Results colour-coded for transmembrane structure

The current colourscheme of the alignment is for **transmembrane structure type**.

The transmembrane structure for each sequence is represented by a colour. If a sequence in the alignment has no colours assigned, this means that no prediction was possible for that sequence (if this was requested).
The colour assignment is:

TM SEGMENT (T)   You have selected to perform transmembrane structure prediction using **PHOBIUS** (Kall et. al, 2005).

```
                        . . . . . . . . . 10 . . . . . . . . . 20 . . . . . . . . . 30 . . . . . . . . . 40 . . . . . . . . . 50
(PRED)  gi_13633932_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_118573879_sp ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13633915_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_341942042_sp ---------- ---------- ---------- ---------- ----------
(PRED)  gi_82121811_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_21264062_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959533_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959566_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959559_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13633872_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959539_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_21264049_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_66774168_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959527_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_51338669_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_60414603_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_117949830_sp ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13633871_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13633914_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_75041393_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_110826300_sp ---------- ---------- ---------- ---------- ----------
(PRED)  gi_21264050_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_341942043_sp ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959528_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959561_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_116256078_sp ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959531_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959540_sp_ MFRSKRSGLV RRLWRSRVVP DREEGSG-GG GGVDEDGSLG SRAEPAPRAR
(PRED)  gi_115502451_sp MFRSKRSGLV RRLWRSRVVP DREEGGSGGG GGGDEDGSLG SRAEPAPRAR
(PRED)  gi_13959573_sp_ MFRSKRSGLV RRLWRSRVIP ERDGGDGNGQ SSERNATAVT AEG-------
(PRED)  gi_13959541_sp_ MFRTKRSALV RRLWRSRAPG GEDEEEGVGG GGGG--GELR GEG-------
(PRED)  gi_13959538_sp_ MFRTKRSALV RRLWRSRAPG GEDEEEGAGG GGGG--GELR GEG-------
(PRED)  gi_13959529_sp_ MFRTKRSALV RRLWRSRAPG GEDEEEGVGG GGGG--GGLR GEG-------

                        . . . . . . . . . 60 . . . . . . . . . 70 . . . . . . . . . 80 . . . . . . . . . 90 . . . . . . . . . 100
(PRED)  gi_13633932_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_118573879_sp ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13633915_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_341942042_sp ---------- ---------- ---------- ---------- ----------
(PRED)  gi_82121811_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_21264062_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959533_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959566_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959559_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13633872_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959539_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_21264049_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_66774168_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959527_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_51338669_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_60414603_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_117949830_sp ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13633871_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13633914_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_75041393_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_110826300_sp ---------- ---------- ---------- ---------- ----------
(PRED)  gi_21264050_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_341942043_sp ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959528_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959561_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_116256078_sp ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959531_sp_ ---------- ---------- ---------- ---------- ----------
(PRED)  gi_13959540_sp_ EGGGCSRSEV RSVAPRRPRD AVGPRGAAIA GRRRRTGGLP RPVSESGAGA
```

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(PRED) gi_115502451_sp EGGGCGRSEV  RPVAPRRPRD  AVGQRGAQGA  GRRRRAGGPP  RPMSEPGAGA
(PRED) gi_13959573_sp_ ----------  ----------  ----------  ----------  ----------
(PRED) gi_13959541_sp_ ----------  ----------  ----------  ----------  ----------
(PRED) gi_13959538_sp_ ----------  ----------  ----------  ----------  ----------
(PRED) gi_13959529_sp_ ----------  ----------  ----------  ----------  ----------


                       .........110.........120.........130.........140.........150
(PRED) gi_13633932_sp_ ----------  ----------  -----M---N  VTSLFS----  ----------
(PRED) gi_118573879_sp ----------  ----------  -----M---N  VTSLFS----  ----------
(PRED) gi_13633915_sp_ ----------  ----------  -----M---N  VTSLFS----  ----------
(PRED) gi_341942042_sp ----------  ----------  -----M---N  VTSLFS----  ----------
(PRED) gi_82121811_sp_ ----------  ----------  -----M--TS  MASLFS----  ----------
(PRED) gi_21264062_sp_ ----------  ----------  -----M--TS  MSSLFS----  ----------
(PRED) gi_13959533_sp_ ----------  ----------  -----M--TS  MASLFS----  ----------
(PRED) gi_13959566_sp_ ----------  ----------  -----M--TS  MASLFS----  ----------
(PRED) gi_13959559_sp_ ----------  ----------  -----M--TS  MASLFS----  ----------
(PRED) gi_13633872_sp_ ----------  ----------  -----M---N  VTSLFS----  ----------
(PRED) gi_13959539_sp_ ----------  ----------  --MHST--TP  ISSLFS----  ----------
(PRED) gi_21264049_sp_ ----------  ----------  -----M---N  VTSLFS----  ----------
(PRED) gi_66774168_sp_ ----------  ----------  --MHPS--TP  ISSLFS----  ----------
(PRED) gi_13959527_sp_ ----------  ----------  --MHPS--TP  ISSLFS----  ----------
(PRED) gi_51338669_sp_ ----------  ----------  ----------  MSSILP----  ----------
(PRED) gi_60414603_sp_ ----------  ----------  ----------  MSSILP----  ----------
(PRED) gi_117949830_sp ----------  ----------  ----------  MSSILP----  ----------
(PRED) gi_13633871_sp_ ----------  ----------  ----------  MSSILP----  ----------
(PRED) gi_13633914_sp_ ----------  ----------  ----------  MSSILP----  ----------
(PRED) gi_75041393_sp_ ----------  ----------  ----------  MSSILP----  ----------
(PRED) gi_110826300_sp ----------  ----------  ----------  MSSILP----  ----------
(PRED) gi_21264050_sp_ ----------  ----------  ----------  MSSILP----  ----------
(PRED) gi_341942043_sp ----------  ----------  --MDNMSITN  TPTSND----  ----------
(PRED) gi_13959528_sp_ ----------  ----------  --MDNMSITN  TPTSND----  ----------
(PRED) gi_13959561_sp_ ----------  ----------  --MDNMSITN  TPTSND----  ----------
(PRED) gi_116256078_sp ----------  ----------  --MDNMSITN  TPTSND----  ----------
(PRED) gi_13959531_sp_ ----------  ----------  --MDNMSITN  TPTSND----  ----------
(PRED) gi_13959540_sp_ GGSPLDVAEP  GGPGWLPESD  CETVTCCLFS  ERDAAGAPRD  SGDPQARQSP
(PRED) gi_115502451_sp GSSLLDVAEP  GGPGWLPESD  CETVTCCLFS  ERDAAGAPRD  ASDPLAGAAL
(PRED) gi_13959573_sp_ -------QRM  AQPRRAQEGE  GRPVRCCLFA  ERPGPELPPP  PPPPPPGG--
(PRED) gi_13959541_sp_ -------ATD  GRAYGAGGGG  AGRAGCCLGK  AVRGAK----  ----------
(PRED) gi_13959538_sp_ -------ATD  SRAHGAGGGG  PGRAGCCLGK  AVRGAK----  ----------
(PRED) gi_13959529_sp_ -------ATD  GRAYGAGGGG  AGRAGCCLGK  AVRGAK----  ----------


                       .........160.........170.........180.........190.........200
(PRED) gi_13633932_sp_ --------FT  SPAVKRLLGW  KQ--------  ------GDEE  EKWAEKAVDA
(PRED) gi_118573879_sp --------FT  SPAVKRLLGW  KQ--------  ------GDEE  EKWAEKAVDA
(PRED) gi_13633915_sp_ --------FT  SPAVKRLLGW  KQ--------  ------GDEE  EKWAEKAVDA
(PRED) gi_341942042_sp --------FT  SPAVKRLLGW  KQ--------  ------GDEE  EKWAEKAVDA
(PRED) gi_82121811_sp_ --------FT  SPAVKRLLGW  KQ--------  ------GDEE  EKWAEKAVDA
(PRED) gi_21264062_sp_ --------FT  SPAVKRLLGW  KQ--------  ------GDEE  EKWAEKAVDA
(PRED) gi_13959533_sp_ --------FT  SPAVKRLLGW  KQ--------  ------GDEE  EKWAEKAVDA
(PRED) gi_13959566_sp_ --------FT  SPAVKRLLGW  KQ--------  ------GDEE  EKWAEKAVDA
(PRED) gi_13959559_sp_ --------FT  SPAVKRLLGW  KQ--------  ------GDEE  EKWAEKAVDA
(PRED) gi_13633872_sp_ --------FT  SPAVKRLLGW  KQ--------  ------GDEE  EKWAEKAVDA
(PRED) gi_13959539_sp_ --------FT  SPAVKRLLGW  KQ--------  ------GDEE  EKWAEKAVDS
(PRED) gi_21264049_sp_ --------FT  SPAVKRLLGW  KQ--------  ------GDEE  EKWAEKAVDA
(PRED) gi_66774168_sp_ --------FT  SPAVKRLLGW  KQ--------  ------GDEE  EKWAEKAVDS
(PRED) gi_13959527_sp_ --------FT  SPAVKRLLGW  KQ--------  ------GDEE  EKWAEKAVDS
(PRED) gi_51338669_sp_ --------FT  PPIVKRLLGW  KK--------  ---GEQNGQE  EKWCEKAVKS
(PRED) gi_60414603_sp_ --------FT  PPIVKRLLGW  KK--------  ---GEQNGQE  EKWCEKAVKS
(PRED) gi_117949830_sp --------FT  PPVVKRLLGW  KKSAGGSG-G  AGGGEQNGQE  EKWCEKAVKS
(PRED) gi_13633871_sp_ --------FT  PPVVKRLLGW  KKSAGGSG-G  AGGGEQNGQE  EKWCEKAVKS
(PRED) gi_13633914_sp_ --------FT  PPVVKRLLGW  KKSAGGSG-G  AGGGEQNGQE  EKWCEKAVKS
(PRED) gi_75041393_sp_ --------FT  PPVVKRLLGW  KKSAGGSG-G  AGGGEQNGQE  EKWCEKAVKS
(PRED) gi_110826300_sp --------FT  PPVVKRLLGW  KKSAGGSG-G  AGGGEQNGQE  EKWCEKAVKS
(PRED) gi_21264050_sp_ --------FT  PPVVKRLLGW  KKSASGSSGA  GGGGEQNGQE  EKWCEKAVKS
(PRED) gi_341942043_sp --------AC  LSIVHSLMCH  RQ--------  ------GGES  ETFAKRAIES
(PRED) gi_13959528_sp_ --------AC  LSIVHSLMCH  RQ--------  ------GGES  ETFAKRAIES
(PRED) gi_13959561_sp_ --------AC  LSIVHSLMCH  RQ--------  ------GGES  ETFAKRAIES
(PRED) gi_116256078_sp --------AC  LSIVHSLMCH  RQ--------  ------GGES  ETFAKRAIES
(PRED) gi_13959531_sp_ --------AC  LSIVHSLMCH  RQ--------  ------GGES  ETFAKRAIES
(PRED) gi_13959540_sp_ EPEEGGGPRS  REARSRLLLL  ----------  ----------  EQELKTVTYS
(PRED) gi_115502451_sp EP--AGGGRS  REARSRLLLL  ----------  ----------  EQELKTVTYS
(PRED) gi_13959573_sp_ --------AS  PPGPGGGEAR  SR--------  ------LVLL  ERELKAVTYA
(PRED) gi_13959541_sp_ --------GH  HHPHPPTSGA  GA--------  ------AGGA  EADLKALTHS
(PRED) gi_13959538_sp_ --------GH  HHPHPPAAGA  GA--------  ------AGGA  EADLKALTHS
(PRED) gi_13959529_sp_ --------GH  HHPHPPSSGA  GA--------  ------AGGA  EADLKALTHS
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Results colour-coded for transmembrane structure

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              . . . . . . . . . 210 . . . . . . . . . 220 . . . . . . . . . 230 . . . . . . . . . 240 . . . . . . . . . 250
(PRED) gi_13633932_sp_ LVKKLKKKKG  AMEELEKALS  CPG-QPSNCV  TIP-------  ----------
(PRED) gi_118573879_sp LVKKLKKKKG  AMEELEKALS  CPG-QPSNCV  TIP-------  ----------
(PRED) gi_13633915_sp_ LVKKLKKKKG  AMEELEKALS  CPG-QPSNCV  TIP-------  ----------
(PRED) gi_341942042_sp LVKKLKKKKG  AMEELEKALS  CPG-QPSNCV  TIP-------  ----------
(PRED) gi_82121811_sp_ LVKKLKKKKG  AMEELEKALS  SPG-QPSKCV  TIP-------  ----------
(PRED) gi_21264062_sp_ LVKKLKKKKG  AMEDLEKALS  SPG-QPSKCV  TIP-------  ----------
(PRED) gi_13959533_sp_ LVKKLKKKKG  AMEELEKALS  SPG-QPSKCV  TIP-------  ----------
(PRED) gi_13959566_sp_ LVKKLKKKKG  AMEELEKALS  SPG-QPSKCV  TIP-------  ----------
(PRED) gi_13959559_sp_ LVKKLKKKKG  AMEELEKALS  SPG-QPSKCV  TIP-------  ----------
(PRED) gi_13633872_sp_ LVKKLKKKKG  AMEELEKALS  CPG-QPSNCV  TIP-------  ----------
(PRED) gi_13959539_sp_ LVKKLKKKKG  AMDELERALS  CPG-QPSKCV  TIP-------  ----------
(PRED) gi_21264049_sp_ LVKKLKKKKG  AMEELERALS  CPG-QPSNCV  TIP-------  ----------
(PRED) gi_66774168_sp_ LVKKLKKKKG  AMDELERALS  CPG-QPSNCV  TIP-------  ----------
(PRED) gi_13959527_sp_ LVKKLKKKKG  AMDELERALS  CPG-QPSKCV  TIP-------  ----------
(PRED) gi_51338669_sp_ LVKKLKK-TG  QLDELEKAIT  TQN-VNTKCI  TIP-------  ----------
(PRED) gi_60414603_sp_ LVKKLKK-TG  QLDELEKAIT  TQN-INTKCI  TIP-------  ----------
(PRED) gi_117949830_sp LVKKLKK-TG  RLDELEKAIT  TQN-CNTKCV  TIPSTCSEIW  GLSTANTVDQ
(PRED) gi_13633871_sp_ LVKKLKK-TG  RLDELEKAIT  TQN-CNTKCV  TIPSTCSEIW  GLSTANTVDQ
(PRED) gi_13633914_sp_ LVKKLKK-TG  RLDELEKAIT  TQN-CNTKCV  TIPSTCSEIW  GLSTPNTIDQ
(PRED) gi_75041393_sp_ LVKKLKK-TG  RLDELEKAIT  TQN-CNTKCV  TIPSTCSEIW  GLSTPNTIDQ
(PRED) gi_110826300_sp LVKKLKK-TG  RLDELEKAIT  TQN-CNTKCV  TIPSTCSEIW  GLSTPNTIDQ
(PRED) gi_21264050_sp_ LVKKLKK-TG  QLDELEKAIT  TQN-RNTKCV  TIPSNCSEIW  GLSTPNTIEQ
(PRED) gi_341942043_sp LVKKLKEKKD  ELDSLITAIT  TNGAHPSKCV  TIQ-------  ----------
(PRED) gi_13959528_sp_ LVKKLKEKKD  ELDSLITAIT  TNGAHPSKCV  TIQ-------  ----------
(PRED) gi_13959561_sp_ LVKKLKEKKD  ELDSLITAIT  TNGAHPSKCV  TIQ-------  ----------
(PRED) gi_116256078_sp LVKKLKEKKD  ELDSLITAIT  TNGAHPSKCV  TIQ-------  ----------
(PRED) gi_13959531_sp_ LVKKLKEKKD  ELDSLITAIT  TNGAHPSKCV  TIQ-------  ----------
(PRED) gi_13959540_sp_ LLKRLKE--R  SLDTLLEAVE  SRGGVPGGCV  LVP-------  ----------
(PRED) gi_115502451_sp LLKRLKE--R  SLDTLLEAVE  SRGGVPGGCV  LVP-------  ----------
(PRED) gi_13959573_sp_ LLKRLKE--R  SLHSLLQAVE  SRGGTPGGCV  LVA-------  ----------
(PRED) gi_13959541_sp_ VLKKLKE--R  QLELLLQAVE  SRGGTRTACL  LLP-------  ----------
(PRED) gi_13959538_sp_ VLKKLKE--R  QLELLLQAVE  SRGGTRTACL  LLP-------  ----------
(PRED) gi_13959529_sp_ VLKKLKE--R  QLELLLQAVE  SRGGTRTACL  LLP-------  ----------


              . . . . . . . . . 260 . . . . . . . . . 270 . . . . . . . . . 280 . . . . . . . . . 290 . . . . . . . . . 300
(PRED) gi_13633932_sp_ ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_118573879_sp ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_13633915_sp_ ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_341942042_sp ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_82121811_sp_ ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_21264062_sp_ ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_13959533_sp_ ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_13959566_sp_ ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_13959559_sp_ ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_13633872_sp_ ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_13959539_sp_ ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_21264049_sp_ ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_66774168_sp_ ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_13959527_sp_ ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_51338669_sp_ ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_60414603_sp_ ----------  ---RSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_117949830_sp WDTTGLYSFS  EQTRSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_13633871_sp_ WDTTGLYSFS  EQTRSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_13633914_sp_ WDTTGLYSFS  EQTRSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_75041393_sp_ WDTTGLYSFS  EQTRSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_110826300_sp WDTTGLYSFS  EQTRSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_21264050_sp_ WDTSGLYSYP  DQTRSLDGRL  ----------  -QVS-HRKGL  PH--------
(PRED) gi_341942043_sp ----------  ---RTLDGRL  ----------  -QVA-GRKGF  PH--------
(PRED) gi_13959528_sp_ ----------  ---RTLDGRL  ----------  -QVA-GRKGF  PH--------
(PRED) gi_13959561_sp_ ----------  ---RTLDGRL  ----------  -QVA-GRKGF  PH--------
(PRED) gi_116256078_sp ----------  ---RTLDGRL  ----------  -QVA-GRKGF  PH--------
(PRED) gi_13959531_sp_ ----------  ---RTLDGRL  ----------  -QVA-GRKGF  PH--------
(PRED) gi_13959540_sp_ ----------  ------RADL  ----------  -RL-GGQPAP  PQ--------
(PRED) gi_115502451_sp ----------  ------RADL  ----------  -RL-GGQPAP  PQ--------
(PRED) gi_13959573_sp_ ----------  ------RGEL  ----------  -RLGAARRPP  PH--------
(PRED) gi_13959541_sp_ ----------  ---GRLDCRL  GPGAPASAQP  AQP-PSSYSL  P---------
(PRED) gi_13959538_sp_ ----------  ---GRLDCRL  ----------  -GP-GAPAGA  QPAQPPSSYS
(PRED) gi_13959529_sp_ ----------  ---GRLDCRL  GPGAPASAQP  AQP-PSSYSL  P---------


              . . . . . . . . . 310 . . . . . . . . . 320 . . . . . . . . . 330 . . . . . . . . . 340 . . . . . . . . . 350
(PRED) gi_13633932_sp_ --VIYCRVWR  WPDLQSHHEL  KPLECCE-FP  FGSKQKEVCI  NPYHYKRVES
(PRED) gi_118573879_sp --VIYCRVWR  WPDLQSHHEL  KPLECCE-FP  FGSKQKEVCI  NPYHYKRVES
(PRED) gi_13633915_sp_ --VIYCRVWR  WPDLQSHHEL  KPLECCE-FP  FGSKQKEVCI  NPYHYKRVES
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Results colour-coded for transmembrane structure

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(PRED) gi_341942042_sp--VIYCRVWR   WPDLQSHHEL   KPLECCE-FP   FGSKQKEVCI   NPYHYKRVES
(PRED) gi_82121811_sp_--VIYCRVWR   WPDLQSHHEL   KPLDICE-FP   FGSKQKEVCI   NPYHYKRVES
(PRED) gi_21264062_sp_--VIYCRVWR   WPDLQSHHEL   KPLEVCE-YP   FGSKQKEVCI   NPYHYKRVES
(PRED) gi_13959533_sp_--VIYCRVWR   WPDLQSHHEL   KPLDICE-FP   FGSKQKEVCI   NPYHYKRVES
(PRED) gi_13959566_sp_--VIYCRVWR   WPDLQSHHEL   KPLDICE-FP   FGSKQKEVCI   NPYHYKRVES
(PRED) gi_13959559_sp_--VIYCRVWR   WPDLQSHHEL   KPLDICE-FP   FGSKQKEVCI   NPYHYKRVES
(PRED) gi_13633872_sp_--VIYCRVWR   WPDLQSHHEL   KPLECCE-FP   FGSKQKEVCI   NPYHYKRVES
(PRED) gi_13959539_sp_--VIYCRVWR   WPDLQSHHEL   KPLECCE-FP   FGSKQKEVCI   NPYHYRRVET
(PRED) gi_21264049_sp_--VIYCRVWR   WPDLQSHHEL   KALECCE-FP   FGSKQKDVCI   NPYHYKRVDS
(PRED) gi_66774168_sp_--VIYCRVWR   WPDLQSHHEL   KPLECCE-FP   FGSKQKEVCI   NPYHYRRVET
(PRED) gi_13959527_sp_--VIYCRVWR   WPDLQSHHEL   KPLECCE-FP   FGSKQKEVCI   NPYHYRRVET
(PRED) gi_51338669_sp_--VIYCRLWR   WPDLHSHHEL   RAMELCE-FA   FNMKKDEVCV   NPYHYQRVET
(PRED) gi_60414603_sp_--VIYCRLWR   WPDLHSHHEL   RAMEMCE-YA   FNMKKDEVCV   NPYHYQRVET
(PRED) gi_117949830_sp--VIYCRLWR   WPDLHSHHEL   KAIENCE-YA   FNLKKDEVCV   NPYHYQRVET
(PRED) gi_13633871_sp_--VIYCRLWR   WPDLHSHHEL   KAIENCE-YA   FSLKKDEVCV   NPYHYQRVET
(PRED) gi_13633914_sp_--VIYCRLWR   WPDLHSHHEL   KAIENCE-YA   FNLKKDEVCV   NPYHYQRVET
(PRED) gi_75041393_sp_--VIYCRLWR   WPDLHSHHEL   KAIENCE-YA   FNLKEDEVCV   NPYHYQRVET
(PRED) gi_110826300_sp--VIYCRLWR   WPDLHSHHEL   KAIENCE-YA   FNLKKDEVCV   NPYHYQRVET
(PRED) gi_21264050_sp_--VIYCRLWR   WPDLHSHHEL   RAIETCE-YA   FNLKKDEVCV   NPYHYQRVET
(PRED) gi_341942043_sp--VIYARLWR   WPDLH-KNEL   KHVKYCQ-YA   FDLKCDSVCV   NPYHYERVVS
(PRED) gi_13959528_sp_--VIYARLWR   WPDLH-KNEL   KHVKYCQ-YA   FDLKCDSVCV   NPYHYERVVS
(PRED) gi_13959561_sp_--VIYARLWR   WPDLH-KNEL   KHVKYCQ-YA   FDLKCDSVCV   NPYHYERVVS
(PRED) gi_116256078_sp--VIYARLWR   WPDLH-KNEL   KHVKYCQ-YA   FDLKCDSVCV   NPYHYERVVS
(PRED) gi_13959531_sp_--VIYARLWR   WPDLH-KNEL   KHVKYCQ-YA   FDLKCDSVCV   NPYHYERVVS
(PRED) gi_13959540_sp_--LLLGRLFR   WPDLQHAVEL   KPLCGCHSFT   AAADGPTVCC   NPYHFSRLCG
(PRED) gi_115502451_sp--LLLGRLFR   WPDLQHAVEL   KPLCGCHSFA   AAADGPTVCC   NPYHFSRLCG
(PRED) gi_13959573_sp_--LLLGKLFR   WPDLQHPAEL   KALCECQ-SF   GAADGPTVCC   NPYHFSRLCG
(PRED) gi_13959541_sp_--LLLCKVFR   WPDLRHSSEV   KRLCCCE-SY   GKINPELVCC   NPHHLSRLCE
(PRED) gi_13959538_sp_LPLLLCKVFR   WPDLRHSSEV   KRLCCCE-SY   GKINPELVCC   NPHHLSRLCE
(PRED) gi_13959529_sp_--LLLCKVFR   WPDLRHSSEV   KRLCCCE-SY   GKINPELVCC   NPHHLSRLCE


                       ........ 360........ 370........ 380........ 390........ 400
(PRED) gi_13633932_sp_PVLPPVLVPR   HSEYNPQHSL   LAQFRNL---   ---------G   -QNEPHMPHN
(PRED) gi_118573879_spPVLPPVLVPR   HSEYNPQHSL   LAQFRNL---   ---------G   -QNEPHMPLN
(PRED) gi_13633915_sp_PVLPPVLVPR   HSEYNPQHSL   LAQFRNL---   ---------G   -QNEPHMPLN
(PRED) gi_341942042_spPVLPPVLVPR   HSEYNPQHSL   LAQFRNL---   ---------G   -QNEPHMPLN
(PRED) gi_82121811_sp_PVLPPVLVPR   HSEFNPQHSL   LVQFRNL---   ---------S   -HNEPHMPHN
(PRED) gi_21264062_sp_PVLPPVLVPR   HSEFNPQHSL   LVQFRNL---   ---------S   -HNEPHMPLN
(PRED) gi_13959533_sp_PVLPPVLVPR   HNEFNPQHSL   LVQFRNL---   ---------S   -HNEPHMPQN
(PRED) gi_13959566_sp_PVLPPVLVPR   HNEFNPQHSL   LVQFRNL---   ---------S   -HNEPHMPQN
(PRED) gi_13959559_sp_PVLPPVLVPR   HNEFNPQHSL   LVQFRNL---   ---------S   -HNEPHMPQN
(PRED) gi_13633872_sp_PVLPPVLVPR   HSEYNPQHSL   LAQFRNL---   ---------G   -QNEPHMPLN
(PRED) gi_13959539_sp_PVLPPVLVPR   HSEYNPQLSL   LAKFRSA---   ---------S   LHSEPLMPHN
(PRED) gi_21264049_sp_PVLPPVLVPR   NSEFNAKLSM   LPRFRNP---   ---------L   HQTEPPMPQN
(PRED) gi_66774168_sp_PVLPPVLVPR   HSEYNPQLSL   LAKFRSA---   ---------S   LHSEPLMPHN
(PRED) gi_13959527_sp_PVLPPVLVPR   HSEYNPQLSL   LAKFRSA---   ---------S   LHSEPLMPHN
(PRED) gi_51338669_sp_PVLPPVLVPR   HTEIPAEFPP   LDDY------   ----------   ---SHSIPEN
(PRED) gi_60414603_sp_PVLPPVLVPR   HTEIPAEFPP   LDDY------   ----------   ---SHSIPEN
(PRED) gi_117949830_spPVLPPVLVPR   HTEILTELPP   LDDY------   ----------   ---THSIPEN
(PRED) gi_13633871_sp_PVLPPVLVPR   HTEILTELPP   LDDY------   ----------   ---THSIPEN
(PRED) gi_13633914_sp_PVLPPVLVPR   HTEILTELPP   LDDY------   ----------   ---THSIPEN
(PRED) gi_75041393_sp_PVLPPVLVPR   HTEILTELPP   LDDY------   ----------   ---THSIPEN
(PRED) gi_110826300_spPVLPPVLVPR   HTEILTELPP   LDDY------   ----------   ---THSIPEN
(PRED) gi_21264050_sp_PVLPPVLVPR   HTEILTELPP   LDDY------   ----------   ---TNSIPEN
(PRED) gi_341942043_spPGIDLSGLTL   QSN-APSMLV   KDEYVHDFEG   QPSLPTEGHS   IQTIQHPPSN
(PRED) gi_13959528_sp_PGIDLSGLTL   QSNAPPSMLV   KDEYVHDFEG   QPSLPTEGHS   IQTIQHPPSN
(PRED) gi_13959561_sp_PGIDLSGLTL   QSNAPSSMMV   KDEYVHDFEG   QPSLSTEGHS   IQTIQHPPSN
(PRED) gi_116256078_spPGIDLSGLTL   QSNAPPSMLV   KDEYVHDFEG   QPSLSTEGHS   IQTIQHPPSN
(PRED) gi_13959531_sp_PGIDLSGLTL   QSNAPSGMLV   KDEYVHDFEG   QPSLATEGHS   IQTIQHPPSN
(PRED) gi_13959540_sp_PESPP---PP   YSRLSPP---   ----------   ----------   -----DQYKP
(PRED) gi_115502451_spPESPP---PP   YSRLSPR---   ----------   ----------   -----DEYKP
(PRED) gi_13959573_sp_PESPP---PP   YSRLSPN---   ----------   ----------   -----DEQKP
(PRED) gi_13959541_sp_LESPP---PP   YSRYPMD---   ----------   ----------   -----FLKPT
(PRED) gi_13959538_sp_LESPP---PP   YSRYPMD---   ----------   ----------   -----FLKPT
(PRED) gi_13959529_sp_LESPP---PP   YSRYPMD---   ----------   ----------   -----FLKPT


                       ........ 410........ 420........ 430........ 440........ 450
(PRED) gi_13633932_sp_ATFPDSFQQP   NSHPFPHSPN   ------SSYP   NSPGSSSSTY   PHSPAS----
(PRED) gi_118573879_spATFPDSFQQP   NSHPFPHSPN   ------SSYP   NSPGSSSSTY   PHSPTS----
(PRED) gi_13633915_sp_ATFPDSFQQP   NSHPFPHSPN   ------SSYP   NSPGSSSSTY   PHSPTS----
(PRED) gi_341942042_spATFPDSFQQP   NSHPFPHSPN   ------SSYP   NSPGGSSSTY   PHSPTS----
(PRED) gi_82121811_sp_ATFPDSFQQP   NSTPFSISPN   ------SPYP   PSPA--SSTY   PSSPAS----
(PRED) gi_21264062_sp_ATFPESFQQH   SGGSSFPISP   ------NSPY   PPSPASSGTY   PNSPAS----
(PRED) gi_13959533_sp_ATFPDSFHQP   NSTPFPLSPN   ------SPYP   PSPA--SSTY   PNSPAS----
(PRED) gi_13959566_sp_ATFPDSFHQP   NNTPFPLSPN   ------SPYP   PSPA--SSTY   PNSPAS----
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Results colour-coded for transmembrane structure   4

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(PRED) gi_13959559_sp_ATFPDSFHQP  NNAPFPLSPN  ------SPYP  PSPA--SSTY  PNSPAS----
(PRED) gi_13633872_sp_ATFPDSFQQP  HSHPFAQYPN  ------SSYP  NSPGSSSSTY  PHSPTS----
(PRED) gi_13959539_sp_ATYPDSFQQP  PCSALPPSPS  ------HAFS  QSPC--TASY  PHSPGS----
(PRED) gi_21264049_sp_ATFPDSFPQQ  PANALPFTPN  SPTNSYPSSP  NSGTGSTATF  PHSPSS----
(PRED) gi_66774168_sp_ATYPDSFQQS  LCPAP-----  ----------  ----------  ----------
(PRED) gi_13959527_sp_ATYPDSFQQS  LGPAP-----  ----------  ----------  ----------
(PRED) gi_51338669_sp_TNFPAGI-EP  QSNI-PETPP  ------PGYL  SEDG--ETSD  HQMNHS----
(PRED) gi_60414603_sp_TNFPAGI-EP  QSNYIPETPP  ------PGYL  SEDG--ETSD  HQMNPS----
(PRED) gi_117949830_spTNFPAGI-EP  QSNYIPETPP  ------PGYI  SEDG--ETSD  QQLNQS----
(PRED) gi_13633871_sp_TNFPAGI-EP  QSNYIPETPP  ------PGYI  SEDG--ETSD  QQLNQS----
(PRED) gi_13633914_sp_TNFPAGI-EP  QSNYIPETPP  ------PGYI  SEDG--ETSD  QQLNQS----
(PRED) gi_75041393_sp_TNFPAGI-EP  QSNYIPETPP  ------PGYI  SEDG--ETSD  QQLNQS----
(PRED) gi_110826300_spTNFPAGI-EP  QSNYIPETPP  ------PGYI  SEDG--ETSD  QQLNQS----
(PRED) gi_21264050_sp_TNFPTGI-EP  PNNYIPETPP  ------PGYI  SEDG--EASD  QQMNQS----
(PRED) gi_341942043_spRASTETYSAP  ALLAPAESNA  TSTTNFPNIP  VASTSQPASI  LAGSHSEGLL
(PRED) gi_13959528_sp_RASTETYSAP  ALLAPSESNA  TSTTNFPNIP  VASTSQPASI  LAGSHSEGLL
(PRED) gi_13959561_sp_RASTETYSTP  ALLAPSESNA  TSTANFPNIP  VASTSQPASI  LGGSHSEGLL
(PRED) gi_116256078_spRASTETYSTP  ALLAPSESNA  TSTTNFPNIP  VASTSQPASI  LAGSHSEGLL
(PRED) gi_13959531_sp_RASTETYSTP  ALLAPSESNA  TSTTNFPNIP  VASTSQPASI  LAGSHSEGLL
(PRED) gi_13959540_sp_LDLSDSTLSY  TETEATNSL-  ----------  ----------  ----------
(PRED) gi_115502451_spLDLSDSTLSY  TETEATNSL-  ----------  ----------  ----------
(PRED) gi_13959573_sp_LDLSDSTLSY  TETEATNSP-  ----------  ----------  ----------
(PRED) gi_13959541_sp_AGCPDAVPSS  AETGGTN---  ----------  ----------  ----------
(PRED) gi_13959538_sp_ADCPDAVPSS  AETGGTN---  ----------  ----------  ----------
(PRED) gi_13959529_sp_ADCPDAVPSS  DETGGTN---  ----------  ----------  ----------


                 .........460.........470.........480.........490.........500
(PRED) gi_13633932_sp_---SDPGSPF  QMPADTPPPA  YLPPEDQMTH  DTSQPMDT--  -NMMAPGIHP
(PRED) gi_118573879_sp---SDPGSPF  QMPADTPPPA  YLPPEDPMTQ  DGSQPMDT--  -NMMAPSLPS
(PRED) gi_13633915_sp_---SDPGSPF  QMPADTPPPA  YLPPEDPMTQ  DGSQPMDT--  -NMMAPPLPS
(PRED) gi_341942042_sp---SDPGSPF  QMPADTPPPA  YLPPEDPMAQ  DGSQPMDT--  -NMMAPPLPA
(PRED) gi_82121811_sp_---SGPSSPF  QLPADTPPPA  YMPPDDQMGQ  DNSQSMDTS-  -NTMIPQIMP
(PRED) gi_21264062_sp_---SGPSSPF  QLPADTPPPA  YMPPDEQMGQ  DGSQSMETG-  -SSLAPQ---
(PRED) gi_13959533_sp_---SGPGSPF  QLPADTPPPA  YMPPDDQMGQ  DNSQPMDTS-  -NNMIPQIMP
(PRED) gi_13959566_sp_---SGPGSPF  QLPADTPPPA  YMPPDDQMGQ  DNSQPMDTS-  -NNMIPQIMP
(PRED) gi_13959559_sp_---SGPGSPF  QLPADTPPPA  YMPPDDQMAP  DNSQPMDTS-  -SNMIPQTMP
(PRED) gi_13633872_sp_---SDPGSPF  QMPADTPPPA  YLPPEDPMAQ  DGSQPMDTNM  TNMTAPTLPA
(PRED) gi_13959539_sp_--PSEPESPY  QHSVDTPPLP  YHATEASETQ  SG-QPVDA--  --TADRHVVL
(PRED) gi_21264049_sp_---SDPGSPF  QMP-ETPPPA  YMPPEEPMTQ  DCPQPMDTN-  -LLAPNLPLE
(PRED) gi_66774168_sp_-----PSSPG  HVFPQSPCPT  SYPHSPGSPS  ESDSPYQH--  ----------
(PRED) gi_13959527_sp_-----PSSPG  HVFPQSPCPT  SYPQSPGSPS  ESDSPYQH--  ----------
(PRED) gi_51338669_sp_---MDAGSPN  -LSPNPMSPA  HNN-------  ----------  ----------
(PRED) gi_60414603_sp_---MDAGSPN  -LSPNPMSPA  HNN-------  ----------  ----------
(PRED) gi_117949830_sp---MDTGSPA  ELSPTTLSPV  NHS-------  ----------  ----------
(PRED) gi_13633871_sp_---MDTGSPA  ELSPTTLSPV  NHS-------  ----------  ----------
(PRED) gi_13633914_sp_---MDTGSPA  ELSPTTLSPV  NHS-------  ----------  ----------
(PRED) gi_75041393_sp_---MDTGSPA  ELSPTTLSPV  NHS-------  ----------  ----------
(PRED) gi_110826300_sp---MDTGSPA  ELSPTTLSPV  NHS-------  ----------  ----------
(PRED) gi_21264050_sp_---MDTGSPA  ELSPSTLSPV  NHG-------  ----------  ----------
(PRED) gi_341942043_spQIASGPQPGQ  QQNGFTAQPA  TYHHNSTTTW  TGSRTAPYTP  NLPHHQNGHL
(PRED) gi_13959528_sp_QIASGPQPGQ  QQNGFTAQPA  TYHHNSTTTW  TGSRTAPYTP  NLPHHQNGHL
(PRED) gi_13959561_sp_QIASGPQPGQ  QQNGFTGQPA  TYHHNSTTTW  TGSRTAPYTP  NLPHHQNGHL
(PRED) gi_116256078_spQIASGPQPGQ  QQNGFTGQPA  TYHHNSTTTW  TGGRTAPYTP  NLPHHQNGHL
(PRED) gi_13959531_sp_QIASGPQPGQ  QQNGFTGQPA  TYHHNSTTTW  TGSRTAPYPP  NLPHHQNGHL
(PRED) gi_13959540_sp_-----ITAPG  EFSDASMS--  ----------  ----------  ----------
(PRED) gi_115502451_sp-----ITAPG  EFSDASTS--  ----------  ----------  ----------
(PRED) gi_13959573_sp_-----NVTPG  EFSDASTS--  ----------  ----------  ----------
(PRED) gi_13959541_sp_-----YLAPG  GLSDSQLL--  ----------  ----------  ----------
(PRED) gi_13959538_sp_-----YLAPG  GLSDSQLL--  ----------  ----------  ----------
(PRED) gi_13959529_sp_-----YLAPG  GLSDSQLL--  ----------  ----------  ----------


                 .........510.........520.........530.........540.........550
(PRED) gi_13633932_sp_D---------  -------IHR  GDVQA--VAY  EEPKHWCSIV  YYELNNRVGE
(PRED) gi_118573879_spE---------  -------INR  GDVQA--VAY  EEPKHWCSIV  YYELNNRVGE
(PRED) gi_13633915_sp_E---------  -------INR  GDVQA--VAY  EEPKHWCSIV  YYELNNRVGE
(PRED) gi_341942042_spE---------  -------ISR  GDVQA--VAY  EEPKHWCSIV  YYELNNRVGE
(PRED) gi_82121811_sp_N---------  -------IST  RDVQP--VAY  EEPKHWCSIV  YYELNNRVGE
(PRED) gi_21264062_sp_N---------  -------MPR  GDVQP--VEY  QEPSHWCSIV  YYELNNRVGE
(PRED) gi_13959533_sp_S---------  -------ISS  RDVQP--VAY  EEPKHWCSIV  YYELNNRVGE
(PRED) gi_13959566_sp_S---------  -------ISS  RDVQP--VAY  EEPKHWCSIV  YYELNNRVGE
(PRED) gi_13959559_sp_S---------  -------ISS  RDVQP--VAY  EEPKHWCSIV  YYELNNRVGE
(PRED) gi_13633872_sp_E---------  -------INR  GDVQA--VAY  EEPKHWCSIV  YYELNNRVGE
(PRED) gi_13959539_sp_S---------  -------IPN  GDFRP--VCY  EEPQHWCSVA  YYELNNRVGE
(PRED) gi_21264049_sp_I---------  -------SNR  TDVHP--VAY  QEPKHWCSIV  YYELNNRVGE
(PRED) gi_66774168_sp_----------  ----------  SDFRP--VCY  EEPQHWCSVA  YYELNNRVGE
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Results colour-coded for transmembrane structure

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(PRED) gi_13959527_sp_----------  ----------  SDFRP--VCY  EEPLHWCSVA  YYELNNRVGE
(PRED) gi_51338669_sp_----------  ----------  LDLQP--VTY  CEPAFWCSIS  YYELNQRVGE
(PRED) gi_60414603_sp_----------  ----------  LDLQP--VTY  CEPAFWCSIS  YYELNQRVGE
(PRED) gi_117949830_sp----------  ----------  LDLQP--VTY  SEPAFWCSIA  YYELNQRVGE
(PRED) gi_13633871_sp_----------  ----------  LDLQP--VTY  SEPAFWCSIA  YYELNQRVGE
(PRED) gi_13633914_sp_----------  ----------  LDLQP--VTY  SEPAFWCSIA  YYELNQRVGE
(PRED) gi_75041393_sp_----------  ----------  LDLQP--VTY  SEPAFWCSIA  YYELNQRVGE
(PRED) gi_110826300_sp----------  ----------  LDLQP--VTY  SEPAFWCSIA  YYELNQRVGE
(PRED) gi_21264050_sp_----------  ----------  MDLQP--VTY  SEPAFWCSIA  YYELNQRVGE
(PRED) gi_341942043_spQHHPPMPPHP  GHYWPV-HNE  LAFQPPISNH  PAPEYWCSIA  YFEMDVQVGE
(PRED) gi_13959528_sp_QHHPPMPPHP  GHYWPV-HNE  LAFQPPISNH  PAPEYWCSIA  YFEMDVQVGE
(PRED) gi_13959561_sp_QHHPPMPPHP  GHYWPV-HNE  LAFQPPISNH  PAPEYWCSIA  YFEMDVQVGE
(PRED) gi_116256078_spQHHPPMPPHP  GHYWPPVHNE  LAFQPPISNH  PAPEYWCSIA  YFEMDVQVGE
(PRED) gi_13959531_sp_QHHPPMPPHP  GHYWPV-HNE  LAFQPPISNH  PAPEYWCSIA  YFEMDVQVGE
(PRED) gi_13959540_sp_----------  ----------  -------PDA  TKPSHWCSVA  YWEHRTRVGR
(PRED) gi_115502451_sp----------  ----------  -------PDA  TKPSHWCSVA  YWEHRTRVGR
(PRED) gi_13959573_sp_----------  ----------  -------PDA  VKRSHWCNVA  YWEHRTRVGR
(PRED) gi_13959541_sp_----------  ----------  -------LEP  GDRSHWCVVA  YWEEKTRVGR
(PRED) gi_13959538_sp_----------  ----------  -------LEP  GDRSHWCVVA  YWEEKTRVGR
(PRED) gi_13959529_sp_----------  ----------  -------LEP  GDRSHWCVVA  YWEEKTRVGR


                  .........560.........570.........580.........590.........600
(PRED) gi_13633932_sp_AFHASST--S  ILVDGFTDPS  NNKNRFCLGL  LSNVNRNSTI  ENTRRHIGKG
(PRED) gi_118573879_spAFHASST--S  VLVDGFTDPS  NNKNRFCLGL  LSNVNRNSTI  ENTRRHIGKG
(PRED) gi_13633915_sp_AFHASST--S  VLVDGFTDPS  NNKNRFCLGL  LSNVNRNSTI  ENTRRHIGKG
(PRED) gi_341942042_spAFHASST--S  VLVDGFTDPS  NNKNRFCLGL  LSNVNRNSTI  ENTRRHIGKG
(PRED) gi_82121811_sp_AFHASST--S  VLVDGFTDPS  NNKNRFCLGL  LSNVNRNSTI  ENTRRHIGKG
(PRED) gi_21264062_sp_AYHASST--S  VLVDGFTDPS  NNKNRFCLGL  LSNVNRNSTI  ENTRRHIGKG
(PRED) gi_13959533_sp_AFHASST--S  VLVDGFTDPA  NNKSRFCLGL  LSNVNRNSTI  ENTRRHIGKG
(PRED) gi_13959566_sp_AFHASST--S  VLVDGFTDPS  NNKSRFCLGL  LSNVNRNSTI  ENTRRHIGKG
(PRED) gi_13959559_sp_AFHASST--S  VLVDGFTDPS  NNKSRFCLGL  LSNVNRNSTI  ENTRRHIGKG
(PRED) gi_13633872_sp_RFHASST--S  VLVDGFTDPS  NNKNRFCLGL  LSNVNRNSTI  ENTRRHIGKG
(PRED) gi_13959539_sp_TFQASSR--S  VLIDGFTDPS  NNRNRFCLGL  LSNVNRNSTI  ENTRRHIGKG
(PRED) gi_21264049_sp_AFLASST--S  VLVDGFTDPS  NNRNRFCLGL  LSNVNRNSTI  ENTRRHIGKG
(PRED) gi_66774168_sp_TFQASSR--S  VLIDGFTDPS  NNRNRFCLGL  LSNVNRNSTI  ENTRRHIGKG
(PRED) gi_13959527_sp_TFQASSR--S  VLIDGFTDPS  NNRNRFCLGL  LSNVNRNSTI  ENTRRHIGKG
(PRED) gi_51338669_sp_TFHASQP--S  MTVDGFTDPS  NS-ERFCLGL  LSNVNRNAAV  ELTRRHIGRG
(PRED) gi_60414603_sp_TFHASQP--S  MTVDGFTDPS  NS-ERFCLGL  LSNVNRNAAV  ELTRRHIGRG
(PRED) gi_117949830_spTFHASQP--S  LTVDGFTDPS  NS-ERFCLGL  LSNVNRNATV  EMTRRHIGRG
(PRED) gi_13633871_sp_TFHASQP--S  LTVDGFTDPS  NS-ERFCLGL  LSNVNRNATV  EMTRRHIGRG
(PRED) gi_13633914_sp_TFHASQP--S  LTVDGFTDPS  NS-ERFCLGL  LSNVNRNATV  EMTRRHIGRG
(PRED) gi_75041393_sp_TFHASQP--S  LTVDGFTDPS  NS-ERFCLGL  LSNVNRNATV  EMTRRHIGRG
(PRED) gi_110826300_spTFHASQP--S  LTVDGFTDPS  NS-ERFCLGL  LSNVNRNATV  EMTRRHIGRG
(PRED) gi_21264050_sp_TFHASQP--S  LTVDGFTDPS  NS-ERFCLGL  LSNVNRNATV  EMTRRHIGRG
(PRED) gi_341942043_spTFKVPSSCPV  VTVDGYVDPS  GG-DRFCLGQ  LSNVHRTEAI  ERARLHIGKG
(PRED) gi_13959528_sp_TFKVPSSCPI  VTVDGYVDPS  GG-DRFCLGQ  LSNVHRTEAI  ERARLHIGKG
(PRED) gi_13959561_sp_TFKVPSSCPI  VTVDGYVDPS  GG-DRFCLGQ  LSNVHRTEAI  ERARLHIGKG
(PRED) gi_116256078_spTFKVPSSCPI  VTVDGYVDPS  GG-DRFCLGQ  LSNVHRTEAI  ERARLHIGKG
(PRED) gi_13959531_sp_TFKVPSSCPI  VTVDGYVDPS  GG-DRFCLGQ  LSNVHRTEAI  ERARLHIGKG
(PRED) gi_13959540_sp_LYAVY----D  QAVSIFYDLP  QG-SGFCLGQ  LNLEQRSESV  RRTRSKIGFG
(PRED) gi_115502451_spLYAVY----D  QAVSIFYDLP  QG-SGFCLGQ  LNLEQRSESV  RRTRSKIGFG
(PRED) gi_13959573_sp_LYTVY----E  QSVSIFYDLP  QG-NGFCLGQ  LNLENRSETV  RRTRSKIGYG
(PRED) gi_13959541_sp_LYCVQ----E  PSLDIFYDLP  QG-NGFCLGQ  LNSDNKSQLV  QKVRSKIGCG
(PRED) gi_13959538_sp_LYCVQ----E  PSLDIFYDLP  QG-NGFCLGQ  LNSDNKSQLV  QKVRSKIGCG
(PRED) gi_13959529_sp_LYCVQ----E  PSLDIFYDLP  QG-NGFCLGQ  LNSDNKSQLV  QKVRSKIGCG


                  .........610.........620.........630.........640.........650
(PRED) gi_13633932_sp_VHLYYVG-GE  VYAECLSDSS  IFVQSRNCNY  HHGFHPT-TV  CKIPSGCSLK
(PRED) gi_118573879_spVHLYYVG-GE  VYAECLSDSS  IFVQSRNCNY  HHGFHPT-TV  CKIPSGCSLK
(PRED) gi_13633915_sp_VHLYYVG-GE  VYAECLSDSS  IFVQSRNCNY  HHGFHPT-TV  CKIPSGCSLK
(PRED) gi_341942042_spVHLYYVG-GE  VYAECLSDSS  IFVQSRNCNY  HHGFHPT-TV  CKIPSGCSLK
(PRED) gi_82121811_sp_VHLYYVG-GE  VYAECLSDSS  IFVQSRNCNY  HHGFHPT-TV  CKIPSGCSLK
(PRED) gi_21264062_sp_VHLYYVG-GE  VYAECLSDTS  IFVQSRNCNY  HHGFHPT-TV  CKIPSGCSLK
(PRED) gi_13959533_sp_VHLYYVG-GE  VYAECLSDSS  IFVQSRNCNF  HHGFHPT-TV  CKIPSSCSLK
(PRED) gi_13959566_sp_VHLYYVG-GE  VYAECLSDSS  IFVQSRNCNF  HHGFHPT-TV  CKIPSSCSLK
(PRED) gi_13959559_sp_VHLYYVG-GE  VYAECLSDSS  IFVQSRNCNF  HHGFHPT-TV  CKIPSSCSLK
(PRED) gi_13633872_sp_VHLYYVG-GE  VYAECLSDSS  IFVQSRNCNY  HHGFHPT-TV  CKIPSGCSLK
(PRED) gi_13959539_sp_VHLYYVG-GE  VYAECVSDSS  IFVQSRNCNY  QHGFHPA-TV  CKIPSGCSLK
(PRED) gi_21264049_sp_VHLYYVG-GE  VYAECLSDSS  IFVQSRNCNY  HHGFHPT-TV  CKIPSRCSLK
(PRED) gi_66774168_sp_VHLYYVG-GE  VYAECVSDSS  IFVQSRNCNY  QHGFHPA-TV  CKIPSGCSLK
(PRED) gi_13959527_sp_VHLYYVG-GE  VYAECVSDSS  IFVQSRNCNY  QHGFHPA-TV  CKIPSGCSLK
(PRED) gi_51338669_sp_VRLYYIG-GE  VFAECLSDSA  IFVQSPNCNQ  RYGWHPA-TV  CKIPPGCNLK
(PRED) gi_60414603_sp_VRLYYIG-GE  VFAECLSDSA  IFVQSPNCNQ  RYGWHPA-TV  CKIPPGCNLK
(PRED) gi_117949830_spVRLYYIG-GE  VFAECLSDSA  IFVQSPNCNQ  RYGWHPA-TV  CKIPPGCNLK
(PRED) gi_13633871_sp_VRLYYIG-GE  VFAECLSDSA  IFVQSPNCNQ  RYGWHPA-TV  CKIPPGCNLK
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(PRED) gi_13633914_sp_VRLYYIG-GE  VFAECLSDSA  IFVQSPNCNQ  RYGWHPA-TV  CKIPPGCNLK
(PRED) gi_75041393_sp_VRLYYIG-GE  VFAECLSDSA  IFVQSPNCNQ  RYGWHPA-TV  CKIPPGCNLK
(PRED) gi_110826300_spVRLYYIG-GE  VFAECLSDSA  IFVQSPNCNQ  RYGWHPA-TV  CKIPPGCNLK
(PRED) gi_21264050_sp_VRLYYIG-GE  VFAECLSDSA  IFVQSPNCNQ  RYGWHPA-TV  CKIPPGCNLK
(PRED) gi_341942043_spVQLECKGEGD  VWVRCLSDHA  VFVQSYYLDR  EAGRAPGDAV  HKIYPSAYIK
(PRED) gi_13959528_sp_VQLECKGEGD  VWVRCLSDHA  VFVQSYYLDR  EAGRAPGDAV  HKIYPSAYIK
(PRED) gi_13959561_sp_VQLECKGEGD  VWVRCLSDHA  VFVQSYYLDR  EAGRAPGDAV  HKIYPSAYIK
(PRED) gi_116256078_spVQLECKGEGD  VWVRCLSDHA  VFVQSYYLDR  EAGRAPGDAV  HKIYPSAYIK
(PRED) gi_13959531_sp_VQLECKGEGD  VWVRCLSDHA  VFVQSYYLDR  EAGRAPGDAV  HKIYPSAYIK
(PRED) gi_13959540_sp_ILLSKEP-DG  VWAYNRGEHP  IFVNSPTLDA  PGG-RAL-VV  RKVPPGYSIK
(PRED) gi_115502451_spILLSKEP-DG  VWAYNRGEHP  IFVNSPTLDA  PGG-RAL-VV  RKVPPGYSIK
(PRED) gi_13959573_sp_ILLSKEP-DG  VWAYNRSEHP  IFVNSPTLDI  PNC-RTL-IV  RKVMPGYSIK
(PRED) gi_13959541_sp_IQLTREV-DG  VWVYNRSSYP  IFIKSATLDN  PDS-RTL-LV  HKVFPGFSIK
(PRED) gi_13959538_sp_IQLTREV-DG  VWVYNRSSYP  IFIKSATLDN  PDS-RTL-LV  HKVFPGFSIK
(PRED) gi_13959529_sp_IQLTREV-DG  VWVYNRSSYP  IFIKSATLDN  PDS-RTL-LV  HKVFPGFSIK


                .........660.........670.........680.........690.........700
(PRED) gi_13633932_sp_IFNNQEFAQL  ----LAQSVN  HGFET-----  ----------  ----------
(PRED) gi_118573879_spIFNNQEFAQL  ----LAQSVN  HGFET-----  ----------  ----------
(PRED) gi_13633915_sp_IFNNQEFAQL  ----LAQSVN  HGFET-----  ----------  ----------
(PRED) gi_341942042_spIFNNQEFAQL  ----LAQSVN  HGFET-----  ----------  ----------
(PRED) gi_82121811_sp_IFNNQEFAQL  ----LAQSVN  HGFEA-----  ----------  ----------
(PRED) gi_21264062_sp_IFNNQEFAQL  ----LAQSVN  HGFEA-----  ----------  ----------
(PRED) gi_13959533_sp_IFNNQEFAQL  ----LAQSVN  HGFEA-----  ----------  ----------
(PRED) gi_13959566_sp_IFNNQEFAQL  ----LAQSVN  HGFEA-----  ----------  ----------
(PRED) gi_13959559_sp_IFNNQEFAQL  ----LAQSVN  HGFEA-----  ----------  ----------
(PRED) gi_13633872_sp_IFNNQEFAQL  ----LAQSVN  HGFET-----  ----------  ----------
(PRED) gi_13959539_sp_VFNNQLFAQL  ----LAQSVH  HGFEV-----  ----------  ----------
(PRED) gi_21264049_sp_IFNNQEFAEL  ----LAQSVN  HGFEA-----  ----------  ----------
(PRED) gi_66774168_sp_VFNNQLFAQL  ----LAQSVH  HGFEV-----  ----------  ----------
(PRED) gi_13959527_sp_VFNNQLFAQL  LAQLLAQSVH  HGFEV-----  ----------  ----------
(PRED) gi_51338669_sp_IFNNQEFAAL  ----LAQSVN  QGFEA-----  ----------  ----------
(PRED) gi_60414603_sp_IFNNQEFAAL  ----LAQSVN  QGFEA-----  ----------  ----------
(PRED) gi_117949830_spIFNNQEFAAL  ----LAQSVN  QGFEA-----  ----------  ----------
(PRED) gi_13633871_sp_IFNNQEFAAL  ----LAQSVN  QGFEA-----  ----------  ----------
(PRED) gi_13633914_sp_IFNNQEFAAL  ----LAQSVN  QGFEA-----  ----------  ----------
(PRED) gi_75041393_sp_IFNNQEFAAL  ----LAQSVN  QGFEA-----  ----------  ----------
(PRED) gi_110826300_spIFNNQGFAAL  ----LAQSVN  QGFEA-----  ----------  ----------
(PRED) gi_21264050_sp_IFNNQEFAAL  ----LAQSVN  QGFEA-----  ----------  ----------
(PRED) gi_341942043_spVFDLRQCHRQ  ----MQQQAA  TAQAAAAAQA  AAVAGNIPGP  GSVGGIAPAI
(PRED) gi_13959528_sp_VFDLRQCHRQ  ----MQQQAA  TAQAAAAAQA  AAVAGNIPGP  GSVGGIAPAI
(PRED) gi_13959561_sp_VFDLRQCHRQ  ----MQQQAA  TAQAAAAAQA  AAVAGNIPGP  GSVGGIAPAI
(PRED) gi_116256078_spVFDLRQCHRQ  ----MQQQAA  TAQAAAAAQA  AAVAGNIPGP  GSVGGIAPAI
(PRED) gi_13959531_sp_VFDLRQCHRQ  ----MQQQAA  TAQAAAAAQA  AAVAGNIPGP  GSVGGIAPAI
(PRED) gi_13959540_sp_VFDFERSGLL  ----QHADAA  HG--------  ----------  ----------
(PRED) gi_115502451_spVF-DFERSGL  ----QHAPEP  DA--------  ----------  ----------
(PRED) gi_13959573_sp_VFDYEKSCLL  ----QHTAEL  DY--------  ----------  ----------
(PRED) gi_13959541_sp_AFDYEKAYSL  ----QRPNDH  EF--------  ----------  ----------
(PRED) gi_13959538_sp_AFDYEKAYSL  ----QRPNDH  EF--------  ----------  ----------
(PRED) gi_13959529_sp_AFDYEKAYSL  ----QRPNDH  EF--------  ----------  ----------


                .........710.........720.........730.........740.........750
(PRED) gi_13633932_sp_---------V  YELTKMCTLR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
(PRED) gi_118573879_sp---------V  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
(PRED) gi_13633915_sp_---------V  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
(PRED) gi_341942042_sp---------V  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
(PRED) gi_82121811_sp_---------V  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEVHLHGP
(PRED) gi_21264062_sp_---------V  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
(PRED) gi_13959533_sp_---------V  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
(PRED) gi_13959566_sp_---------V  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
(PRED) gi_13959559_sp_---------V  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
(PRED) gi_13633872_sp_---------E  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
(PRED) gi_13959539_sp_---------V  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
(PRED) gi_21264049_sp_---------V  YELTKMCTIR  MSFVKGWGAK  YHRQDVTSTP  CWIEIHLHGP
(PRED) gi_66774168_sp_---------V  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
(PRED) gi_13959527_sp_---------V  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
(PRED) gi_51338669_sp_---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
(PRED) gi_60414603_sp_---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
(PRED) gi_117949830_sp---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
(PRED) gi_13633871_sp_---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
(PRED) gi_13633914_sp_---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
(PRED) gi_75041393_sp_---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
(PRED) gi_110826300_sp---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
(PRED) gi_21264050_sp_---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
(PRED) gi_341942043_spSLSAAAGIGV  DDLRRLCILR  MSFVKGWGPD  YPRQSIKETP  CWIEIHLHRA
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Results colour-coded for transmembrane structure

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(PRED)  gi_13959528_sp_ SLSAAAGIGV  DDLRRLCILR  MSFVKGWGPD  YPRQSIKETP  CWIEIHLHRA
(PRED)  gi_13959561_sp_ SLSAAAGIGV  DDLRRLCILR  MSFVKGWGPD  YPRQSIKETP  CWIEIHLHRA
(PRED)  gi_116256078_sp SLSAAAGIGV  DDLRRLCILR  MSFVKGWGPD  YPRQSIKETP  CWIEIHLHRA
(PRED)  gi_13959531_sp_ SLSAAAGIGV  DDLRRLCILR  MSFVKGWGPD  YPRQSIKETP  CWIEIHLHRA
(PRED)  gi_13959540_sp_ ---------P  ---YDPHSVR  ISFAKGWGPC  YSRQFITSCP  CWLEILLNNH
(PRED)  gi_115502451_sp ---------A  DGPYDPNSVR  ISFAKGWGPC  YSRQFITSCP  CWLEILLNNP
(PRED)  gi_13959573_sp_ ---------A  DGPYDPNSVR  ISFAKGWGPC  YSRQFITSCP  CWLEILLSNN
(PRED)  gi_13959541_sp_ ---------M  QQPWTGFTVQ  ISFVKGWGQC  YTRQFISSCP  CWLEVIFNSR
(PRED)  gi_13959538_sp_ ---------M  QQPWTGFTVQ  ISFVKGWGQC  YTRQFISSCP  CWLEVIFNSR
(PRED)  gi_13959529_sp_ ---------M  QQPWTGFTVQ  ISFVKGWGQC  YTRQFISSCP  CWLEVIFNSR


                    . . . . . . . . . 760 . . . . . . . . . 770 . .
(PRED)  gi_13633932_sp_ LQWLDKVLTQ  MGSPHNPISS  VS
(PRED)  gi_118573879_sp LQWLDKVLTQ  MGSPHNPISS  VS
(PRED)  gi_13633915_sp_ LQWLDKVLTQ  MGSPHNPISS  VS
(PRED)  gi_341942042_sp LQWLDKVLTQ  MGSPHNPISS  VS
(PRED)  gi_82121811_sp_ LQWLDKVLTQ  MGSPLNPISS  VS
(PRED)  gi_21264062_sp_ LQWLDKVLTQ  MGSPLNPISS  VS
(PRED)  gi_13959533_sp_ LQWLDKVLTQ  MGSPLNPISS  VS
(PRED)  gi_13959566_sp_ LQWLDKVLTQ  MGSPLNPISS  VS
(PRED)  gi_13959559_sp_ LQWLDKVLTQ  MGSPLNPISS  VS
(PRED)  gi_13633872_sp_ LQWLDKVLTQ  MGSPHNPISS  VS
(PRED)  gi_13959539_sp_ LQWLDKVLTQ  MGSPHNPISS  VS
(PRED)  gi_21264049_sp_ LQWLDKVLTQ  MGSPHNPISS  VS
(PRED)  gi_66774168_sp_ LQWLDKVLTQ  MGSPHNPISS  VS
(PRED)  gi_13959527_sp_ LQWLDKVLTQ  MGSPHNPISS  VS
(PRED)  gi_51338669_sp_ LQWLDKVLTQ  MGSPSIRCSS  VS
(PRED)  gi_60414603_sp_ LQWLDKVLTQ  MGSPSIRCSS  VS
(PRED)  gi_117949830_sp LQWLDKVLTQ  MGSPSVRCSS  MS
(PRED)  gi_13633871_sp_ LQWLDKVLTQ  MGSPSVRCSS  MS
(PRED)  gi_13633914_sp_ LQWLDKVLTQ  MGSPSVRCSS  MS
(PRED)  gi_75041393_sp_ LQWLDKVLTQ  MGSPSVRCSS  MS
(PRED)  gi_110826300_sp LQWLDKVLTQ  MGSPSVRCSS  MS
(PRED)  gi_21264050_sp_ LQWLDKVLTQ  MGSPSVRCSS  MS
(PRED)  gi_341942043_sp LQLLDEVLHT  MPIA-DP-QP  LD
(PRED)  gi_13959528_sp_ LQLLDEVLHT  MPIA-DP-QP  LD
(PRED)  gi_13959561_sp_ LQLLDEVLHT  MPIA-DP-QP  LD
(PRED)  gi_116256078_sp LQLLDEVLHT  MPIA-DP-QP  LD
(PRED)  gi_13959531_sp_ LQLLDEVLHT  MPIA-DP-QP  LD
(PRED)  gi_13959540_sp_ R---------  ----------  --
(PRED)  gi_115502451_sp R---------  ----------  --
(PRED)  gi_13959573_sp_ R---------  ----------  --
(PRED)  gi_13959541_sp_ ----------  ----------  --
(PRED)  gi_13959538_sp_ ----------  ----------  --
(PRED)  gi_13959529_sp_ ----------  ----------  --
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