





18 gi 5802814GagProPolEnvProt	11.3%	NSPTICQ-----TFVGRALQPVREKFSDCYIIHYIDDILCAAETKDKLIDCYTFLQAEVANAGLAIASD
19 gi 257758ReverseTranscript	30.3%	NSPTLFG-----ETLQQDLIPFRASHPNCTLLQ-----
20 gi 3600064polymerase	18.5%	NNPTICQ-----TFVGRALQPVREKFSDCYIIHYIDDILCAAETKDKLIDCYTFLQAEVANAGLAIASD
21 gi 52000844HERK18pol	18.8%	NSPTICQ-----TFVGRALQPVREKFSDCYIIHYIDDILCAAETKDKLIDCYTFLQAEVANAGLAIASD
22 gi 3600071polymerase	19.0%	NNPTICQ-----TFVGRALQPVREKFSDCYIIHYIDDILCAAETKDKLIDCYTFLQAEVANAGLAIASD
23 gi 3600069polymerase	19.0%	NSPTICQ-----TFVGRALQPVREKFSDCYIIHYIDDILCAAETKDKLIDCYTFLQAEVANAGLAIASD
24 gi 3600067polymerase	18.5%	NSPTICQ-----TFVGRALQPVREKFSDCYIIHYIDDILCAAETKDKLIDCYTFLQAEVANAGLAIASD
25 gi 52000847HERK19pol	18.6%	NSPTICQ-----TFVGRALQPVREKFSDCYIIHYIDDILCAAEMKDKLIDCYTFLQAEVANAGLAIASD
26 gi 5802810GagProPol	11.0%	NSPTICQ-----TFVGRALQPVREKFSDCYIIHYIDDILCAAETKDKLIDCYTFLQAEVASAGLAIASD
27 gi 110811564ReverseTranscriptase	18.0%	NSPTICQ-----TFVGRALQPVREKFSDCYIIHYIDDILCAAETKDKLIDCYTFLQAEVANAGLAIASD
28 gi 21913258polprotein	17.6%	NSPAICQ-----LYVDQAVEPVRQQCPKVQILHYMDDLITAESESHLMEAYKLLLLYLEKVGLQVAPE
29 gi 52001473HERK10pol	18.0%	NSPTICQ-----TFVGRALQPVREKFSDCYIIHYIDDILCAAETKDKLIDCYTFLQAEVANAGLAIASD
30 gi 5802819GagProPol	11.0%	NSPTICQ-----TFVGRALQPVREKFSDCYIIHYIDDILCAAETKDKLIDCYTFLQAEVANAGLAIASD
consensus/100%		.....
consensus/90%		NsPTIht p.lspslp.h.tp..tshllp.....
consensus/80%		NSPTIht phluRslQPs+p+h.sChllphhDDILhut.otsthcshshL.tcItssGhtlupc
consensus/70%		NSPTICQ TFVGRALQPVREKFSDCYIIHYIDDILCAAET+DKLIDCYTFLQAEVASAGLAIASD

	401	.	] 420
1 lc Query_ProteinA	100.0%	-----	
2 gi 30269262polprotein	15.1%	KAQICRPQVRYLGFITRQGE	
3 gi 1034619561HERK9polX1	19.2%	-----	
4 gi 767881134HERK18polX2	20.7%	KAQICRPQ-----	
5 gi 767881132HERK18polX1	19.4%	KAQICRPQVRYLGFITRQGE	
6 gi 68164966polprecursor	32.6%	-----	
7 gi 5802821GagProPolProtein	11.3%	KIQTSTPF-HYLGMQI----	
8 gi 52000770HERK113Pol	18.4%	KIQTSTPF-HYLGMQI----	
9 gi 13021825polymerase	18.0%	KIQTSTPF-HYLGMQI----	
10 gi 13021822polymerase	18.0%	KIQTSTPF-HYLGMQI----	
11 gi 52000839HERK6pol	18.0%	KIQTSTPF-HYLGMQI----	
12 gi 118572691HERK9pol	12.9%	-----	
13 gi 52000773HERK7pol	18.0%	KIQTSTPF-HYLGMQI----	
14 gi 52000846HERK11pol	18.4%	KIQTSTPF-HYLGMQI----	
15 gi 52000774HERK25pol	18.4%	KIQTSTPF-HYLGMQI----	
16 gi 52000771HERK8pol	18.4%	KIQTSTPF-HYLGMQI----	
17 gi 3600073polymerase	19.0%	KIQTSTPF-HYLGMQI----	
18 gi 5802814GagProPolEnvProt	11.3%	KIQTSTPF-HYLGMQI----	
19 gi 257758ReverseTranscript	30.3%	-----	
20 gi 3600064polymerase	18.5%	KIQTSTPF-HYLGMQI----	
21 gi 52000844HERK18pol	18.8%	KIQTSTPF-HYLGMQI----	
22 gi 3600071polymerase	19.0%	KIQTSTPF-HYLGMQI----	
23 gi 3600069polymerase	19.0%	KIQTSTPF-HYLGMQI----	
24 gi 3600067polymerase	18.5%	KIQTSTPF-HYLGMQI----	
25 gi 52000847HERK19pol	18.6%	KIQTSTPF-HYLEMQI----	
26 gi 5802810GagProPol	11.0%	KIQTSTPF-HYLGMQI----	
27 gi 110811564ReverseTranscriptase	18.0%	KIQTSTPF-HYLGMQI----	
28 gi 21913258polprotein	17.6%	RIQKGEVV-QYLGLKVT---	
29 gi 52001473HERK10pol	18.0%	KIQTSTPF-HYLGMQI----	
30 gi 5802819GagProPol	11.0%	KIQTSTPF-HYLGMQI----	
consensus/100%		.....	
consensus/90%		.....	
consensus/80%		KhQhspP. pYLthpl	
consensus/70%		KIQTSTPF HYLGMQI	

Reference sequence (1): lcl|Query\_ProteinB  
Identities normalised by aligned length.  
Colored by: identity + property

```
1 [ . . . . . : . . . . . 80
1 lcl|Query_ProteinB 100.0% -----MGQVWGLVHFTLELFHT-----GNEEEQEYSEVTEEVTEHVYLPAKAKAAKEG
2 gi|767899321HERK8gag 36.5% MDVEVWEEVGSTLKKAYKGAEDIPITVMSVWALIHSTLEAFHTDDEEEGDKEERECDNVAAEEIKEQIRQLKE--TQEG
3 gi|768005179HERK8gag 36.5% MDVEVWEEVGSALKKAYKGAEDIPITVMSVWALIHSTLEAFHTDDEEEGDKEERECDNVAAEEIKEQIRQLKE--TQEG
4 gi|119623778hCG2040478 51.1% -----VRWGAWKHRVTMGQVWALVRSTLELFHTDDEEEG-----EYDEVTEEVTEQVYLPAKAKVAQEE
consensus/100% .....hhpVWuLl+.TLEhFHT....G....EhspVsEElpEplh.PhKt..spEt
consensus/90% .....hhpVWuLl+.TLEhFHT....G....EhspVsEElpEplh.PhKt..spEt
consensus/80% .....hhpVWuLl+.TLEhFHT....G....EhspVsEElpEplh.PhKt..spEt
consensus/70% .....h+.GA.ch.lThhpWAlLHSTLEhFHTDDEEEGscEEpEhDpVsEElpEQlh.PhKt..sQEG
```

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81 . . . . . 1 . . . . . : . . . . . 160
1 lcl|Query_ProteinB 100.0% EIHYPYSAPPYY-FDED--DPPHLSFLEDTGQKVIAPVTVRAAPHVTALSSIQAGIQQARQEGDLEAWQFPVRIHPPDQ
2 gi|767899321HERK8gag 36.5% EACPCPSAPPQYL-EDREWPDPLDLSFLEDTERKVVSPATVRAAPRVTLSSIQAGIQQARREGNLEAWKFPVRIHPPDQ
3 gi|768005179HERK8gag 36.5% EACPCPSAPPQYL-EDREWPDPLDLSFLEDTEQKVVSPATVRAEPRVTALSSIQAGIQQARREGNLEAWKFPVRIHPPDQ
4 gi|119623778hCG2040478 51.1% EVHYPYSAPPHYFEEKEWPDPPDLSFLEDTGKRVVAPVT---EQHLERLLSVLFRQEFSLDERVI-----
consensus/100% EhpPhPSAPP.Yh.-c-.DP.cLSFLEDTtpKVluPs...t.+lptL.Sl.ht.p.uR.-tp1.....
consensus/90% EhpPhPSAPP.Yh.-c-.DP.cLSFLEDTtpKVluPs...t.+lptL.Sl.ht.p.uR.-tp1.....
consensus/80% EhpPhPSAPP.Yh.-c-.DP.cLSFLEDTtpKVluPs...t.+lptL.Sl.ht.p.uR.-tp1.....
consensus/70% EspPhPSAPPpYh ED+EWDPD.DLSFLEDTtpKVluPsTVRatP+VTALSSIQAGIQQARpEGsLEAWpFPVRIHPPDQ
```

```
161 . . . . . 2 . . . . . . . . . . 240
1 lcl|Query_ProteinB 100.0% QGNIIATFEPFPFKSQETP*-----
2 gi|767899321HERK8gag 36.5% QGNVMAFTEAFPFKLLNEFKQAINQYGRSPFVWGLSKNVATSSQMIPIDGTLLEPVWLLLSFYSLRPGGQMKLLFKLP
3 gi|768005179HERK8gag 36.5% QGNVMAFTEAFPFKLLNEFKQAINQYGRSPFVWGLSKNVATSSQMIPIDGTLLEPVWLLLSFYSLRPGGQMKLLFKLP
4 gi|119623778hCG2040478 51.1% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% QGNlHATFESFPFK..pp.....
```

```
241 ] 250
1 lcl|Query_ProteinB 100.0% -----
2 gi|767899321HERK8gag 36.5% AVHKFNLQLM
3 gi|768005179HERK8gag 36.5% AVHKFNLQLM
4 gi|119623778hCG2040478 51.1% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....
```

Reference sequence (1): lcl|Query\_ProteinC-Transcript1and3  
Identities normalised by aligned length.  
Colored by: identity + property

```
1 [ . . . . . : . . . . . 80
-----
1 lcl|Query_ProteinC-Transcript1and3 100.0%
2 gi|119588514hCG2040415 17.9% -----KRGCSFFPALQPGPSVLSDGKEWPPGSIHYNIILQLDLFCRKREGKWSKI
3 gi|1034610826LOC107985332 12.6% MGNQSSVPPQDSPLGCILRNWDKFDQPALKRKRLLVFCNTVWPKYE-LEGQEAWPVGGSLNVNTIILQLDLYVCRQRKMWSEV
4 gi|119612025hCG1647242 12.5% MTQEPSAIM-----
5 gi|8272464gag 11.2% MGNIPPKAK-TPLRCILENWDQCDTQLTRKKRFIFFCSTAWPQYP-LQGRETWLPEGSINYNIILQLDLFCRKREGKMWSEV
6 gi|119605352hCG1789547 15.2%
consensus/100%
consensus/90%
consensus/80%
consensus/70%

81 . . . . . : . . . . . 160
-----
1 lcl|Query_ProteinC-Transcript1and3 100.0%
2 gi|119588514hCG2040415 17.9% PYVQAFFSLKENTLCKACNLYPTGGPLSLLPYPSLPI-APLPINDKTPLISPAQKAT--SKEISKGPQKPLGYQ----
3 gi|1034610826LOC107985332 12.6% PYVQTFMILRENPDFCKGCKIDP----ALLAILSRPLQRPPGGFNDFLVNPQPPLPETKEKEQAPPAPSSLYRTLSSL
4 gi|119612025hCG1647242 12.5% -----REVPEMVNLIKGTGDI
5 gi|8272464gag 11.2% PYVQTFFLRDNSQLCKKCGLCPTGSPSPPPYSPVPPPTSSTNKDPPLTQTVQKEI--DKGVNNEPKSANIPR----
6 gi|119605352hCG1789547 15.2%
consensus/100%
consensus/90%
consensus/80%
consensus/70%

161 . . . . . 2 . . . . . 240
-----
1 lcl|Query_ProteinC-Transcript1and3 100.0%
2 gi|119588514hCG2040415 17.9% -----LCPLQAVGGEEH-----VPFSLSDLKQIKAEELGKFSDNPDYIDVLQGLGQTFDLTWRDVMLL
3 gi|1034610826LOC107985332 12.6% HGSASTYTRSPGSRSGICLLPVV-SRPVGPVQVQVPSMQDLSQVKEGLGKFSENPGKFLGFRKLTTLTFELTWKDVAIL
4 gi|119612025hCG1647242 12.5% HNTE-----
5 gi|8272464gag 11.2% -----LCPLQAVRGGEGFPARVPVFPFSLSDLKQIKIDLGKFSNDPDGYIDVLQGLGQSFDLTWRDIMLL
6 gi|119605352hCG1789547 15.2%
consensus/100%
consensus/90%
consensus/80%
consensus/70%

241 . . . . . 3 . . . . . 320
-----
1 lcl|Query_ProteinC-Transcript1and3 100.0%
2 gi|119588514hCG2040415 17.9% -----MCIMEGFCRT
3 gi|1034610826LOC107985332 12.6% LDQTLAFNEKNVALAAAEFGDTWYLSQVNDMPAEERDKFPTGQEAIPSDPHWDPDSHDGWSHKHLLTCVLEGLRRI
4 gi|119612025hCG1647242 12.5% LGQTLGLEERQTIWEAARQCGDELHLADAN-----YPVATAVPLQDPNWDYDTPAGICARNHMLLCLIEGMKRS
5 gi|8272464gag 11.2% -----IQNDNGKVNLAGAKYRAPVGG-----LKATSTAARL
6 gi|119605352hCG1789547 15.2% LNQTLTPNERSAAVTAAREFGDLWYLSQVNNRMTTEERTT-PTGQAVPSVDPHWDTESEHGDWCHKHLLTCVLEGLRRT
consensus/100%
consensus/90%
consensus/80%
consensus/70%
hphhpsht+
hphhpsht+

321 . . . . . : . . . . . 4 400
-----
1 lcl|Query_ProteinC-Transcript1and3 100.0%
2 gi|119588514hCG2040415 17.9% KTKPLNYTKLSMIDE-----VF DENPAAFLERLREALVKHTCLSPDSVEGQLTLKDKFITQAAPDLRRKLQKRALG
3 gi|1034610826LOC107985332 12.6% RKMPMSYSVMSTITQ-----GKEENPSAFLKRLWKALRKYTSLSPNSVEGQLILKDKFITQSATDIRRKLQKRVLG
4 gi|119612025hCG1647242 12.5% QVKPVNYNKLATIDQ-----GPHENPTAFLELQETLIKHTNLDPGSEPGQLVLDKDFLTAAPDIRRKLRLMLALG
5 gi|8272464gag 11.2% KTRVSGFLGKGSLLTPDSSSELGPLGKEENPSAFLERLREALRKYTSLSPKLEGLILKDKFITQSTADIRRKLQKQALG
6 gi|119605352hCG1789547 15.2% RKKPMNYSMMSTITQ-----GKEENPTAFDLRLREALRKHSTLSPDSIEGQLILKDKFITQSAADIRKNFK----
consensus/100%
consensus/90%
consensus/80%
consensus/70%
htc+FloQuSSDIR+php
htc+FloQuSSDIR+php
phhs.sa.hhu.lsp s.cENPsAFLcRL.csLhKaTsLsPtS.EGQhLkD+FITQuAsDIR+kLph..IG
phhs.sa.hhu.lsp s.cENPsAFLcRL.csLhKaTsLsPtS.EGQhLkD+FITQuAsDIR+kLph..IG

401 . . . . . : . . . . . 480
-----
1 lcl|Query_ProteinC-Transcript1and3 100.0%
2 gi|119588514hCG2040415 17.9% PDSTLEDLLKVATLVFYNTDRE----AQERERKYRKDTEALMAT-----R-
3 gi|1034610826LOC107985332 12.6% PEQNL EALLNLATSVFYNRYQEEQ----AEKEKRDQRKAAALVMAL-----R-
4 gi|119612025hCG1647242 12.5% TRAPMSEILKFASSVFNDRDQDRDRAERKEKQKEERQAQLLAAL-----QVHQPPPQCPKDTFFPGNCYCGKPG
5 gi|8272464gag 11.2% PEQNL ETLNLATFVFNDRDQEEQ----AQKEKQDQRKAAALVMAL-----R-
6 gi|119605352hCG1789547 15.2% -----SLP
PQTNQQLLDTFMVMYNNCDLKEG----KRRQSEKWKQAKIMAAIIGDVLNARRASKENLKGHKDKASRDSFCCKKSG
consensus/100%
consensus/90%
consensus/80%
consensus/70%
th
th
spts.ptlLphh..Va.Np..c..cccpp.c+.tthlhAh t..
spts.ptlLphh..Va.Np..c..cccpp.c+.tthlhAh t..

481 . . . . . 5 . . . . . : . . . . . 560
-----
1 lcl|Query_ProteinC-Transcript1and3 100.0%
2 gi|119588514hCG2040415 17.9% -----QAH--KPQNSQGT PVNY*-----
3 gi|1034610826LOC107985332 12.6% -----QTNLGG-----
4 gi|119612025hCG1647242 12.5% HWKANCYPGRGPKCTACPLCRKLRWYKENCPCESQKGP-----
5 gi|8272464gag 11.2% -----QTNIDGSERTETEQAHLLEGLLIKDGEP EIHDCQIIVQTYATRDDL
6 gi|119605352hCG1789547 15.2% HWAKG--YTKPLPGQCCKGKTSHPY-WRTDCPCATMGLGQKTLAVQKEELED-----
consensus/100%
```

consensus/90% .....  
consensus/80% ..... .psp.....  
consensus/70% ..... .psp.....

561 . . . . . 6 . . . . . 640  
1 lcl|Query\_ProteinC-Transcript1and3 100.0% -----  
2 gi|119588514hCG2040415 17.9% -----  
3 gi|1034610826LOC107985332 12.6% -----  
4 gi|119612025hCG1647242 12.5% LEVPLTNPDLNLYTDGSSVVENGIRRAGYAIVSDVTILESKPLVPGTSAQLAELVALTRALELGKGIINVYTDISKYAYL  
5 gi|8272464gag 11.2% -----  
6 gi|119605352hCG1789547 15.2% -----  
consensus/100% .....  
consensus/90% .....  
consensus/80% .....  
consensus/70% .....

641 : . . . . . 7 . . . . . 720  
1 lcl|Query\_ProteinC-Transcript1and3 100.0% -----  
2 gi|119588514hCG2040415 17.9% -----  
3 gi|1034610826LOC107985332 12.6% -----  
4 gi|119612025hCG1647242 12.5% ILHAHAAIWKWEFLTSGNPHGCHREVMELLHMVQETKEVGVLVHYQSHQNGKERGEQQRKQLAESCIPFAALKIFFNII  
5 gi|8272464gag 11.2% -----  
6 gi|119605352hCG1789547 15.2% -----  
consensus/100% .....  
consensus/90% .....  
consensus/80% .....  
consensus/70% .....

721 . . . . . : . . . . . 8 800  
1 lcl|Query\_ProteinC-Transcript1and3 100.0% -----  
2 gi|119588514hCG2040415 17.9% -----  
3 gi|1034610826LOC107985332 12.6% -----  
4 gi|119612025hCG1647242 12.5% ASQLTHNNADIGTAGDCDLKQLKMSAYTTSCLMGVQGGPLPPSAPSLNCPFRSSGKVGSRKDRRPEPWSRYQVIRSPS  
5 gi|8272464gag 11.2% -----  
6 gi|119605352hCG1789547 15.2% -----  
consensus/100% .....  
consensus/90% .....  
consensus/80% .....  
consensus/70% .....

801 . . . . . : ] 857  
1 lcl|Query\_ProteinC-Transcript1and3 100.0% -----  
2 gi|119588514hCG2040415 17.9% -----  
3 gi|1034610826LOC107985332 12.6% -----  
4 gi|119612025hCG1647242 12.5% RCPLRTPLLPSGVRRSVKPAGLPVPAELKAKISQEHRRRQRRWRPDLALSPLGEP  
5 gi|8272464gag 11.2% -----  
6 gi|119605352hCG1789547 15.2% -----  
consensus/100% .....  
consensus/90% .....  
consensus/80% .....  
consensus/70% .....

Reference sequence (1): lcl|Query\_ProteinCTranscript2  
Identities normalised by aligned length.  
Colored by: identity + property

```
1 [ . . . . . : . . . . . 80
1 lcl|Query_ProteinCTranscript2 100.0% -----
2 gi|119588514hCG2040415 16.4% -----KRGCSFFPALQPGPSVLSGDEKWPPEGSIHYNIILQLDLFCRREGKWS
3 gi|1034610826LOC107985332 13.8% MGNSQSVVQD--SPLGCILRNWDKFDQPALKRKRLVFLCNTVWP-KYELEGQEAWPVGGSLNVNTILQLLDVYCRQQRKWS
4 gi|119612025hCG1647242 12.3% -----
5 gi|8272464gag 12.4% ---MGNIPPKAKTPLRCILENWDQCDTQTLRKKRFFFCSTAWP-QYPLQGRETWLPEGSINYNIILQLDLFCRKEGKWS
6 gi|119605352hCG1789547 19.6% -----
  consensus/100% -----
  consensus/90% -----
  consensus/80% -----
  consensus/70% -----

81 . . . . . : . . . . . 160
1 lcl|Query_ProteinCTranscript2 100.0% -----
2 gi|119588514hCG2040415 16.4% KIPYVQAFVFLKENTKLCKACNLYPTGGPLSLLPYPSLPI-APLPINDKTPILSPAQKATSKESKGPQKPLGYQLCPLQ
3 gi|1034610826LOC107985332 13.8% EVPVYQTFMILRENPDFCKGCKIDP----ALLAILSRPLQRPQPGGFNDFLVNPPQPLPETKEKEQAPPAPSSLYRTL
4 gi|119612025hCG1647242 12.3% -----
5 gi|8272464gag 12.4% EVPVYQTFVFLRDNSQLCKKCGLCPTGSPQSPPPYSPVPPPTPSSTNKDPLTQTVQKEIDKGVNNEPKSANIPRLCPLQ
6 gi|119605352hCG1789547 19.6% -----
  consensus/100% -----
  consensus/90% -----
  consensus/80% -----
  consensus/70% -----

161 . . . . . 2 . . . . . 240
1 lcl|Query_ProteinCTranscript2 100.0% -----
2 gi|119588514hCG2040415 16.4% AVGGEEH-----VPSLSDLKQIKAEKGFSDNPDRYIDVLQGLGQTFDLTWRDVML
3 gi|1034610826LOC107985332 13.8% SLHGSASTYTRSPGPRSGICLLPVVSRVPGVPVQVQVPSMQDLSQVKEGLGKFSENPGKFLGFRKLTTFELTWKDVAI
4 gi|119612025hCG1647242 12.3% -----M
5 gi|8272464gag 12.4% AVRGGEF-----GPARVPVPSLSDLKQIKIDLKGFSDNPDGYIDVLQGLGQSFDLTWRDVML
6 gi|119605352hCG1789547 19.6% -----
  consensus/100% -----
  consensus/90% -----
  consensus/80% -----
  consensus/70% -----

241 : . . . . . 3 . . . . . 320
1 lcl|Query_ProteinCTranscript2 100.0% -----
2 gi|119588514hCG2040415 16.4% LLDQTLAFNEKNVALAAQEFGDTWYLSQVND--RMPAEERDKFPTGQEAIPSMDPHPDSDHGDWSHKHLLTCVLEGL
3 gi|1034610826LOC107985332 13.8% LLGQTLSEERQTIWEAARQCDELHLADANY-----PVGATAVPLQDPNWDYDTPAGICARNHMLLCLIEGM
4 gi|119612025hCG1647242 12.3% TQEPSAIMREVPEMNILKGTGDIHNTEIQNDNGKVNLAGAKYRAPVQQLKATS-----TAARLKTRVSGFL
5 gi|8272464gag 12.4% LLNQLTLPNERSAAVTAAREFGDLWYLSQVNN--RMTTEERTT-PTGQAVPSVDPHWDTESEHGDWCHKHLTCVLEGL
6 gi|119605352hCG1789547 19.6% -----
  consensus/100% -----
  consensus/90% -----
  consensus/80% -----
  consensus/70% -----
  hp1.thh
  hp1.thh

321 : . . . . . 4 400
1 lcl|Query_ProteinCTranscript2 100.0% CRTKTKPLNYTKLSMIDEVFDENPAFLERLREALVKHTCLSPDSVFGQLTLKDKFITQAAAPDLRRKLRKRALGPDSTLE
2 gi|119588514hCG2040415 16.4% RRIRKMPMSYSVMSTITQKKEENPSAFLKRLWKALRKYTSLSPNSVFGQLTLKDKFITQSAADIRRLKQKRVLGPEQNL
3 gi|1034610826LOC107985332 13.8% KRSQVKPVNKNLATIDQGPHEPTAFLERLQETLIKHTNLDPGSPEGLVLDKDFITQAAAPDIRRLRMLALGTRAPMS
4 gi|119612025hCG1647242 12.3% GKGSLLTPDSSSELGPL--GKEENPSAFLERLREALRKYTSLSPKSLFGQLTLKDKFITQSTADIRRLKQKQALGPEQNL
5 gi|8272464gag 12.4% RKTRKPKMNSMMSTITQKKEENPTAFLDRLREALRKYTSLSPDSVFGQLTLKDKFITQSAADIRKNFKSLP-----
6 gi|119605352hCG1789547 19.6% -----MAKHFIQSAPDIRHKLHLKQLGIPQTNQN
  consensus/100% -----
  consensus/90% -----
  consensus/80% -----
  consensus/70% -----
  ht+cFloQussDLR+php
  ht+cFloQussDLR+php
  t+.phhs.s.s.hu.l.s.cENPSAFLcRL.csLhKaTsLsPtS.EGQLhLKD+FITQuAsDIR+kLpphsIGspts.p
  t+.phhs.s.s.hu.l.s.cENPSAFLcRL.csLhKaTsLsPtS.EGQLhLKD+FITQuAsDIR+kLpphsIGspts.p

401 : . . . . . 480
1 lcl|Query_ProteinCTranscript2 100.0% DLLKVATLVFYNTDLWEESDCRFPQNDAPISRKQLRPVIIHIRTAVRCTSSDRGGDIEEGQGSAGK--RAWSLAKA--
2 gi|119588514hCG2040415 16.4% ALLNLATSVFYNRYQEEQAE-----KEKRQDKAAALVMALRQTNLGG-----
3 gi|1034610826LOC107985332 13.8% EILKFASSVFNRYRQDERDR-----AERKEKQKEERQAQLLAALQVHQPDPGKPKDFFPGN-CYQCG-KPGHWKANC
4 gi|119612025hCG1647242 12.3% TLLNLATVFNRYRQEEQAE-----KEKQDKRKAALVMALRQTNIDGSETEQANHLEGLLIKDGPEIEH--
5 gi|8272464gag 12.4% -----
6 gi|119605352hCG1789547 19.6% QLLDTMFMVYNNCDLKEGKR--KQSEEKWQAKIMAAIGDVLNARRASKENLKGHKDKASRDSFCFKC-KSGHWAAGYT
  consensus/100% -----
  consensus/90% -----
  consensus/80% -----
  consensus/70% -----
  tllphh..Va.Np...Ettp .....ptK..t.h.htlh.Ahp.pp.s
  tllphh..Va.Np...Ettp .....ptK..t.h.htlh.Ahp.pp.s

481 . . . . . 5 . . . . . 560
1 lcl|Query_ProteinCTranscript2 100.0% -----PPLGLCPQT*-----
2 gi|119588514hCG2040415 16.4% -----
3 gi|1034610826LOC107985332 13.8% YGPRGEKPTACPLCRKRLRYWKENCPESQKGP-----
4 gi|119612025hCG1647242 12.3% -----DCQQIIVQTYATRDDLLVPLTNPDLNLYTDGSSVVENGIRRAGYAIIVSDVTILESKPLVPGTSAQLAELVALT
```

```

5 gi|8272464gag 12.4% -----
6 gi|119605352hCG1789547 19.6% KPLPG--PCCQCKGTSHPY-WRTDCPCATMGLGQKTLAVQKEELDED-----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

561 . . . 6 . . . 640
1 lcl|Query_ProteinCTranscript2 100.0% -----
2 gi|119588514hCG2040415 16.4% -----
3 gi|1034610826LOC107985332 13.8% -----
4 gi|119612025hCG1647242 12.3% RALELGKGKIINVYTDISKYAYLILHAHAAIWKEWFLTSGNPHGCHREVMELLHMVQETKEVGLHYQSHQNGKERGEQQ
5 gi|8272464gag 12.4% -----
6 gi|119605352hCG1789547 19.6% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

641 : . . . 7 . . . 720
1 lcl|Query_ProteinCTranscript2 100.0% -----
2 gi|119588514hCG2040415 16.4% -----
3 gi|1034610826LOC107985332 13.8% -----
4 gi|119612025hCG1647242 12.3% RKQLAESCIPIFAALKIFFNIIASQLTHNNADIGTAGDCDLKQLKMSAYTTSCLMGVQGGGLPLPPSAPSLNCLFRRSGK
5 gi|8272464gag 12.4% -----
6 gi|119605352hCG1789547 19.6% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

721 . . . : . . . . . ] 799
1 lcl|Query_ProteinCTranscript2 100.0% -----
2 gi|119588514hCG2040415 16.4% -----
3 gi|1034610826LOC107985332 13.8% -----
4 gi|119612025hCG1647242 12.3% VGSRKDRRPEPWSRYQVIRSPSRCPLRTPLLPSGVRRSVKPAGLPVPAELKAKISQEHSRRRQRRWRPDLALSPLGEP
5 gi|8272464gag 12.4% -----
6 gi|119605352hCG1789547 19.6% -----
consensus/100% .....
consensus/90% .....
consensus/80% .....
consensus/70% .....

```