## **The FASTA results**

### 1. TYMP (TP) alignment between

```
Query: NCBI Reference Sequence: NP_ 001244917.1; thymidine phosphorylase isoform 1
precursor [Homo sapiens]

Sbjct: NCBI Reference Sequence: XP_ 015362361.1; PREDICTED: thymidine phosphorylase,
partial [Marmota marmota marmota]


Identities       Positives        Gaps
266/310(86%)     286/310(92%)     0/310(0%)

Query  28   DPSPEPKQLPELIRMKRDGGRLSEADIRGFVAAVVNGSAQGAQIGAMLMAIRLRGMDLEE  87
            D  P  KQLP LIR KRDGGRLSE DI+GF++AVV GSAQGAQIGAMLMAIRL+GMDLEE
Sbjct  28   DSMPGAKQLPVLIRRKRDGGRLSEEDIKGFISAVVEGSAQGAQIGAMLMAIRLQGMDLEE  87

Query  88   TSVLTQALAQSGQQLEWPEAWRQQLVDKHSTGGVGDKVSLVLAPALAACGCKVPMISGRG  147
            TS LTQA+A+SG+QL+WP AW QQLVDKHSTGGVGDKVSL+LAPALAACGCKVPMISGRG
Sbjct  88   TSALTQAMARSGEQLQWPAAWHQQLVDKHSTGGVGDKVSLILAPALAACGCKVPMISGRG  147

Query  148  LGHTGGTLDKLESIPGFNVIQSPEQMQVLLDQAGCCIVGQSEQLVPADGILYAARDVTAT  207
            LGHTGGTLDKLESIPGFNVIQSP+QMQVLL+Q GCCIVGQS++LVPADGILYAARDVTAT
Sbjct  148  LGHTGGTLDKLESIPGFNVIQSPQQMQVLLEQVGCCIVGQSKELVPADGILYAARDVTAT  207

Query  208  VDSLPLITASILSKKLVEGLSALVVDVKFGGAAVFPNQEQARELAKTLVGVGASLGLRVA  267
            VDSLPLITASILSKK VEGLSALV+DVKFGGAAVFP+QE+ARELA+ LVGVGA LGLRVA
Sbjct  208  VDSLPLITASILSKKAVEGLSALVIDVKFGGAAVFPDQEKARELARALVGVGADLGLRVA  267

Query  268  AALTAMDKPLGRCVGHALEVEEALLCMDGAGPPDLRDLVTTLGGALLWLSGHAGTQAQGA  327
            AALTAMD PLGR VGH LEVEEALLC+DG GPPDLRDLVT LGG LLWLSGHAG+ AQG
Sbjct  268  AALTAMDNPLGRNVGHTLEVEEALLCLDGTGPPDLRDLVTRLGGVLLWLSGHAGSSAQGT  327

Query  328  ARVAAALDDG  337
            AR+A ALDDG
Sbjct  328  ARIATALDDG  337
```

## 2. UGT1A1 alignment between

```
Query: NCBI Reference Sequence: NP_000454.1; UDP-glucuronosyltransferase 1-1
precursor [Homo sapiens]

Sbjct: NCBI Reference Sequence: XP_015337083.1; PREDICTED: UDP-
glucuronosyltransferase 1-1 isoform X2 [Marmota marmota marmota]


Identities       Positives        Gaps
433/533(81%)     472/533(88%)     0/533(0%)

Query  1    MAVESQGGRPLVLGLLLCVLGPVVSHAGKILLIPVDGSHWLSMLGAIQQLQQRGHEIVVL  60
            MAV SQG   L+LGLLLCVL P +SHA K+L+IPVDGSHWLSM+G IQQLQ+RGHE+VV+
Sbjct  1    MAVVSQGPCTLLLGLLLCVLNPSISHAEKLLIIPVDGSHWLSMVGVIQQLQKRGHEMVVI  60

Query  61   APDASLYIRDGAFYTLKTYPVPFQREDVKESFVSLGHNVFENDSFLQRVIKTYKKIKKDS  120
             P+AS++I++ +FY+LK YPVPFQ+EDV+ SF  LG   FEN  FLQ V K Y+K +KDS
Sbjct  61   TPEASIHIKEASFYSLKKYPVPFQKEDVETSFAELGFYAFENVPFLQGVAKMYEKAQKDS  120

Query  121  AMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIVAQYLSLPTVFFLHALPCSLE  180
            A+LLSGCSHLLHNKE MASL ES FD +LTDPFLPC  IVAQYL LP V FL+ALPC L+
Sbjct  121  AVLLSGCSHLLHNKEFMASLVESDFDAVLTDPFLPCGSIVAQYLDLPAVNFLNALPCGLD  180

Query  181  FEATQCPNPFSYVPRPLSSHSDHMTFLQRVKNMLIAFSQNFLCDVVYSPYATLASEFLQR  240
             +ATQCP+P SYVPR LSS+SDHMTFLQRVKNMLIA  +NFLC +VYSPYA LAS+ LQR
Sbjct  181  LKATQCPSPLSYVPRALSSNSDHMTFLQRVKNMLIALLENFLCSMVYSPYAALASQVLQR  240

Query  241  EVTVQDLLSSASVWLFRSDFVKDYPRPIMPNMVFVGGINCLHQNPLSQEFEAYINASGEH  300
            ++T+QDLLSSASVWL R DFVKDYP PIMPNMVFVGGINCLH  P+SQEFEAY+NASGEH
Sbjct  241  DLTLQDLLSSASVWLMRKDFVKDYPMPIMPNMVFVGGINCLHTKPISQEFEAYVNASGEH  300

Query  301  GIVVFSLGSMVSEIPEKKAMAIADALGKIPQTVLWRYTGTRPSNLANNTILVKWLPQNDL  360
            GIVVFSLGSMVSEIPEKKAM IADALG+IPQTVLWRYTGT PSNLA NT LVKWLPQNDL
Sbjct  301  GIVVFSLGSMVSEIPEKKAMEIADALGRIPQTVLWRYTGTPPSNLAKNTKLVKWLPQNDL  360

Query  361  LGHPMTRAFITHAGSHGVYESICNGVPMVMMPLFGDQMDNAKRMETKGAGVTLNVLEMTS  420
            LGHP TRAFITHAGSHGVYE ICNGVPMVMMPLFGDQMDNAKRMET+GAGVTLNVLEMTS
Sbjct  361  LGHPKTRAFITHAGSHGVYEGICNGVPMVMMPLFGDQMDNAKRMETRGAGVTLNVLEMTS  420

Query  421  EDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKGAPHLRPAAHD  480
            +DL NALKAVINDKSYKENIMRLS LHKDRP+EPLDLAVFWVEFVMRHKGAPHLRPAAHD
Sbjct  421  DDLANALKAVINDKSYKENIMRLSRLHKDRPIEPLDLAVFWVEFVMRHKGAPHLRPAAHD  480

Query  481  LTWYQYHSLDVIGFLLAVVLTVAFITFKCCAYGYRKCLGKKGRVKKAHKSKTH  533
            LTWYQYHSLDVIGFLLA+VL VAFI FKCCAYG RKC GKKG VKK HKSK H
Sbjct  481  LTWYQYHSLDVIGFLLAIVLGVAFIAFKCCAYGCRKCFGKKGSVKKGHKSKAH  533
```

3. UGT1A9 alignment between

```
Query: NCBI Reference Sequence: NP_066307.1; UDP-glucuronosyltransferase 1-9
precursor [Homo sapiens]

Sbjct: NCBI Reference Sequence: XP_015337084.1; PREDICTED: UDP-
glucuronosyltransferase 1-9 isoform X3 [Marmota marmota marmota]


Identities        Positives         Gaps
429/521(82%)      463/521(88%)      0/521(0%)

Query  10   LPLCVCLLLTCGFAEAGKLLVVPMDGSHWFTMRSVVEKLILRGHEVVVVMPEVSWQLGRS  69
            LPLCVCLLL    A+AGKLLVVPMDGSHWFTMRSVVEKL+ RG+EVV VMPEVSWQLG+S
Sbjct  10   LPLCVCLLLASSSAQAGKLLVVPMDGSHWFTMRSVVEKLVHRGNEVVAVMPEVSWQLGQS  69

Query  70   LNCTVKTYSTSYTLEDLDREFKAFAHAQWKAQVRSIYSLLMGSYNDIFDLFFSNCRSLFK  129
            LN TVKTYSTSYTLEDLDR F  F   QWK   +S+YS  MGS    FD+ FS CRSLF
Sbjct  70   LNFTVKTYSTSYTLEDLDRGFNFFVDTQWKTPEQSMYSAAMGSSKAFFDITFSRCRSLFN  129

Query  130  DKKLVEYLKESSFDAVFLDPFDNCGLIVAKYFSLPSVVFARGILCHYLEEGAQCPAPLSY  189
            DKKLVEYLKE+SFDAVFLDPFD CGL+VAKYFSLPSVVFAR + C++LE+GAQCP+PLSY
Sbjct  130  DKKLVEYLKETSFDAVFLDPFDVCGLVVAKYFSLPSVVFARVVFCNFLEDGAQCPSPLSY  189

Query  190  VPRILLGFSDAMTFKERVRNHIMHLEEHLLCHRFFKNALEIASEILQTPVTEYDLYSHTS  249
            VPR+ L  SDA++F ER+RNH+ +LEE+L C  FF+ ALE+ASEIL+TPVT  DL+S  S
Sbjct  190  VPRVFLMSSDALSFMERIRNHLNYLEEYLFCPYFFQTALEVASEILRTPVTIGDLFSQIS  249

Query  250  IWLLRTDFVLDYPKPVMPNMIFIGGINCHQGKPLPMEFEAYINASGEHGIVVFSLGSMVS  309
            IWLLRTDFVL+YP+PVMPNMIF+GGINCHQ KPLP EFEAY+NASGEHGIVVFSLGSMVS
Sbjct  250  IWLLRTDFVLEYPRPVMPNMIFVGGINCHQRKPLPKEFEAYVNASGEHGIVVFSLGSMVS  309

Query  310  EIPEKKAMAIADALGKIPQTVLWRYTGTRPSNLANNTILVKWLPQNDLLGHPMTRAFITH  369
            EIPEKKAM IADALG+IPQTVLWRYTGT PSNLA NT LVKWLPQNDLLGHP TRAFITH
Sbjct  310  EIPEKKAMEIADALGRIPQTVLWRYTGTPPSNLAKNTKLVKWLPQNDLLGHPKTRAFITH  369

Query  370  AGSHGVYESICNGVPMVMMPLFGDQMDNAKRMETKGAGVTLNVLEMTSEDLENALKAVIN  429
            AGSHGVYE ICNGVPMVMMPLFGDQMDNAKRMET+GAGVTLNVLEMTS+DL NALKAVIN
Sbjct  370  AGSHGVYEGICNGVPMVMMPLFGDQMDNAKRMETRGAGVTLNVLEMTSDDLANALKAVIN  429

Query  430  DKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVI  489
            DKSYKENIMRLS LHKDRP+EPLDLAVFWVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVI
Sbjct  430  DKSYKENIMRLSRLHKDRPIEPLDLAVFWVEFVMRHKGAPHLRPAAHDLTWYQYHSLDVI  489

Query  490  GFLLAVVLTVAFITFKCCAYGYRKCLGKKGRVKKAHKSKTH  530
            GFLLA+VL VAFI FKCCAYG RKC GKKG VKK HKSK H
Sbjct  490  GFLLAIVLGVAFIAFKCCAYGCRKCFGKKGSVKKGHKSKAH  530
```

4. UGT2B4 alignment between

```
Query: NCBI Reference Sequence: NP_066962.2; UDP-glucuronosyltransferase 2B4 isoform
1 precursor [Homo sapiens]

Sbjct: NCBI Reference Sequence: XP_015337650.1 PREDICTED: UDP-glucuronosyltransferase
2B4-like [Marmota marmota marmota]


Identities       Positives        Gaps
54/115(47%)      60/115(52%)      44/115(38%)
Query  250  MAKADIWLIRNYWDFQFPHPLLPNVEFVGGLHCKPAKPLPKEMEEFVQSSGENGVVVFSL  309
            MAKADIWLI  YWD +F H  LPNV+ VGGLHC+PAK LP
Sbjct  1    MAKADIWLICTYWDLEFSHSTLPNVDIVGGLHCRPAKSLP--------------------  40

Query  310  GSMVSNTSEERANVIASALAKIPQKVLWRFDGNKPDTLGLNTRLYKWIPQNDLLG  364
                                    K+LWRFDG KPDTLGLN +LYKWIP+ DLLG
Sbjct  41   ------------------------KILWRFDGKKPDTLGLNIQLYKWIPKGDLLG  71
```

## 5. UGT2B4 alignment (alternative)

```
Query: NCBI Reference Sequence: NP_066962.2; UDP-glucuronosyltransferase 2B4 isoform
1 precursor [Homo sapiens]

Sbjct: NCBI Reference Sequence: XP_015360783.1; PREDICTED: UDP-
glucuronosyltransferase 2B15-like [Marmota marmota marmota]


Identities       Positives        Gaps
388/530(73%)     455/530(85%)     2/530(0%)

Query  1     MSMKWTSALLLIQLSCYFSSGSCGKVLVWPTEFSHWMNIKTILDELVQRGHEVTVLASSA  60
             MS+K  S LLLIQL CYFSSGSCGKVLVWPTE+SHW+NIK ILDEL+QRGHEVTVL S+A
Sbjct  1     MSVKRNSVLLLIQLMCYFSSGSCGKVLVWPTEYSHWINIKAILDELLQRGHEVTVLTSTA  60

Query  61    SISFDPNSPSTLKFEVYPVSLTKTEFEDIIKQLVKRWA-ELPKDTFWSYFSQVQEIMWTF  119
             SI  +PN+ S + FEVYP   +K   E+   + +  W  + PKD FW ++S VQ++   +
Sbjct  61    SILINPNTTSAINFEVYPAPSSKQHLEERFSKWIHEWIYDTPKDDFWEFYSLVQKVFKDY  120

Query  120   NDILRKFCKDIVSNKKLMKKLQESRFDVVLADAVFPFGELLAELLKIPFVYSLRFSPGYA  179
             +D + + C+++V NKKLM KL ES+FDVVLADAV P GELLAELLKIPFVY+LRF+ GY
Sbjct  121   SDTIEQLCRNVVLNKKLMMKLHESKFDVVLADAVGPCGELLAELLKIPFVYTLRFTFGYT  180

Query  180   IEKHSGGLLFPPSYVPVVMSELSDQMTFIERVKNMIYVLYFEFWFQIFDMKKWDQFYSEV  239
              EK+SGGL  PPSYVP+VMSELSDQMTF+ERVKN +Y+LYF+FWFQIFD+K+W+QFYSEV
Sbjct  181   YEKYSGGLTVPPSYVPIVMSELSDQMTFMERVKNTVYMLYFDFWFQIFDVKRWNQFYSEV  240

Query  240   LGRPTTLSETMAKADIWLIRNYWDFQFPHPLLPNVEFVGGLHCKPAKPLPKEMEEFVQSS  299
             LGRPTT+ ETM KAD WLIR YWD +FP PLLPN +FVGGLHCKPAKPLPKEMEEFVQSS
Sbjct  241   LGRPTTIYETMGKADFWLIRTYWDLEFPRPLLPNFDFVGGLHCKPAKPLPKEMEEFVQSS  300

Query  300   GENGVVVFSLGSMVSNTSEERANVIASALAKIPQKVLWRFDGNKPDTLGLNTRLYKWIPQ  359
             GENG+VVFSLG+MVSN  EE+AN+IA ALA+IPQKV+WRF+G KPD LG NT++Y+WIPQ
Sbjct  301   GENGIVVFSLGTMVSNMPEEKANMIAFALAQIPQKVIWRFNGKKPDKLGPNTQIYEWIPQ  360

Query  360   NDLLGHPKTRAFITHGGANGIYEAIYHGIPMVGVPLFADQPDNIAHMKAKGAAVSLDFHT  419
             NDLLGHPKT+AFITHGG NG+YEAIYHG+PMVG+PLFADQPDNIAH+KAKGAA+ LD+
Sbjct  361   NDLLGHPKTKAFITHGGTNGVYEAIYHGVPMVGIPLFADQPDNIAHVKAKGAAIRLDYRI  420

Query  420   MSSTDLLNALKTVINDPLYKENAMKLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVA  479
             ++S DLL AL+ VINDP YKENAM+LSRI HDQPVKPLDRAVFWIEFVMRHKGAKHL+VA
Sbjct  421   LTSADLLKALRMVINDPSYKENAMELSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLQVA  480

Query  480   AHDLTWFQYHSLDVTGFLLACVATVIFIITK-CLFCVWKFVRTGKKGKRD  528
             AHDL+WFQY+SLDV GFLLACVATV+FII+K CLFC   F +TGKK KR+
Sbjct  481   AHDLSWFQYYSLDVIGFLLACVATVMFIISKCCLFCFQMFFKTGKKEKRE  530
```

### 6. UGT2B15 alignment between

Query: NCBI Reference Sequence: NP_001067.2; UDP-glucuronosyltransferase 2B15 precursor [Homo sapiens]

Sbjct: NCBI Reference Sequence: XP_015360783.1; PREDICTED: UDP-glucuronosyltransferase 2B15-like [Marmota marmota marmota]

```
Identities       Positives        Gaps
392/530(74%)     459/530(86%)     0/530(0%)

Query  1    MSLKWTSVFLLIQLSCYFSSGSCGKVLVWPTEYSHWINMKTILEELVQRGHEVTVLTSSA  60
            MS+K  SV LLIQL CYFSSGSCGKVLVWPTEYSHWIN+K IL+EL+QRGHEVTVLTS+A
Sbjct  1    MSVKRNSVLLLIQLMCYFSSGSCGKVLVWPTEYSHWINIKAILDELLQRGHEVTVLTSTA  60

Query  61   STLVNASKSSAIKLEVYPTSLTKNYLEDSLLKILDRWIYGVSKNTFWSYFSQLQELCWEY  120
            S L+N + +SAI  EVYP   +K +LE+   K +  WIY   K+ FW ++S +Q++  +Y
Sbjct  61   SILINPNTTSAINFEVYPAPSSKQHLEERFSKWIHEWIYDTPKDDFWEFYSLVQKVFKDY  120

Query  121  YDYSNKLCKDAVLNKKLMMKLQESKFDVILADALNPCGELLAELFNIPFLYSLRFSVGYT  180
             D   +LC++ VLNKKLMMKL ESKFDV+LADA+ PCGELLAEL  IPF+Y+LRF+ GYT
Sbjct  121  SDTIEQLCRNVVLNKKLMMKLHESKFDVVLADAVGPCGELLAELLKIPFVYTLRFTFGYT  180

Query  181  FEKNGGGFLFPPSYVPVVMSELSDQMIFMERIKNMIHMLYFDFWFQIYDLKKWDQFYSEV  240
            +EK  GG   PPSYVP+VMSELSDQM FMER+KN ++MLYFDFWFQI+D+K+W+QFYSEV
Sbjct  181  YEKYSGGLTVPPSYVPIVMSELSDQMTFMERVKNTVYMLYFDFWFQIFDVKRWNQFYSEV  240

Query  241  LGRPTTLFETMGKAEMWLIRTYWDFEFPRPFLPNVDFVGGLHCKPAKPLPKEMEEFVQSS  300
            LGRPTT++ETMGKA+ WLIRTYWD EFPRP LPN DFVGGLHCKPAKPLPKEMEEFVQSS
Sbjct  241  LGRPTTIYETMGKADFWLIRTYWDLEFPRPLLPNFDFVGGLHCKPAKPLPKEMEEFVQSS  300

Query  301  GENGIVVFSLGSMISNMSEESANMIASALAQIPQKVLWRFDGKKPNTLGSNTRLYKWLPQ  360
            GENGIVVFSLG+M+SNM EE ANMIA ALAQIPQKV+WRF+GKKP+ LG NT++Y+W+PQ
Sbjct  301  GENGIVVFSLGTMVSNMPEEKANMIAFALAQIPQKVIWRFNGKKPDKLGPNTQIYEWIPQ  360

Query  361  NDLLGHPKTKAFITHGGTNGIYEAIYHGIPMVGIPLFADQHDNIAHMKAKGAALSVDIRT  420
            NDLLGHPKTKAFITHGGTNG+YEAIYHG+PMVGIPLFADQ DNIAH+KAKGAA+ +D R
Sbjct  361  NDLLGHPKTKAFITHGGTNGVYEAIYHGVPMVGIPLFADQPDNIAHVKAKGAAIRLDYRI  420

Query  421  MSSRDLLNALKSVINDPVYKENVMKLSRIHHDQPMKPLDRAVFWIEFVMRHKGAKHLRVA  480
            ++S DLL AL+ VINDP YKEN M+LSRI HDQP+KPLDRAVFWIEFVMRHKGAKHL+VA
Sbjct  421  LTSADLLKALRMVINDPSYKENAMELSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLQVA  480

Query  481  AHNLTWIQYHSLDVIAFLLACVATVIFIITKFCLFCFRKLAKKGKKKKRD  530
            AH+L+W QY+SLDVI FLLACVATV+FII+K CLFCF+   K GKK+KR+
Sbjct  481  AHDLSWFQYYSLDVIGFLLACVATVMFIISKCCLFCFQMFFKTGKKEKRE  530
```

## 7. GUSB (β-glucuronidase) alignment between

```
Query: >NP_000172.2; beta-glucuronidase isoform 1 precursor [Homo sapiens]

Sbjct: >XP_015346866.1; PREDICTED: beta-glucuronidase [Marmota marmota marmota]


Identities       Positives        Gaps
471/575(82%)     514/575(89%)     1/575(0%)

Query  77   MPVPSSFNDISQDWRLRHFVGWVWYEREVILPERWTQDLRTRVVLRIGSAHSYAIVWVNG  136
            MPVPSSFND+ QD +LR FVGWVWYERE +LP+RWTQDL TRVVLRIGSAH YAIVWVNG
Sbjct  1    MPVPSSFNDVGQDAQLRSFVGWVWYEREAVLPQRWTQDLGTRVVLRIGSAHYYAIVWVNG  60

Query  137  VDTLEHEGGYLPFEADISNLVQVGPLPSRLRITIAINNTLTPTTLPPGTIQYLTDTSKYP  196
            V   EHEGG+LPFEADIS LVQ GPL S  RITIAINNTLTP TLPPGTI Y TDTSKYP
Sbjct  61   VHVAEHEGGHLPFEADISKLVQSGPL-SSCRITIAINNTLTPHTLPPGTILYKTDTSKYP  119

Query  197  KGYFVQNTYFDFFNYAGLQRSVLLYTTPTTYIDDITVTTSVEQDSGLVNYQISVKGSNLF  256
            KGYFVQ+  FDFFNYAGL RSV LYTTPTTYIDDITVTT V+QD+GLVNYQI  +GS
Sbjct  120  KGYFVQDINFDFFNYAGLHRSVTLYTTPTTYIDDITVTTGVDQDTGLVNYQIFTQGSEHV  179

Query  257  KLEVRLLDAENKVVANGTGTQGQLKVPGVSLWWPYLMHERPAYLYSLEVQLTAQTSLGPV  316
            +L+VRLLDA+ +VVA+G+G QGQL+VP   LWWPYLMHE PAYLYSLEV++TAQT  GPV
Sbjct  180  QLDVRLLDADGRVVADGSGGQGQLQVPAAHLWWPYLMHEHPAYLYSLEVRMTAQTEAGPV  239

Query  317  SDFYTLPVGIRTVAVTKSQFLINGKPFYFHGVNKHEDADIRGKGFDWPLLVKDFNLLRWL  376
            +DFYTLPVGIRTVAVT+SQFLINGKPFYFHGVNKHED+D+RGKGFDW LL+KDFNLLRWL
Sbjct  240  ADFYTLPVGIRTVAVTESQFLINGKPFYFHGVNKHEDSDVRGKGFDWALLMKDFNLLRWL  299

Query  377  GANAFRTSHYPYAEEVMQMCDRYGIVVIDECPGVGLALPQFFNNVSLHHHMQVMEEVVRR  436
            GANAFRTSHYPYAEEVMQ+CDRYGIVVIDECPGVG+ LPQ + N SL HH+QVMEE+VRR
Sbjct  300  GANAFRTSHYPYAEEVMQLCDRYGIVVIDECPGVGIVLPQSYGNASLQHHLQVMEELVRR  359

Query  437  DKNHPAVVMWSVANEPASHLESAGYYLKMVIAHTKSLDPSRPVTFVSNSNYAADKGAPYV  496
            DKNHPA+VMWSVANEP S L+ AGYYLK VIAHTK+LDP+RPVTFV+NSN+  D GAPYV
Sbjct  360  DKNHPAIVMWSVANEPTSSLKPAGYYLKTVIAHTKALDPTRPVTFVTNSNFEGDLGAPYV  419

Query  497  DVICLNSYYSWYHDYGHLELIQLQLATQFENWYKKYQKPIIQSEYGAETIAGFHQDPPLM  556
            DVIC+NSYYSWYHDYGHLE+IQLQL TQFE WY+ Y KPIIQSEYGAETIAGFH+DPPLM
Sbjct  420  DVICVNSYYSWYHDYGHLEVIQLQLRTQFEGWYRTYHKPIIQSEYGAETIAGFHEDPPLM  479

Query  557  FTEEYQKSLLEQYHLGLDQKRRKYVVGELIWNFADFMTEQSPTRVLGNKKGIFTRQRQPK  616
            FTEEYQKSLLEQYHL LDQKR++YVVGELIWNFADFMT QSP R +GN+KGIFTRQRQPK
Sbjct  480  FTEEYQKSLLEQYHLVLDQKRKEYVVGELIWNFADFMTNQSPQRPVGNRKGIFTRQRQPK  539

Query  617  SAAFLLRERYWKIANETRYPHSVAKSQCLENSLFT  651
            SAAFLLRERYWK+ANETRY  SVAKSQCL N  FT
Sbjct  540  SAAFLLRERYWKLANETRYHPSVAKSQCLGNGPFT  574
```