BLAST ® » blastn suite » RID-ZZN22EJY01R

BLAST Results

Questions/comments

Job title: Nucleotide Sequence (25 letters)

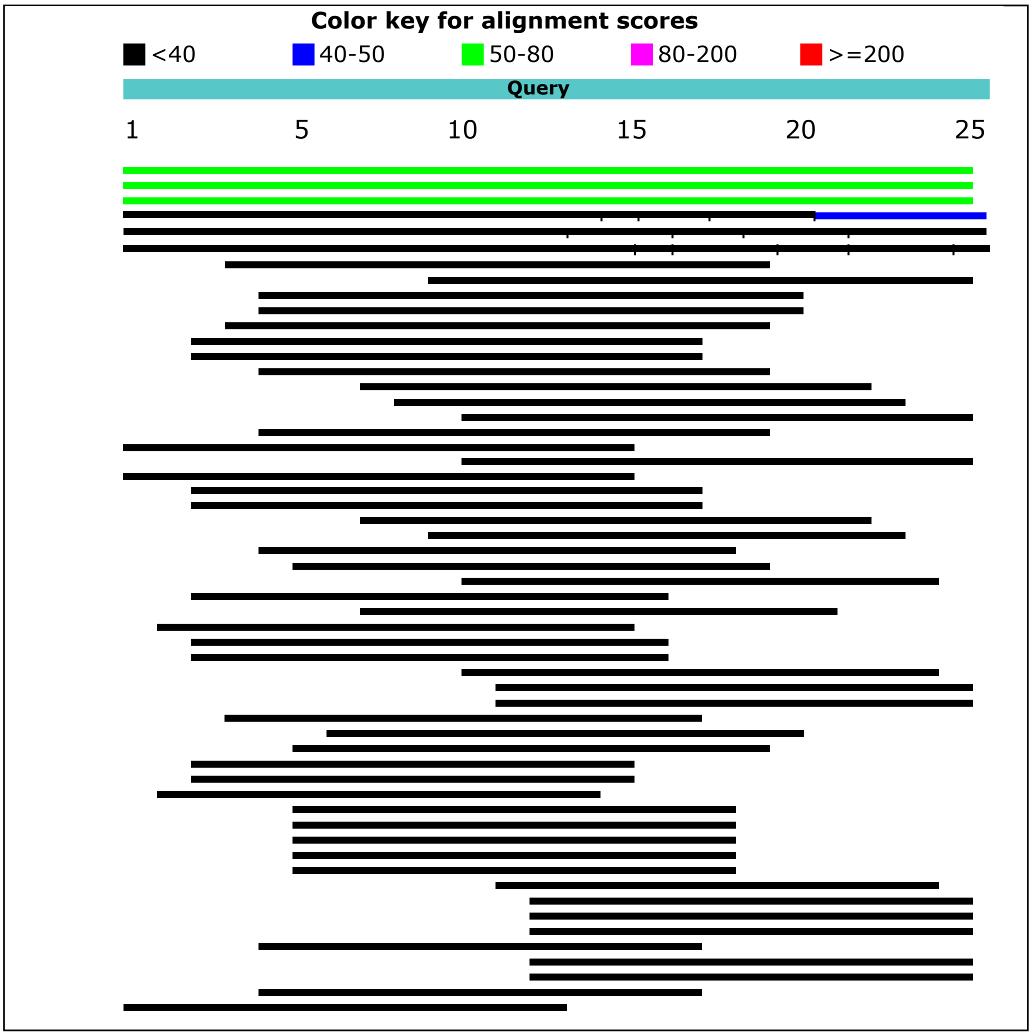
RID ZZN22EJY01R (Expires on 11-30 18:57 pm)

Query ID lcl|Query_15267
Description None
Molecule type nucleic acid
Query Length 25

Database Name Human G+T (2 databases)
Description
Program BLASTN 2.8.1+

Graphic Summary

Distribution of the top 200 Blast Hits on 100 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Transcripts						
Homo sapiens eukaryotic translation initiation factor 4 gamma 2 (EIF4G2), transcript variant 3, mRNA	50.1	50.1	100%	2e-05	100%	NM_001172705.1
Homo sapiens eukaryotic translation initiation factor 4 gamma 2 (EIF4G2), transcript variant 1, mRNA	50.1	50.1	100%	2e-05	100%	NM_001418.3
Homo sapiens eukaryotic translation initiation factor 4 gamma 2 (EIF4G2), transcript variant 2, mRNA	50.1	50.1	100%	2e-05	100%	NM_001042559.2
PREDICTED: Homo sapiens uncharacterized LOC107987115 (LOC107987115), ncRNA	30.2	30.2	60%	21	100%	XR_001746892.1
PREDICTED: Homo sapiens lysine demethylase 3B (KDM3B), transcript variant X2, mRNA	30.2	30.2	60%	21	100%	XM_011543489.2
PREDICTED: Homo sapiens uncharacterized LOC105373397 (LOC105373397), ncRNA	28.2	28.2	56%	84	100%	XR_001739259.2
PREDICTED: Homo sapiens long intergenic non-protein coding RNA 345 (LINC00345), transcript variant X3, ncRNA	28.2	28.2	56%	84	100%	XR_002957523.1
Homo sapiens chromosome 10 open reading frame 53 (C10orf53), transcript variant 1, mRNA	28.2	28.2	56%	84	100%	NM_182554.3
Homo sapiens chromosome 10 open reading frame 53 (C10orf53), transcript variant 2, mRNA	28.2	28.2	56%	84	100%	NM_001042427.2
Homo sapiens DAPK1 intronic transcript 1 (DAPK1-IT1), long non-coding RNA	28.2	28.2	56%	84	100%	NR_146781.1
Homo sapiens purine rich element binding protein G (PURG), transcript variant C, mRNA	28.2	28.2	56%	84	100%	NM_001323311.1
Homo sapiens purine rich element binding protein G (PURG), transcript variant A, mRNA	28.2	28.2	56%	84	100%	NM_013357.2
PREDICTED: Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant X2, mRNA	26.3	26.3	52%	332	100%	XM_024447161.1
PREDICTED: Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant X1, mRNA	26.3	26.3	52%	332	100%	XM_024447160.1
PREDICTED: Homo sapiens armadillo repeat containing 12 (ARMC12), transcript variant X1, mRNA	26.3	26.3	52%	332	100%	XM_017010435.2
PREDICTED: Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant X7, mRNA	26.3	26.3	52%	332	100%	XM_011524192.3
PREDICTED: Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant X5, misc_RNA	26.3	26.3	52%	332	100%	XR_001752401.2
PREDICTED: Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant X4, misc_RNA	26.3	26.3	52%	332	100%	XR_002957946.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant X3, misc_RNA	26.3	26.3	52%	332	100%	XR_002957945.1
PREDICTED: Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant X2, misc_RNA	26.3	26.3	52%	332	100%	XR_002957944.1
PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X3, mRNA	26.3	26.3	52%	332	100%	XM_017020381.2
PREDICTED: Homo sapiens splicing factor 1 (SF1), transcript variant X13, mRNA	26.3	26.3	52%	332	100%	XM_024448680.1
PREDICTED: Homo sapiens splicing factor 1 (SF1), transcript variant X10, mRNA	26.3	26.3	52%	332	100%	XM_017018249.2
Homo sapiens methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2 like (MTHFD2L), transcript variant 7, mRNA	26.3	26.3	52%	332	100%	NM_001351329.1
Homo sapiens DnaJ heat shock protein family (Hsp40) member C21 (DNAJC21), transcript variant 3, mRNA	26.3	26.3	52%	332	100%	NM_001348420.1
Homo sapiens splicing factor 1 (SF1), transcript variant 7, mRNA	26.3	26.3	52%	332	100%	NM_001346409.1
Homo sapiens splicing factor 1 (SF1), transcript variant 5, mRNA	26.3	26.3	52%	332	100%	NM_001178031.2
PREDICTED: Homo sapiens DnaJ heat shock protein family (Hsp40) member C21 (DNAJC21), transcript variant X1, mRNA	26.3	26.3	52%	332	100%	XM_011513965.2
PREDICTED: Homo sapiens uncharacterized LOC105377576 (LOC105377576), transcript variant X6, ncRNA	26.3	26.3	52%	332	100%	XR_001741934.1
PREDICTED: Homo sapiens uncharacterized LOC105377576 (LOC105377576), transcript variant X5, ncRNA	26.3	26.3	52%	332	100%	XR_001741933.1
PREDICTED: Homo sapiens uncharacterized LOC105377576 (LOC105377576), transcript variant X4, ncRNA	26.3	26.3	52%	332	100%	XR_001741932.1
PREDICTED: Homo sapiens uncharacterized LOC105377576 (LOC105377576), transcript variant X3, ncRNA	26.3	26.3	52%	332	100%	XR_001741931.1
PREDICTED: Homo sapiens uncharacterized LOC105377576 (LOC105377576), transcript variant X1, ncRNA	26.3	26.3	52%	332	100%	XR_001741930.1
PREDICTED: Homo sapiens uncharacterized LOC105371082 (LOC105371082), transcript variant X1, ncRNA	26.3	26.3	52%	332	100%	XR_933073.2
PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X11, mRNA	26.3	26.3	52%	332	100%	XM_005266250.3
PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X10, mRNA	26.3	26.3	52%	332	100%	XM_005266249.3
PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X9, mRNA	26.3	26.3	52%	332	100%	XM_017020383.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X8, mRNA	26.3	26.3	52%	332	100%	XM_017020382.1
PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X7, mRNA	26.3	26.3	52%	332	100%	XM_005266248.3
PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X5, mRNA	26.3	26.3	52%	332	100%	XM_011534906.2
PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X1, mRNA	26.3	26.3	52%	332	100%	XM_011534903.2
PREDICTED: Homo sapiens uncharacterized LOC107984457 (LOC107984457), ncRNA	26.3	26.3	52%	332	100%	XR_001749428.1
PREDICTED: Homo sapiens uncharacterized LOC105378256 (LOC105378256), ncRNA	26.3	26.3	52%	332	100%	XR_945331.2
PREDICTED: Homo sapiens uncharacterized LOC105369957 (LOC105369957), transcript variant X8, ncRNA	26.3	26.3	52%	332	100%	XR_001749299.1
PREDICTED: Homo sapiens uncharacterized LOC105369957 (LOC105369957), transcript variant X6, ncRNA	26.3	26.3	52%	332	100%	XR_945302.2
PREDICTED: Homo sapiens uncharacterized LOC105369957 (LOC105369957), transcript variant X5, ncRNA	26.3	26.3	52%	332	100%	XR_945301.2
PREDICTED: Homo sapiens uncharacterized LOC105369957 (LOC105369957), transcript variant X4, ncRNA	26.3	26.3	52%	332	100%	XR_945300.2
PREDICTED: Homo sapiens uncharacterized LOC105369957 (LOC105369957), transcript variant X3, ncRNA	26.3	26.3	52%	332	100%	XR_945299.2
PREDICTED: Homo sapiens uncharacterized LOC105369957 (LOC105369957), transcript variant X2, ncRNA	26.3	26.3	52%	332	100%	XR_001749298.1
PREDICTED: Homo sapiens uncharacterized LOC105369957 (LOC105369957), transcript variant X1, ncRNA	26.3	26.3	52%	332	100%	XR_001749297.1
PREDICTED: Homo sapiens splicing factor 1 (SF1), transcript variant X12, mRNA	26.3	26.3	52%	332	100%	XM_017018251.1
PREDICTED: Homo sapiens splicing factor 1 (SF1), transcript variant X11, mRNA	26.3	26.3	52%	332	100%	XM_017018250.1
PREDICTED: Homo sapiens splicing factor 1 (SF1), transcript variant X6, mRNA	26.3	26.3	52%	332	100%	XM_017018245.1
PREDICTED: Homo sapiens splicing factor 1 (SF1), transcript variant X1, mRNA	26.3	26.3	52%	332	100%	XM_017018244.1
PREDICTED: Homo sapiens translation initiation factor IF-2-like (LOC107985115), mRNA	26.3	26.3	52%	332	100%	XM_017003072.1
PREDICTED: Homo sapiens uncharacterized LOC105370550 (LOC105370550), transcript variant X6, ncRNA	26.3	26.3	52%	332	100%	XR_943987.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: Homo sapiens uncharacterized LOC105370550 (LOC105370550), transcript variant X1, ncRNA	26.3	26.3	52%	332	100%	XR_943980.1
PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X4, mRNA	26.3	26.3	52%	332	100%	XM_011534905.1
PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X2, mRNA	26.3	26.3	52%	332	100%	XM_011534904.1
PREDICTED: Homo sapiens splicing factor 1 (SF1), transcript variant X2, mRNA	26.3	26.3	52%	332	100%	XM_011545244.1
Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant 3, mRNA	26.3	26.3	52%	332	100%	NM_001288986.1
Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant 2, mRNA	26.3	26.3	52%	332	100%	NM_007168.3
Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant 1, mRNA	26.3	26.3	52%	332	100%	NM_001288985.1
Genomic sequences[show first]						
Homo sapiens chromosome 11, GRCh38.p12 Primary Assembly	40.1	874	100%	0.022	100%	NC_000011.10
Homo sapiens chromosome 13, GRCh38.p12 Primary Assembly	36.2	789	100%	0.34	100%	NC_000013.11
Homo sapiens chromosome 8, GRCh38.p12 Primary Assembly	34.2	1187	100%	1.4	100%	NC_000008.11
Homo sapiens chromosome 1, GRCh38.p12 Primary Assembly	32.2	1874	100%	5.4	100%	NC_000001.11
Homo sapiens chromosome 5, GRCh38.p12 Primary Assembly	32.2	1476	100%	5.4	100%	NC_000005.10
Homo sapiens chromosome 6, GRCh38.p12 Primary Assembly	32.2	1536	100%	5.4	100%	NC_000006.12
Homo sapiens chromosome 9, GRCh38.p12 Primary Assembly	32.2	1067	96%	5.4	100%	NC_000009.12
Homo sapiens chromosome 2, GRCh38.p12 Primary Assembly	32.2	1865	100%	5.4	100%	NC_000002.12
Homo sapiens chromosome 12 genomic patch of type FIX, GRCh38.p12 PATCHES HG23_PATCH	30.2	30.2	60%	21	100%	NW_009646204.1
Homo sapiens chromosome 3, GRCh38.p12 Primary Assembly	30.2	1320	100%	21	100%	NC_000003.12
Homo sapiens chromosome 10, GRCh38.p12 Primary Assembly	30.2	1086	100%	21	100%	NC_000010.11
Homo sapiens chromosome 18, GRCh38.p12 Primary Assembly	30.2	407	96%	21	100%	NC_000018.10
Homo sapiens chromosome 19, GRCh38.p12 Primary Assembly	30.2	137	92%	21	100%	NC_000019.10
Homo sapiens chromosome 20, GRCh38.p12 Primary Assembly	30.2	377	100%	21	100%	NC_000020.11
Homo sapiens chromosome X, GRCh38.p12 Primary Assembly	30.2	1207	100%	21	100%	NC_000023.11
Homo sapiens chromosome 4, GRCh38.p12 Primary Assembly	30.2	1322	100%	21	100%	NC_000004.12
Homo sapiens chromosome 12, GRCh38.p12 Primary Assembly	30.2	1007	100%	21	100%	NC_000012.12
Homo sapiens chromosome 14, GRCh38.p12 Primary Assembly	30.2	670	100%	21	100%	NC_000014.9

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens chromosome 17, GRCh38.p12 Primary Assembly	30.2	722	100%	21	100%	NC_000017.11
Homo sapiens chromosome 3 genomic patch of type FIX, GRCh38.p12 PATCHES HG2236_PATCH	28.2	28.2	56%	84	100%	NW_017363813.1
Homo sapiens chromosome 7, GRCh38.p12 Primary Assembly	28.2	1171	100%	84	100%	NC_000007.14
Homo sapiens chromosome 15, GRCh38.p12 Primary Assembly	28.2	664	100%	84	100%	NC_000015.10
Homo sapiens chromosome 21, GRCh38.p12 Primary Assembly	28.2	319	96%	84	100%	NC_000021.9
Homo sapiens chromosome 16 genomic scaffold, GRCh38.p12 alternate locus group ALT_REF_LOCI_1 HSCHR16_1_CTG1	28.2	28.2	56%	84	100%	NT_187607.1
Homo sapiens chromosome 16, GRCh38.p12 Primary Assembly	28.2	610	100%	84	100%	NC_000016.10
Homo sapiens chromosome 22, GRCh38.p12 Primary Assembly	28.2	216	96%	84	100%	NC_000022.11
Homo sapiens chromosome 17 genomic scaffold, GRCh38.p12 alternate locus group ALT_REF_LOCI_1 HSCHR17_7_CTG4	28.2	54.5	56%	84	100%	NT_187614.1
Homo sapiens chromosome Y, GRCh38.p12 Primary Assembly	26.3	157	88%	332	100%	NC_000024.10
Homo sapiens chromosome 6 genomic scaffold, GRCh38.p12 alternate locus group ALT_REF_LOCI_7 HSCHR6_MHC_SSTO_CTG1	26.3	26.3	68%	332	94%	NT_167249.2
Homo sapiens chromosome 6 genomic scaffold, GRCh38.p12 alternate locus group ALT_REF_LOCI_6 HSCHR6_MHC_QBL_CTG1	26.3	26.3	68%	332	94%	NT_167248.2
Homo sapiens chromosome 6 genomic scaffold, GRCh38.p12 alternate locus group ALT_REF_LOCI_4 HSCHR6_MHC_MANN_CTG1	26.3	26.3	68%	332	94%	NT_167246.2
Homo sapiens chromosome 6 genomic scaffold, GRCh38.p12 alternate locus group ALT_REF_LOCI_3 HSCHR6_MHC_DBB_CTG1	26.3	26.3	68%	332	94%	NT_167245.2
Homo sapiens chromosome 6 genomic scaffold, GRCh38.p12 alternate locus group ALT_REF_LOCI_2 HSCHR6_MHC_COX_CTG1	26.3	26.3	68%	332	94%	NT_113891.3
Homo sapiens chromosome 12 genomic scaffold, GRCh38.p12 alternate locus group ALT_REF_LOCI_2 HSCHR12_3_CTG2	26.3	26.3	52%	332	100%	NT_187658.1
Homo sapiens chromosome 6 genomic scaffold, GRCh38.p12 alternate locus group ALT_REF_LOCI_1 HSCHR6_MHC_APD_CTG1	26.3	26.3	68%	332	94%	NT_167244.2
Homo sapiens chromosome 11 genomic scaffold, GRCh38.p12 alternate locus group ALT_REF_LOCI_1 HSCHR11_1_CTG2	26.3	26.3	52%	332	100%	NT_187581.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens chromosome 14 unlocalized genomic scaffold, GRCh38.p12 Primary Assembly HSCHR14_CTG1_UNLOCALIZED	26.3	26.3	52%	332	100%	NT_113796.3

Alignments

Homo sapiens eukaryotic translation initiation factor 4 gamma 2 (EIF4G2), transcript variant 3, mRNA
Sequence ID: **NM_001172705.1** Length: 4028 Number of Matches: 1
Range 1: 1341 to 1365

Score	Expect	Identities	Gaps	Strand	Frame
50.1 bits(25)	2e-05()	25/25(100%)	0/25(0%)	Plus/Plus	

Features:

```
Query  1     AGCCAAGTCCTTAATGGATCAGTAC  25
             |||||||||||||||||||||||||
Sbjct  1341  AGCCAAGTCCTTAATGGATCAGTAC  1365
```

Homo sapiens eukaryotic translation initiation factor 4 gamma 2 (EIF4G2), transcript variant 1, mRNA
Sequence ID: **NM_001418.3** Length: 3911 Number of Matches: 1
Range 1: 1224 to 1248

Score	Expect	Identities	Gaps	Strand	Frame
50.1 bits(25)	2e-05()	25/25(100%)	0/25(0%)	Plus/Plus	

Features:

```
Query  1     AGCCAAGTCCTTAATGGATCAGTAC  25
             |||||||||||||||||||||||||
Sbjct  1224  AGCCAAGTCCTTAATGGATCAGTAC  1248
```

Homo sapiens eukaryotic translation initiation factor 4 gamma 2 (EIF4G2), transcript variant 2, mRNA
Sequence ID: **NM_001042559.2** Length: 3797 Number of Matches: 1
Range 1: 1224 to 1248

Score	Expect	Identities	Gaps	Strand	Frame
50.1 bits(25)	2e-05()	25/25(100%)	0/25(0%)	Plus/Plus	

Features:

```
Query  1     AGCCAAGTCCTTAATGGATCAGTAC  25
             |||||||||||||||||||||||||
Sbjct  1224  AGCCAAGTCCTTAATGGATCAGTAC  1248
```

PREDICTED: Homo sapiens uncharacterized LOC107987115 (LOC107987115), ncRNA
Sequence ID: **XR_001746892.1** Length: 2828 Number of Matches: 1
Range 1: 404 to 418

Score	Expect	Identities	Gaps	Strand	Frame
30.2 bits(15)	21()	15/15(100%)	0/15(0%)	Plus/Minus	

Features:

```
Query  1    AGCCAAGTCCTTAAT  15
            |||||||||||||||
Sbjct  418  AGCCAAGTCCTTAAT  404
```

PREDICTED: Homo sapiens lysine demethylase 3B (KDM3B), transcript variant X2, mRNA
Sequence ID: **XM_011543489.2** Length: 6987 Number of Matches: 1
Range 1: 504 to 518

Score	Expect	Identities	Gaps	Strand	Frame
30.2 bits(15)	21()	15/15(100%)	0/15(0%)	Plus/Minus	

Features:

```
Query  11   TTAATGGATCAGTAC  25
            |||||||||||||||
Sbjct  518  TTAATGGATCAGTAC  504
```

PREDICTED: Homo sapiens uncharacterized LOC105373397 (LOC105373397), ncRNA
Sequence ID: **XR_001739259.2** Length: 4099 Number of Matches: 1
Range 1: 751 to 764

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Minus	

Features:

```
Query  8    TCCTTAATGGATCA  21
            ||||||||||||||
Sbjct  764  TCCTTAATGGATCA  751
```

PREDICTED: Homo sapiens long intergenic non-protein coding RNA 345 (LINC00345), transcript variant X3, ncRNA
Sequence ID: **XR_002957523.1** Length: 1175 Number of Matches: 1
Range 1: 309 to 322

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Minus	

Features:

```
Query  2    GCCAAGTCCTTAAT  15
            ||||||||||||||
Sbjct  322  GCCAAGTCCTTAAT  309
```

Homo sapiens chromosome 10 open reading frame 53 (C10orf53), transcript variant 1, mRNA
Sequence ID: **NM_182554.3** Length: 2186 Number of Matches: 1
Range 1: 266 to 279

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Minus	

Features:

```
Query  3    CCAAGTCCTTAATG  16
            ||||||||||||||
Sbjct  279  CCAAGTCCTTAATG  266
```

Homo sapiens chromosome 10 open reading frame 53 (C10orf53), transcript variant 2, mRNA
Sequence ID: **NM_001042427.2** Length: 3280 Number of Matches: 1
Range 1: 266 to 279

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Minus	

Features:

```
Query  3    CCAAGTCCTTAATG  16
            ||||||||||||||
Sbjct  279  CCAAGTCCTTAATG  266
```

Homo sapiens DAPK1 intronic transcript 1 (DAPK1-IT1), long non-coding RNA
Sequence ID: **NR_146781.1** Length: 702 Number of Matches: 1
Range 1: 441 to 454

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Minus	

Features:

```
Query  11   TTAATGGATCAGTA  24
            ||||||||||||||
Sbjct  454  TTAATGGATCAGTA  441
```

Homo sapiens purine rich element binding protein G (PURG), transcript variant C, mRNA
Sequence ID: **NM_001323311.1** Length: 2076 Number of Matches: 1

Range 1: 1219 to 1232

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Minus	

Features:

```
Query  12    TAATGGATCAGTAC  25
             ||||||||||||||
Sbjct  1232  TAATGGATCAGTAC  1219
```

Homo sapiens purine rich element binding protein G (PURG), transcript variant A, mRNA
Sequence ID: **NM_013357.2** Length: 1972 Number of Matches: 1
Range 1: 1115 to 1128

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Minus	

Features:

```
Query  12    TAATGGATCAGTAC  25
             ||||||||||||||
Sbjct  1128  TAATGGATCAGTAC  1115
```

PREDICTED: Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant X2, mRNA
Sequence ID: **XM_024447161.1** Length: 1924 Number of Matches: 1
Range 1: 643 to 655

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  3    CCAAGTCCTTAAT  15
            |||||||||||||
Sbjct  643  CCAAGTCCTTAAT  655
```

PREDICTED: Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant X1, mRNA
Sequence ID: **XM_024447160.1** Length: 3675 Number of Matches: 1
Range 1: 645 to 657

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  3    CCAAGTCCTTAAT  15
            |||||||||||||
Sbjct  645  CCAAGTCCTTAAT  657
```

PREDICTED: Homo sapiens armadillo repeat containing 12 (ARMC12), transcript variant X1, mRNA
Sequence ID: **XM_017010435.2** Length: 2744 Number of Matches: 1
Range 1: 1361 to 1373

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  2     GCCAAGTCCTTAA  14
             |||||||||||||
Sbjct  1361  GCCAAGTCCTTAA  1373
```

PREDICTED: Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant X7, mRNA
Sequence ID: **XM_011524192.3** Length: 3494 Number of Matches: 1
Range 1: 257 to 269

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  6    AGTCCTTAATGGA  18
            |||||||||||||
Sbjct  257  AGTCCTTAATGGA  269
```

PREDICTED: Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant X5, misc_RNA
Sequence ID: **XR_001752401.2** Length: 6000 Number of Matches: 1
Range 1: 257 to 269

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  6    AGTCCTTAATGGA  18
            |||||||||||||
Sbjct  257  AGTCCTTAATGGA  269
```

PREDICTED: Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant X4, misc_RNA
Sequence ID: **XR_002957946.1** Length: 7228 Number of Matches: 1
Range 1: 257 to 269

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  6    AGTCCTTAATGGA  18
            |||||||||||||
Sbjct  257  AGTCCTTAATGGA  269
```

PREDICTED: Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant X3, misc_RNA
Sequence ID: **XR_002957945.1** Length: 9928 Number of Matches: 1
Range 1: 257 to 269

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  6    AGTCCTTAATGGA  18
            |||||||||||||
Sbjct  257  AGTCCTTAATGGA  269
```

PREDICTED: Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant X2, misc_RNA
Sequence ID: **XR_002957944.1** Length: 5910 Number of Matches: 1
Range 1: 257 to 269

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  6    AGTCCTTAATGGA  18
            |||||||||||||
Sbjct  257  AGTCCTTAATGGA  269
```

PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X3, mRNA
Sequence ID: **XM_017020381.2** Length: 9948 Number of Matches: 1
Range 1: 4292 to 4304

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  12    TAATGGATCAGTA  24
             |||||||||||||
Sbjct  4292  TAATGGATCAGTA  4304
```

PREDICTED: Homo sapiens splicing factor 1 (SF1), transcript variant X13, mRNA
Sequence ID: **XM_024448680.1** Length: 2643 Number of Matches: 1

Range 1: 1492 to 1504

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  13    AATGGATCAGTAC  25
             |||||||||||||
Sbjct  1492  AATGGATCAGTAC  1504
```

PREDICTED: Homo sapiens splicing factor 1 (SF1), transcript variant X10, mRNA
Sequence ID: **XM_017018249.2** Length: 5206 Number of Matches: 1
Range 1: 3416 to 3428

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  13    AATGGATCAGTAC  25
             |||||||||||||
Sbjct  3416  AATGGATCAGTAC  3428
```

Homo sapiens methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2 like (MTHFD2L), transcript variant 7, mRNA
Sequence ID: **NM_001351329.1** Length: 2388 Number of Matches: 1
Range 1: 1754 to 1766

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  13    AATGGATCAGTAC  25
             |||||||||||||
Sbjct  1754  AATGGATCAGTAC  1766
```

Homo sapiens DnaJ heat shock protein family (Hsp40) member C21 (DNAJC21), transcript variant 3, mRNA
Sequence ID: **NM_001348420.1** Length: 6122 Number of Matches: 1
Range 1: 3358 to 3370

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  5     AAGTCCTTAATGG  17
             |||||||||||||
Sbjct  3358  AAGTCCTTAATGG  3370
```

Homo sapiens splicing factor 1 (SF1), transcript variant 7, mRNA
Sequence ID: **NM_001346409.1** Length: 2873 Number of Matches: 1
Range 1: 1714 to 1726

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  13    AATGGATCAGTAC  25
             |||||||||||||
Sbjct  1714  AATGGATCAGTAC  1726
```

Homo sapiens splicing factor 1 (SF1), transcript variant 5, mRNA
Sequence ID: **NM_001178031.2** Length: 3366 Number of Matches: 1
Range 1: 1570 to 1582

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  13    AATGGATCAGTAC  25
             |||||||||||||
Sbjct  1570  AATGGATCAGTAC  1582
```

PREDICTED: Homo sapiens DnaJ heat shock protein family (Hsp40) member C21 (DNAJC21), transcript variant X1, mRNA
Sequence ID: **XM_011513965.2** Length: 6300 Number of Matches: 1
Range 1: 3546 to 3558

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  5     AAGTCCTTAATGG  17
             |||||||||||||
Sbjct  3546  AAGTCCTTAATGG  3558
```

PREDICTED: Homo sapiens uncharacterized LOC105377576 (LOC105377576), transcript variant X6, ncRNA
Sequence ID: **XR_001741934.1** Length: 5699 Number of Matches: 1
Range 1: 1318 to 1330

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  1     AGCCAAGTCCTTA  13
             |||||||||||||
Sbjct  1318  AGCCAAGTCCTTA  1330
```

PREDICTED: Homo sapiens uncharacterized LOC105377576 (LOC105377576), transcript variant X5, ncRNA
Sequence ID: **XR_001741933.1** Length: 5723 Number of Matches: 1
Range 1: 1318 to 1330

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  1     AGCCAAGTCCTTA  13
             |||||||||||||
Sbjct  1318  AGCCAAGTCCTTA  1330
```

PREDICTED: Homo sapiens uncharacterized LOC105377576 (LOC105377576), transcript variant X4, ncRNA
Sequence ID: **XR_001741932.1** Length: 5780 Number of Matches: 1
Range 1: 1318 to 1330

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  1     AGCCAAGTCCTTA  13
             |||||||||||||
Sbjct  1318  AGCCAAGTCCTTA  1330
```

PREDICTED: Homo sapiens uncharacterized LOC105377576 (LOC105377576), transcript variant X3, ncRNA
Sequence ID: **XR_001741931.1** Length: 5783 Number of Matches: 1
Range 1: 1318 to 1330

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  1     AGCCAAGTCCTTA  13
             |||||||||||||
Sbjct  1318  AGCCAAGTCCTTA  1330
```

PREDICTED: Homo sapiens uncharacterized LOC105377576 (LOC105377576), transcript variant X1, ncRNA
Sequence ID: **XR_001741930.1** Length: 6329 Number of Matches: 1

Range 1: 1318 to 1330

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  1     AGCCAAGTCCTTA  13
             |||||||||||||
Sbjct  1318  AGCCAAGTCCTTA  1330
```

PREDICTED: Homo sapiens uncharacterized LOC105371082 (LOC105371082), transcript variant X1, ncRNA

Sequence ID: **XR_933073.2** Length: 1399 Number of Matches: 1
Range 1: 288 to 300

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  1    AGCCAAGTCCTTA  13
            |||||||||||||
Sbjct  288  AGCCAAGTCCTTA  300
```

PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X11, mRNA

Sequence ID: **XM_005266250.3** Length: 5673 Number of Matches: 1
Range 1: 4264 to 4276

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  12    TAATGGATCAGTA  24
             |||||||||||||
Sbjct  4264  TAATGGATCAGTA  4276
```

PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X10, mRNA

Sequence ID: **XM_005266249.3** Length: 5757 Number of Matches: 1
Range 1: 4264 to 4276

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  12    TAATGGATCAGTA  24
             |||||||||||||
Sbjct  4264  TAATGGATCAGTA  4276
```

PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X9, mRNA

Sequence ID: **XM_017020383.1** Length: 9948 Number of Matches: 1
Range 1: 4292 to 4304

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  12    TAATGGATCAGTA  24
             |||||||||||||
Sbjct  4292  TAATGGATCAGTA  4304
```

PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X8, mRNA

Sequence ID: **XM_017020382.1** Length: 9760 Number of Matches: 1
Range 1: 4104 to 4116

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  12    TAATGGATCAGTA  24
             |||||||||||||
Sbjct  4104  TAATGGATCAGTA  4116
```

PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X7, mRNA
Sequence ID: **XM_005266248.3** Length: 9813 Number of Matches: 1
Range 1: 4157 to 4169

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  12    TAATGGATCAGTA  24
             |||||||||||||
Sbjct  4157  TAATGGATCAGTA  4169
```

PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X5, mRNA
Sequence ID: **XM_011534906.2** Length: 10088 Number of Matches: 1
Range 1: 4432 to 4444

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  12    TAATGGATCAGTA  24
             |||||||||||||
Sbjct  4432  TAATGGATCAGTA  4444
```

PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X1, mRNA
Sequence ID: **XM_011534903.2** Length: 9916 Number of Matches: 1
Range 1: 4260 to 4272

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  12    TAATGGATCAGTA  24
             |||||||||||||
Sbjct  4260  TAATGGATCAGTA  4272
```

PREDICTED: Homo sapiens uncharacterized LOC107984457 (LOC107984457), ncRNA
Sequence ID: **XR_001749428.1** Length: 1218 Number of Matches: 1
Range 1: 842 to 854

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  4    CAAGTCCTTAATG  16
            |||||||||||||
Sbjct  842  CAAGTCCTTAATG  854
```

PREDICTED: Homo sapiens uncharacterized LOC105378256 (LOC105378256), ncRNA
Sequence ID: **XR_945331.2** Length: 973 Number of Matches: 1
Range 1: 106 to 118

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  13   AATGGATCAGTAC  25
            |||||||||||||
Sbjct  106  AATGGATCAGTAC  118
```

PREDICTED: Homo sapiens uncharacterized LOC105369957 (LOC105369957), transcript variant X8, ncRNA
Sequence ID: **XR_001749299.1** Length: 3382 Number of Matches: 1

Range 1: 1294 to 1306

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  10    CTTAATGGATCAG  22
             |||||||||||||
Sbjct  1294  CTTAATGGATCAG  1306
```

PREDICTED: Homo sapiens uncharacterized LOC105369957 (LOC105369957), transcript variant X6, ncRNA
Sequence ID: **XR_945302.2** Length: 2606 Number of Matches: 1
Range 1: 394 to 406

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  10   CTTAATGGATCAG  22
            |||||||||||||
Sbjct  394  CTTAATGGATCAG  406
```

PREDICTED: Homo sapiens uncharacterized LOC105369957 (LOC105369957), transcript variant X5, ncRNA
Sequence ID: **XR_945301.2** Length: 2918 Number of Matches: 1
Range 1: 706 to 718

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  10   CTTAATGGATCAG  22
            |||||||||||||
Sbjct  706  CTTAATGGATCAG  718
```

PREDICTED: Homo sapiens uncharacterized LOC105369957 (LOC105369957), transcript variant X4, ncRNA
Sequence ID: **XR_945300.2** Length: 3027 Number of Matches: 1
Range 1: 815 to 827

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  10   CTTAATGGATCAG  22
            |||||||||||||
Sbjct  815  CTTAATGGATCAG  827
```

PREDICTED: Homo sapiens uncharacterized LOC105369957 (LOC105369957), transcript variant X3, ncRNA
Sequence ID: **XR_945299.2** Length: 3000 Number of Matches: 1
Range 1: 788 to 800

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  10   CTTAATGGATCAG  22
            |||||||||||||
Sbjct  788  CTTAATGGATCAG  800
```

PREDICTED: Homo sapiens uncharacterized LOC105369957 (LOC105369957), transcript variant X2, ncRNA
Sequence ID: **XR_001749298.1** Length: 3579 Number of Matches: 1
Range 1: 1367 to 1379

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  10    CTTAATGGATCAG  22
             |||||||||||||
Sbjct  1367  CTTAATGGATCAG  1379
```

PREDICTED: Homo sapiens uncharacterized LOC105369957 (LOC105369957), transcript variant X1, ncRNA
Sequence ID: **XR_001749297.1** Length: 3506 Number of Matches: 1
Range 1: 1294 to 1306

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  10    CTTAATGGATCAG  22
             |||||||||||||
Sbjct  1294  CTTAATGGATCAG  1306
```

PREDICTED: Homo sapiens splicing factor 1 (SF1), transcript variant X12, mRNA
Sequence ID: **XM_017018251.1** Length: 3284 Number of Matches: 1
Range 1: 1494 to 1506

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  13    AATGGATCAGTAC  25
             |||||||||||||
Sbjct  1494  AATGGATCAGTAC  1506
```

PREDICTED: Homo sapiens splicing factor 1 (SF1), transcript variant X11, mRNA
Sequence ID: **XM_017018250.1** Length: 3429 Number of Matches: 1
Range 1: 1639 to 1651

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  13    AATGGATCAGTAC  25
             |||||||||||||
Sbjct  1639  AATGGATCAGTAC  1651
```

PREDICTED: Homo sapiens splicing factor 1 (SF1), transcript variant X6, mRNA
Sequence ID: **XM_017018245.1** Length: 3333 Number of Matches: 1
Range 1: 1543 to 1555

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  13    AATGGATCAGTAC  25
             |||||||||||||
Sbjct  1543  AATGGATCAGTAC  1555
```

PREDICTED: Homo sapiens splicing factor 1 (SF1), transcript variant X1, mRNA
Sequence ID: **XM_017018244.1** Length: 3256 Number of Matches: 1
Range 1: 1462 to 1474

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  13    AATGGATCAGTAC  25
             |||||||||||||
Sbjct  1462  AATGGATCAGTAC  1474
```

PREDICTED: Homo sapiens translation initiation factor IF-2-like (LOC107985115), mRNA
Sequence ID: **XM_017003072.1** Length: 3834 Number of Matches: 1

Range 1: 1804 to 1816

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  10    CTTAATGGATCAG  22
             |||||||||||||
Sbjct  1804  CTTAATGGATCAG  1816
```

PREDICTED: Homo sapiens uncharacterized LOC105370550 (LOC105370550), transcript variant X6, ncRNA
Sequence ID: **XR_943987.1** Length: 2410 Number of Matches: 1
Range 1: 230 to 242

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  12   TAATGGATCAGTA  24
            |||||||||||||
Sbjct  230  TAATGGATCAGTA  242
```

PREDICTED: Homo sapiens uncharacterized LOC105370550 (LOC105370550), transcript variant X1, ncRNA
Sequence ID: **XR_943980.1** Length: 2503 Number of Matches: 1
Range 1: 230 to 242

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  12   TAATGGATCAGTA  24
            |||||||||||||
Sbjct  230  TAATGGATCAGTA  242
```

PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X4, mRNA
Sequence ID: **XM_011534905.1** Length: 9870 Number of Matches: 1
Range 1: 4214 to 4226

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  12    TAATGGATCAGTA  24
             |||||||||||||
Sbjct  4214  TAATGGATCAGTA  4226
```

PREDICTED: Homo sapiens A-kinase anchoring protein 11 (AKAP11), transcript variant X2, mRNA
Sequence ID: **XM_011534904.1** Length: 10112 Number of Matches: 1
Range 1: 4456 to 4468

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  12    TAATGGATCAGTA  24
             |||||||||||||
Sbjct  4456  TAATGGATCAGTA  4468
```

PREDICTED: Homo sapiens splicing factor 1 (SF1), transcript variant X2, mRNA
Sequence ID: **XM_011545244.1** Length: 2824 Number of Matches: 1
Range 1: 1462 to 1474

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  13    AATGGATCAGTAC  25
             |||||||||||||
Sbjct  1462  AATGGATCAGTAC  1474
```

Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant 3, mRNA
Sequence ID: **NM_001288986.1** Length: 5836 Number of Matches: 1
Range 1: 265 to 277

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  6    AGTCCTTAATGGA  18
            |||||||||||||
Sbjct  265  AGTCCTTAATGGA  277
```

Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant 2, mRNA
Sequence ID: **NM_007168.3** Length: 5731 Number of Matches: 1
Range 1: 265 to 277

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  6    AGTCCTTAATGGA  18
            |||||||||||||
Sbjct  265  AGTCCTTAATGGA  277
```

Homo sapiens ATP binding cassette subfamily A member 8 (ABCA8), transcript variant 1, mRNA
Sequence ID: **NM_001288985.1** Length: 6012 Number of Matches: 1
Range 1: 426 to 438

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

```
Query  6    AGTCCTTAATGGA  18
            |||||||||||||
Sbjct  426  AGTCCTTAATGGA  438
```

Homo sapiens chromosome 11, GRCh38.p12 Primary Assembly
Sequence ID: **NC_000011.10** Length: 135086622 Number of Matches: 32
Range 1: 10803277 to 10803296

Score	Expect	Identities	Gaps	Strand	Frame
40.1 bits(20)	0.022()	20/20(100%)	0/20(0%)	Plus/Minus	

Features:
eukaryotic translation initiation factor 4 gamma 2 isoform 2eukaryotic translation initiation factor 4 gamma 2 isoform 1

```
Query  6         AGTCCTTAATGGATCAGTAC  25
                 ||||||||||||||||||||
Sbjct  10803296  AGTCCTTAATGGATCAGTAC  10803277
```

Range 2: 4900949 to 4900965

Score	Expect	Identities	Gaps	Strand	Frame
34.2 bits(17)	1.4()	17/17(100%)	0/17(0%)	Plus/Plus	

Features:
18066 bp at 5' side: olfactory receptor 51T16405 bp at 3' side: olfactory receptor 51A7

```
Query  8        TCCTTAATGGATCAGTA  24
                |||||||||||||||||
Sbjct  4900949  TCCTTAATGGATCAGTA  4900965
```

Range 3: 123004143 to 123004157

Score	Expect	Identities	Gaps	Strand	Frame
30.2 bits(15)	21()	15/15(100%)	0/15(0%)	Plus/Minus	

Features:
22472 bp at 5' side: brain-specific homeobox protein homolog53577 bp at 3' side: heat shock cognate 71 kDa protein isoform 2

```
Query  7          GTCCTTAATGGATCA  21
                  |||||||||||||||
Sbjct  123004157  GTCCTTAATGGATCA  123004143
```

Range 4: 58832558 to 58832571

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Plus	

Features:
108062 bp at 5' side: glycine N-acyltransferase isoform b1858 bp at 3' side: glycine N-acyltransferase-like protein 2 isoform X1

```
Query  1         AGCCAAGTCCTTAA  14
                 ||||||||||||||
Sbjct  58832558  AGCCAAGTCCTTAA  58832571
```

Range 5: 110494633 to 110494646

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Plus	

Features:
32165 bp at 5' side: adrenodoxin, mitochondrial precursor84724 bp at 3' side: rho GTPase-activating protein 20 isoform 4

```
Query  4          CAAGTCCTTAATGG  17
                  ||||||||||||||
Sbjct  110494633  CAAGTCCTTAATGG  110494646
```

Range 6: 13108068 to 13108081

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Minus	

Features:
96968 bp at 5' side: ras association domain-containing protein 10168944 bp at 3' side: aryl hydrocarbon receptor nuclear translocator-like prote...

```
Query  10        CTTAATGGATCAGT  23
                 ||||||||||||||
Sbjct  13108081  CTTAATGGATCAGT  13108068
```

Range 7: 109815450 to 109815463

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Minus	

Features:
391223 bp at 5' side: uncharacterized protein C11orf87 isoform X2277737 bp at 3' side: probable ribonuclease ZC3H12C isoform X1

```
Query  10         CTTAATGGATCAGT  23
                  ||||||||||||||
Sbjct  109815463  CTTAATGGATCAGT  109815450
```

Range 8: 5102631 to 5102643

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
32134 bp at 5' side: olfactory receptor 52E129049 bp at 3' side: olfactory receptor 52A5

```
Query  10       CTTAATGGATCAG  22
                |||||||||||||
Sbjct  5102631  CTTAATGGATCAG  5102643
```

Range 9: 6742286 to 6742298

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
58990 bp at 5' side: 39S ribosomal protein L17, mitochondrial25709 bp at 3' side: olfactory receptor 2AG2

```
Query  10       CTTAATGGATCAG  22
                |||||||||||||
Sbjct  6742286  CTTAATGGATCAG  6742298
```

Range 10: 15807133 to 15807145

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
101852 bp at 5' side: uncharacterized protein LOC102724957 isoform X1165664 bp at 3' side: transcription factor SOX-6 isoform 3

```
Query  4         CAAGTCCTTAATG  16
                 |||||||||||||
Sbjct  15807133  CAAGTCCTTAATG  15807145
```

Range 11: 26763789 to 26763801

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
42075 bp at 5' side: sodium-coupled monocarboxylate transporter 2 isoform X4230726 bp at 3' side: fin bud initiation factor homolog precursor

```
Query  8         TCCTTAATGGATC  20
                 |||||||||||||
Sbjct  26763789  TCCTTAATGGATC  26763801
```

Range 12: 37382844 to 37382856

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
723658 bp at 5' side: uncharacterized protein C11orf74 isoform a2731514 bp at 3' side: leucine-rich repeat-containing protein 4C isoform X1

```
Query  4         CAAGTCCTTAATG  16
                 |||||||||||||
Sbjct  37382844  CAAGTCCTTAATG  37382856
```

Range 13: 46910169 to 46910181

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
low-density lipoprotein receptor-related protein 4 precursorlow-density lipoprotein receptor-related protein 4 isofor...

```
Query  5         AAGTCCTTAATGG  17
                 |||||||||||||
Sbjct  46910169  AAGTCCTTAATGG  46910181
```

Range 14: 47430975 to 47430987

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
4696 bp at 5' side: 26S proteasome regulatory subunit 6A isoform X16800 bp at 3' side: 43 kDa receptor-associated protein of the synapse isoform X1

```
Query  1         AGCCAAGTCCTTA  13
                 |||||||||||||
Sbjct  47430975  AGCCAAGTCCTTA  47430987
```

Range 15: 49867398 to 49867410

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
658989 bp at 5' side: glutamate carboxypeptidase 2 isoform X585013 bp at 3' side: olfactory receptor 4C13

```
Query  4         CAAGTCCTTAATG  16
                 |||||||||||||
Sbjct  49867398  CAAGTCCTTAATG  49867410
```

Range 16: 58732811 to 58732823

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:

8315 bp at 5' side: glycine N-acyltransferase isoform b101606 bp at 3' side: glycine N-acyltransferase-like protein 2 isoform X1

```
Query  10        CTTAATGGATCAG  22
                 |||||||||||||
Sbjct  58732811  CTTAATGGATCAG  58732823
```

Range 17: 75474387 to 75474399

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
glycerophosphodiester phosphodiesterase domain-containing...glycerophosphodiester phosphodiesterase domain-containing...

```
Query  3         CCAAGTCCTTAAT  15
                 |||||||||||||
Sbjct  75474387  CCAAGTCCTTAAT  75474399
```

Range 18: 93753858 to 93753870

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
ester hydrolase C11orf54 isoform X1ester hydrolase C11orf54 isoform b

```
Query  12        TAATGGATCAGTA  24
                 |||||||||||||
Sbjct  93753858  TAATGGATCAGTA  93753870
```

Range 19: 94208996 to 94209008

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
28127 bp at 5' side: pannexin-1 isoform X196629 bp at 3' side: sperm-egg fusion protein Juno precursor

```
Query  9         CCTTAATGGATCA  21
                 |||||||||||||
Sbjct  94208996  CCTTAATGGATCA  94209008
```

Range 20: 104788029 to 104788041

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
750016 bp at 5' side: protein DDI1 homolog 1156712 bp at 3' side: caspase-4 isoform alpha precursor

```
Query  2          GCCAAGTCCTTAA  14
                  |||||||||||||
Sbjct  104788029  GCCAAGTCCTTAA  104788041
```

Range 21: 107955514 to 107955526

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
ras-related protein Rab-39A

```
Query  10         CTTAATGGATCAG  22
                  |||||||||||||
Sbjct  107955514  CTTAATGGATCAG  107955526
```

Range 22: 121598740 to 121598752

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
sortilin-related receptor preproproteinsortilin-related receptor isoform X1

```
Query  2          GCCAAGTCCTTAA  14
                  |||||||||||||
Sbjct  121598740  GCCAAGTCCTTAA  121598752
```

Range 23: 134071411 to 134071423

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
junctional adhesion molecule C isoform 1 precursorjunctional adhesion molecule C isoform 2 precursor

```
Query  11         TTAATGGATCAGT  23
                  |||||||||||||
Sbjct  134071411  TTAATGGATCAGT  134071423
```

Range 24: 134922115 to 134922127

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
534456 bp at 5' side: galactosylgalactosylxylosylprotein 3-beta-glucuronosyltra...

```
Query  1          AGCCAAGTCCTTA  13
                  |||||||||||||
Sbjct  134922115  AGCCAAGTCCTTA  134922127
```

Range 25: 2331034 to 2331046

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
13129 bp at 5' side: tetraspanin-32 isoform X846504 bp at 3' side: CD81 antigen isoform 1

```
Query  1        AGCCAAGTCCTTA  13
                |||||||||||||
Sbjct  2331046  AGCCAAGTCCTTA  2331034
```

Range 26: 28149643 to 28149655

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
probable methyltransferase-like protein 15 isoform X1probable methyltransferase-like protein 15 isoform X4

```
Query  8         TCCTTAATGGATC  20
                 |||||||||||||
Sbjct  28149655  TCCTTAATGGATC  28149643
```

Range 27: 31902546 to 31902558

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
96135 bp at 5' side: paired box protein Pax-6 isoform c188639 bp at 3' side: reticulocalbin-1 precursor

```
Query  10        CTTAATGGATCAG  22
                 |||||||||||||
Sbjct  31902558  CTTAATGGATCAG  31902546
```

Range 28: 73043825 to 73043841

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	16/17(94%)	0/17(0%)	Plus/Minus	

Features:
F-BAR and double SH3 domains protein 2F-BAR and double SH3 domains protein 2 isoform X1

```
Query  4         CAAGTCCTTAATGGATC  20
                 |||||||| ||||||||
Sbjct  73043841  CAAGTCCTCAATGGATC  73043825
```

Range 29: 78307466 to 78307478

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
GRB2-associated-binding protein 2 isoform aGRB2-associated-binding protein 2 isoform X1

```
Query  2         GCCAAGTCCTTAA  14
                 |||||||||||||
Sbjct  78307478  GCCAAGTCCTTAA  78307466
```

Range 30: 83533788 to 83533800

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
disks large homolog 2 isoform X21disks large homolog 2 isoform X26

```
Query  4         CAAGTCCTTAATG  16
                 |||||||||||||
Sbjct  83533800  CAAGTCCTTAATG  83533788
```

Range 31: 88784257 to 88784269

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
metabotropic glutamate receptor 5 isoform X2metabotropic glutamate receptor 5 isoform b precursor

```
Query  12        TAATGGATCAGTA  24
                 |||||||||||||
Sbjct  88784269  TAATGGATCAGTA  88784257
```

Range 32: 105346366 to 105346378

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
206640 bp at 5' side: caspase recruitment domain-containing protein 18264620 bp at 3' side: glutamate receptor 4 isoform X5

```
Query  7          GTCCTTAATGGAT  19
                  |||||||||||||
Sbjct  105346378  GTCCTTAATGGAT  105346366
```

Homo sapiens chromosome 13, GRCh38.p12 Primary Assembly
Sequence ID: **NC_000013.11** Length: 114364328 Number of Matches: 29
Range 1: 93670071 to 93670088

Score	Expect	Identities	Gaps	Strand	Frame
36.2 bits(18)	0.34()	18/18(100%)	0/18(0%)	Plus/Minus	

Features:
glypican-6 precursorglypican-6 isoform X1

```
Query  4         CAAGTCCTTAATGGATCA  21
                 ||||||||||||||||||
Sbjct  93670088  CAAGTCCTTAATGGATCA  93670071
```

Range 2: 41967183 to 41967197

Score	Expect	Identities	Gaps	Strand	Frame
30.2 bits(15)	21()	15/15(100%)	0/15(0%)	Plus/Plus	

Features:
6168 bp at 5' side: von Willebrand factor A domain-containing protein 8 isofo...81577 bp at 3' side: diacylglycerol kinase eta isoform 2

```
Query  3         CCAAGTCCTTAATGG  17
                 |||||||||||||||
Sbjct  41967183  CCAAGTCCTTAATGG  41967197
```

Range 3: 36831797 to 36831811

Score	Expect	Identities	Gaps	Strand	Frame
30.2 bits(15)	21()	15/15(100%)	0/15(0%)	Plus/Minus	

Features:
4044 bp at 5' side: regulatory factor X-associated protein16865 bp at 3' side: mothers against decapentaplegic homolog 9 isoform b

```
Query  2         GCCAAGTCCTTAATG  16
                 |||||||||||||||
Sbjct  36831811  GCCAAGTCCTTAATG  36831797
```

Range 4: 40068575 to 40068588

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Plus	

Features:
317482 bp at 5' side: conserved oligomeric Golgi complex subunit 6 isoform 1490935 bp at 3' side: forkhead box protein O1

```
Query  6         AGTCCTTAATGGAT  19
                 ||||||||||||||
Sbjct  40068575  AGTCCTTAATGGAT  40068588
```

Range 5: 52600685 to 52600698

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Plus	

Features:
125544 bp at 5' side: cytoskeleton-associated protein 2 isoform X241795 bp at 3' side: heterogeneous nuclear ribonucleoprotein A1-like 2

```
Query  2         GCCAAGTCCTTAAT  15
                 ||||||||||||||
Sbjct  52600685  GCCAAGTCCTTAAT  52600698
```

Range 6: 23209326 to 23209339

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Minus	

Features:
gamma-sarcoglycan isoform X1gamma-sarcoglycan isoform X2

```
Query  5         AAGTCCTTAATGGA  18
                 ||||||||||||||
Sbjct  23209339  AAGTCCTTAATGGA  23209326
```

Range 7: 28998746 to 28998759

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Minus	

Features:
280748 bp at 5' side: solute carrier family 46 member 3 isoform a precursor25910 bp at 3' side: microtubule-associated tumor suppressor candidate 2 isofo...

```
Query  5         AAGTCCTTAATGGA  18
                 ||||||||||||||
Sbjct  28998759  AAGTCCTTAATGGA  28998746
```

Range 8: 97885183 to 97885196

Score	Expect	Identities	Gaps	Strand	Frame
28.2 bits(14)	84()	14/14(100%)	0/14(0%)	Plus/Minus	

Features:
420741 bp at 5' side: ras-related protein Rap-2a precursor84585 bp at 3' side: importin-5

```
Query  6         AGTCCTTAATGGAT  19
                 ||||||||||||||
Sbjct  97885196  AGTCCTTAATGGAT  97885183
```

Range 9: 29521088 to 29521100

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
high affinity cationic amino acid transporter 1high affinity cationic amino acid transporter 1 isoform X2

```
Query  3         CCAAGTCCTTAAT  15
                 |||||||||||||
Sbjct  29521088  CCAAGTCCTTAAT  29521100
```

Range 10: 35469452 to 35469464

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
neurobeachin isoform X3neurobeachin isoform 1

```
Query  12        TAATGGATCAGTA  24
                 |||||||||||||
Sbjct  35469452  TAATGGATCAGTA  35469464
```

Range 11: 39339007 to 39339019

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
291081 bp at 5' side: NHL repeat-containing protein 3 isoform b4917 bp at 3' side: LHFPL tetraspan subfamily member 6 protein precursor

```
Query  3         CCAAGTCCTTAAT  15
                 |||||||||||||
Sbjct  39339007  CCAAGTCCTTAAT  39339019
```

Range 12: 42302834 to 42302846

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
A-kinase anchor protein 11 isoform X1A-kinase anchor protein 11 isoform X3

```
Query  12        TAATGGATCAGTA  24
                 |||||||||||||
Sbjct  42302834  TAATGGATCAGTA  42302846
```

Range 13: 76861325 to 76861337

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
978223 bp at 5' side: LMO7 downstream neighbor protein isoform X123834 bp at 3' side: BTB/POZ domain-containing protein KCTD12

```
Query  3         CCAAGTCCTTAAT  15
                 |||||||||||||
Sbjct  76861325  CCAAGTCCTTAAT  76861337
```

Range 14: 76984746 to 76984762

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	16/17(94%)	0/17(0%)	Plus/Plus	

Features:
26761 bp at 5' side: cis-aconitate decarboxylase7190 bp at 3' side: ceroid-lipofuscinosis neuronal protein 5

```
Query  2         GCCAAGTCCTTAATGGA  18
                 ||||||||||| |||||
Sbjct  76984746  GCCAAGTCCTTTATGGA  76984762
```

Range 15: 81570671 to 81570683

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
1232966 bp at 5' side: protein sprouty homolog 22308734 bp at 3' side: SLIT and NTRK-like protein 1 precursor

```
Query  12        TAATGGATCAGTA  24
                 |||||||||||||
Sbjct  81570671  TAATGGATCAGTA  81570683
```

Range 16: 91165182 to 91165202

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	19/21(90%)	0/21(0%)	Plus/Plus	

Features:
3486917 bp at 5' side: SLIT and NTRK-like protein 5 isoform X1233845 bp at 3' side: glypican-5 isoform X3

```
Query  5         AAGTCCTTAATGGATCAGTAC  25
                 ||||| |||||||| ||||||
Sbjct  91165182  AAGTCATTAATGGAACAGTAC  91165202
```

Range 17: 102931738 to 102931750

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
55835 bp at 5' side: DNA repair protein complementing XP-G cells114383 bp at 3' side: ileal sodium/bile acid cotransporter

```
Query  9          CCTTAATGGATCA  21
                  |||||||||||||
Sbjct  102931738  CCTTAATGGATCA  102931750
```

Range 18: 106008722 to 106008734

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
518641 bp at 5' side: D-amino acid oxidase activator isoform 3484306 bp at 3' side: ephrin-B2 precursor

```
Query  5          AAGTCCTTAATGG  17
                  |||||||||||||
Sbjct  106008722  AAGTCCTTAATGG  106008734
```

Range 19: 108568026 to 108568038

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Plus	

Features:
261088 bp at 5' side: tumor necrosis factor ligand superfamily member 13B isofo...61807 bp at 3' side: unconventional myosin-XVI isoform 1

```
Query  13         AATGGATCAGTAC  25
                  |||||||||||||
Sbjct  108568026  AATGGATCAGTAC  108568038
```

Range 20: 32332564 to 32332576

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
breast cancer type 2 susceptibility protein

```
Query  12        TAATGGATCAGTA  24
                 |||||||||||||
Sbjct  32332576  TAATGGATCAGTA  32332564
```

Range 21: 39494356 to 39494368

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
LHFPL tetraspan subfamily member 6 protein precursorLHFPL tetraspan subfamily member 6 protein isoform X1

```
Query  4         CAAGTCCTTAATG  16
                 |||||||||||||
Sbjct  39494368  CAAGTCCTTAATG  39494356
```

Range 22: 44792903 to 44792915

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
216829 bp at 5' side: TSC22 domain family protein 1 isoform X4148291 bp at 3' side: nuclear fragile X mental retardation-interacting protein 1

```
Query  3         CCAAGTCCTTAAT  15
                 |||||||||||||
Sbjct  44792915  CCAAGTCCTTAAT  44792903
```

Range 23: 66128159 to 66128171

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
2295166 bp at 5' side: keratin-associated protein 21-1176484 bp at 3' side: protocadherin-9 isoform 4 precursor

```
Query  2         GCCAAGTCCTTAA  14
                 |||||||||||||
Sbjct  66128171  GCCAAGTCCTTAA  66128159
```

Range 24: 75536472 to 75536484

Score	Expect	Identities	Gaps	Strand	Frame

26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
COMM domain-containing protein 6 isoform aCOMM domain-containing protein 6 isoform b

```
Query  3          CCAAGTCCTTAAT  15
                  |||||||||||||
Sbjct  75536484   CCAAGTCCTTAAT  75536472
```

Range 25: 93483004 to 93483016

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
glypican-6 precursor

```
Query  1          AGCCAAGTCCTTA  13
                  |||||||||||||
Sbjct  93483016   AGCCAAGTCCTTA  93483004
```

Range 26: 100212404 to 100212416

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
propionyl-CoA carboxylase alpha chain, mitochondrial isof...propionyl-CoA carboxylase alpha chain, mitochondrial isof...

```
Query  10          CTTAATGGATCAG  22
                   |||||||||||||
Sbjct  100212416   CTTAATGGATCAG  100212404
```

Range 27: 111688507 to 111688523

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	16/17(94%)	0/17(0%)	Plus/Minus	

Features:
51904 bp at 5' side: uncharacterized protein LOC107983958325638 bp at 3' side: peptidyl-prolyl cis-trans isomerase CYP95-like

```
Query  6           AGTCCTTAATGGATCAG  22
                   ||||||| |||||||||
Sbjct  111688523   AGTCCTTCATGGATCAG  111688507
```

Range 28: 111773778 to 111773794

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	16/17(94%)	0/17(0%)	Plus/Minus	

Features:
137175 bp at 5' side: uncharacterized protein LOC107983958240367 bp at 3' side: peptidyl-prolyl cis-trans isomerase CYP95-like

```
Query  6           AGTCCTTAATGGATCAG  22
                   ||||||| |||||||||
Sbjct  111773794   AGTCCTTCATGGATCAG  111773778
```

Range 29: 112404726 to 112404738

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	332()	13/13(100%)	0/13(0%)	Plus/Minus	

Features:
sperm acrosome-associated protein 7 isoform X1sperm acrosome-associated protein 7 isoform X5

```
Query  1           AGCCAAGTCCTTA  13
                   |||||||||||||
Sbjct  112404738   AGCCAAGTCCTTA  112404726
```

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