Multiple sequence alignment

Block 1 (positions 1–80)

```
Turt1             MAFVRCSIFILLLGIWPLVWA-SDSVEPSFDHQLNSPESKDGKERIDGSLIPLVSSPSSSSLSSSSSPLTPSSPSSSVAT   79
Turt2             -MLLKNGSFLFLSLLFLCVTWNSVSGSDNIDSPFNQQILDSHEIKSNESYFLDNQRSIIPLSTSPKFNKKNNIYSN        75
Dpul              -----------MAVLMTVLAYCQP--------------------------ASAAATAVTDDDELMAR                 30
Phum              MNARIIQNFLLFSFAFSFVLSSAEIVIPIRRNIEDSNISVSSILTNYSTTVTDSDKSSSDDYHHHQGNNYVSNRENYVIN    80
Aaeg              MNTIRIGTLVLLMLNIYFSYADPGVKSDVTKNIRDKRDHYYSEGSNFNPLLDTDGTSKVANDVPTDNDDGEDDALVSLDD    80
Smar              --MMNFRGIWSLRLSIFIIFF                                                               19
Amel              --MIIHSIFLLMVSITLVIA      EESDNVLFDKRAPTGHQEMQGKQNSASLNSENF                         51
Nvit              PAAARLRATTMLLTLLTLGVSAQHSMTTTINGQTDRDSEIILETKAPQEPEELDGYQASQALDSTKHLREPSSSYLLLLT    80
Bmor              --MGTYRACLVFLILQVISIA      TAQEMIKRIPQGFLGMRGKKHEDDSSE                              46
Dmel              ---MRPLSGLIALALLLLLLTAPSSAAD    TETESSGSPLTPGAEEPRR                                 45
Tcas              HYYTITRVYLFSPLSILTMHSTTITTAVVLATIYVVCAAEDHHKRAPSGFTGVRGKKSIPDYSTGNSDSDSIPELKDIVS    80
Lmig              --MCRVGALLLLAALMSADPA    AAQRQEAGEPRAAAPFLGMRTAAAAADADGGAADGL                        55
Rpro              --MPVGSLLVMSCVLAACLA                                                                18
Znev                                                                                                   0
Znev2             TPRVRCRACAVLVVTLSLVAV           VLCAPEESPKRAPSGFLGVRGKKDSAFVSEEAYNDV                 57
Tcas8509_10-290   -YYTITRVYLFSPLSILTMHSTTITTAVVLATIYVVCAAEDHHKRAPSGFTGVRGKKSIPDYSTGNSDSDSIPELKDIVS    79
```

Consensus: M X M M R I R A L L L L X L L X L L V L A X X I S X A D V X X X I Y X X C A A E D X E K R A P S G F L G X R G K K S S X D L S S G N S D X D X S X E L X X X V X

Block 2 (positions 81–160)

```
Turt1             LLNSNNNNLYDLYGTKGNSYLATSADENEKNFADDYV-VDLPGRRFIPLRGRKDDFFHPRSDSFYTAFRKKAA---FTGM   155
Turt2             --NVKENNFYDLYGIRESTY----SPENGNNL----IDLPGRKFIQL----DQHLNDWI---RRRSA----FNGM        129
Dpul              --QTRGLVLRSWRNAQQQT--HSADKTPSAKVAEPILPQKEA-MVFNGLPISMRLVLLQHLAGY----DKRTPSRAFLGM   101
Phum              KENINKRNRMSFTGMRGKK---ENNNDIILDNYNEPCKGKRAP-LAFHGMRGKKSD--EYETKW-----TKPPFGLNFL   148
Aaeg              EFHYFHPNPDS--GVEGKLNYDWNNDDTNENRLDVGKKRAP-SGFLGLRGK-------YYYNG-AKRVP-SGFTGM      146
Smar              --------FGPIFGQQVQSLNDKIKNMQLDEDNLLRKSR-NVFMGMRGKKMSMDQDRDLQRAATSIKRIN--GFMAM     85
Amel              --GIFKRALMGFQGVRGKK---SIINDVKNELFPEDIN-KRAP-MGFQGMRGKKAS---FDDEYYK---RAP-MGFQGM   116
Nvit              EELDKRASMRGFQGMRGKK----SVDPTSSFLAGYSSKRAP-MGFQGMRGKKSSADLEEDAYY--K-RAP-MGFQGM    148
Bmor              --QYYKRKPQFFVGVKGKKFYDYLEN-PDGYF----KRAP-LGFTGVRGKKEDMSSEYQYYPYEALK-RDGLIGQIEY   115
Dmel              --VVKRAPTSSFIGMRGKK---DEEHDTSEGNWLGSGPDKKAP-LAFVGLRGKKFIPINRLSDVLQSLRLRDSLQDFFDR   120
Tcas              DLAVDKRAPSGFMGMRGKKFSLWEGTYPDGVF----KRAP-SGFMGMRGKKDMEFANYADEYIK---RAP-SGFMGM    148
Lmig              --LEKRAPSLGFHGVRGKK----DDLQELED-----KRAPSLGFHGVRGKKDDANGLDDDDF----DKRAPMRGFQSV   118
Rpro              ---QERRAMGFVGMRGKK----DTPDMEEY-----KRAPSMGFQGVRGKKDDLIGEPDDTFLEEFK-RAPAMGFQGM    82
Znev              --MEKRAPAMGFQGVRGKK---DD-----KRGPSMGFHGMRGKKDA---DSRAEFLQELK-RAPSMGFMGM          57
Znev2             --MEKRAPAMGFQGVRGKK---DD-----KRGPSMGFHGMRGKKDA---DSRAEFLQELK-RAPSMGFMGM          114
Tcas8509_10-290   DLAVDKRAPSGFMGMRGKKFSLWEGTYPDGVF----KRAP-SGFMGMRGKKDMEFANYADE----IKRAP-SGFMGM   147
```

Consensus: X L N V K R R X P M G F Q G X R G K K F X D W X D D X P X G N F L E D X L X K R A P S M G F H G M R G K K D D X F X E Y D D E Y X Q E L K K R A P S M G F M G M

Block 3 (positions 161–240)

```
Turt1             RGKK-------MDLSSPVNNRQGALIRNMMNR-                   NGYGAMDDSPLIS---FANLNDVGAYK    204
Turt2             RGKK-------VNLPLPSSPYTLRNSF                         GIYHWNRTND-LIVKRA              165
Dpul              RGKKSPPGADALTMEDNQL-DDASGWPQGDI-LPDTYYFGPAPQKKKMHGKFLGMRGKKMMNGTAFIPNWRERYIYQ    176
Phum              PTNQLLITSGLFEDGDDILEYPEYTNIKKENS-ESMIGDDDVTVKRSPY-SFQGMRGKKGSVD--MNLKRT           215
Aaeg              RGNKNSIHNIFDEVENPYI-FPGD          KRAK-GFLGMRGKKQPSG--MNRWSN                       214
Smar              RGKK-SLEEILDEIKKKTTRFQDSRSKDVYLIQNILDKKDELLGEWEKRAPM-GFYGTRGKKIILD-ALLDKRGV       131
Amel              RGKK-SLEEILDEIKKKTTRFQDSRSKDVYLIQNILDKKDELLGEWEKRAPM-GFYGTRGKKIILD-ALLDKRGV       188
Nvit              RGKKSAIEEVLEELEKRAMGFQGMRGKKSPEP   SVWNKRAPM-GFQGMRGKKSSFLDELLEKRAL              211
Bmor              TSAE-HINDGQYPILNDILEYLQKLERQETNSDTNETEEQRITNEVEKRAANMQFYGVRGKKSVDNPPYLSIRGK-     189
Dmel              VAGR----DGSAVGKRAPTGFTGMRGKRPALLGDDDAEADEATELQQKRAPVNSFVGMRGKKDVSHQHYYDLRGKQQRFA 196
Tcas              RGKKDYDSSSSQLDKRAPMGFMGMRGKKDYDE-         IADEKRAPS-GFFGMRGKKMPRQAGFFGMRGKKYPYQ   216
Lmig              RGKKEAEVEDAELGDGDYLQLAGLPYREDYDAADSDGEELQLDDPWQKRALK-GFFGTRGKKAPQA-GFYGVRGKKGPSG  196
Rpro              RGKK----TPAMGFMGMRGKKDSDY-     GWDKRAPASGFFGMRGKKAPAS-GFFGMRGKKGPS              138
Znev              RGKKEALDFDYFDKRAPSLGFQGMRGRRDGEYDEDLEAGLQDAEEFSKRAPAAGFFGTRGKKVPAN-GFFGTRGKKGPS-  135
Znev2             RGKKEALDFDYFDKRAPSLGFQGMRGRRDGEYDEDLEAGLQDAEEFSKRAPAAGFFGTRGKKVPAN-GFFGTRGKKGPS-  192
Tcas8509_10-290   RGKKDYDSSSSQLDKRAPMGFMGMRGKKDYDE-        EKRAPS-GFFGMRGKKMPRQAGFFGMRGKKYPYQ       212
```

Consensus: R G K K E A I X X D S F X D K R P X L G F Q G M R G X K D Y D Y D X D L E E X L Q D X E E W E K R A P X A G F F G M R G K K X P A D A G F F G X R G K K G P X Q

Block 4 (positions 241–~312)

```
Turt1             RSRPFAAMRGKRS-                       IQTSNLLPF-----FANLNDVGAYK                       226
Turt2             -RPFAAMLGKRY-                        ALRRGKARFYASRG-                                 190
Dpul              EPNSFMGMRGKRSPTDYQFFNDDIIVDEELPDVDSKVSPRRSQERTPI-                                   224
Phum              --MGFLGMRGKKVPE--MLWHTDNKYDKREPQMSFFGMKG---KKAQSGFFGMRGKKQSYFNGNDDGKKTL            279
Aaeg              DYTSYFGMQGNKEPLGSDKIYSQLNRMNWPVNDRLQMDRT-PPKRVPNGFLGVRGKK--WTDTIYDE                 278
Smar              -SKFFAMRGKRD                                                                        142
Amel              MDFIGLQRKKDTTDDYLDYAINPFDYEKRSTDFQDVESESFKRAPMGFHGMRGKRDAYQDMRNRGSNFP               257
Nvit              -LGFHGMRGKKN       GVAELAYEPADMDGYV---EKRPMMMGFHGMRGKRSAFYGRQEEQQQ                   266
Bmor              ----FIGVRGKKD        VKNSNGKEIKFLLSRPFPKRRGQMGFFGMRGKK-WIDGMNDPRY                    241
Dmel              DFSKFVAVRGKKS-DLEGNGVGIGDDHEQALVHPWLYLWGEKRAPNGFLGMRGKRPALFE----                    255
Tcas              FRGKFVGVRGKKA--    SPDDYYNVDLDTVGQEL-DLNQLMLLLTENEGESDIWNGNNEVGQYSQ                  276
Lmig              FYSGFYGVRGKKAPSGFHGVRGKKEDGAPAPDLDSLLYYL-NTKKAPVGFYGTRGK-KSWAP-                     256
Rpro              -SAFFGMRGKKAPSGFMGVRGKRD         SPDDLNHLLGLGDRGLKRFAGLSDSFGKRPAELL                  198
Znev              -AGFFAMRGKKAPSGFMEYQG       PPVDLDTLLNYLPGSKKAPIGFLGTRGK-KDWPTQQVVASSEG             197
Znev2             -AGFFAMRGKKAPSGFMEYQG       PPVDLDTLLNYLPGSKKAPIGFLGTRGK-KDWPTQQVVASSEG             254
Tcas8509_10-290   FRGKFVGVRGKKA--      SPDDYYNVDLDTVGQEL-DLNQLMLLLTENEGESDIWNGNNEVGQYSQ                272
```

Consensus: F X S G F F G M R G K K A P S G F M E X X G X X P D D Y X P V D L D T L L Q Y L P G L K R A P X G F L G M R G K X X X W P X X X E V G X Y X X