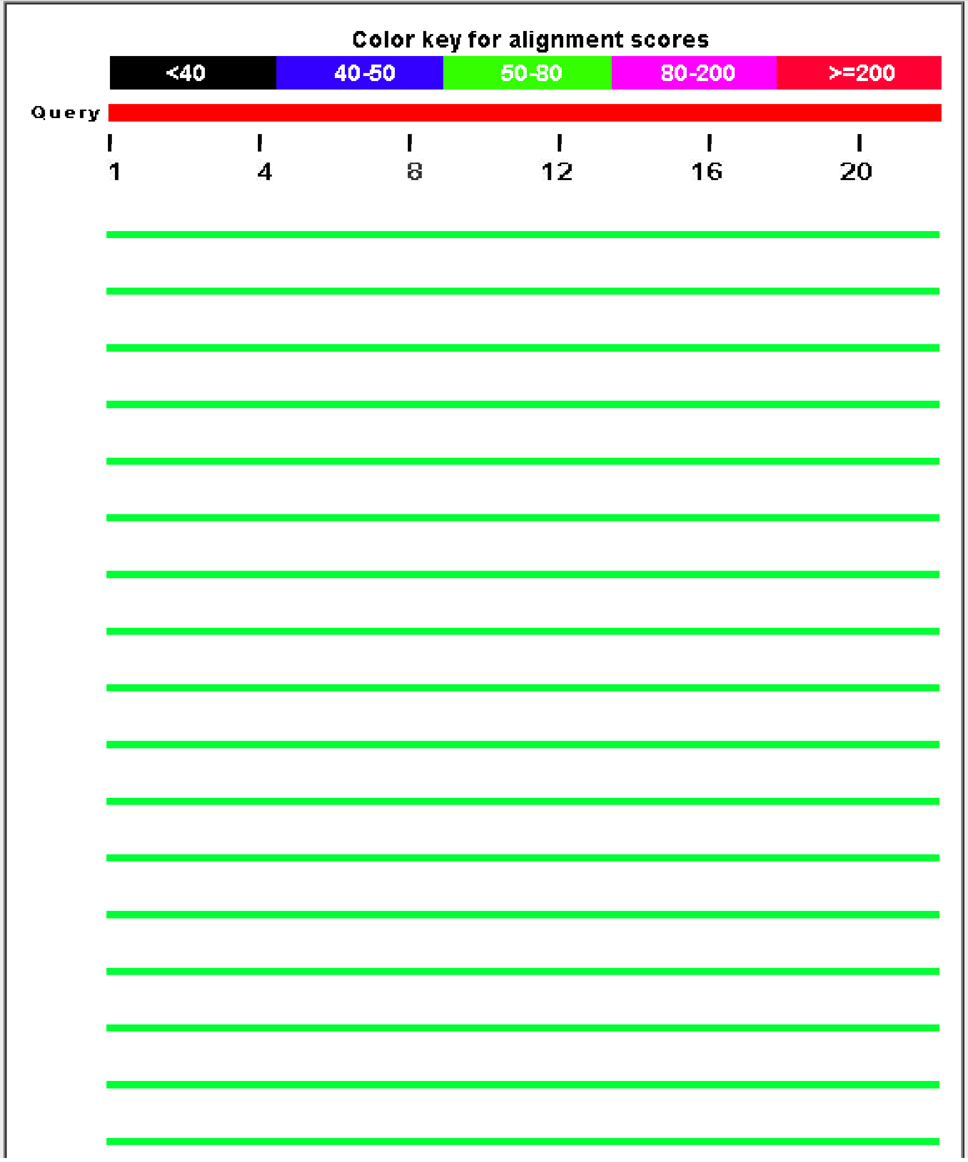
Graphic Summary

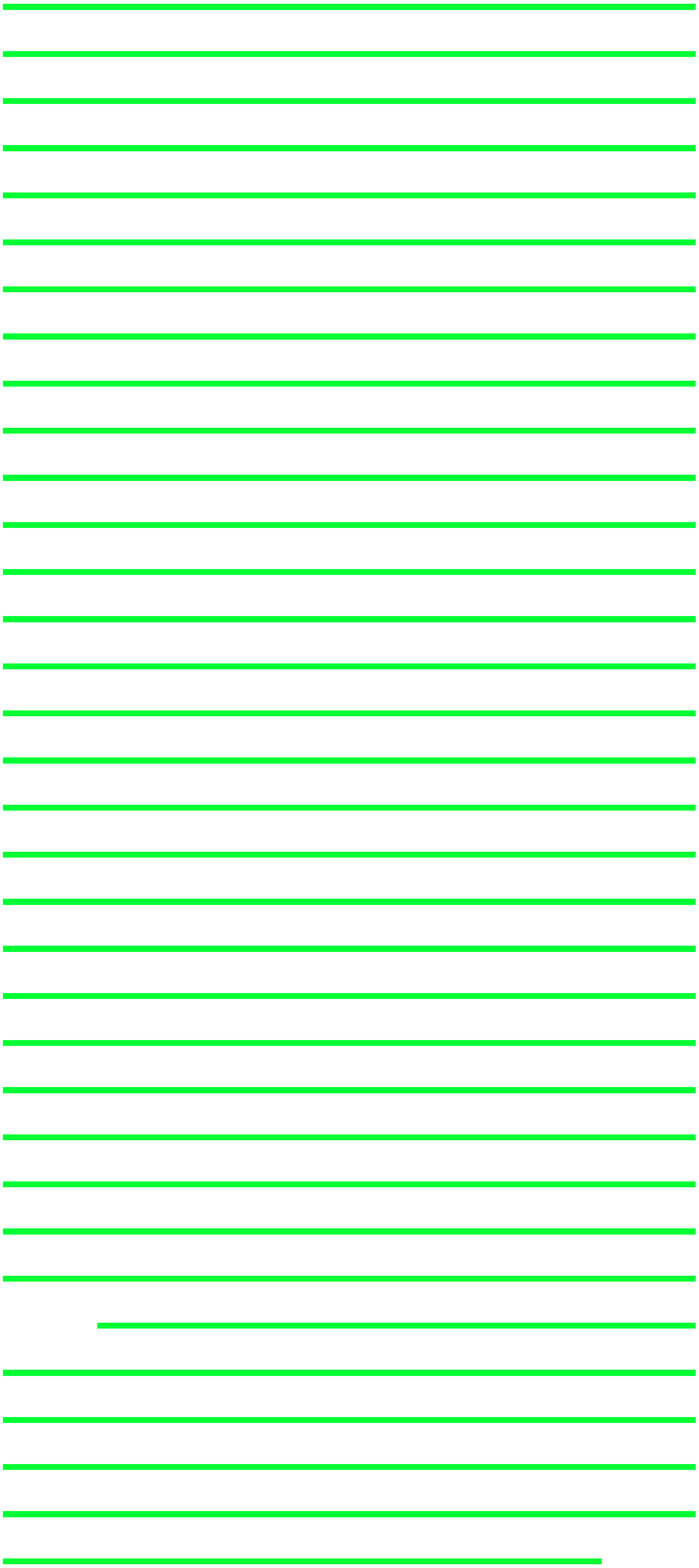
Show Conserved Domains

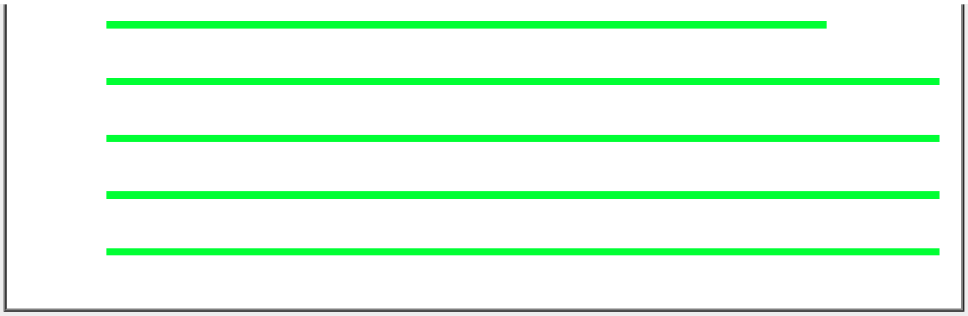
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	sex hormone binding globulin [Homo sapiens]	72.7	72.7	100%	3e-13	95%	ABY68001.1
☐	PREDICTED: sex hormone-binding globulin isoform X6 [Homo sapiens]	72.7	72.7	100%	4e-13	95%	XP_005256822.1
☐	sex hormone binding globulin [Homo sapiens]	72.7	72.7	100%	4e-13	95%	ABY67999.1
☐	sex steroid-binding protein [Homo sapiens]	72.7	72.7	100%	4e-13	95%	CAA29234.1
☐	PREDICTED: sex hormone-binding globulin isoform X5 [Rhinopithecus roxella	72.7	72.7	100%	4e-13	95%	XP_010360686.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Papio anubis]	72.7	72.7	100%	4e-13	95%	XP_009187837.1
☐	PREDICTED: sex hormone-binding globulin isoform X6 [Pan paniscus]	72.7	72.7	100%	4e-13	95%	XP_008960682.1
☐	PREDICTED: sex hormone-binding globulin isoform X6 [Chlorocebus sabaeu	72.7	72.7	100%	4e-13	95%	XP_008008379.1
☐	sex hormone-binding globulin isoform 7 [Homo sapiens]	72.7	72.7	100%	4e-13	95%	NP_001276045.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Pan paniscus]	72.7	72.7	100%	4e-13	95%	XP_003810122.1
☐	sex hormone-binding globulin isoform 4 precursor [Homo sapiens]	72.7	72.7	100%	4e-13	95%	NP_001139753.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Rhinopithecus roxella	72.7	72.7	100%	4e-13	95%	XP_010360685.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Pan paniscus]	72.7	72.7	100%	4e-13	95%	XP_008960680.1
☐	sex hormone-binding globulin isoform 5 [Homo sapiens]	72.7	72.7	100%	4e-13	95%	NP_001276042.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Rhinopithecus roxella	72.7	72.7	100%	4e-13	95%	XP_010360684.1
☐	PREDICTED: sex hormone-binding globulin isoform X5 [Chlorocebus sabaeu	72.7	72.7	100%	4e-13	95%	XP_008008377.1
☐	PREDICTED: sex hormone-binding globulin isoform X7 [Homo sapiens]	72.7	72.7	100%	4e-13	95%	XP_006721632.1
☐	unnamed protein product [Homo sapiens]	72.7	72.7	100%	4e-13	95%	CAA29309.1
☐	unnamed protein product [Homo sapiens]	72.7	72.7	100%	4e-13	95%	CAA28987.1
☐	sex hormone-binding globulin isoform 2 precursor [Homo sapiens]	72.7	72.7	100%	4e-13	95%	NP_001139751.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Chlorocebus sabaeu	72.7	72.7	100%	4e-13	95%	XP_008008372.1
☐	SHBG protein [Homo sapiens]	72.7	72.7	100%	4e-13	95%	AAH69597.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Rhinopithecus roxella	72.7	72.7	100%	4e-13	95%	XP_010360683.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Papio anubis]	72.7	72.7	100%	4e-13	95%	XP_009187836.1
☐	sex hormone-binding globulin [synthetic construct]	72.7	72.7	100%	4e-13	95%	AAX36263.1
☐	sex hormone-binding globulin [Homo sapiens]	72.7	72.7	100%	4e-13	95%	AAC18778.1
☐	sex hormone-binding globulin isoform 1 precursor [Homo sapiens]	72.7	72.7	100%	4e-13	95%	NP_001031.2
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Pan paniscus]	72.7	72.7	100%	4e-13	95%	XP_003810120.1
☐	Sex hormone-binding globulin [Macaca mulatta]	72.7	72.7	100%	4e-13	95%	EHH24482.1

☐	PREDICTED: sex hormone-binding globulin isoform X1 [Rhinopithecus roxella	72.7	72.7	100%	4e-13	95%	XP_010360681.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Papio anubis]	72.7	72.7	100%	4e-13	95%	XP_009187834.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Chlorocebus sabaeu	72.7	72.7	100%	4e-13	95%	XP_008008371.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding globulin-like [N	72.7	72.7	100%	4e-13	95%	XP_002808160.1
☐	uncharacterized protein LOC101864774 [Macaca fascicularis]	72.7	72.7	100%	4e-13	95%	NP_001270513.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Chlorocebus sabaeu	72.7	72.7	100%	4e-13	95%	XP_008008369.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Chlorocebus sabaeu	72.7	72.7	100%	4e-13	95%	XP_008008368.1
☐	PREDICTED: sex hormone-binding globulin isoform 4 [Gorilla gorilla gorilla]	69.8	69.8	100%	4e-12	91%	XP_004058549.1
☐	PREDICTED: sex hormone-binding globulin isoform 3 [Gorilla gorilla gorilla]	69.8	69.8	100%	4e-12	91%	XP_004058548.1
☐	PREDICTED: sex hormone-binding globulin isoform 1 [Gorilla gorilla gorilla]	69.8	69.8	100%	4e-12	91%	XP_004058546.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding globulin [Pong	68.1	68.1	100%	2e-11	91%	XP_009249533.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Saimiri boliviensis bo	67.7	67.7	100%	2e-11	86%	XP_010338103.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Callithrix jacchus]	67.7	67.7	100%	2e-11	86%	XP_008994833.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Callithrix jacchus]	67.7	67.7	100%	2e-11	86%	XP_008994832.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Callithrix jacchus]	67.7	67.7	100%	2e-11	86%	XP_002747998.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Saimiri boliviensis bo	67.7	67.7	100%	2e-11	86%	XP_003929225.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding globulin [Noma	63.0	63.0	86%	9e-10	95%	XP_004091565.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Balaenoptera acutoro	58.7	58.7	100%	2e-08	77%	XP_007166454.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Balaenoptera acutoro	58.7	58.7	100%	2e-08	77%	XP_007166453.1
☐	sex hormone-binding globulin precursor [Oryctolagus cuniculus]	58.3	58.3	100%	3e-08	77%	NP_001075839.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding globulin [Otole	58.3	58.3	100%	3e-08	77%	XP_003791316.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding globulin [Phys	57.9	57.9	86%	5e-08	84%	XP_007131043.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding globulin [Orcin	57.9	57.9	86%	5e-08	84%	XP_004266952.1
☐	PREDICTED: sex hormone-binding globulin isoform X5 [Loxodonta africana]	57.5	57.5	100%	6e-08	77%	XP_010594887.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Tarsius syrichta]	57.5	57.5	100%	6e-08	73%	XP_008060529.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Loxodonta africana]	57.5	57.5	100%	6e-08	77%	XP_010594883.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Loxodonta africana]	57.5	57.5	100%	6e-08	77%	XP_010594886.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Loxodonta africana]	57.5	57.5	100%	6e-08	77%	XP_010594885.1
☐	PREDICTED: sex hormone-binding globulin [Trichechus manatus latirostris]	57.5	57.5	100%	6e-08	77%	XP_004376080.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Tarsius syrichta]	57.5	57.5	100%	6e-08	73%	XP_008060527.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Tarsius syrichta]	57.5	57.5	100%	7e-08	73%	XP_008060526.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Jaculus jaculus]	55.8	55.8	95%	2e-07	76%	XP_004669275.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Jaculus jaculus]	55.8	55.8	95%	2e-07	76%	XP_004669274.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Jaculus jaculus]	55.8	55.8	95%	2e-07	76%	XP_004669273.1
☐	PREDICTED: sex hormone-binding globulin isoform X5 [Eptesicus fuscus]	55.4	55.4	100%	3e-07	68%	XP_008151730.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Myotis davidii]	55.4	55.4	100%	3e-07	68%	XP_006761714.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Eptesicus fuscus]	55.4	55.4	100%	3e-07	68%	XP_008151727.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Myotis lucifugus]	55.4	55.4	100%	3e-07	68%	XP_006107895.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Lipotes vexillifer]	55.4	55.4	86%	3e-07	79%	XP_007457850.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Eptesicus fuscus]	55.4	55.4	100%	3e-07	68%	XP_008151725.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Myotis lucifugus]	55.4	55.4	100%	3e-07	68%	XP_006107894.1
☐	Sex hormone-binding globulin [Myotis brandtii]	55.4	55.4	100%	3e-07	68%	EPQ15483.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Eptesicus fuscus]	55.4	55.4	100%	3e-07	68%	XP_008151729.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Myotis lucifugus]	55.4	55.4	100%	3e-07	68%	XP_006107893.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Lipotes vexillifer]	55.4	55.4	86%	3e-07	79%	XP_007457849.1

☐	PREDICTED: sex hormone-binding globulin [Tursiops truncatus]	55.4	55.4	86%	3e-07	79%	XP_004310675.1
☐	Sex hormone-binding globulin [Myotis davidii]	55.4	55.4	100%	3e-07	68%	ELK31809.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Myotis lucifugus]	55.4	55.4	100%	3e-07	68%	XP_006107892.1
☐	PREDICTED: sex hormone-binding globulin-like isoform X4 [Myotis brandtii]	55.4	55.4	100%	3e-07	68%	XP_005878824.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Galeopterus variegat	54.9	54.9	100%	4e-07	73%	XP_008572063.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding globulin [Ptero	54.5	54.5	81%	6e-07	83%	XP_006927039.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding globulin [Sus s	54.1	54.1	100%	9e-07	73%	XP_005669285.1
☐	PREDICTED: sex hormone-binding globulin-like isoform 2 [Ailuropoda melanc	54.1	54.1	100%	9e-07	68%	XP_002924481.1
☐	PREDICTED: sex hormone-binding globulin [Ursus maritimus]	54.1	54.1	100%	9e-07	68%	XP_008686192.1
☐	PREDICTED: sex hormone-binding globulin-like isoform 1 [Ailuropoda melanc	54.1	54.1	100%	9e-07	68%	XP_002924480.1
☐	PREDICTED: sex hormone-binding globulin [Orycteropus afer afer]	53.7	53.7	100%	1e-06	77%	XP_007950448.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Ictidomys tridecemlin	53.7	53.7	100%	1e-06	73%	XP_005332872.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Ictidomys tridecemlin	53.7	53.7	100%	1e-06	73%	XP_005332871.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Ictidomys tridecemlin	53.7	53.7	100%	1e-06	73%	XP_005332870.1
☐	PREDICTED: sex hormone-binding globulin isoformX1 [Canis lupus familiaris]	52.4	52.4	100%	3e-06	68%	XP_003639094.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Camelus dromedariu	52.0	52.0	86%	4e-06	74%	XP_010994821.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Camelus bactrianus]	52.0	52.0	86%	4e-06	74%	XP_010964222.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Camelus dromedariu	52.0	52.0	86%	4e-06	74%	XP_010994820.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Camelus bactrianus]	52.0	52.0	86%	4e-06	74%	XP_010964221.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Camelus ferus]	52.0	52.0	86%	4e-06	74%	XP_006175877.1
☐	PREDICTED: sex hormone-binding globulin [Vicugna pacos]	52.0	52.0	86%	4e-06	74%	XP_006218840.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Camelus dromedariu	52.0	52.0	86%	5e-06	74%	XP_010994819.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Camelus bactrianus]	52.0	52.0	86%	5e-06	74%	XP_010964220.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Camelus ferus]	52.0	52.0	86%	5e-06	74%	XP_006175876.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Camelus dromedariu	52.0	52.0	86%	5e-06	74%	XP_010994818.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Camelus bactrianus]	52.0	52.0	86%	5e-06	74%	XP_010964219.1

Alignments

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sex hormone binding globulin [Homo sapiens]

Sequence ID: gb|ABY68001.1| **Length:** 206 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 185 to 206 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.7 bits(164)	3e-13	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1    RSHEIWTHSCPQSPGDGTDASH  22
            RSHEIWTHSCPQSPG+GTDASH
Sbjct  185  RSHEIWTHSCPQSPGNGTDASH  206
```

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PREDICTED: sex hormone-binding globulin isoform X6 [Homo sapiens]

Sequence ID: ref|XP_005256822.1| **Length:** 233 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 212 to 233 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.7 bits(164)	4e-13	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1    RSHEIWTHSCPQSPGDGTDASH  22
            RSHEIWTHSCPQSPG+GTDASH
Sbjct  212  RSHEIWTHSCPQSPGNGTDASH  233
```

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sex hormone binding globulin [Homo sapiens]

Sequence ID: gb|ABY67999.1| **Length:** 260 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 239 to 260 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.7 bits(164)	4e-13	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1    RSHEIWTHSCPQSPGDGTDASH  22
            RSHEIWTHSCPQSPG+GTDASH
Sbjct  239  RSHEIWTHSCPQSPGNGTDASH  260
```

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sex steroid-binding protein [Homo sapiens]

Sequence ID: emb|CAA29234.1| **Length:** 282 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 261 to 282 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.7 bits(164)	4e-13	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1    RSHEIWTHSCPQSPGDGTDASH  22
            RSHEIWTHSCPQSPG+GTDASH
Sbjct  261  RSHEIWTHSCPQSPGNGTDASH  282
```

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PREDICTED: sex hormone-binding globulin isoform X5 [Rhinopithecus roxellana]

Sequence ID: ref|XP_010360686.1| **Length:** 286 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 265 to 286 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
72.7 bits(164)	4e-13	21/22(95%)	22/22(100%)	0/22(0%)

```
Query  1    RSHEIWTHSCPQSPGDGTDASH  22
            RSHEIWTHSCPQSPG+GTDASH
Sbjct  265  RSHEIWTHSCPQSPGNGTDASH  286
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BE8A8FGM015

Your search parameters were adjusted to search for a short input sequence.

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How to read this page Blast report description

SHBG_RSHEIWTHSCPQSPGNGTDASH_NonMod

RID BE8A8FGM015 (Expires on 01-16 09:09 am)

Query ID lcl|1124
Description None
Molecule type amino acid
Query Length 22

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Program BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

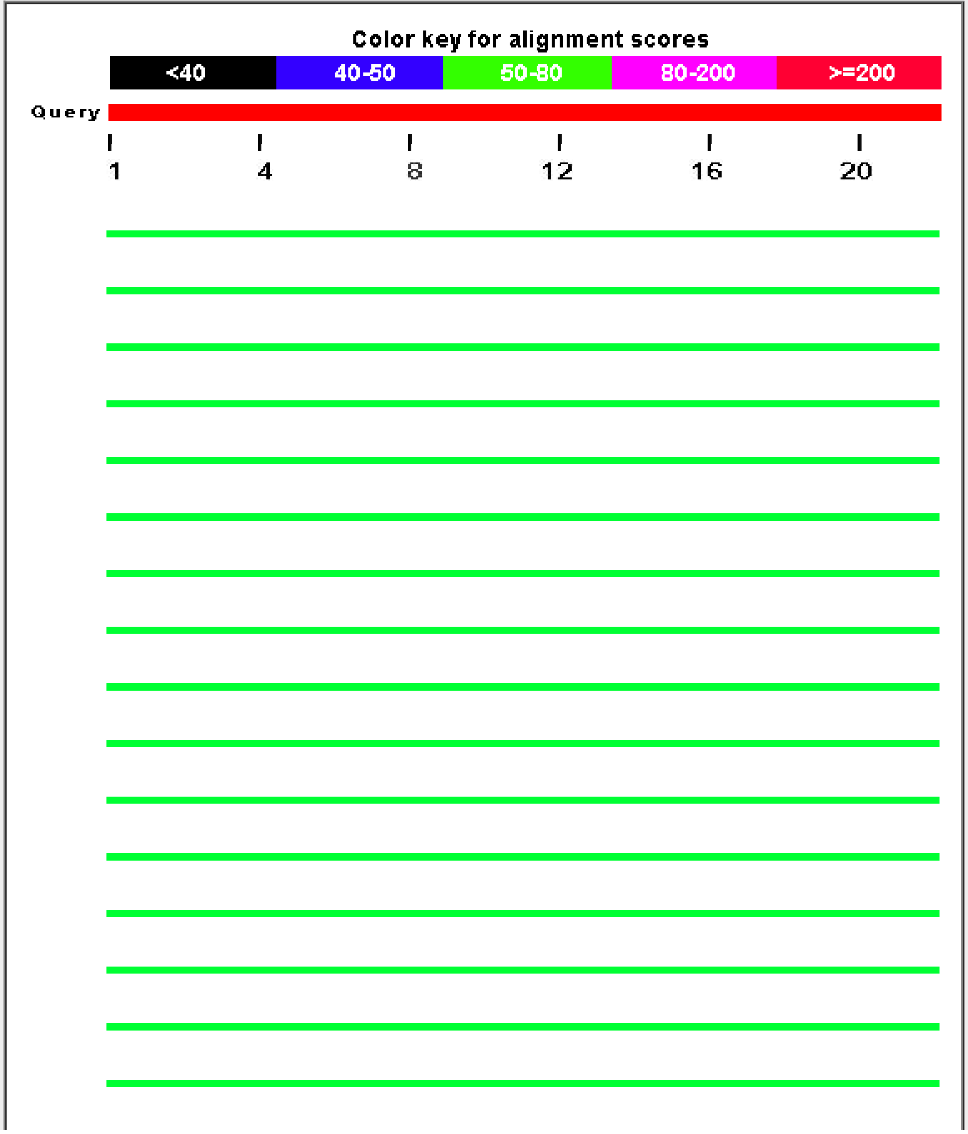
Graphic Summary

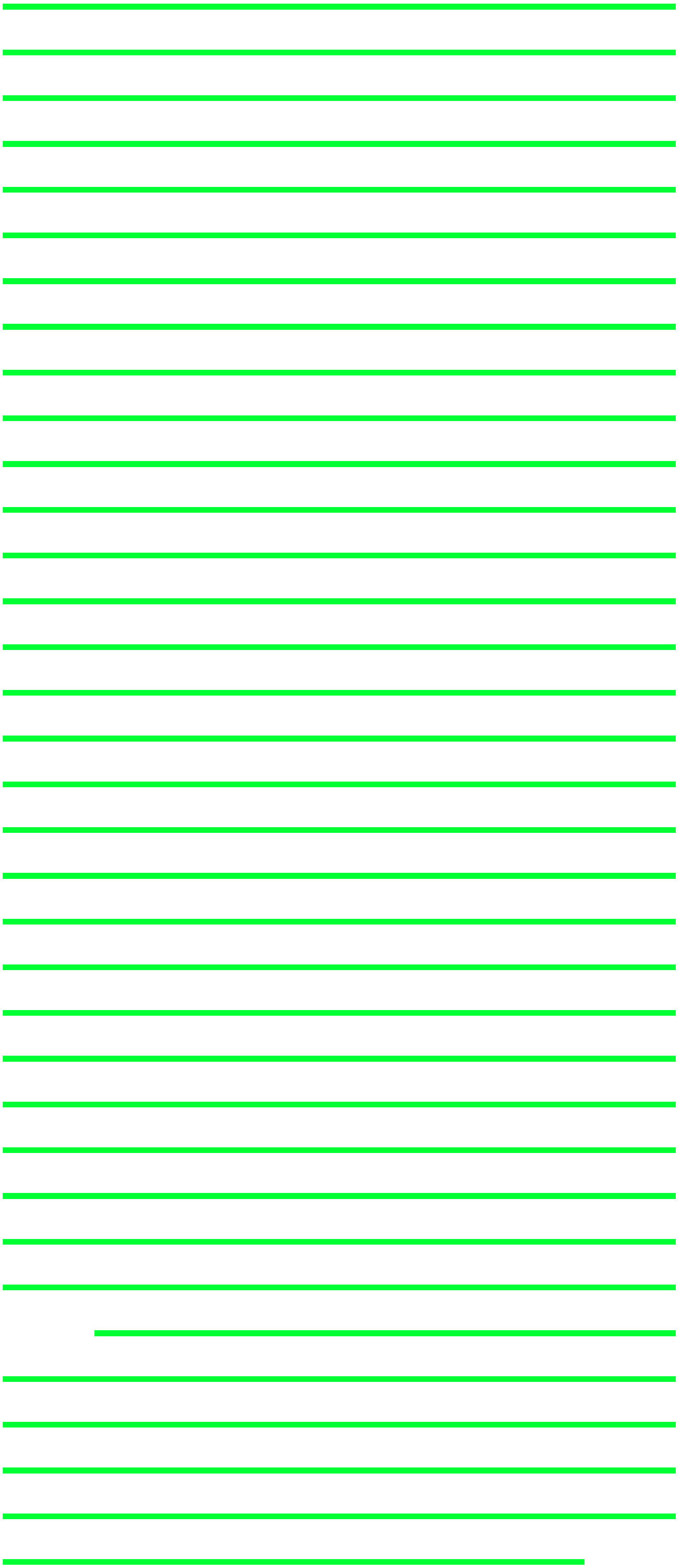
Show Conserved Domains

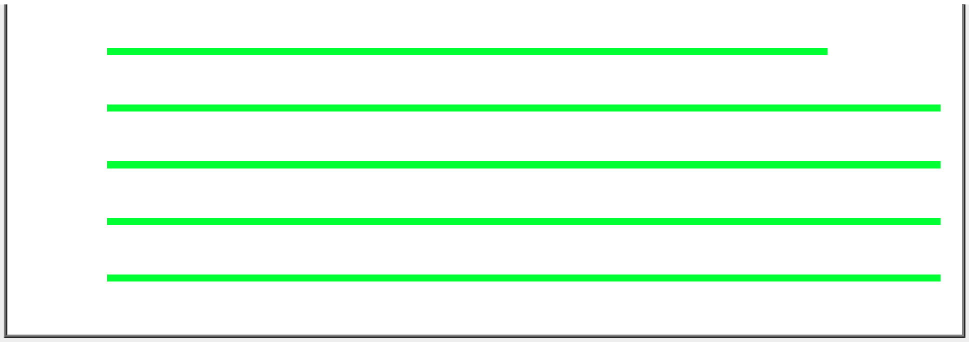
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊖Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	sex hormone binding globulin [Homo sapiens]	75.3	75.3	100%	4e-14	100%	gi|165873764|ABY68001.1
☐	PREDICTED: sex hormone-binding globulin isoform X6 [Homo sapi	75.3	75.3	100%	5e-14	100%	gi|530410575|XP_005256822.1
☐	sex hormone binding globulin [Homo sapiens]	75.3	75.3	100%	5e-14	100%	gi|165873760|ABY67999.1
☐	sex steroid-binding protein [Homo sapiens]	75.3	75.3	100%	5e-14	100%	gi|825718|CAA29234.1
☐	PREDICTED: sex hormone-binding globulin isoform X5 [Rhinopithe	75.3	75.3	100%	5e-14	100%	gi|724818518|XP_010360686.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Papio anul	75.3	75.3	100%	5e-14	100%	gi|685595645|XP_009187837.1
☐	PREDICTED: sex hormone-binding globulin isoform X6 [Pan panisc	75.3	75.3	100%	5e-14	100%	gi|675705950|XP_008960682.1
☐	PREDICTED: sex hormone-binding globulin isoform X6 [Chlorocebu	75.3	75.3	100%	5e-14	100%	gi|635087572|XP_008008379.1
☐	sex hormone-binding globulin isoform 7 [Homo sapiens]	75.3	75.3	100%	5e-14	100%	gi|574288369|NP_001276045.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Pan panisc	75.3	75.3	100%	5e-14	100%	gi|397477529|XP_003810122.1
☐	sex hormone-binding globulin isoform 4 precursor [Homo sapiens]	75.3	75.3	100%	5e-14	100%	gi|226371613|NP_001139753.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Rhinopithe	75.3	75.3	100%	5e-14	100%	gi|724818515|XP_010360685.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Pan panisc	75.3	75.3	100%	5e-14	100%	gi|675705940|XP_008960680.1
☐	sex hormone-binding globulin isoform 5 [Homo sapiens]	75.3	75.3	100%	5e-14	100%	gi|574287849|NP_001276042.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Rhinopithe	75.3	75.3	100%	5e-14	100%	gi|724818512|XP_010360684.1
☐	PREDICTED: sex hormone-binding globulin isoform X5 [Chlorocebu	75.3	75.3	100%	5e-14	100%	gi|635087568|XP_008008377.1
☐	PREDICTED: sex hormone-binding globulin isoform X7 [Homo sapi	75.3	75.3	100%	5e-14	100%	gi|578830017|XP_006721632.1
☐	unnamed protein product [Homo sapiens]	75.3	75.3	100%	5e-14	100%	gi|1335306|CAA29309.1
☐	unnamed protein product [Homo sapiens]	75.3	75.3	100%	6e-14	100%	gi|36448|CAA28987.1
☐	sex hormone-binding globulin isoform 2 precursor [Homo sapiens]	75.3	75.3	100%	6e-14	100%	gi|226371775|NP_001139751.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Chlorocebu	75.3	75.3	100%	6e-14	100%	gi|635087558|XP_008008372.1
☐	SHBG protein [Homo sapiens]	75.3	75.3	100%	6e-14	100%	gi|47479685|AAH69597.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Rhinopithe	75.3	75.3	100%	6e-14	100%	gi|724818509|XP_010360683.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Papio anul	75.3	75.3	100%	6e-14	100%	gi|685595643|XP_009187836.1
☐	sex hormone-binding globulin [synthetic construct]	75.3	75.3	100%	6e-14	100%	gi|60813500|AAX36263.1
☐	sex hormone-binding globulin [Homo sapiens]	75.3	75.3	100%	6e-14	100%	gi|338075|AAC18778.1
☐	sex hormone-binding globulin isoform 1 precursor [Homo sapiens]	75.3	75.3	100%	6e-14	100%	gi|7382460|NP_001031.2
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Pan panisc	75.3	75.3	100%	6e-14	100%	gi|397477525|XP_003810120.1
☐							

	Sex hormone-binding globulin [Macaca mulatta]	75.3	75.3	100%	6e-14	100%	gi|355568201|EHH24482.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Rhinopithe	75.3	75.3	100%	6e-14	100%	gi|724818503|XP_010360681.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Papio anub	75.3	75.3	100%	6e-14	100%	gi|685595639|XP_009187834.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Chlorocebu	75.3	75.3	100%	6e-14	100%	gi|635087556|XP_008008371.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding glob	75.3	75.3	100%	6e-14	100%	gi|297271824|XP_002808160.1
☐	uncharacterized protein LOC101864774 [Macaca fascicularis]	75.3	75.3	100%	6e-14	100%	gi|545686862|NP_001270513.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Chlorocebu	75.3	75.3	100%	6e-14	100%	gi|635087554|XP_008008369.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Chlorocebu	75.3	75.3	100%	6e-14	100%	gi|635087552|XP_008008368.1
☐	PREDICTED: sex hormone-binding globulin isoform 4 [Gorilla gorill	72.3	72.3	100%	5e-13	95%	gi|426383969|XP_004058549.1
☐	PREDICTED: sex hormone-binding globulin isoform 3 [Gorilla gorill	72.3	72.3	100%	6e-13	95%	gi|426383967|XP_004058548.1
☐	PREDICTED: sex hormone-binding globulin isoform 1 [Gorilla gorill	72.3	72.3	100%	6e-13	95%	gi|426383963|XP_004058546.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding glob	70.6	70.6	100%	2e-12	95%	gi|686752223|XP_009249533.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Saimiri boli	70.2	70.2	100%	3e-12	91%	gi|725571085|XP_010338103.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Callithrix ja	70.2	70.2	100%	3e-12	91%	gi|675658295|XP_008994833.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Callithrix ja	70.2	70.2	100%	3e-12	91%	gi|675658293|XP_008994832.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Callithrix ja	70.2	70.2	100%	3e-12	91%	gi|296201365|XP_002747998.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Saimiri boli	70.2	70.2	100%	3e-12	91%	gi|403274954|XP_003929225.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding glob	65.5	65.5	86%	1e-10	100%	gi|441662099|XP_004091565.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Balaenopte	61.3	61.3	100%	3e-09	82%	gi|594623652|XP_007166454.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Balaenopte	61.3	61.3	100%	3e-09	82%	gi|594623650|XP_007166453.1
☐	sex hormone-binding globulin precursor [Oryctolagus cuniculus]	60.9	60.9	100%	5e-09	82%	gi|126723743|NP_001075839.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding glob	60.9	60.9	100%	5e-09	82%	gi|395836756|XP_003791316.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding glob	60.4	60.4	86%	6e-09	89%	gi|593708274|XP_007131043.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding glob	60.4	60.4	86%	6e-09	89%	gi|465992477|XP_004266952.1
☐	PREDICTED: sex hormone-binding globulin isoform X5 [Loxodonta	60.0	60.0	100%	8e-09	82%	gi|731501491|XP_010594887.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Tarsius syr	60.0	60.0	100%	8e-09	77%	gi|640808027|XP_008060529.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Loxodonta	60.0	60.0	100%	8e-09	82%	gi|731501482|XP_010594883.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Loxodonta	60.0	60.0	100%	9e-09	82%	gi|731501488|XP_010594886.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Loxodonta	60.0	60.0	100%	9e-09	82%	gi|731501486|XP_010594885.1
☐	PREDICTED: sex hormone-binding globulin [Trichechus manatus la	60.0	60.0	100%	9e-09	82%	gi|471371144|XP_004376080.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Tarsius syr	60.0	60.0	100%	9e-09	77%	gi|640808023|XP_008060527.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Tarsius syr	60.0	60.0	100%	9e-09	77%	gi|640808021|XP_008060526.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Jaculus jac	58.3	58.3	95%	3e-08	81%	gi|507571348|XP_004669275.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Jaculus jac	58.3	58.3	95%	3e-08	81%	gi|507571346|XP_004669274.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Jaculus jac	58.3	58.3	95%	3e-08	81%	gi|507571344|XP_004669273.1
☐	PREDICTED: sex hormone-binding globulin isoform X5 [Eptesicus f	57.9	57.9	100%	4e-08	73%	gi|641723756|XP_008151730.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Myotis dav	57.9	57.9	100%	4e-08	73%	gi|584083885|XP_006761714.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Eptesicus f	57.9	57.9	100%	4e-08	73%	gi|641723750|XP_008151727.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Myotis luci	57.9	57.9	100%	4e-08	73%	gi|558212270|XP_006107895.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Lipotes ve	57.9	57.9	86%	4e-08	84%	gi|602691440|XP_007457850.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Eptesicus f	57.9	57.9	100%	4e-08	73%	gi|641723748|XP_008151725.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Myotis luci	57.9	57.9	100%	5e-08	73%	gi|558212266|XP_006107894.1
☐	Sex hormone-binding globulin [Myotis brandtii]	57.9	57.9	100%	5e-08	73%	gi|521033698|EPQ15483.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Eptesicus f	57.9	57.9	100%	5e-08	73%	gi|641723754|XP_008151729.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Myotis luci	57.9	57.9	100%	5e-08	73%	gi|558212261|XP_006107893.1

☐	PREDICTED: sex hormone-binding globulin isoform X1 [Lipotes vex	57.9	57.9	86%	5e-08	84%	gi|602691438|XP_007457849.1
☐	PREDICTED: sex hormone-binding globulin [Tursiops truncatus]	57.9	57.9	86%	5e-08	84%	gi|470595418|XP_004310675.1
☐	Sex hormone-binding globulin [Myotis davidii]	57.9	57.9	100%	5e-08	73%	gi|432105615|ELK31809.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Myotis luci	57.9	57.9	100%	5e-08	73%	gi|558212256|XP_006107892.1
☐	PREDICTED: sex hormone-binding globulin-like isoform X4 [Myotis	57.9	57.9	100%	5e-08	73%	gi|554569120|XP_005878824.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding glob	57.1	57.1	81%	9e-08	89%	gi|586535218|XP_006927039.1
☐	PREDICTED: LOW QUALITY PROTEIN: sex hormone-binding glob	56.6	56.6	100%	1e-07	77%	gi|545860218|XP_005669285.1
☐	PREDICTED: sex hormone-binding globulin-like isoform 2 [Ailuropo	56.6	56.6	100%	1e-07	73%	gi|301778205|XP_002924481.1
☐	PREDICTED: sex hormone-binding globulin [Ursus maritimus]	56.6	56.6	100%	1e-07	73%	gi|670990414|XP_008686192.1
☐	PREDICTED: sex hormone-binding globulin-like isoform 1 [Ailuropo	56.6	56.6	100%	1e-07	73%	gi|301778203|XP_002924480.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Galeopteru	56.2	56.2	100%	2e-07	73%	gi|667274663|XP_008572063.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Ictidomys t	56.2	56.2	100%	2e-07	77%	gi|532094390|XP_005332872.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Ictidomys t	56.2	56.2	100%	2e-07	77%	gi|532094388|XP_005332871.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Ictidomys t	56.2	56.2	100%	2e-07	77%	gi|532094386|XP_005332870.1
☐	PREDICTED: sex hormone-binding globulin [Orycteropus afer afer]	55.4	55.4	100%	3e-07	77%	gi|634880093|XP_007950448.1
☐	PREDICTED: sex hormone-binding globulin isoformX1 [Canis lupus	54.9	54.9	100%	5e-07	73%	gi|359319496|XP_003639094.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Camelus d	54.5	54.5	86%	6e-07	79%	gi|744613691|XP_010994821.1
☐	PREDICTED: sex hormone-binding globulin isoform X4 [Camelus b	54.5	54.5	86%	6e-07	79%	gi|743739556|XP_010964222.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Camelus d	54.5	54.5	86%	6e-07	79%	gi|744613688|XP_010994820.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Camelus b	54.5	54.5	86%	6e-07	79%	gi|743739554|XP_010964221.1
☐	PREDICTED: sex hormone-binding globulin isoform X3 [Camelus fe	54.5	54.5	86%	6e-07	79%	gi|560898873|XP_006175877.1
☐	PREDICTED: sex hormone-binding globulin [Vicugna pacos]	54.5	54.5	86%	6e-07	79%	gi|560993445|XP_006218840.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Camelus d	54.5	54.5	86%	6e-07	79%	gi|744613685|XP_010994819.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Camelus b	54.5	54.5	86%	6e-07	79%	gi|743739552|XP_010964220.1
☐	PREDICTED: sex hormone-binding globulin isoform X2 [Camelus fe	54.5	54.5	86%	6e-07	79%	gi|560898871|XP_006175876.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Camelus d	54.5	54.5	86%	6e-07	79%	gi|744613682|XP_010994818.1
☐	PREDICTED: sex hormone-binding globulin isoform X1 [Camelus b	54.5	54.5	86%	6e-07	79%	gi|743739550|XP_010964219.1

Alignments

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sex hormone binding globulin [Homo sapiens]

Sequence ID: gi|165873764|gb|ABY68001.1| **Length:** 206 **Number of Matches:** 1

Range 1: 185 to 206 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.3 bits(170)	4e-14	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1    RSHEIWTHSCPQSPGNGTDASH  22
           RSHEIWTHSCPQSPGNGTDASH
Sbjct  185  RSHEIWTHSCPQSPGNGTDASH  206
```

Related Information

Gene - associated gene details

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PREDICTED: sex hormone-binding globulin isoform X6 [Homo sapiens]

Sequence ID: gi|530410575|ref|XP_005256822.1| **Length:** 233 **Number of Matches:** 1

Range 1: 212 to 233 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.3 bits(170)	5e-14	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1    RSHEIWTHSCPQSPGNGTDASH  22
```

Related Information

Gene - associated gene details

```
                 RSHEIWTHSCPQSPGNGTDASH
Sbjct  212  RSHEIWTHSCPQSPGNGTDASH  233
```

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sex hormone binding globulin [Homo sapiens]

Sequence ID: gi|165873760|gb|ABY67999.1| **Length:** 260 **Number of Matches:** 1

Range 1: 239 to 260 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.3 bits(170)	5e-14	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1    RSHEIWTHSCPQSPGNGTDASH  22
            RSHEIWTHSCPQSPGNGTDASH
Sbjct  239  RSHEIWTHSCPQSPGNGTDASH  260
```

Related Information

Gene - associated gene details

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sex steroid-binding protein [Homo sapiens]

Sequence ID: gi|825718|emb|CAA29234.1| **Length:** 282 **Number of Matches:** 1

Range 1: 261 to 282 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.3 bits(170)	5e-14	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1    RSHEIWTHSCPQSPGNGTDASH  22
            RSHEIWTHSCPQSPGNGTDASH
Sbjct  261  RSHEIWTHSCPQSPGNGTDASH  282
```

Related Information

Gene - associated gene details

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PREDICTED: sex hormone-binding globulin isoform X5 [Rhinopithecus roxellana]

Sequence ID: gi|724818518|ref|XP_010360686.1| **Length:** 286 **Number of Matches:** 1

Range 1: 265 to 286 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
75.3 bits(170)	5e-14	22/22(100%)	22/22(100%)	0/22(0%)

```
Query  1    RSHEIWTHSCPQSPGNGTDASH  22
            RSHEIWTHSCPQSPGNGTDASH
Sbjct  265  RSHEIWTHSCPQSPGNGTDASH  286
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

BLAST ® *Basic Local Alignment Search Tool*

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NCBI/ BLAST/ blastp suite/ **Formatting Results - BVM52HEP01R**

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit   Save Search Strategies   ▷Formatting options   ▷Download   How to read this page   Blast report description

THBS1_KKVSCPIMPCSDATVPDGECCPRC_Mod

RID	BVM52HEP01R (Expires on 01-21 10:50 am)		
Query ID	lcl|115247	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	24	**Program**	BLASTP 2.2.30+ ▷Citation

Other reports: ▷Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

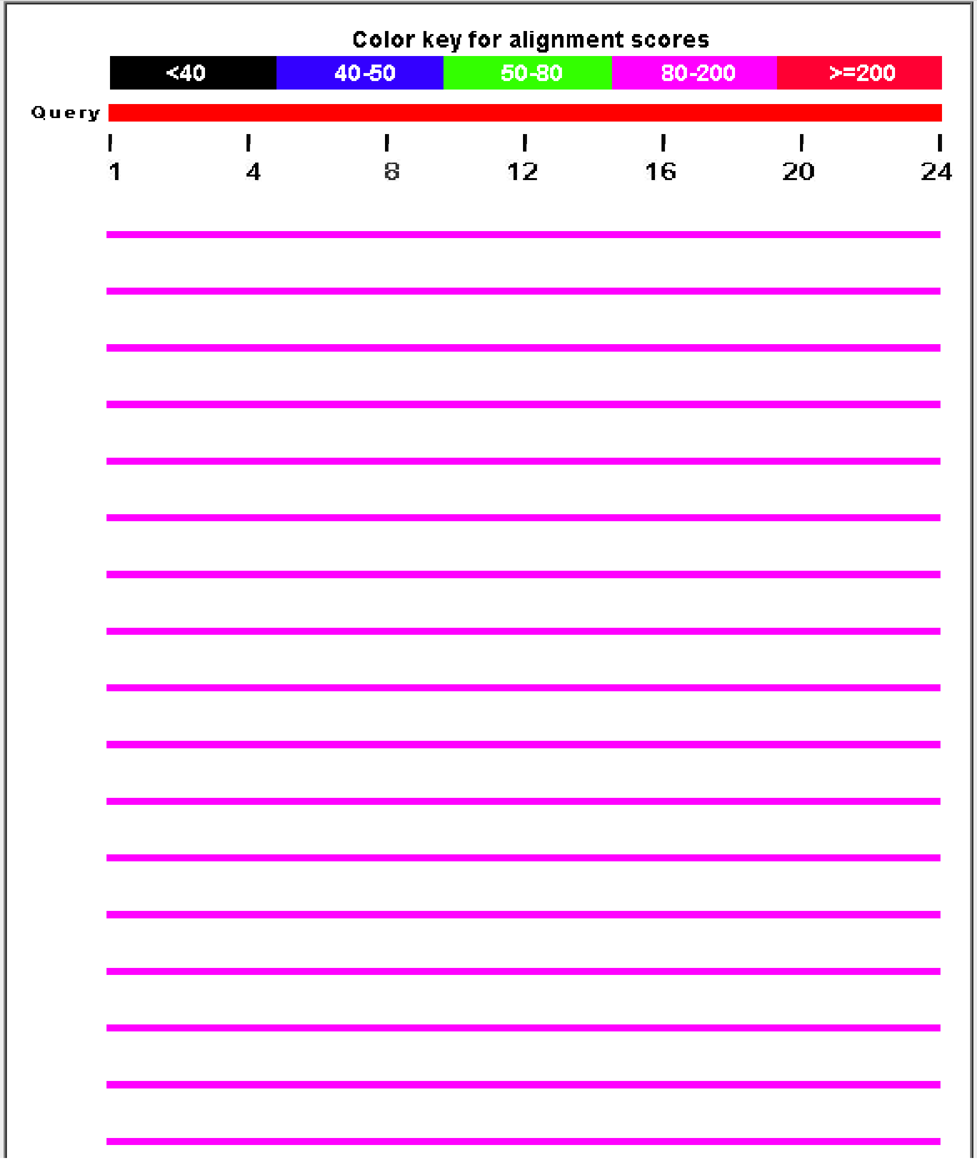
Graphic Summary

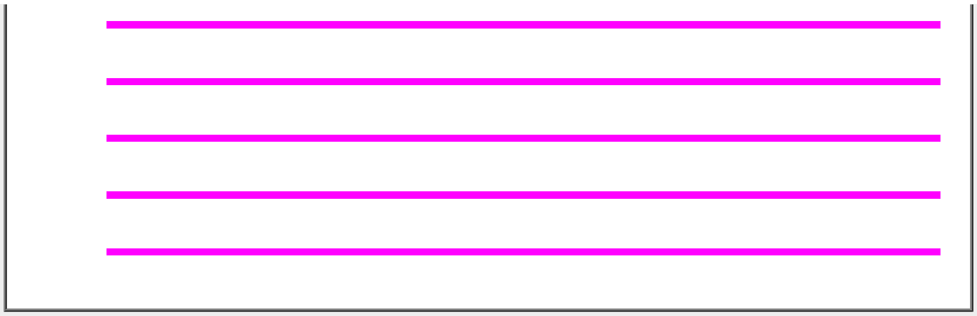
Show Conserved Domains

No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments





Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	thrombospondin 1 [Sus scrofa]	82.1	82.1	100%	3e-16	96%	AAV38110.1
☐	Thrombospondin [Homo sapiens]	82.1	82.1	100%	3e-16	96%	AAA61237.1
☐	thrombospondin [Homo sapiens]	82.1	82.1	100%	3e-16	96%	AAA36741.1
☐	THBS1 protein [Homo sapiens]	82.1	82.1	100%	4e-16	96%	AAH28145.1
☐	thrombospondin [Mus musculus domesticus]	82.1	82.1	100%	4e-16	96%	AAA40431.1
☐	thrombospondin 1 [Rattus norvegicus]	82.1	82.1	100%	4e-16	96%	EDL79850.1
☐	thrombospondin 1, isoform CRA_a [Mus musculus]	82.1	82.1	100%	4e-16	96%	EDL27901.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Eptesicus fuscus]	82.1	82.1	100%	4e-16	96%	XP_008141208.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Orycteropus afer afer]	82.1	82.1	100%	4e-16	96%	XP_007938654.1
☐	unnamed protein product [Homo sapiens]	82.1	82.1	100%	4e-16	96%	BAG65509.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Leptonychotes weddellii]	82.1	82.1	100%	4e-16	96%	XP_006742087.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Pantholops hodgsonii]	82.1	82.1	100%	4e-16	96%	XP_005978527.1
☐	PREDICTED: thrombospondin-1 isoform 2 [Ovis aries]	82.1	82.1	100%	4e-16	96%	XP_004010485.1
☐	PREDICTED: thrombospondin-1 [Macaca mulatta]	82.1	82.1	100%	4e-16	96%	XP_001093770.2
☐	Thrombospondin-1 [Bos mutus]	82.1	82.1	100%	4e-16	96%	ELR61299.1
☐	thrombospondin 1, isoform CRA_b [Mus musculus]	82.1	82.1	100%	4e-16	96%	EDL27902.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Camelus bactria	82.1	82.1	100%	4e-16	96%	XP_010963427.1
☐	PREDICTED: thrombospondin-1 [Equus przewalskii]	82.1	82.1	100%	4e-16	96%	XP_008527173.1
☐	PREDICTED: thrombospondin-1 [Camelus dromedarius]	82.1	82.1	100%	4e-16	96%	XP_010987639.1
☐	PREDICTED: thrombospondin-1 [Bos mutus]	82.1	82.1	100%	4e-16	96%	XP_005889010.1
☐	PREDICTED: thrombospondin-1 [Myotis davidii]	82.1	82.1	100%	4e-16	96%	XP_006778160.1
☐	PREDICTED: thrombospondin-1 [Sorex araneus]	82.1	82.1	100%	4e-16	96%	XP_004609618.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Ursus maritimus	82.1	82.1	100%	4e-16	96%	XP_008700482.1
☐	hypothetical protein PANDA_001089 [Ailuropoda melanoleuca]	82.1	82.1	100%	4e-16	96%	EFB13827.1
☐	PREDICTED: thrombospondin-1 [Ochotona princeps]	82.1	82.1	100%	4e-16	96%	XP_004578240.1
☐	Thrombospondin-1 [Macaca fascicularis]	82.1	82.1	100%	4e-16	96%	EHH62970.1
☐	PREDICTED: thrombospondin-1 [Loxodonta africana]	82.1	82.1	100%	4e-16	96%	XP_010596632.1
☐	PREDICTED: thrombospondin-1 [Galeopterus variegatus]	82.1	82.1	100%	4e-16	96%	XP_008564332.1
☐	PREDICTED: thrombospondin-1 isoform X4 [Cricetulus griseus]	82.1	82.1	100%	4e-16	96%	XP_007627125.1

☐	PREDICTED: thrombospondin-1 [Bison bison bison]	82.1	82.1	100%	4e-16	96%	XP_010846231.1
☐	PREDICTED: thrombospondin-1 [Rhinopithecus roxellana]	82.1	82.1	100%	4e-16	96%	XP_010358095.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Eptesicus fuscus]	82.1	82.1	100%	4e-16	96%	XP_008141207.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Tarsius syrichta]	82.1	82.1	100%	4e-16	96%	XP_008051911.1
☐	PREDICTED: thrombospondin-1 [Chlorocebus sabaeus]	82.1	82.1	100%	4e-16	96%	XP_008015274.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Orycteropus afer afer]	82.1	82.1	100%	4e-16	96%	XP_007938653.1
☐	PREDICTED: thrombospondin-1 [Callithrix jacchus]	82.1	82.1	100%	4e-16	96%	XP_002753603.1
☐	thrombospondin 1 precursor [Sus scrofa]	82.1	82.1	100%	4e-16	96%	NP_001231465.1
☐	thrombospondin 1 [Mus musculus]	82.1	82.1	100%	4e-16	96%	AAA53063.1
☐	PREDICTED: thrombospondin-1 isoform X3 [Cricetulus griseus]	82.1	82.1	100%	4e-16	96%	XP_007627124.1
☐	PREDICTED: thrombospondin-1 [Lipotes vexillifer]	82.1	82.1	100%	4e-16	96%	XP_007460252.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Balaenoptera acutorostrata scan	82.1	82.1	100%	4e-16	96%	XP_007180483.1
☐	PREDICTED: thrombospondin-1 [Physeter catodon]	82.1	82.1	100%	4e-16	96%	XP_007103269.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Panthera tigris a	82.1	82.1	100%	4e-16	96%	XP_007081705.1
☐	PREDICTED: thrombospondin-1 [Pteropus alecto]	82.1	82.1	100%	4e-16	96%	XP_006920568.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Leptonychotes weddellii]	82.1	82.1	100%	4e-16	96%	XP_006742086.1
☐	unnamed protein product [Homo sapiens]	82.1	82.1	100%	4e-16	96%	CAA28370.1
☐	PREDICTED: thrombospondin-1 [Vicugna pacos]	82.1	82.1	100%	4e-16	96%	XP_006201694.1
☐	PREDICTED: thrombospondin-1 [Camelus ferus]	82.1	82.1	100%	4e-16	96%	XP_006176662.1
☐	PREDICTED: thrombospondin-1 [Myotis lucifugus]	82.1	82.1	100%	4e-16	96%	XP_006087569.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Pantholops hodgsonii]	82.1	82.1	100%	4e-16	96%	XP_005978526.1
☐	PREDICTED: thrombospondin-1 [Myotis brandtii]	82.1	82.1	100%	4e-16	96%	XP_005860295.1
☐	PREDICTED: thrombospondin-1 [Macaca fascicularis]	82.1	82.1	100%	4e-16	96%	XP_005559204.1
☐	PREDICTED: thrombospondin-1 [Ictidomys tridecemlineatus]	82.1	82.1	100%	4e-16	96%	XP_005316445.1
☐	PREDICTED: thrombospondin-1 [Mustela putorius furo]	82.1	82.1	100%	4e-16	96%	XP_004751131.1
☐	PREDICTED: thrombospondin-1 [Dasypus novemcinctus]	82.1	82.1	100%	4e-16	96%	XP_004481433.1
☐	PREDICTED: thrombospondin-1 [Ceratotherium simum simum]	82.1	82.1	100%	4e-16	96%	XP_004421456.1
☐	PREDICTED: thrombospondin-1 [Odobenus rosmarus divergens]	82.1	82.1	100%	4e-16	96%	XP_004400502.1
☐	PREDICTED: thrombospondin-1 [Orcinus orca]	82.1	82.1	100%	4e-16	96%	XP_004274061.1
☐	PREDICTED: thrombospondin-1 [Gorilla gorilla gorilla]	82.1	82.1	100%	4e-16	96%	XP_004056005.1
☐	PREDICTED: thrombospondin-1 isoform 1 [Ovis aries]	82.1	82.1	100%	4e-16	96%	XP_004010484.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Mus musculus]	82.1	82.1	100%	4e-16	96%	XP_006499215.1
☐	RecName: Full=Thrombospondin-1; Flags: Precursor [Mus musculus]	82.1	82.1	100%	4e-16	96%	P35441.1
☐	precursor polypeptide (AA -31 to 1139) [Homo sapiens]	82.1	82.1	100%	4e-16	96%	CAA32889.1
☐	thrombospondin-1 precursor [Bos taurus]	82.1	82.1	100%	4e-16	96%	NP_776621.1
☐	PREDICTED: thrombospondin-1 [Felis catus]	82.1	82.1	100%	4e-16	96%	XP_003987333.1
☐	PREDICTED: thrombospondin-1 [Saimiri boliviensis boliviensis]	82.1	82.1	100%	4e-16	96%	XP_003935780.1
☐	PREDICTED: thrombospondin-1 [Papio anubis]	82.1	82.1	100%	4e-16	96%	XP_003900802.1
☐	PREDICTED: thrombospondin-1 [Pan paniscus]	82.1	82.1	100%	4e-16	96%	XP_003826603.1
☐	PREDICTED: thrombospondin-1 [Otolemur garnettii]	82.1	82.1	100%	4e-16	96%	XP_003791750.1
☐	PREDICTED: thrombospondin-1 [Canis lupus familiaris]	82.1	82.1	100%	4e-16	96%	XP_544610.3
☐	PREDICTED: thrombospondin-1 [Pan troglodytes]	82.1	82.1	100%	4e-16	96%	XP_510294.3
☐	PREDICTED: thrombospondin-1 isoform 1 [Nomascus leucogenys]	82.1	82.1	100%	4e-16	96%	XP_003266759.1
☐	PREDICTED: thrombospondin-1-like [Ailuropoda melanoleuca]	82.1	82.1	100%	4e-16	96%	XP_002913278.1
☐	PREDICTED: thrombospondin-1 [Pongo abelii]	82.1	82.1	100%	4e-16	96%	XP_002825327.1

☐	TPA: thrombospondin 1 precursor [Bos taurus]	82.1	82.1	100%	4e-16	96%	DAA25420.1
☐	thrombospondin-1 precursor [synthetic construct]	82.1	82.1	100%	4e-16	96%	BAG10999.1
☐	unnamed protein product [Homo sapiens]	82.1	82.1	100%	4e-16	96%	BAF84328.1
☐	PREDICTED: thrombospondin-1 [Equus caballus]	82.1	82.1	100%	4e-16	96%	XP_001503649.1
☐	thrombospondin-1 precursor [Homo sapiens]	82.1	82.1	100%	4e-16	96%	NP_003237.2
☐	thrombospondin-1 precursor [Rattus norvegicus]	82.1	82.1	100%	4e-16	96%	NP_001013080.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Bos taurus]	82.1	82.1	100%	4e-16	96%	XP_010807460.1
☐	PREDICTED: thrombospondin-1 [Fukomys damarensis]	82.1	82.1	100%	4e-16	96%	XP_010622953.1
☐	PREDICTED: thrombospondin-1 [Nannospalax galili]	82.1	82.1	100%	4e-16	96%	XP_008823512.1
☐	PREDICTED: thrombospondin-1-like [Oryctolagus cuniculus]	82.1	82.1	100%	4e-16	96%	XP_008250683.1
☐	PREDICTED: thrombospondin-1 [Oryctolagus cuniculus]	82.1	82.1	100%	4e-16	96%	XP_002717845.1
☐	thrombospondin-1 precursor [Mus musculus]	82.1	82.1	100%	4e-16	96%	NP_035710.2
☐	PREDICTED: thrombospondin-1 [Erinaceus europaeus]	82.1	82.1	100%	4e-16	96%	XP_007528982.1
☐	PREDICTED: thrombospondin-1 [Elephantulus edwardii]	82.1	82.1	100%	4e-16	96%	XP_006883092.1
☐	PREDICTED: thrombospondin-1 [Microtus ochrogaster]	82.1	82.1	100%	4e-16	96%	XP_005364295.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Heterocephalus glaber]	82.1	82.1	100%	4e-16	96%	XP_004896133.1
☐	PREDICTED: thrombospondin-1 [Octodon degus]	82.1	82.1	100%	4e-16	96%	XP_004623473.1
☐	PREDICTED: thrombospondin-1 [Jaculus jaculus]	82.1	82.1	100%	4e-16	96%	XP_004660826.1
☐	Thrombospondin 1 [Mus musculus]	82.1	82.1	100%	4e-16	96%	AAH42422.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Peromyscus ma	82.1	82.1	100%	4e-16	96%	XP_006979294.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Tupaia chinensis	82.1	82.1	100%	4e-16	96%	XP_006158770.1
☐	PREDICTED: thrombospondin-1 [Mesocricetus auratus]	82.1	82.1	100%	4e-16	96%	XP_005064576.1
☐	Thrombospondin-1 [Tupaia chinensis]	82.1	82.1	100%	4e-16	96%	ELW48182.1
☐	PREDICTED: thrombospondin-1 isoform X3 [Mustela putorius furo]	82.1	82.1	100%	4e-16	96%	XP_004796564.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Tarsius syrichta]	82.1	82.1	100%	4e-16	96%	XP_008051910.1
☐	Thrombospondin-1 [Pteropus alecto]	82.1	82.1	100%	4e-16	96%	ELK05556.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

thrombospondin 1 [Sus scrofa]

Sequence ID: gb|AAV38110.1| **Length:** 249 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 141 to 164 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.1 bits(186)	3e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    KKVSCPIMPCSDATVPDGECCPRC  24
            KKVSCPIMPCS+ATVPDGECCPRC
Sbjct  141  KKVSCPIMPCSNATVPDGECCPRC  164
```

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Thrombospondin, partial [Homo sapiens]

Sequence ID: gb|AAA61237.1| **Length:** 376 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 349 to 372 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.1 bits(186)	3e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    KKVSCPIMPCSDATVPDGECCPRC  24
            KKVSCPIMPCS+ATVPDGECCPRC
Sbjct  349  KKVSCPIMPCSNATVPDGECCPRC  372
```

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thrombospondin, partial [Homo sapiens]

Sequence ID: gb|AAA36741.1| **Length:** 397 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 349 to 372 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.1 bits(186)	3e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    KKVSCPIMPCSDATVPDGECCPRC  24
            KKVSCPIMPCS+ATVPDGECCPRC
Sbjct  349  KKVSCPIMPCSNATVPDGECCPRC  372
```

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THBS1 protein, partial [Homo sapiens]

Sequence ID: gb|AAH28145.1| **Length:** 401 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 349 to 372 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.1 bits(186)	4e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    KKVSCPIMPCSDATVPDGECCPRC  24
            KKVSCPIMPCS+ATVPDGECCPRC
Sbjct  349  KKVSCPIMPCSNATVPDGECCPRC  372
```

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thrombospondin, partial [Mus musculus domesticus]

Sequence ID: gb|AAA40431.1| **Length:** 490 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 349 to 372 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
82.1 bits(186)	4e-16	23/24(96%)	24/24(100%)	0/24(0%)

```
Query  1    KKVSCPIMPCSDATVPDGECCPRC  24
            KKVSCPIMPCS+ATVPDGECCPRC
Sbjct  349  KKVSCPIMPCSNATVPDGECCPRC  372
```

Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

How to read this page Blast report description

THBS1_KKVSCPIMPCSNATVPDGECCPRC_NonMod

RID BE8AGHTS015 (Expires on 01-16 09:09 am)

Query ID	lcl|7223	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	24		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

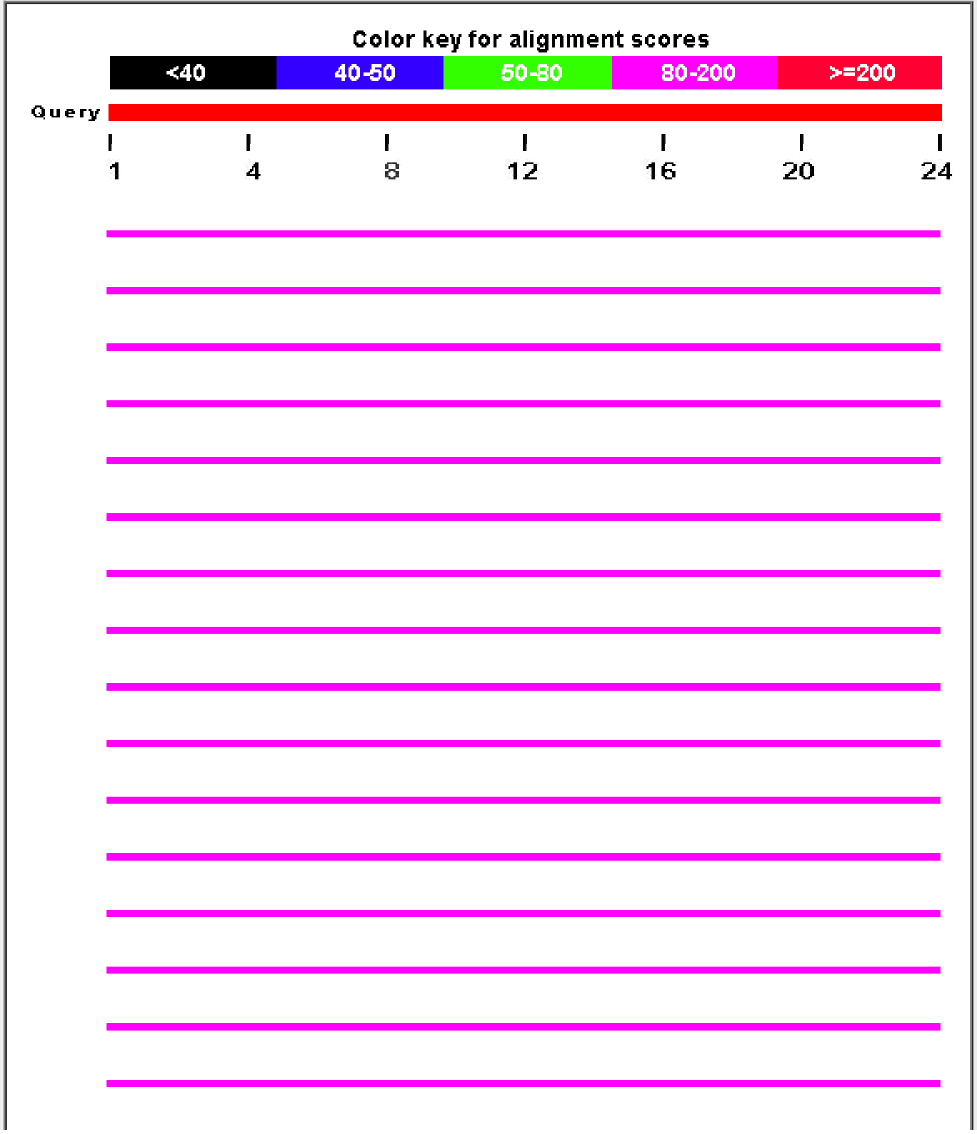
Graphic Summary

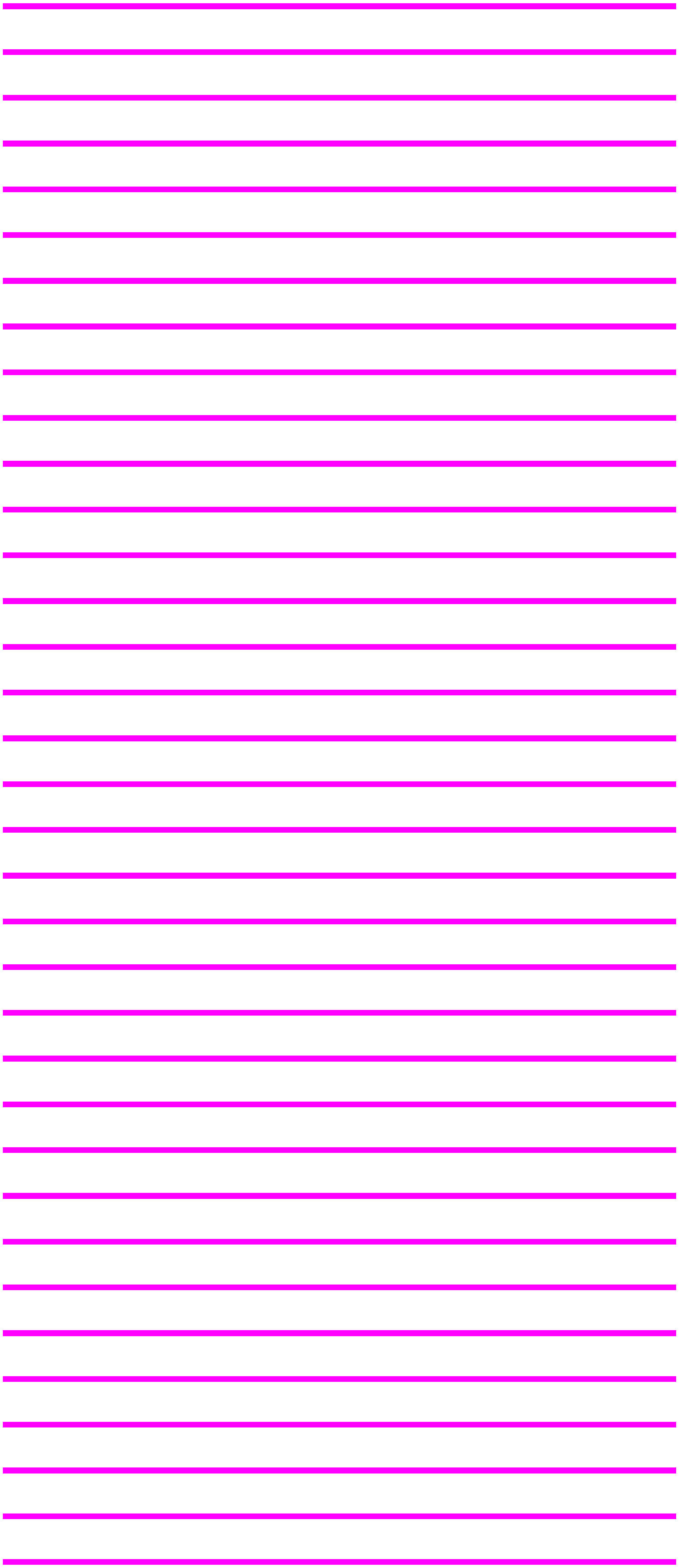
Show Conserved Domains

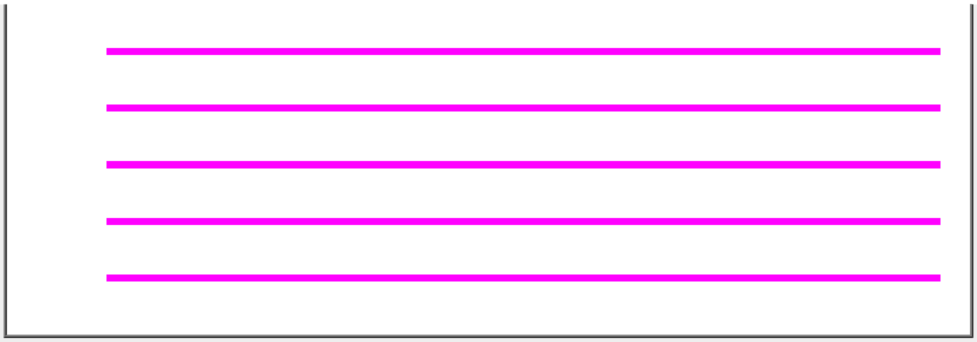
No putative conserved domains have been detected

Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







⊟ Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	thrombospondin 1 [Sus scrofa]	84.6	84.6	100%	4e-17	100%	gi|54694859|AAV38110.1
☐	Thrombospondin [Homo sapiens]	84.6	84.6	100%	5e-17	100%	gi|553801|AAA61237.1
☐	thrombospondin [Homo sapiens]	84.6	84.6	100%	5e-17	100%	gi|538354|AAA36741.1
☐	THBS1 protein [Homo sapiens]	84.6	84.6	100%	5e-17	100%	gi|118600432|AAH28145.1
☐	thrombospondin [Mus musculus domesticus]	84.6	84.6	100%	5e-17	100%	gi|554390|AAA40431.1
☐	thrombospondin 1 [Rattus norvegicus]	84.6	84.6	100%	5e-17	100%	gi|149022956|EDL79850.1
☐	thrombospondin 1, isoform CRA_a [Mus musculus]	84.6	84.6	100%	5e-17	100%	gi|148695954|EDL27901.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Eptesicus fuscus]	84.6	84.6	100%	5e-17	100%	gi|641704796|XP_008141208.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Orycteropus afer afer]	84.6	84.6	100%	5e-17	100%	gi|634847136|XP_007938654.1
☐	unnamed protein product [Homo sapiens]	84.6	84.6	100%	5e-17	100%	gi|194388250|BAG65509.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Leptonychotes wedde	84.6	84.6	100%	5e-17	100%	gi|585180878|XP_006742087.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Pantholops hodgsonii]	84.6	84.6	100%	5e-17	100%	gi|556766553|XP_005978527.1
☐	PREDICTED: thrombospondin-1 isoform 2 [Ovis aries]	84.6	84.6	100%	5e-17	100%	gi|426232960|XP_004010485.1
☐	PREDICTED: thrombospondin-1 [Macaca mulatta]	84.6	84.6	100%	5e-17	100%	gi|297296130|XP_001093770.2
☐	Thrombospondin-1 [Bos mutus]	84.6	84.6	100%	5e-17	100%	gi|440911658|ELR61299.1
☐	thrombospondin 1, isoform CRA_b [Mus musculus]	84.6	84.6	100%	5e-17	100%	gi|148695955|EDL27902.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Came	84.6	84.6	100%	5e-17	100%	gi|743738078|XP_010963427.1
☐	PREDICTED: thrombospondin-1 [Equus przewalskii]	84.6	84.6	100%	5e-17	100%	gi|664739742|XP_008527173.1
☐	PREDICTED: thrombospondin-1 [Camelus dromedarius]	84.6	84.6	100%	5e-17	100%	gi|744592369|XP_010987639.1
☐	PREDICTED: thrombospondin-1 [Bos mutus]	84.6	84.6	100%	5e-17	100%	gi|555953675|XP_005889010.1
☐	PREDICTED: thrombospondin-1 [Myotis davidii]	84.6	84.6	100%	5e-17	100%	gi|584039099|XP_006778160.1
☐	PREDICTED: thrombospondin-1 [Sorex araneus]	84.6	84.6	100%	5e-17	100%	gi|505828620|XP_004609618.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Ursus	84.6	84.6	100%	5e-17	100%	gi|671019315|XP_008700482.1
☐	hypothetical protein PANDA_001089 [Ailuropoda melanoleuca]	84.6	84.6	100%	5e-17	100%	gi|281338243|EFB13827.1
☐	PREDICTED: thrombospondin-1 [Ochotona princeps]	84.6	84.6	100%	5e-17	100%	gi|504130905|XP_004578240.1
☐	Thrombospondin-1 [Macaca fascicularis]	84.6	84.6	100%	5e-17	100%	gi|355777934|EHH62970.1
☐	PREDICTED: thrombospondin-1 [Loxodonta africana]	84.6	84.6	100%	5e-17	100%	gi|731505698|XP_010596632.1
☐	PREDICTED: thrombospondin-1 [Galeopterus variegatus]	84.6	84.6	100%	5e-17	100%	gi|667251967|XP_008564332.1
☐							

	PREDICTED: thrombospondin-1 isoform X4 [Cricetulus griseus]	84.6	84.6	100%	5e-17	100%	gi|625271143|XP_007627125.1
☐	PREDICTED: thrombospondin-1 [Bison bison bison]	84.6	84.6	100%	5e-17	100%	gi|742157428|XP_010846231.1
☐	PREDICTED: thrombospondin-1 [Rhinopithecus roxellana]	84.6	84.6	100%	5e-17	100%	gi|724808372|XP_010358095.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Eptesicus fuscus]	84.6	84.6	100%	5e-17	100%	gi|641704794|XP_008141207.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Tarsius syrichta]	84.6	84.6	100%	5e-17	100%	gi|640792006|XP_008051911.1
☐	PREDICTED: thrombospondin-1 [Chlorocebus sabaeus]	84.6	84.6	100%	5e-17	100%	gi|635136734|XP_008015274.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Orycteropus afer afer]	84.6	84.6	100%	5e-17	100%	gi|634847133|XP_007938653.1
☐	PREDICTED: thrombospondin-1 [Callithrix jacchus]	84.6	84.6	100%	5e-17	100%	gi|296214225|XP_002753603.1
☐	thrombospondin 1 precursor [Sus scrofa]	84.6	84.6	100%	5e-17	100%	gi|347300340|NP_001231465.1
☐	thrombospondin 1 [Mus musculus]	84.6	84.6	100%	5e-17	100%	gi|567240|AAA53063.1
☐	PREDICTED: thrombospondin-1 isoform X3 [Cricetulus griseus]	84.6	84.6	100%	5e-17	100%	gi|625271141|XP_007627124.1
☐	PREDICTED: thrombospondin-1 [Lipotes vexillifer]	84.6	84.6	100%	5e-17	100%	gi|602696403|XP_007460252.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Balaenoptera acutoros	84.6	84.6	100%	5e-17	100%	gi|594664699|XP_007180483.1
☐	PREDICTED: thrombospondin-1 [Physeter catodon]	84.6	84.6	100%	5e-17	100%	gi|593713526|XP_007103269.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Panth	84.6	84.6	100%	5e-17	100%	gi|591310271|XP_007081705.1
☐	PREDICTED: thrombospondin-1 [Pteropus alecto]	84.6	84.6	100%	5e-17	100%	gi|586531321|XP_006920568.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Leptonychotes wedde	84.6	84.6	100%	5e-17	100%	gi|585180876|XP_006742086.1
☐	unnamed protein product [Homo sapiens]	84.6	84.6	100%	5e-17	100%	gi|37138|CAA28370.1
☐	PREDICTED: thrombospondin-1 [Vicugna pacos]	84.6	84.6	100%	5e-17	100%	gi|560958468|XP_006201694.1
☐	PREDICTED: thrombospondin-1 [Camelus ferus]	84.6	84.6	100%	5e-17	100%	gi|560900504|XP_006176662.1
☐	PREDICTED: thrombospondin-1 [Myotis lucifugus]	84.6	84.6	100%	5e-17	100%	gi|558119542|XP_006087569.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Pantholops hodgsonii]	84.6	84.6	100%	5e-17	100%	gi|556766551|XP_005978526.1
☐	PREDICTED: thrombospondin-1 [Myotis brandtii]	84.6	84.6	100%	5e-17	100%	gi|554531033|XP_005860295.1
☐	PREDICTED: thrombospondin-1 [Macaca fascicularis]	84.6	84.6	100%	5e-17	100%	gi|544442455|XP_005559204.1
☐	PREDICTED: thrombospondin-1 [Ictidomys tridecemlineatus]	84.6	84.6	100%	5e-17	100%	gi|532061120|XP_005316445.1
☐	PREDICTED: thrombospondin-1 [Mustela putorius furo]	84.6	84.6	100%	5e-17	100%	gi|511854421|XP_004751131.1
☐	PREDICTED: thrombospondin-1 [Dasypus novemcinctus]	84.6	84.6	100%	5e-17	100%	gi|488592374|XP_004481433.1
☐	PREDICTED: thrombospondin-1 [Ceratotherium simum simum]	84.6	84.6	100%	5e-17	100%	gi|478494216|XP_004421456.1
☐	PREDICTED: thrombospondin-1 [Odobenus rosmarus divergens]	84.6	84.6	100%	5e-17	100%	gi|472361819|XP_004400502.1
☐	PREDICTED: thrombospondin-1 [Orcinus orca]	84.6	84.6	100%	5e-17	100%	gi|466029792|XP_004274061.1
☐	PREDICTED: thrombospondin-1 [Gorilla gorilla gorilla]	84.6	84.6	100%	5e-17	100%	gi|426378604|XP_004056005.1
☐	PREDICTED: thrombospondin-1 isoform 1 [Ovis aries]	84.6	84.6	100%	5e-17	100%	gi|426232958|XP_004010484.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Mus musculus]	84.6	84.6	100%	5e-17	100%	gi|568916267|XP_006499215.1
☐	RecName: Full=Thrombospondin-1; Flags: Precursor [Mus musculu	84.6	84.6	100%	5e-17	100%	gi|549134|P35441.1
☐	precursor polypeptide (AA -31 to 1139) [Homo sapiens]	84.6	84.6	100%	5e-17	100%	gi|37465|CAA32889.1
☐	thrombospondin-1 precursor [Bos taurus]	84.6	84.6	100%	5e-17	100%	gi|41386685|NP_776621.1
☐	PREDICTED: thrombospondin-1 [Felis catus]	84.6	84.6	100%	5e-17	100%	gi|410961529|XP_003987333.1
☐	PREDICTED: thrombospondin-1 [Saimiri boliviensis boliviensis]	84.6	84.6	100%	5e-17	100%	gi|403289260|XP_003935780.1
☐	PREDICTED: thrombospondin-1 [Papio anubis]	84.6	84.6	100%	5e-17	100%	gi|402873929|XP_003900802.1
☐	PREDICTED: thrombospondin-1 [Pan paniscus]	84.6	84.6	100%	5e-17	100%	gi|397512548|XP_003826603.1
☐	PREDICTED: thrombospondin-1 [Otolemur garnettii]	84.6	84.6	100%	5e-17	100%	gi|395837664|XP_003791750.1
☐	PREDICTED: thrombospondin-1 [Canis lupus familiaris]	84.6	84.6	100%	5e-17	100%	gi|345794639|XP_544610.3
☐	PREDICTED: thrombospondin-1 [Pan troglodytes]	84.6	84.6	100%	5e-17	100%	gi|332843483|XP_510294.3
☐	PREDICTED: thrombospondin-1 isoform 1 [Nomascus leucogenys]	84.6	84.6	100%	5e-17	100%	gi|332235127|XP_003266759.1
☐	PREDICTED: thrombospondin-1-like [Ailuropoda melanoleuca]	84.6	84.6	100%	5e-17	100%	gi|301754930|XP_002913278.1

☐	PREDICTED: thrombospondin-1 [Pongo abelii]	84.6	84.6	100%	5e-17	100%	gi|297696281|XP_002825327.1
☐	TPA: thrombospondin 1 precursor [Bos taurus]	84.6	84.6	100%	5e-17	100%	gi|296483305|DAA25420.1
☐	thrombospondin-1 precursor [synthetic construct]	84.6	84.6	100%	5e-17	100%	gi|168278042|BAG10999.1
☐	unnamed protein product [Homo sapiens]	84.6	84.6	100%	5e-17	100%	gi|158256710|BAF84328.1
☐	PREDICTED: thrombospondin-1 [Equus caballus]	84.6	84.6	100%	5e-17	100%	gi|149692076|XP_001503649.1
☐	thrombospondin-1 precursor [Homo sapiens]	84.6	84.6	100%	5e-17	100%	gi|40317626|NP_003237.2
☐	thrombospondin-1 precursor [Rattus norvegicus]	84.6	84.6	100%	5e-17	100%	gi|61556835|NP_001013080.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Bos taurus]	84.6	84.6	100%	5e-17	100%	gi|741940058|XP_010807460.1
☐	PREDICTED: thrombospondin-1 [Fukomys damarensis]	84.6	84.6	100%	5e-17	100%	gi|731217228|XP_010622953.1
☐	PREDICTED: thrombospondin-1 [Nannospalax galili]	84.6	84.6	100%	5e-17	100%	gi|674104645|XP_008823512.1
☐	PREDICTED: thrombospondin-1-like [Oryctolagus cuniculus]	84.6	84.6	100%	5e-17	100%	gi|655897852|XP_008250683.1
☐	PREDICTED: thrombospondin-1 [Oryctolagus cuniculus]	84.6	84.6	100%	5e-17	100%	gi|291403258|XP_002717845.1
☐	thrombospondin-1 precursor [Mus musculus]	84.6	84.6	100%	5e-17	100%	gi|47059073|NP_035710.2
☐	PREDICTED: thrombospondin-1 [Erinaceus europaeus]	84.6	84.6	100%	5e-17	100%	gi|617628577|XP_007528982.1
☐	PREDICTED: thrombospondin-1 [Elephantulus edwardii]	84.6	84.6	100%	5e-17	100%	gi|585648801|XP_006883092.1
☐	PREDICTED: thrombospondin-1 [Microtus ochrogaster]	84.6	84.6	100%	5e-17	100%	gi|532042932|XP_005364295.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Heterocephalus glabe	84.6	84.6	100%	5e-17	100%	gi|512885023|XP_004896133.1
☐	PREDICTED: thrombospondin-1 [Octodon degus]	84.6	84.6	100%	5e-17	100%	gi|507615991|XP_004623473.1
☐	PREDICTED: thrombospondin-1 [Jaculus jaculus]	84.6	84.6	100%	5e-17	100%	gi|507554090|XP_004660826.1
☐	Thrombospondin 1 [Mus musculus]	84.6	84.6	100%	5e-17	100%	gi|27502731|AAH42422.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Perom	84.6	84.6	100%	5e-17	100%	gi|589933009|XP_006979294.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Tupaia	84.6	84.6	100%	5e-17	100%	gi|562860786|XP_006158770.1
☐	PREDICTED: thrombospondin-1 [Mesocricetus auratus]	84.6	84.6	100%	5e-17	100%	gi|524920590|XP_005064576.1
☐	Thrombospondin-1 [Tupaia chinensis]	84.6	84.6	100%	5e-17	100%	gi|444706864|ELW48182.1
☐	PREDICTED: thrombospondin-1 isoform X3 [Mustela putorius furo]	84.6	84.6	100%	5e-17	100%	gi|511956507|XP_004796564.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Tarsius syrichta]	84.6	84.6	100%	5e-17	100%	gi|640792004|XP_008051910.1
☐	Thrombospondin-1 [Pteropus alecto]	84.6	84.6	100%	5e-17	100%	gi|431896138|ELK05556.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

thrombospondin 1 [Sus scrofa]

Sequence ID: gi|54694859|gb|AAV38110.1| **Length:** 249 **Number of Matches:** 1

Range 1: 141 to 164 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.6 bits(192)	4e-17	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KKVSCPIMPCSNATVPDGECCPRC  24
            KKVSCPIMPCSNATVPDGECCPRC
Sbjct  141  KKVSCPIMPCSNATVPDGECCPRC  164
```

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

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Thrombospondin, partial [Homo sapiens]

Sequence ID: gi|553801|gb|AAA61237.1| **Length:** 376 **Number of Matches:** 1

Range 1: 349 to 372 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.6 bits(192)	5e-17	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KKVSCPIMPCSNATVPDGECCPRC  24
```

Related Information

Gene - associated gene details

```
                 KKVSCPIMPCSNATVPDGECCPRC
Sbjct  349  KKVSCPIMPCSNATVPDGECCPRC  372
```

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thrombospondin, partial [Homo sapiens]

Sequence ID: gi|538354|gb|AAA36741.1| **Length:** 397 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 349 to 372 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.6 bits(192)	5e-17	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KKVSCPIMPCSNATVPDGECCPRC  24
            KKVSCPIMPCSNATVPDGECCPRC
Sbjct  349  KKVSCPIMPCSNATVPDGECCPRC  372
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

THBS1 protein, partial [Homo sapiens]

Sequence ID: gi|118600432|gb|AAH28145.1| **Length:** 401 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 349 to 372 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.6 bits(192)	5e-17	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KKVSCPIMPCSNATVPDGECCPRC  24
            KKVSCPIMPCSNATVPDGECCPRC
Sbjct  349  KKVSCPIMPCSNATVPDGECCPRC  372
```

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thrombospondin, partial [Mus musculus domesticus]

Sequence ID: gi|554390|gb|AAA40431.1| **Length:** 490 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 349 to 372 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
84.6 bits(192)	5e-17	24/24(100%)	24/24(100%)	0/24(0%)

```
Query  1    KKVSCPIMPCSNATVPDGECCPRC  24
            KKVSCPIMPCSNATVPDGECCPRC
Sbjct  349  KKVSCPIMPCSNATVPDGECCPRC  372
```

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Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download How to read this page Blast report description

THBS1_KVVDSTTGPGEHLRN_Mod

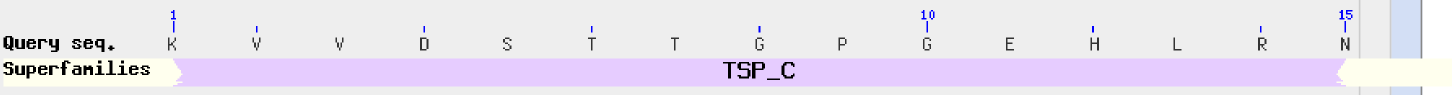
RID	BVM5BJ6801R (Expires on 01-21 10:51 am)		
Query ID	lcl|118520	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	**Program**	BLASTP 2.2.30+ Citation
Query Length	15		

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

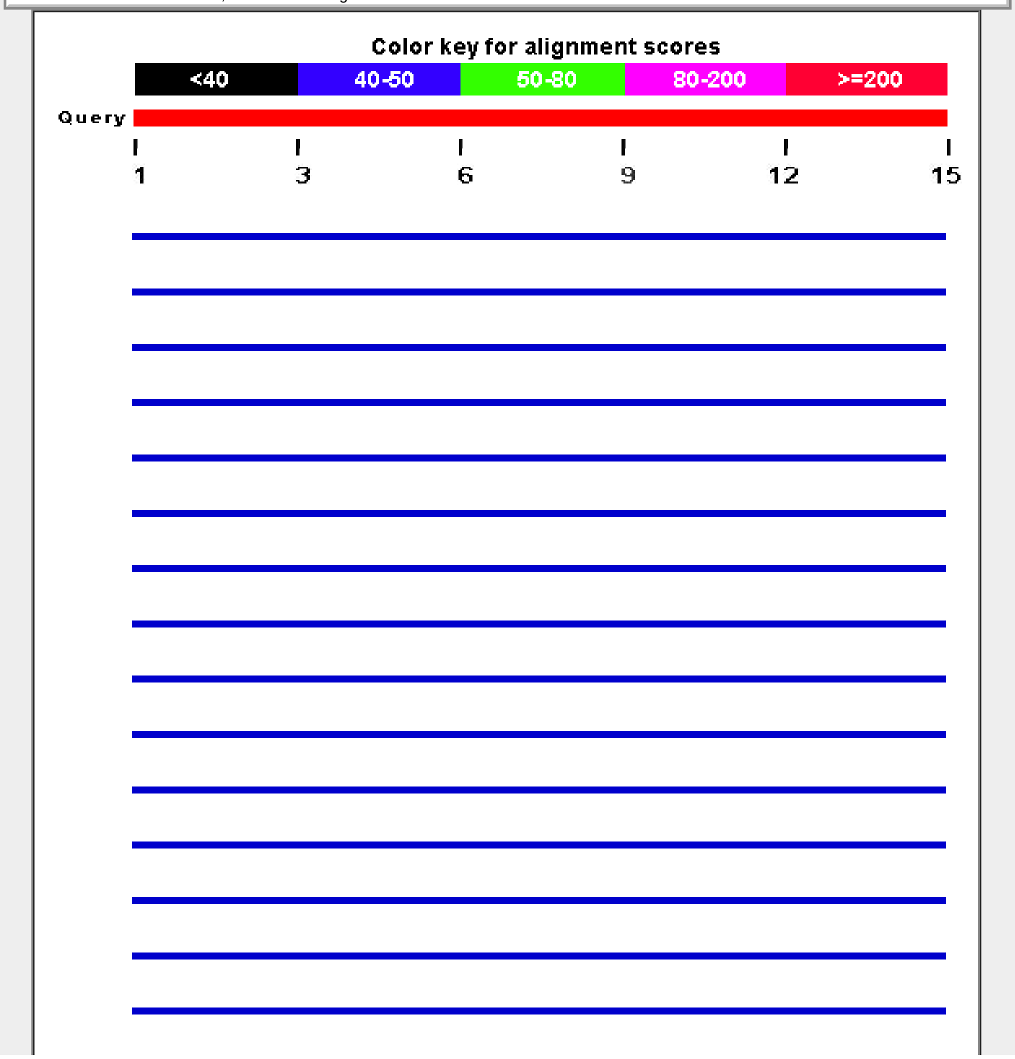
Show Conserved Domains

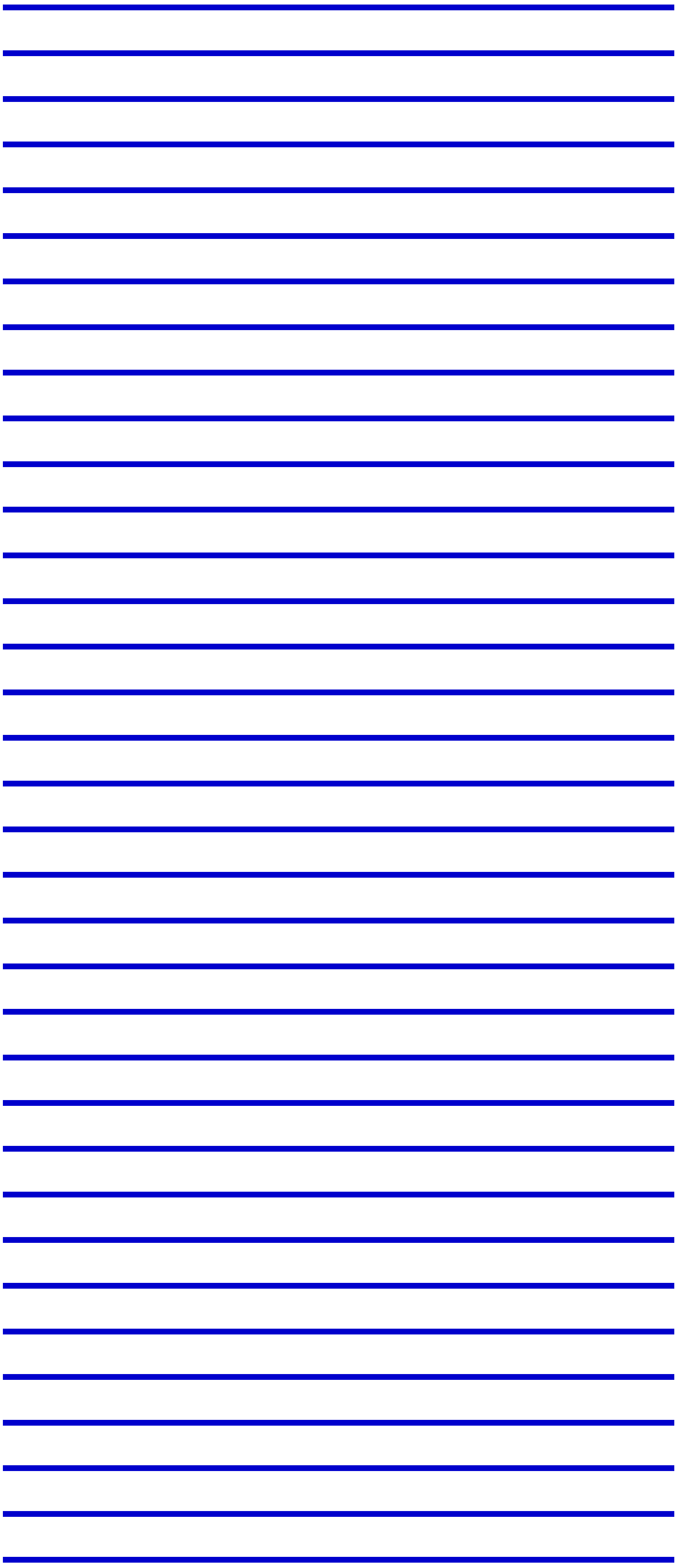
Putative conserved domains have been detected, click on the image below for detailed results.

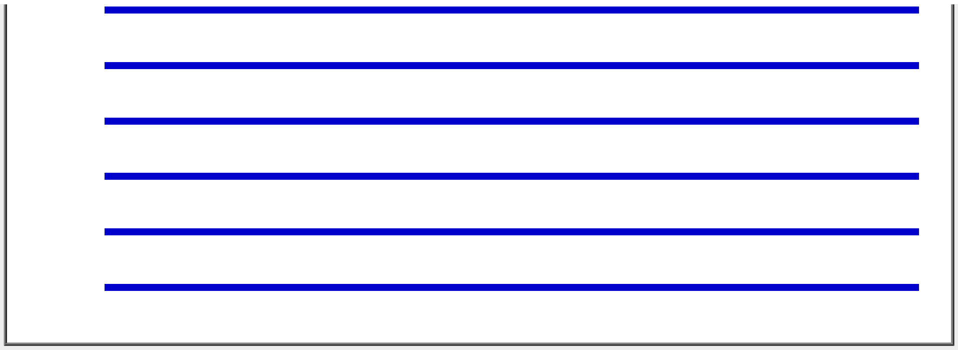


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	thrombospondin [Homo sapiens]	46.9	46.9	100%	8e-05	93%	AAB59366.1
☐	Thrombospondin-1 [Calypte anna]	46.9	46.9	100%	9e-05	93%	KFO95071.1
☐	PREDICTED: thrombospondin-1-like [Taeniopygia guttata]	46.9	46.9	100%	1e-04	93%	XP_002188235.2
☐	unnamed protein product [Mus musculus]	46.9	46.9	100%	1e-04	93%	BAE37804.1
☐	unnamed protein product [Mus musculus]	46.9	46.9	100%	1e-04	93%	BAE37878.1
☐	unnamed protein product [Oncorhynchus mykiss]	46.9	46.9	100%	1e-04	93%	CDQ99562.1
☐	unnamed protein product [Oncorhynchus mykiss]	46.9	46.9	100%	1e-04	93%	CDQ96481.1
☐	thrombospondin [Bos taurus]	46.9	46.9	100%	1e-04	93%	CAA60950.1
☐	Thrombospondin-1 [Cricetulus griseus]	46.9	46.9	100%	1e-04	93%	EGW04306.1
☐	PREDICTED: thrombospondin-1-like [Danio rerio]	46.9	46.9	100%	1e-04	93%	XP_002667003.3
☐	PREDICTED: thrombospondin-1-like [Xiphophorus maculatus]	46.9	46.9	100%	1e-04	93%	XP_005805261.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Latimeria chalumnae]	46.9	46.9	100%	1e-04	93%	XP_005988415.1
☐	PREDICTED: thrombospondin-1-like [Poecilia reticulata]	46.9	46.9	100%	1e-04	93%	XP_008396149.1
☐	PREDICTED: thrombospondin-1 [Ornithorhynchus anatinus]	46.9	46.9	100%	1e-04	93%	XP_007664158.1
☐	thrombospondin 1, isoform CRA_a [Mus musculus]	46.9	46.9	100%	1e-04	93%	EDL27901.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Eptesicus fuscus]	46.9	46.9	100%	1e-04	93%	XP_008141208.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Orycteropus afer afer]	46.9	46.9	100%	1e-04	93%	XP_007938654.1
☐	unnamed protein product [Homo sapiens]	46.9	46.9	100%	1e-04	93%	BAG65509.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Leptonychotes weddellii]	46.9	46.9	100%	1e-04	93%	XP_006742087.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Pantholops hodgsonii]	46.9	46.9	100%	1e-04	93%	XP_005978527.1
☐	PREDICTED: thrombospondin-1 isoform 2 [Ovis aries]	46.9	46.9	100%	1e-04	93%	XP_004010485.1
☐	PREDICTED: thrombospondin-1 [Macaca mulatta]	46.9	46.9	100%	1e-04	93%	XP_001093770.2
☐	PREDICTED: thrombospondin-1-like [Alligator mississippiensis]	46.9	46.9	100%	1e-04	93%	XP_006265214.1
☐	Thrombospondin-1 [Corvus brachyrhynchos]	46.9	46.9	100%	1e-04	93%	KFO63667.1
☐	Thrombospondin-1 [Buceros rhinoceros silvestris]	46.9	46.9	100%	1e-04	93%	KFO88878.1
☐	Thrombospondin-1 [Calypte anna]	46.9	46.9	100%	1e-04	93%	KFO96190.1
☐	Thrombospondin-1 [Nestor notabilis]	46.9	46.9	100%	1e-04	93%	KFQ42080.1
☐	Thrombospondin-1 [Apaloderma vittatum]	46.9	46.9	100%	1e-04	93%	KFP81422.1
☐	Thrombospondin-1 [Charadrius vociferus]	46.9	46.9	100%	1e-04	93%	KGL92027.1

☐	Thrombospondin-1 [Manacus vitellinus]	46.9	46.9	100%	1e-04	93%	KFW75047.1
☐	Thrombospondin-1 [Fulmarus glacialis]	46.9	46.9	100%	1e-04	93%	KFV92396.1
☐	Thrombospondin-1 [Acanthisitta chloris]	46.9	46.9	100%	1e-04	93%	KFP86921.1
☐	Thrombospondin-1 [Podiceps cristatus]	46.9	46.9	100%	1e-04	93%	KFZ68358.1
☐	Thrombospondin-1 [Phalacrocorax carbo]	46.9	46.9	100%	1e-04	93%	KFW95848.1
☐	Thrombospondin-1 [Pygoscelis adeliae]	46.9	46.9	100%	1e-04	93%	KFW65009.1
☐	Thrombospondin-1 [Eurypyga helias]	46.9	46.9	100%	1e-04	93%	KFW04094.1
☐	Thrombospondin-1 [Struthio camelus australis]	46.9	46.9	100%	1e-04	93%	KFV78213.1
☐	Thrombospondin-1 [Gavia stellata]	46.9	46.9	100%	1e-04	93%	KFV55243.1
☐	Thrombospondin-1 [Tyto alba]	46.9	46.9	100%	1e-04	93%	KFV42717.1
☐	Thrombospondin-1 [Tauraco erythrolophus]	46.9	46.9	100%	1e-04	93%	KFU99322.1
☐	Thrombospondin-1 [Pterocles gutturalis]	46.9	46.9	100%	1e-04	93%	KFU96792.1
☐	Thrombospondin-1 [Chaetura pelagica]	46.9	46.9	100%	1e-04	93%	KFU85223.1
☐	Thrombospondin-1 [Nipponia nippon]	46.9	46.9	100%	1e-04	93%	KFR07154.1
☐	Thrombospondin-1 [Opisthocomus hoazin]	46.9	46.9	100%	1e-04	93%	KFR07008.1
☐	Thrombospondin-1 [Pelecanus crispus]	46.9	46.9	100%	1e-04	93%	KFQ61165.1
☐	Thrombospondin-1 [Merops nubicus]	46.9	46.9	100%	1e-04	93%	KFQ17938.1
☐	Thrombospondin-1 [Leptosomus discolor]	46.9	46.9	100%	1e-04	93%	KFQ12753.1
☐	Thrombospondin-1 [Haliaeetus albicilla]	46.9	46.9	100%	1e-04	93%	KFQ05795.1
☐	Thrombospondin-1 [Cariama cristata]	46.9	46.9	100%	1e-04	93%	KFP58732.1
☐	Thrombospondin-1 [Cathartes aura]	46.9	46.9	100%	1e-04	93%	KFP57718.1
☐	Thrombospondin-1 [Colius striatus]	46.9	46.9	100%	1e-04	93%	KFP29490.1
☐	Thrombospondin-1 [Egretta garzetta]	46.9	46.9	100%	1e-04	93%	KFP12089.1
☐	Thrombospondin-1 [Balearica pavonina gibbericeps]	46.9	46.9	100%	1e-04	93%	KFO12753.1
☐	Thrombospondin-1 [Tinamus guttatus]	46.9	46.9	100%	1e-04	93%	KGL85097.1
☐	Thrombospondin-1 [Phaethon lepturus]	46.9	46.9	100%	1e-04	93%	KFQ75928.1
☐	Thrombospondin-1 [Mesitornis unicolor]	46.9	46.9	100%	1e-04	93%	KFQ33396.1
☐	Thrombospondin-1 [Chlamydotis undulata macqueenii]	46.9	46.9	100%	1e-04	93%	KFP35274.1
☐	Thrombospondin-1 [Caprimulgus carolinensis]	46.9	46.9	100%	1e-04	93%	KFZ56796.1
☐	Thrombospondin-1 [Cuculus canorus]	46.9	46.9	100%	1e-04	93%	KFO70201.1
☐	Thrombospondin-1 [Aptenodytes forsteri]	46.9	46.9	100%	1e-04	93%	KFM10485.1
☐	Thrombospondin-1 [Anas platyrhynchos]	46.9	46.9	100%	1e-04	93%	EOB08499.1
☐	Thrombospondin-1 [Bos mutus]	46.9	46.9	100%	1e-04	93%	ELR61299.1
☐	thrombospondin 1, isoform CRA_b [Mus musculus]	46.9	46.9	100%	1e-04	93%	EDL27902.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Camelus bactria	46.9	46.9	100%	1e-04	93%	XP_010963427.1
☐	PREDICTED: thrombospondin-1 [Equus przewalskii]	46.9	46.9	100%	1e-04	93%	XP_008527173.1
☐	PREDICTED: thrombospondin-1 [Acanthisitta chloris]	46.9	46.9	100%	1e-04	93%	XP_009079349.1
☐	PREDICTED: thrombospondin-1 [Corvus brachyrhynchos]	46.9	46.9	100%	1e-04	93%	XP_008637956.1
☐	PREDICTED: thrombospondin-1 [Camelus dromedarius]	46.9	46.9	100%	1e-04	93%	XP_010987639.1
☐	PREDICTED: thrombospondin-1 [Bos mutus]	46.9	46.9	100%	1e-04	93%	XP_005889010.1
☐	Thrombospondin-1 [Chelonia mydas]	46.9	46.9	100%	1e-04	93%	EMP26772.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1-like [Cynoglossus	46.9	46.9	100%	1e-04	93%	XP_008311728.1
☐	PREDICTED: thrombospondin-1 [Echinops telfairi]	46.9	46.9	100%	1e-04	93%	XP_004712753.1
☐	PREDICTED: thrombospondin-1 [Tinamus guttatus]	46.9	46.9	100%	1e-04	93%	XP_010224375.1
☐	PREDICTED: thrombospondin-1 [Chlamydotis undulata macqueenii]	46.9	46.9	100%	1e-04	93%	XP_010113973.1
☐	PREDICTED: thrombospondin-1 [Myotis davidii]	46.9	46.9	100%	1e-04	93%	XP_006778160.1

☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Columba livia]	46.9	46.9	100%	1e-04	93%	XP_005502344.1
☐	PREDICTED: thrombospondin-1 [Sorex araneus]	46.9	46.9	100%	1e-04	93%	XP_004609618.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Ursus maritimus	46.9	46.9	100%	1e-04	93%	XP_008700482.1
☐	PREDICTED: thrombospondin-1 [Callorhinchus milii]	46.9	46.9	100%	1e-04	93%	XP_007886260.1
☐	hypothetical protein PANDA_001089 [Ailuropoda melanoleuca]	46.9	46.9	100%	1e-04	93%	EFB13827.1
☐	PREDICTED: thrombospondin-1-like [Neolamprologus brichardi]	46.9	46.9	100%	1e-04	93%	XP_006792742.1
☐	PREDICTED: thrombospondin-1-like [Haplochromis burtoni]	46.9	46.9	100%	1e-04	93%	XP_005931578.1
☐	PREDICTED: thrombospondin-1-like [Pundamilia nyererei]	46.9	46.9	100%	1e-04	93%	XP_005737355.1
☐	PREDICTED: thrombospondin-1 [Ochotona princeps]	46.9	46.9	100%	1e-04	93%	XP_004578240.1
☐	Thrombospondin-1 [Macaca fascicularis]	46.9	46.9	100%	1e-04	93%	EHH62970.1
☐	thrombospondin-1a precursor [Oreochromis niloticus]	46.9	46.9	100%	1e-04	93%	NP_001266664.1
☐	PREDICTED: thrombospondin-1-like [Larimichthys crocea]	46.9	46.9	100%	1e-04	93%	XP_010748801.1
☐	PREDICTED: thrombospondin-1-like [Larimichthys crocea]	46.9	46.9	100%	1e-04	93%	XP_010738923.1
☐	PREDICTED: thrombospondin-1 [Loxodonta africana]	46.9	46.9	100%	1e-04	93%	XP_010596632.1
☐	PREDICTED: thrombospondin-1 [Caprimulgus carolinensis]	46.9	46.9	100%	1e-04	93%	XP_010164792.1
☐	PREDICTED: thrombospondin-1 [Galeopterus variegatus]	46.9	46.9	100%	1e-04	93%	XP_008564332.1
☐	PREDICTED: thrombospondin-1 [Stegastes partitus]	46.9	46.9	100%	1e-04	93%	XP_008283030.1
☐	PREDICTED: thrombospondin-1 isoform X4 [Cricetulus griseus]	46.9	46.9	100%	1e-04	93%	XP_007627125.1
☐	PREDICTED: thrombospondin-1-like [Takifugu rubripes]	46.9	46.9	100%	1e-04	93%	XP_003971811.1
☐	PREDICTED: thrombospondin-1 [Bison bison bison]	46.9	46.9	100%	1e-04	93%	XP_010846231.1
☐	PREDICTED: thrombospondin-1 [Rhinopithecus roxellana]	46.9	46.9	100%	1e-04	93%	XP_010358095.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Eptesicus fuscus]	46.9	46.9	100%	1e-04	93%	XP_008141207.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Tarsius syrichta]	46.9	46.9	100%	1e-04	93%	XP_008051911.1
☐	PREDICTED: thrombospondin-1 [Chlorocebus sabaeus]	46.9	46.9	100%	1e-04	93%	XP_008015274.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Orycteropus afer afer]	46.9	46.9	100%	1e-04	93%	XP_007938653.1

⊟ Alignments

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thrombospondin, partial [Homo sapiens]

Sequence ID: gb|AAB59366.1| **Length:** 143 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 37 to 51 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	8e-05	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1   KVVDSTTGPGEHLRN  15
           KVV+STTGPGEHLRN
Sbjct  37  KVVNSTTGPGEHLRN  51
```

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Thrombospondin-1, partial [Calypte anna]

Sequence ID: gb|KFO95071.1| **Length:** 172 **Number of Matches:** 1

Related Information

Range 1: 66 to 80 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	9e-05	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1   KVVDSTTGPGEHLRN  15
           KVV+STTGPGEHLRN
Sbjct  66  KVVNSTTGPGEHLRN  80
```

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PREDICTED: thrombospondin-1-like, partial [Taeniopygia guttata]

Sequence ID: ref|XP_002188235.2| **Length:** 245 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 141 to 155 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	1e-04	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    KVVDSTTGPGEHLRN  15
            KVV+STTGPGEHLRN
Sbjct  141  KVVNSTTGPGEHLRN  155
```

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unnamed protein product [Mus musculus]

Sequence ID: dbj|BAE37804.1| **Length:** 259 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 153 to 167 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	1e-04	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    KVVDSTTGPGEHLRN  15
            KVV+STTGPGEHLRN
Sbjct  153  KVVNSTTGPGEHLRN  167
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Mus musculus]

Sequence ID: dbj|BAE37878.1| **Length:** 262 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 156 to 170 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
46.9 bits(103)	1e-04	14/15(93%)	15/15(100%)	0/15(0%)

```
Query  1    KVVDSTTGPGEHLRN  15
            KVV+STTGPGEHLRN
Sbjct  156  KVVNSTTGPGEHLRN  170
```

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NCBI/ BLAST/ blastp suite/ Formatting Results - BVMCU5X601R

Your search parameters were adjusted to search for a short input sequence.

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THBS1_KVVNSTTGPGEHLRN_NonMod

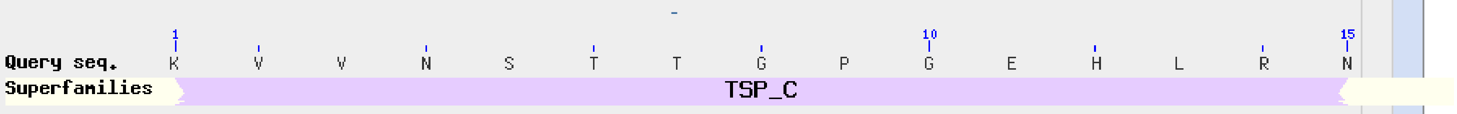
RID	BVMCU5X601R (Expires on 01-21 10:55 am)		
Query ID	lcl|289205	**Database Name**	nr
Description	None	**Description**	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid		
Query Length	15	**Program**	BLASTP 2.2.30+ Citation

Other reports: Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment]

Graphic Summary

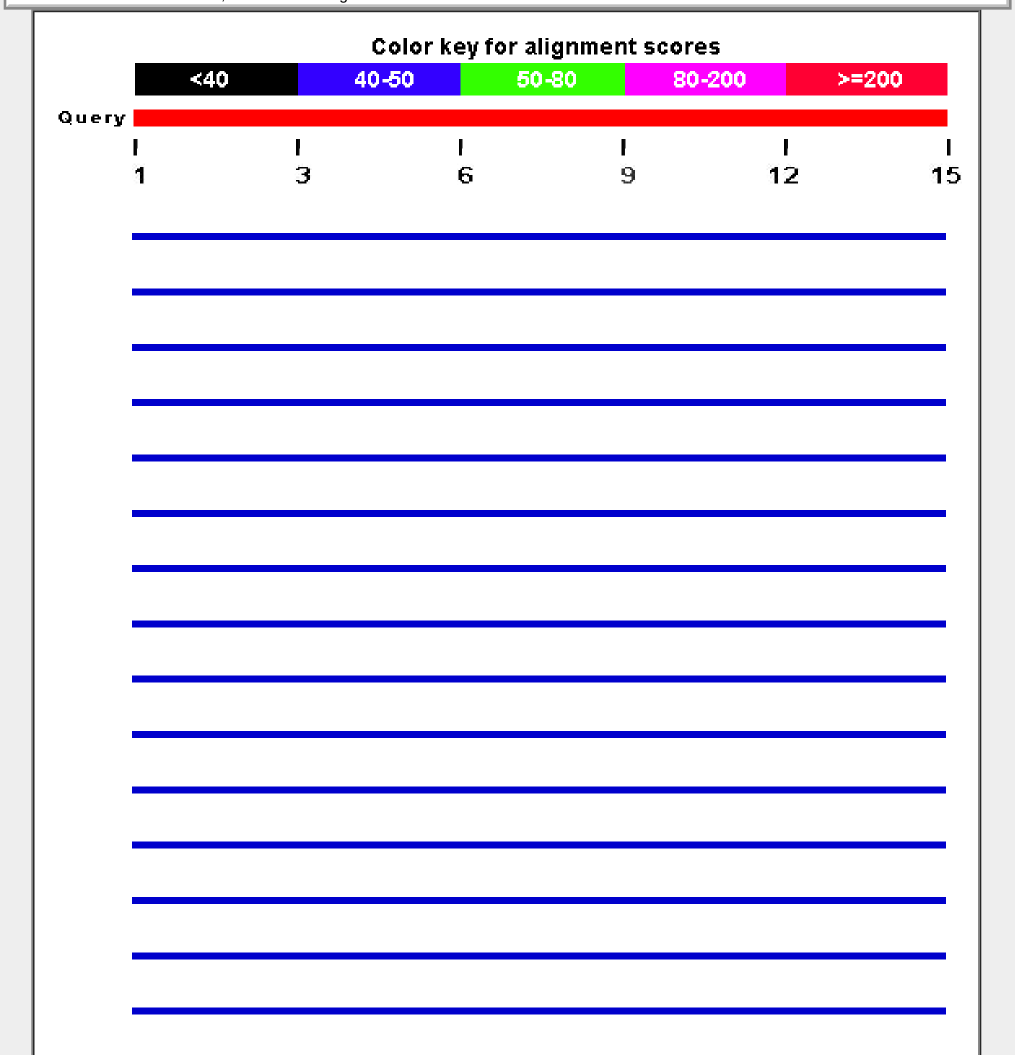
Show Conserved Domains

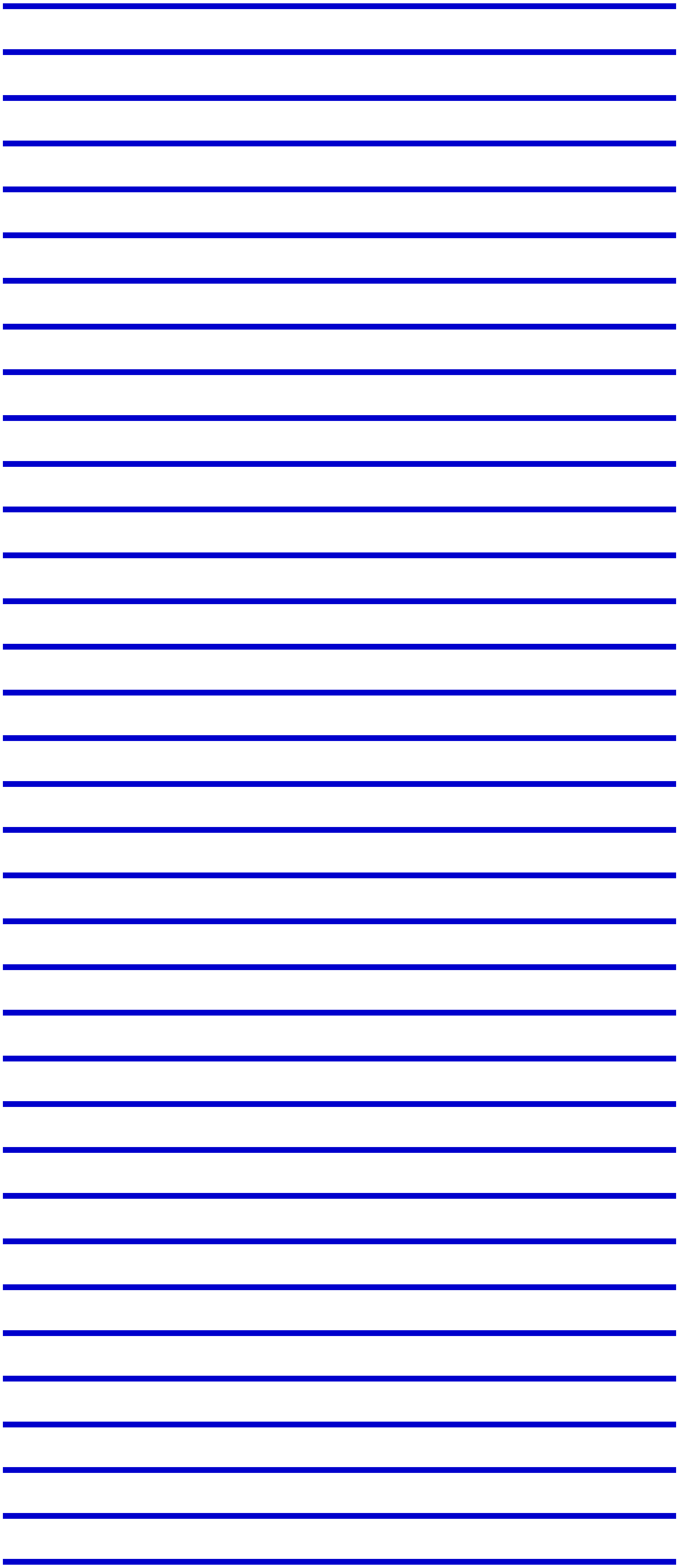
Putative conserved domains have been detected, click on the image below for detailed results.

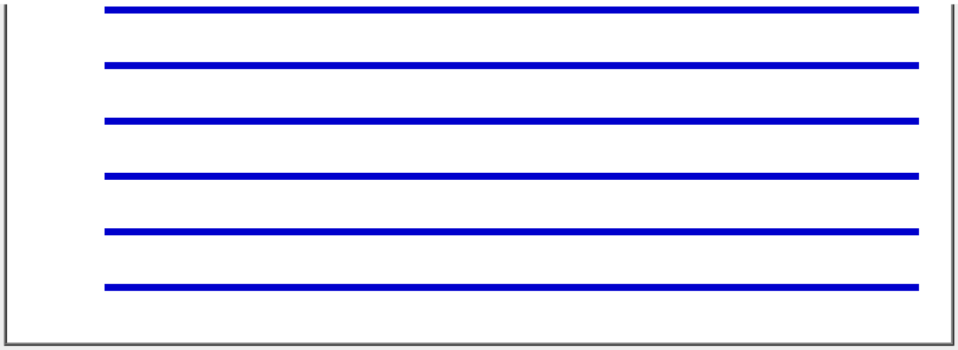


Distribution of 100 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments







Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	thrombospondin [Homo sapiens]	49.4	49.4	100%	1e-05	100%	AAB59366.1
☐	Thrombospondin-1 [Calypte anna]	49.4	49.4	100%	1e-05	100%	KFO95071.1
☐	PREDICTED: thrombospondin-1-like [Taeniopygia guttata]	49.4	49.4	100%	1e-05	100%	XP_002188235.2
☐	unnamed protein product [Mus musculus]	49.4	49.4	100%	1e-05	100%	BAE37804.1
☐	unnamed protein product [Mus musculus]	49.4	49.4	100%	1e-05	100%	BAE37878.1
☐	unnamed protein product [Oncorhynchus mykiss]	49.4	49.4	100%	1e-05	100%	CDQ99562.1
☐	unnamed protein product [Oncorhynchus mykiss]	49.4	49.4	100%	1e-05	100%	CDQ96481.1
☐	thrombospondin [Bos taurus]	49.4	49.4	100%	1e-05	100%	CAA60950.1
☐	Thrombospondin-1 [Cricetulus griseus]	49.4	49.4	100%	1e-05	100%	EGW04306.1
☐	PREDICTED: thrombospondin-1-like [Danio rerio]	49.4	49.4	100%	2e-05	100%	XP_002667003.3
☐	PREDICTED: thrombospondin-1-like [Xiphophorus maculatus]	49.4	49.4	100%	2e-05	100%	XP_005805261.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Latimeria chalumnae]	49.4	49.4	100%	2e-05	100%	XP_005988415.1
☐	PREDICTED: thrombospondin-1-like [Poecilia reticulata]	49.4	49.4	100%	2e-05	100%	XP_008396149.1
☐	PREDICTED: thrombospondin-1 [Ornithorhynchus anatinus]	49.4	49.4	100%	2e-05	100%	XP_007664158.1
☐	thrombospondin 1, isoform CRA_a [Mus musculus]	49.4	49.4	100%	2e-05	100%	EDL27901.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Eptesicus fuscus]	49.4	49.4	100%	2e-05	100%	XP_008141208.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Orycteropus afer afer]	49.4	49.4	100%	2e-05	100%	XP_007938654.1
☐	unnamed protein product [Homo sapiens]	49.4	49.4	100%	2e-05	100%	BAG65509.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Leptonychotes weddellii]	49.4	49.4	100%	2e-05	100%	XP_006742087.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Pantholops hodgsonii]	49.4	49.4	100%	2e-05	100%	XP_005978527.1
☐	PREDICTED: thrombospondin-1 isoform 2 [Ovis aries]	49.4	49.4	100%	2e-05	100%	XP_004010485.1
☐	PREDICTED: thrombospondin-1 [Macaca mulatta]	49.4	49.4	100%	2e-05	100%	XP_001093770.2
☐	PREDICTED: thrombospondin-1-like [Alligator mississippiensis]	49.4	49.4	100%	2e-05	100%	XP_006265214.1
☐	Thrombospondin-1 [Corvus brachyrhynchos]	49.4	49.4	100%	2e-05	100%	KFO63667.1
☐	Thrombospondin-1 [Buceros rhinoceros silvestris]	49.4	49.4	100%	2e-05	100%	KFO88878.1
☐	Thrombospondin-1 [Calypte anna]	49.4	49.4	100%	2e-05	100%	KFO96190.1
☐	Thrombospondin-1 [Nestor notabilis]	49.4	49.4	100%	2e-05	100%	KFQ42080.1
☐	Thrombospondin-1 [Apaloderma vittatum]	49.4	49.4	100%	2e-05	100%	KFP81422.1
☐	Thrombospondin-1 [Charadrius vociferus]	49.4	49.4	100%	2e-05	100%	KGL92027.1

☐	Thrombospondin-1 [Manacus vitellinus]	49.4	49.4	100%	2e-05	100%	KFW75047.1
☐	Thrombospondin-1 [Fulmarus glacialis]	49.4	49.4	100%	2e-05	100%	KFV92396.1
☐	Thrombospondin-1 [Acanthisitta chloris]	49.4	49.4	100%	2e-05	100%	KFP86921.1
☐	Thrombospondin-1 [Podiceps cristatus]	49.4	49.4	100%	2e-05	100%	KFZ68358.1
☐	Thrombospondin-1 [Phalacrocorax carbo]	49.4	49.4	100%	2e-05	100%	KFW95848.1
☐	Thrombospondin-1 [Pygoscelis adeliae]	49.4	49.4	100%	2e-05	100%	KFW65009.1
☐	Thrombospondin-1 [Eurypyga helias]	49.4	49.4	100%	2e-05	100%	KFW04094.1
☐	Thrombospondin-1 [Struthio camelus australis]	49.4	49.4	100%	2e-05	100%	KFV78213.1
☐	Thrombospondin-1 [Gavia stellata]	49.4	49.4	100%	2e-05	100%	KFV55243.1
☐	Thrombospondin-1 [Tyto alba]	49.4	49.4	100%	2e-05	100%	KFV42717.1
☐	Thrombospondin-1 [Tauraco erythrolophus]	49.4	49.4	100%	2e-05	100%	KFU99322.1
☐	Thrombospondin-1 [Pterocles gutturalis]	49.4	49.4	100%	2e-05	100%	KFU96792.1
☐	Thrombospondin-1 [Chaetura pelagica]	49.4	49.4	100%	2e-05	100%	KFU85223.1
☐	Thrombospondin-1 [Nipponia nippon]	49.4	49.4	100%	2e-05	100%	KFR07154.1
☐	Thrombospondin-1 [Opisthocomus hoazin]	49.4	49.4	100%	2e-05	100%	KFR07008.1
☐	Thrombospondin-1 [Pelecanus crispus]	49.4	49.4	100%	2e-05	100%	KFQ61165.1
☐	Thrombospondin-1 [Merops nubicus]	49.4	49.4	100%	2e-05	100%	KFQ17938.1
☐	Thrombospondin-1 [Leptosomus discolor]	49.4	49.4	100%	2e-05	100%	KFQ12753.1
☐	Thrombospondin-1 [Haliaeetus albicilla]	49.4	49.4	100%	2e-05	100%	KFQ05795.1
☐	Thrombospondin-1 [Cariama cristata]	49.4	49.4	100%	2e-05	100%	KFP58732.1
☐	Thrombospondin-1 [Cathartes aura]	49.4	49.4	100%	2e-05	100%	KFP57718.1
☐	Thrombospondin-1 [Colius striatus]	49.4	49.4	100%	2e-05	100%	KFP29490.1
☐	Thrombospondin-1 [Egretta garzetta]	49.4	49.4	100%	2e-05	100%	KFP12089.1
☐	Thrombospondin-1 [Balearica pavonina gibbericeps]	49.4	49.4	100%	2e-05	100%	KFO12753.1
☐	Thrombospondin-1 [Tinamus guttatus]	49.4	49.4	100%	2e-05	100%	KGL85097.1
☐	Thrombospondin-1 [Phaethon lepturus]	49.4	49.4	100%	2e-05	100%	KFQ75928.1
☐	Thrombospondin-1 [Mesitornis unicolor]	49.4	49.4	100%	2e-05	100%	KFQ33396.1
☐	Thrombospondin-1 [Chlamydotis undulata macqueenii]	49.4	49.4	100%	2e-05	100%	KFP35274.1
☐	Thrombospondin-1 [Caprimulgus carolinensis]	49.4	49.4	100%	2e-05	100%	KFZ56796.1
☐	Thrombospondin-1 [Cuculus canorus]	49.4	49.4	100%	2e-05	100%	KFO70201.1
☐	Thrombospondin-1 [Aptenodytes forsteri]	49.4	49.4	100%	2e-05	100%	KFM10485.1
☐	Thrombospondin-1 [Anas platyrhynchos]	49.4	49.4	100%	2e-05	100%	EOB08499.1
☐	Thrombospondin-1 [Bos mutus]	49.4	49.4	100%	2e-05	100%	ELR61299.1
☐	thrombospondin 1, isoform CRA_b [Mus musculus]	49.4	49.4	100%	2e-05	100%	EDL27902.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Camelus bactria	49.4	49.4	100%	2e-05	100%	XP_010963427.1
☐	PREDICTED: thrombospondin-1 [Equus przewalskii]	49.4	49.4	100%	2e-05	100%	XP_008527173.1
☐	PREDICTED: thrombospondin-1 [Acanthisitta chloris]	49.4	49.4	100%	2e-05	100%	XP_009079349.1
☐	PREDICTED: thrombospondin-1 [Corvus brachyrhynchos]	49.4	49.4	100%	2e-05	100%	XP_008637956.1
☐	PREDICTED: thrombospondin-1 [Camelus dromedarius]	49.4	49.4	100%	2e-05	100%	XP_010987639.1
☐	PREDICTED: thrombospondin-1 [Bos mutus]	49.4	49.4	100%	2e-05	100%	XP_005889010.1
☐	Thrombospondin-1 [Chelonia mydas]	49.4	49.4	100%	2e-05	100%	EMP26772.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1-like [Cynoglossus	49.4	49.4	100%	2e-05	100%	XP_008311728.1
☐	PREDICTED: thrombospondin-1 [Echinops telfairi]	49.4	49.4	100%	2e-05	100%	XP_004712753.1
☐	PREDICTED: thrombospondin-1 [Tinamus guttatus]	49.4	49.4	100%	2e-05	100%	XP_010224375.1
☐	PREDICTED: thrombospondin-1 [Chlamydotis undulata macqueenii]	49.4	49.4	100%	2e-05	100%	XP_010113973.1
☐	PREDICTED: thrombospondin-1 [Myotis davidii]	49.4	49.4	100%	2e-05	100%	XP_006778160.1

☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Columba livia]	49.4	49.4	100%	2e-05	100%	XP_005502344.1
☐	PREDICTED: thrombospondin-1 [Sorex araneus]	49.4	49.4	100%	2e-05	100%	XP_004609618.1
☐	PREDICTED: LOW QUALITY PROTEIN: thrombospondin-1 [Ursus maritimus	49.4	49.4	100%	2e-05	100%	XP_008700482.1
☐	PREDICTED: thrombospondin-1 [Callorhinchus milii]	49.4	49.4	100%	2e-05	100%	XP_007886260.1
☐	hypothetical protein PANDA_001089 [Ailuropoda melanoleuca]	49.4	49.4	100%	2e-05	100%	EFB13827.1
☐	PREDICTED: thrombospondin-1-like [Neolamprologus brichardi]	49.4	49.4	100%	2e-05	100%	XP_006792742.1
☐	PREDICTED: thrombospondin-1-like [Haplochromis burtoni]	49.4	49.4	100%	2e-05	100%	XP_005931578.1
☐	PREDICTED: thrombospondin-1-like [Pundamilia nyererei]	49.4	49.4	100%	2e-05	100%	XP_005737355.1
☐	PREDICTED: thrombospondin-1 [Ochotona princeps]	49.4	49.4	100%	2e-05	100%	XP_004578240.1
☐	Thrombospondin-1 [Macaca fascicularis]	49.4	49.4	100%	2e-05	100%	EHH62970.1
☐	thrombospondin-1a precursor [Oreochromis niloticus]	49.4	49.4	100%	2e-05	100%	NP_001266664.1
☐	PREDICTED: thrombospondin-1-like [Larimichthys crocea]	49.4	49.4	100%	2e-05	100%	XP_010748801.1
☐	PREDICTED: thrombospondin-1-like [Larimichthys crocea]	49.4	49.4	100%	2e-05	100%	XP_010738923.1
☐	PREDICTED: thrombospondin-1 [Loxodonta africana]	49.4	49.4	100%	2e-05	100%	XP_010596632.1
☐	PREDICTED: thrombospondin-1 [Caprimulgus carolinensis]	49.4	49.4	100%	2e-05	100%	XP_010164792.1
☐	PREDICTED: thrombospondin-1 [Galeopterus variegatus]	49.4	49.4	100%	2e-05	100%	XP_008564332.1
☐	PREDICTED: thrombospondin-1 [Stegastes partitus]	49.4	49.4	100%	2e-05	100%	XP_008283030.1
☐	PREDICTED: thrombospondin-1 isoform X4 [Cricetulus griseus]	49.4	49.4	100%	2e-05	100%	XP_007627125.1
☐	PREDICTED: thrombospondin-1-like [Takifugu rubripes]	49.4	49.4	100%	2e-05	100%	XP_003971811.1
☐	PREDICTED: thrombospondin-1 [Bison bison bison]	49.4	49.4	100%	2e-05	100%	XP_010846231.1
☐	PREDICTED: thrombospondin-1 [Rhinopithecus roxellana]	49.4	49.4	100%	2e-05	100%	XP_010358095.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Eptesicus fuscus]	49.4	49.4	100%	2e-05	100%	XP_008141207.1
☐	PREDICTED: thrombospondin-1 isoform X2 [Tarsius syrichta]	49.4	49.4	100%	2e-05	100%	XP_008051911.1
☐	PREDICTED: thrombospondin-1 [Chlorocebus sabaeus]	49.4	49.4	100%	2e-05	100%	XP_008015274.1
☐	PREDICTED: thrombospondin-1 isoform X1 [Orycteropus afer afer]	49.4	49.4	100%	2e-05	100%	XP_007938653.1

Alignments

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

thrombospondin, partial [Homo sapiens]

Sequence ID: gb|AAB59366.1| **Length:** 143 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 37 to 51 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1   KVVNSTTGPGEHLRN  15
           KVVNSTTGPGEHLRN
Sbjct  37  KVVNSTTGPGEHLRN  51
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

Thrombospondin-1, partial [Calypte anna]

Sequence ID: gb|KFO95071.1| **Length:** 172 **Number of Matches:** 1

Related Information

Range 1: 66 to 80 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1   KVVNSTTGPGEHLRN  15
           KVVNSTTGPGEHLRN
Sbjct  66  KVVNSTTGPGEHLRN  80
```

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PREDICTED: thrombospondin-1-like, partial [Taeniopygia guttata]

Sequence ID: ref|XP_002188235.2| **Length:** 245 **Number of Matches:** 1

Related Information

Gene - associated gene details

Map Viewer - aligned genomic context

Range 1: 141 to 155 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KVVNSTTGPGEHLRN  15
            KVVNSTTGPGEHLRN
Sbjct  141  KVVNSTTGPGEHLRN  155
```

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unnamed protein product [Mus musculus]

Sequence ID: dbj|BAE37804.1| **Length:** 259 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 153 to 167 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KVVNSTTGPGEHLRN  15
            KVVNSTTGPGEHLRN
Sbjct  153  KVVNSTTGPGEHLRN  167
```

Download GenPept Graphics ▼ Next ▲ Previous Descriptions

unnamed protein product [Mus musculus]

Sequence ID: dbj|BAE37878.1| **Length:** 262 **Number of Matches:** 1

Related Information

Gene - associated gene details

Range 1: 156 to 170 GenPept Graphics

▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps
49.4 bits(109)	1e-05	15/15(100%)	15/15(100%)	0/15(0%)

```
Query  1    KVVNSTTGPGEHLRN  15
            KVVNSTTGPGEHLRN
Sbjct  156  KVVNSTTGPGEHLRN  170
```