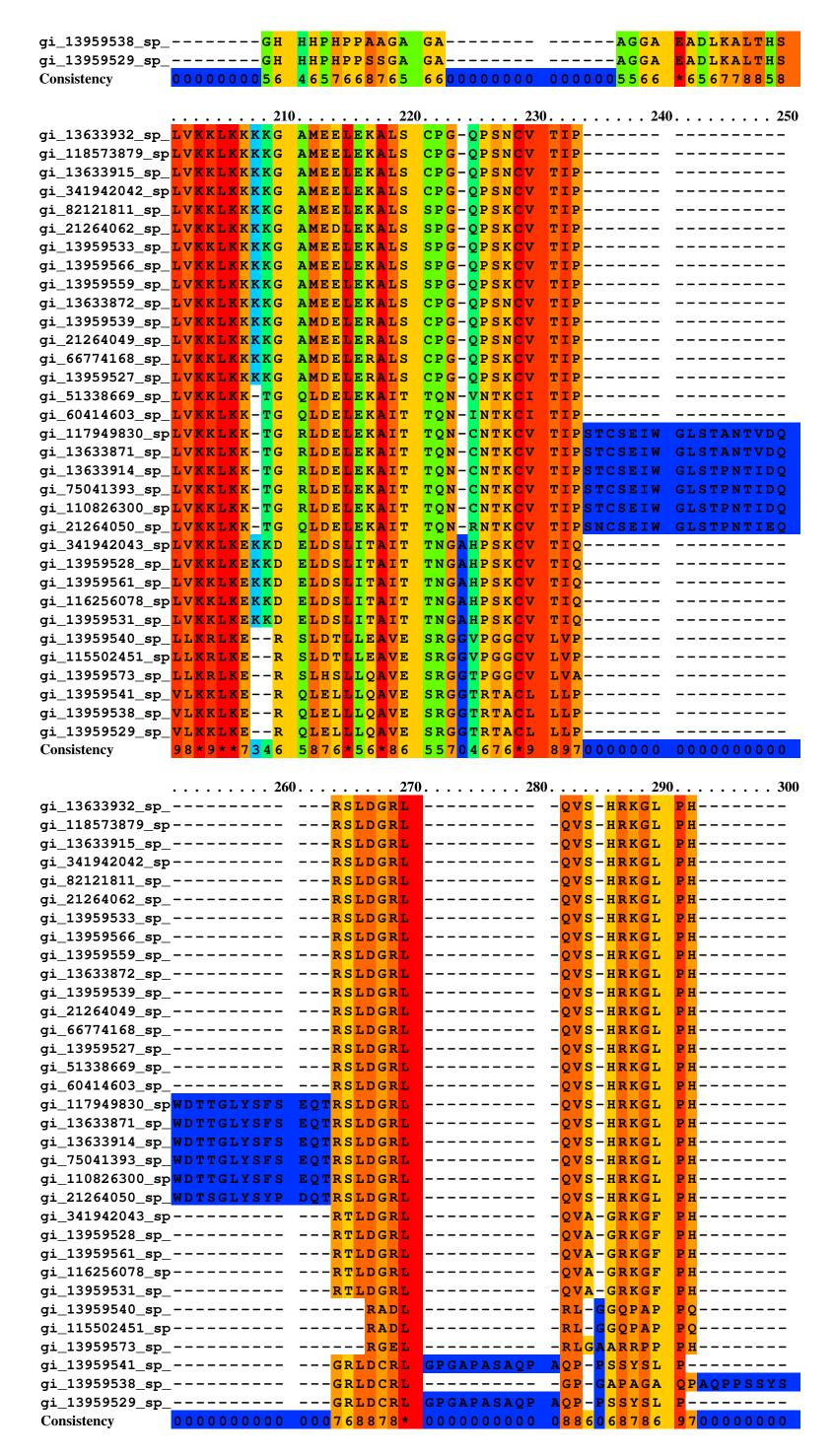# Results colour-coded for amino acid conservation

The current colourscheme of the alignment is for **amino acid conservation**.

The conservation scoring is performed by PRALINE. The scoring scheme works from 0 for the least conserved alignment position, up to 10 for the most conserved alignment position. The colour assignments are:

Unconserved `0 1 2 3 4 5 6 7 8 9 10` **Conserved**

```
                . . . . . . . . . 10 . . . . . . . . . 20 . . . . . . . . . 30 . . . . . . . . . 40 . . . . . . . . . 50
gi_13633932_sp_  ----------  ----------  ----------  ----------  ----------
gi_118573879_sp  ----------  ----------  ----------  ----------  ----------
gi_13633915_sp_  ----------  ----------  ----------  ----------  ----------
gi_341942042_sp  ----------  ----------  ----------  ----------  ----------
gi_82121811_sp_  ----------  ----------  ----------  ----------  ----------
gi_21264062_sp_  ----------  ----------  ----------  ----------  ----------
gi_13959533_sp_  ----------  ----------  ----------  ----------  ----------
gi_13959566_sp_  ----------  ----------  ----------  ----------  ----------
gi_13959559_sp_  ----------  ----------  ----------  ----------  ----------
gi_13633872_sp_  ----------  ----------  ----------  ----------  ----------
gi_13959539_sp_  ----------  ----------  ----------  ----------  ----------
gi_21264049_sp_  ----------  ----------  ----------  ----------  ----------
gi_66774168_sp_  ----------  ----------  ----------  ----------  ----------
gi_13959527_sp_  ----------  ----------  ----------  ----------  ----------
gi_51338669_sp_  ----------  ----------  ----------  ----------  ----------
gi_60414603_sp_  ----------  ----------  ----------  ----------  ----------
gi_117949830_sp  ----------  ----------  ----------  ----------  ----------
gi_13633871_sp_  ----------  ----------  ----------  ----------  ----------
gi_13633914_sp_  ----------  ----------  ----------  ----------  ----------
gi_75041393_sp_  ----------  ----------  ----------  ----------  ----------
gi_110826300_sp  ----------  ----------  ----------  ----------  ----------
gi_21264050_sp_  ----------  ----------  ----------  ----------  ----------
gi_341942043_sp  ----------  ----------  ----------  ----------  ----------
gi_13959528_sp_  ----------  ----------  ----------  ----------  ----------
gi_13959561_sp_  ----------  ----------  ----------  ----------  ----------
gi_116256078_sp  ----------  ----------  ----------  ----------  ----------
gi_13959531_sp_  ----------  ----------  ----------  ----------  ----------
gi_13959540_sp_  MFRSKRSGLV  RRLWRSRVVP  DREEGSG-GG  GGVDEDGSLG  SRAEPAPRAR
gi_115502451_sp  MFRSKRSGLV  RRLWRSRVVP  DREEGSGGG   GGGDEDGSLG  SRAEPAPRAR
gi_13959573_sp_  MFRSKRSGLV  RRLWRSRVIP  ERDGGDGNGQ  SSERNATAVT  AEG-------
gi_13959541_sp_  MFRTKRSALV  RRLWRSRAPG  GEDEEEGVGG  GGGG--GELR  GEG-------
gi_13959538_sp_  MFRTKRSALV  RRLWRSRAPG  GEDEEEGAGG  GGGG--GELR  GEG-------
gi_13959529_sp_  MFRTKRSALV  RRLWRSRAPG  GEDEEEGVGG  GGGG--GGLR  GEG-------
Consistency      0000000000  0000000000  0000000000  0000000000  0000000000

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

```
gi_115502451_sp EGGGCGRSEV RPVAPRRPRD AVGQRGAQGA GRRRRAGGPP RPMSEPGAGA
gi_13959573_sp_ ---------- ---------- ---------- ---------- ----------
gi_13959541_sp_ ---------- ---------- ---------- ---------- ----------
gi_13959538_sp_ ---------- ---------- ---------- ---------- ----------
gi_13959529_sp_ ---------- ---------- ---------- ---------- ----------
Consistency     0000000000 0000000000 0000000000 0000000000 0000000000
```

```
         . . . . . . . . . . 110 . . . . . . . . . . 120 . . . . . . . . . . 130 . . . . . . . . . . 140 . . . . . . . . . . 150
gi_13633932_sp_  ---------- ---------- ------M---N VTSLFS---- ----------
gi_118573879_sp ---------- ---------- ------M---N VTSLFS---- ----------
gi_13633915_sp_  ---------- ---------- ------M---N VTSLFS---- ----------
gi_341942042_sp ---------- ---------- ------M---N VTSLFS---- ----------
gi_82121811_sp_  ---------- ---------- ------M--TS MASLFS---- ----------
gi_21264062_sp_  ---------- ---------- ------M--TS MSSLFS---- ----------
gi_13959533_sp_  ---------- ---------- ------M--TS MASLFS---- ----------
gi_13959566_sp_  ---------- ---------- ------M--TS MASLFS---- ----------
gi_13959559_sp_  ---------- ---------- ------M--TS MASLFS---- ----------
gi_13633872_sp_  ---------- ---------- ------M---N VTSLFS---- ----------
gi_13959539_sp_  ---------- ---------- --MHST--TP ISSLFS---- ----------
gi_21264049_sp_  ---------- ---------- ------M---N VTSLFS---- ----------
gi_66774168_sp_  ---------- ---------- --MHPS--TP ISSLFS---- ----------
gi_13959527_sp_  ---------- ---------- --MHPS--TP ISSLFS---- ----------
gi_51338669_sp_  ---------- ---------- ---------- MSSILP---- ----------
gi_60414603_sp_  ---------- ---------- ---------- MSSILP---- ----------
gi_117949830_sp ---------- ---------- ---------- MSSILP---- ----------
gi_13633871_sp_  ---------- ---------- ---------- MSSILP---- ----------
gi_13633914_sp_  ---------- ---------- ---------- MSSILP---- ----------
gi_75041393_sp_  ---------- ---------- ---------- MSSILP---- ----------
gi_110826300_sp ---------- ---------- ---------- MSSILP---- ----------
gi_21264050_sp_  ---------- ---------- ---------- MSSILP---- ----------
gi_341942043_sp ---------- ---------- --MDNMSITN TPTSND---- ----------
gi_13959528_sp_  ---------- ---------- --MDNMSITN TPTSND---- ----------
gi_13959561_sp_  ---------- ---------- --MDNMSITN TPTSND---- ----------
gi_116256078_sp ---------- ---------- --MDNMSITN TPTSND---- ----------
gi_13959531_sp_  ---------- ---------- --MDNMSITN TPTSND---- ----------
gi_13959540_sp_  GGSPLDVAEP GGPGWLPESD CETVTCCLFS ERDAAGAPRD SGDPQARQSP
gi_115502451_sp GSSLLDVAEP GGPGWLPESD CETVTCCLFS ERDAAGAPRD ASDPLAGAAL
gi_13959573_sp_  -------QRM AQPRRAQEGE GRPVRCCLFA ERPGPELPPP PPPPPPGG--
gi_13959541_sp_  -------ATD GRAYGAGGGG AGRAGCCLGK AVRGAK---- ----------
gi_13959538_sp_  -------ATD SRAHGAGGGG PGRAGCCLGK AVRGAK---- ----------
gi_13959529_sp_  -------ATD GRAYGAGGGG AGRAGCCLGK AVRGAK---- ----------
Consistency     0000000000 0000000000 0000030013 5575450000 0000000000
```

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

Results colour-coded for amino acid conservation   2

```
gi_13959538_sp_---------GH  HHPHPPAAGA  GA--------- ------AGGA  EADLKALTHS
gi_13959529_sp_---------GH  HHPHPPSSGA  GA--------- ------AGGA  EADLKALTHS
Consistency    00000000056  4657668765  6600000000  0000005566  *656778858


             . . . . . . . . . 210 . . . . . . . . . 220 . . . . . . . . . 230 . . . . . . . . . 240 . . . . . . . . . 250
gi_13633932_sp_LVKKLKKKKG  AMEELEKALS  CPG-QPSNCV  TIP------- ----------
gi_118573879_sp LVKKLKKKKG  AMEELEKALS  CPG-QPSNCV  TIP------- ----------
gi_13633915_sp_LVKKLKKKKG  AMEELEKALS  CPG-QPSNCV  TIP------- ----------
gi_341942042_sp LVKKLKKKKG  AMEELEKALS  CPG-QPSNCV  TIP------- ----------
gi_82121811_sp_LVKKLKKKKG  AMEELEKALS  SPG-QPSKCV  TIP------- ----------
gi_21264062_sp_LVKKLKKKKG  AMDELEKALS  SPG-QPSKCV  TIP------- ----------
gi_13959533_sp_LVKKLKKKKG  AMEELEKALS  SPG-QPSKCV  TIP------- ----------
gi_13959566_sp_LVKKLKKKKG  AMEELEKALS  SPG-QPSKCV  TIP------- ----------
gi_13959559_sp_LVKKLKKKKG  AMEELEKALS  SPG-QPSKCV  TIP------- ----------
gi_13633872_sp_LVKKLKKKKG  AMEELEKALS  CPG-QPSNCV  TIP------- ----------
gi_13959539_sp_LVKKLKKKKG  AMDELERALS  CPG-QPSKCV  TIP------- ----------
gi_21264049_sp_LVKKLKKKKG  AMEELERALS  CPG-QPSNCV  TIP------- ----------
gi_66774168_sp_LVKKLKKKKG  AMDELERALS  CPG-QPSKCV  TIP------- ----------
gi_13959527_sp_LVKKLKKKKG  AMDELERALS  CPG-QPSKCV  TIP------- ----------
gi_51338669_sp_LVKKLKK-TG  QLDELEKAIT  TQN-VNTKCI  TIP------- ----------
gi_60414603_sp_LVKKLKK-TG  QLDELEKAIT  TQN-INTKCI  TIP------- ----------
gi_117949830_sp LVKKLKK-TG  RLDELEKAIT  TQN-CNTKCV  TIPSTCSEIW  GLSTANTVDQ
gi_13633871_sp_LVKKLKK-TG  RLDELEKAIT  TQN-CNTKCV  TIPSTCSEIW  GLSTANTVDQ
gi_13633914_sp_LVKKLKK-TG  RLDELEKAIT  TQN-CNTKCV  TIPSTCSEIW  GLSTPNTIDQ
gi_75041393_sp_LVKKLKK-TG  RLDELEKAIT  TQN-CNTKCV  TIPSTCSEIW  GLSTPNTIDQ
gi_110826300_sp LVKKLKK-TG  RLDELEKAIT  TQN-CNTKCV  TIPSTCSEIW  GLSTPNTIDQ
gi_21264050_sp_LVKKLKK-TG  QLDELEKAIT  TQN-RNTKCV  TIPSNCSEIW  GLSTPNTIEQ
gi_341942043_sp LVKKLKEKKD  ELDSLITAIT  TNGAHPSKCV  TIQ------- ----------
gi_13959528_sp_LVKKLKEKKD  ELDSLITAIT  TNGAHPSKCV  TIQ------- ----------
gi_13959561_sp_LVKKLKEKKD  ELDSLITAIT  TNGAHPSKCV  TIQ------- ----------
gi_116256078_sp LVKKLKEKKD  ELDSLITAIT  TNGAHPSKCV  TIQ------- ----------
gi_13959531_sp_LVKKLKEKKD  ELDSLITAIT  TNGAHPSKCV  TIQ------- ----------
gi_13959540_sp_LLKRLKE--R  SLDTLLEAVE  SRGGVPGGCV  LVP------- ----------
gi_115502451_sp LLKRLKE--R  SLDTLLEAVE  SRGGVPGGCV  LVP------- ----------
gi_13959573_sp_LLKRLKE--R  SLHSLLQAVE  SRGGTPGGCV  LVA------- ----------
gi_13959541_sp_VLKKLKE--R  QLELLLQAVE  SRGGTRTACL  LLP------- ----------
gi_13959538_sp_VLKKLKE--R  QLELLLQAVE  SRGGTRTACL  LLP------- ----------
gi_13959529_sp_VLKKLKE--R  QLELLLQAVE  SRGGTRTACL  LLP------- ----------
Consistency    98*9**7346  5876*56*86  55704676*9  8970000000  0000000000


             . . . . . . . . . 260 . . . . . . . . . 270 . . . . . . . . . 280 . . . . . . . . . 290 . . . . . . . . . 300
gi_13633932_sp_----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_118573879_sp----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_13633915_sp_----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_341942042_sp----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_82121811_sp_----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_21264062_sp_----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_13959533_sp_----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_13959566_sp_----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_13959559_sp_----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_13633872_sp_----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_13959539_sp_----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_21264049_sp_----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_66774168_sp_----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_13959527_sp_----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_51338669_sp_----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_60414603_sp_----------  ---RSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_117949830_sp WDTTGLYSFS  EQTRSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_13633871_sp_WDTTGLYSFS  EQTRSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_13633914_sp_WDTTGLYSFS  EQTRSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_75041393_sp_WDTTGLYSFS  EQTRSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_110826300_sp WDTTGLYSFS  EQTRSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_21264050_sp_WDTSGLYSYP  DQTRSLDGRL  ---------- -QVS-HRKGL  PH--------
gi_341942043_sp----------  ---RTLDGRL  ---------- -QVA-GRKGF  PH--------
gi_13959528_sp_----------  ---RTLDGRL  ---------- -QVA-GRKGF  PH--------
gi_13959561_sp_----------  ---RTLDGRL  ---------- -QVA-GRKGF  PH--------
gi_116256078_sp----------  ---RTLDGRL  ---------- -QVA-GRKGF  PH--------
gi_13959531_sp_----------  ---RTLDGRL  GA-------- -QVA-GRKGF  PH--------
gi_13959540_sp_----------  ------RADL  ---------- -RL-GGQPAP  PQ--------
gi_115502451_sp----------  ------RADL  ---------- -RL-GGQPAP  PQ--------
gi_13959573_sp_----------  ------RGEL  ---------- -RLGAARRPP  PH--------
gi_13959541_sp_----------  ---GRLDCRL  GPGAPASAQP  AQP-PSSYSL  P---------
gi_13959538_sp_----------  ---GRLDCRL  ---------- -GP-GAPAGA  QPAQPPSSYS
gi_13959529_sp_----------  ---GRLDCRL  GPGAPASAQP  AQP-PSSYSL  P---------
Consistency    0000000000  0007688878*  0000000000  0886068786  9700000000
```

Results colour-coded for amino acid conservation

```
                          . . . . . . . . 310 . . . . . . . . 320 . . . . . . . . 330 . . . . . . . . 340 . . . . . . . . 350
gi_13633932_sp_  --VIYCRVWR  WPDLQSHHEL  KPLECCE-FP  FGSKQKEVCI  NPYHYKRVES
gi_118573879_sp  --VIYCRVWR  WPDLQSHHEL  KPLECCE-FP  FGSKQKEVCI  NPYHYKRVES
gi_13633915_sp_  --VIYCRVWR  WPDLQSHHEL  KPLECCE-FP  FGSKQKEVCI  NPYHYKRVES
gi_341942042_sp  --VIYCRVWR  WPDLQSHHEL  KPLECCE-FP  FGSKQKEVCI  NPYHYKRVES
gi_82121811_sp_  --VIYCRVWR  WPDLQSHHEL  KPLDICE-FP  FGSKQKEVCI  NPYHYKRVES
gi_21264062_sp_  --VIYCRVWP  WPDLQSHHEL  KPLEVCE-YP  FGSKQKEVCI  NPYHYKRVES
gi_13959533_sp_  --VIYCRVWR  WPDLQSHHEL  KPLDICE-FP  FGSKQKEVCI  NPYHYKRVES
gi_13959566_sp_  --VIYCRVWR  WPDLQSHHEL  KPLDICE-FP  FGSKQKEVCI  NPYHYKRVES
gi_13959559_sp_  --VIYCRVWR  WPDLQSHHEL  KPLDICE-FP  FGSKQKEVCI  NPYHYKRVES
gi_13633872_sp_  --VIYCRVWR  WPDLQSHHEL  KPLECCE-FP  FGSKQKEVCI  NPYHYKRVES
gi_13959539_sp_  --VIYCRVWR  WPDLQSHHEL  KPLECCE-FP  FGSKQKEVCI  NPYHYRRVET
gi_21264049_sp_  --VIYCRVWR  WPDLQSHHEL  KALECCE-FP  FGSKQKDVCI  NPYHYKRVDS
gi_66774168_sp_  --VIYCRVWR  WPDLQSHHEL  KPLECCE-FP  FGSKQKEVCI  NPYHYRRVET
gi_13959527_sp_  --VIYCRVWR  WPDLQSHHEL  KPLECCE-FP  FGSKQKEVCI  NPYHYRRVET
gi_51338669_sp_  --VIYCRLWR  WPDLHSHHEL  RAMELCE-FA  FNMKKDEVCV  NPYHYQRVET
gi_60414603_sp_  --VIYCRLWR  WPDLHSHHEL  RAMEMCE-YA  FNMKKDEVCV  NPYHYQRVET
gi_117949830_sp  --VIYCRLWR  WPDLHSHHEL  KAIENCE-YA  FNLKKDEVCV  NPYHYQRVET
gi_13633871_sp_  --VIYCRLWR  WPDLHSHHEL  KAIENCE-YA  FSLKKDEVCV  NPYHYQRVET
gi_13633914_sp_  --VIYCRLWR  WPDLHSHHEL  KAIENCE-YA  FNLKKDEVCV  NPYHYQRVET
gi_75041393_sp_  --VIYCRLWR  WPDLHSHHEL  KAIENCE-YA  FNLKEDEVCV  NPYHYQRVET
gi_110826300_sp  --VIYCRLWR  WPDLHSHHEL  KAIENCE-YA  FNLKKDEVCV  NPYHYQRVET
gi_21264050_sp_  --VIYCRLWR  WPDLHSHHEL  RAIETCE-YA  FNLKKDEVCV  NPYHYQRVET
gi_341942043_sp  --VIYARLWR  WPDLH-KNEL  KHVKYCQ-YA  FDLKCDSVCV  NPYHYERVVS
gi_13959528_sp_  --VIYARLWR  WPDLH-KNEL  KHVKYCQ-YA  FDLKCDSVCV  NPYHYERVVS
gi_13959561_sp_  --VIYARLWR  WPDLH-KNEL  KHVKYCQ-YA  FDLKCDSVCV  NPYHYERVVS
gi_116256078_sp  --VIYARLWR  WPDLH-KNEL  KHVKYCQ-YA  FDLKCDSVCV  NPYHYERVVS
gi_13959531_sp_  --VIYARLWR  WPDLH-KNEL  KHVKYCQ-YA  FDLKCDSVCV  NPYHYERVVS
gi_13959540_sp_  --LLLGRLFR  WPDLQHAVEL  KPLCGCHSFT  AAADGPTVCC  NPYHFSRLCG
gi_115502451_sp  --LLLGRLFR  WPDLQHAVEL  KPLCGCHSFA  AAADGPTVCC  NPYHFSRLCG
gi_13959573_sp_  --LLLGKLFR  WPDLQHPAEL  KALCECQ-SF  GAADGPTVCC  NPYHFSRLCG
gi_13959541_sp_  --LLLCKVFR  WPDLRHSSEV  KRLCCCE-SY  GKINPELVCC  NPHHLSRLCE
gi_13959538_sp_  LPLLLCKVFR  WPDLRHSSEV  KRLCCCE-SY  GKINPELVCC  NPHHLSRLCE
gi_13959529_sp_  --LLLCKVFR  WPDLRHSSEV  KRLCCCE-SY  GKINPELVCC  NPHHLSRLCE
Consistency      008977988*  ****6566*9  94853*8065  7557456**7  **9*86*856
```

```
                          . . . . . . . . 360 . . . . . . . . 370 . . . . . . . . 380 . . . . . . . . 390 . . . . . . . . 400
gi_13633932_sp_  PVLPPVLVPR  HSEYNPQHSL  LAQFRNL---  ----------G  -QNEPHMPHN
gi_118573879_sp  PVLPPVLVPR  HSEYNPQHSL  LAQFRNL---  ----------G  -QNEPHMPLN
gi_13633915_sp_  PVLPPVLVPR  HSEYNPQHSL  LAQFRNL---  ----------G  -QNEPHMPLN
gi_341942042_sp  PVLPPVLVPR  HSEYNPQHSL  LAQFRNL---  ----------G  -QNEPHMPLN
gi_82121811_sp_  PVLPPVLVPR  HSEFNPQHSL  LVQFRNL---  ----------S  -HNEPHMPHN
gi_21264062_sp_  PVLPPVLVPR  HSEFNPQHSL  LVQFRNL---  ----------S  -HNEPHMPLN
gi_13959533_sp_  PVLPPVLVPR  HNEFNPQHSL  LVQFRNL---  ----------S  -HNEPHMPQN
gi_13959566_sp_  PVLPPVLVPR  HNEFNPQHSL  LVQFRNL---  ----------S  -HNEPHMPQN
gi_13959559_sp_  PVLPPVLVPR  HNEFNPQHSL  LVQFRNL---  ----------S  -HNEPHMPQN
gi_13633872_sp_  PVLPPVLVPR  HSEYNPQHSL  LAQFRNL---  ----------G  -QNEPHMPLN
gi_13959539_sp_  PVLPPVLVPR  HSEYNPQLSL  LAKFRSA---  ----------S  LHSEPLMPHN
gi_21264049_sp_  PVLPPVLVPR  NSEFNAKLSM  LPRFRNP---  ----------L  HQTEPPMPQN
gi_66774168_sp_  PVLPPVLVPR  HSEYNPQLSL  LAKFRSA---  ----------S  LHSEPLMPHN
gi_13959527_sp_  PVLPPVLVPR  HSEYNPQLSL  LAKFRSA---  ----------S  LHSEPLMPHN
gi_51338669_sp_  PVLPPVLVPR  HTEIPAEFPP  LDDY------  -----------  ---SHSIPEN
gi_60414603_sp_  PVLPPVLVPR  HTEIPAEFPP  LDDY------  -----------  ---SHSIPEN
gi_117949830_sp  PVLPPVLVPR  HTEILTELPP  LDDY------  -----------  ---THSIPEN
gi_13633871_sp_  PVLPPVLVPR  HTEILTELPP  LDDY------  -----------  ---THSIPEN
gi_13633914_sp_  PVLPPVLVPR  HTEILTELPP  LDDY------  -----------  ---THSIPEN
gi_75041393_sp_  PVLPPVLVPR  HTEILTELPP  LDDY------  -----------  ---THSIPEN
gi_110826300_sp  PVLPPVLVPR  HTEILTELPP  LDDY------  -----------  ---THSIPEN
gi_21264050_sp_  PVLPPVLVPR  HTEILTELPP  LDDY------  -----------  ---TNSIPEN
gi_341942043_sp  PGIDLSGLTL  QSN-APSMLV  KDEYVHDFEG  QPSLPTEGHS  IQTIQHPPSN
gi_13959528_sp_  PGIDLSGLTL  QSNAPPSMLV  KDEYVHDFEG  QPSLPTEGHS  IQTIQHPPSN
gi_13959561_sp_  PGIDLSGLTL  QSNAPSSMMV  KDEYVHDFEG  QPSLSTEGHS  IQTIQHPPSN
gi_116256078_sp  PGIDLSGLTL  QSNAPPSMLV  KDEYVHDFEG  QPSLSTEGHS  IQTIQHPPSN
gi_13959531_sp_  PGIDLSGLTL  QSNAPSGMLV  KDEYVHDFEG  QPSLATEGHS  IQTIQHPPSN
gi_13959540_sp_  PESPP---PP  YSRLSPP---  ----------  -----------  -----DQYKP
gi_115502451_sp  PESPP---PP  YSRLSPR---  ----------  -----------  -----DEYKP
gi_13959573_sp_  PESPP---PP  YSRLSPN---  ----------  -----------  -----DEQKP
gi_13959541_sp_  LESPP---PP  YSRYPMD---  ----------  -----------  -----FLKPT
gi_13959538_sp_  LESPP---PP  YSRYPMD---  ----------  -----------  -----FLKPT
gi_13959529_sp_  LESPP---PP  YSRYPMD---  ----------  -----------  -----FLKPT
Consistency      8578754585  6775456333  5345221000  0000000002  0223345747
```

```
                          . . . . . . . . 410 . . . . . . . . 420 . . . . . . . . 430 . . . . . . . . 440 . . . . . . . . 450
gi_13633932_sp_  ATFPDSFQQP  NSHPFPHSPN  ------SSYP  NSPGSSSSTY  PHSPAS----
```

Results colour-coded for amino acid conservation

```
gi_118573879_sp ATFPDSFQQP NSHPFPHSPN ------SSYP NSPGSSSSTY PHSPTS----
gi_13633915_sp  ATFPDSFQQP NSHPFPHSPN ------SSYP NSPGSSSSTY PHSPTS----
gi_341942042_sp ATFPDSFQQP NSHPFPHSPN ------SSYP NSPGGSSSTY PHSPTS----
gi_82121811_sp  ATFPDSFQQP NSTPFSISPN ------SPYP PSPA--SSTY PSSPAS----
gi_21264062_sp  ATFPESFQQH SGGSSFPISP ------NSPY PPSPASSGTY PNSPAS----
gi_13959533_sp  ATFPDSFHQP NSTPFPLSPN ------SPYP PSPA--SSTY PNSPAS----
gi_13959566_sp  ATFPDSFHQP NNTPFPLSPN ------SPYP PSPA--SSTY PNSPAS----
gi_13959559_sp  ATFPDSFHQP NNAPFPLSPN ------SPYP PSPA--SSTY PNSPAS----
gi_13633872_sp  ATFPDSFQQP HSHPFAQYPN ------SSYP NSPGSSSSTY PHSPTS----
gi_13959539_sp  ATYPDSFQQP PCSALPPSPS ------HAFS QSPC--TASY PHSPGS----
gi_21264049_sp  ATFPDSFPQQ PANALPFTPN SPTNSYPSSP NSGTGSTATF PHSPSS----
gi_66774168_sp  ATYPDSFQQS LCPAP----- ---------- ---------- ----------
gi_13959527_sp  ATYPDSFQQS LGPAP----- ---------- ---------- ----------
gi_51338669_sp  TNFPAGI-EP QSNI-PETPP -------PGYL SEDG--ETSD HQMNHS----
gi_60414603_sp  TNFPAGI-EP QSNYIPETPP -------PGYL SEDG--ETSD HQMNPS----
gi_117949830_sp TNFPAGI-EP QSNYIPETPP -------PGYI SEDG--ETSD QQLNQS----
gi_13633871_sp  TNFPAGI-EP QSNYIPETPP -------PGYI SEDG--ETSD QQLNQS----
gi_13633914_sp  TNFPAGI-EP QSNYIPETPP -------PGYI SEDG--ETSD QQLNQS----
gi_75041393_sp  TNFPAGI-EP QSNYIPETPP -------PGYI SEDG--ETSD QQLNQS----
gi_110826300_sp TNFPAGI-EP QSNYIPETPP -------PGYI SEDG--ETSD QQLNQS----
gi_21264050_sp  TNFPTGI-EP PNNYIPETPP -------PGYI SEDG--EASD QQMNQS----
gi_341942043_sp RASTETYSAP ALLAPAESNA TSTTNFPNIP VASTSQPASI LAGSHSEGLL
gi_13959528_sp  RASTETYSAP ALLAPSESNA TSTTNFPNIP VASTSQPASI LAGSHSEGLL
gi_13959561_sp  RASTETYSTP ALLAPSESNA TSTANFPNIP VASTSQPASI LGGSHSEGLL
gi_116256078_sp RASTETYSTP ALLAPSESNA TSTTNFPNIP VASTSQPASI LAGSHSEGLL
gi_13959531_sp  RASTETYSTP ALLAPSESNA TSTTNFPNIP VASTSQPASI LAGSHSEGLL
gi_13959540_sp  LDLSDSTLSY TETEATNSL- ---------- ---------- ----------
gi_115502451_sp LDLSDSTLSY TETEATNSL- ---------- ---------- ----------
gi_13959573_sp  LDLSDSTLSY TETEATNSP- ---------- ---------- ----------
gi_13959541_sp  AGCPDAVPSS AETGGTN--- ---------- ---------- ----------
gi_13959538_sp  ADCPDAVPSS AETGGTN--- ---------- ---------- ----------
gi_13959529_sp  ADCPDAVPSS DETGGTN--- ---------- ---------- ----------
Consistency     5557665266 4443343542 0000003232 2333003342 2223250000


..........460.........470.........480.........490.........500

gi_13633932_sp  ---SDPGSPF QMPADTPPPA YLPPEDQMTH DTSQPMDT-- -NMMAPGIHP
gi_118573879_sp ---SDPGSPF QMPADTPPPA YLPPEDPMTQ DGSQPMDT-- -NMMAPSLPS
gi_13633915_sp  ---SDPGSPF QMPADTPPPA YLPPEDPMTQ DGSQPMDT-- -NMMAPPLPS
gi_341942042_sp ---SDPGSPF QMPADTPPPA YLPPEDPMAQ DGSQPMDT-- -NMMAPPLPA
gi_82121811_sp  ---SGPSSPF QLPADTPPPA YMPPDDQMGQ DNSQSMDTS- -NTMIPQIMP
gi_21264062_sp  ---SGPSSPF QLPADTPPPA YMPPDEQMGQ DGSQSMETG- -SSLAPQ---
gi_13959533_sp  ---SGPGSPF QLPADTPPPA YMPPDDQMGQ DNSQPMDTS- -NNMIPQIMP
gi_13959566_sp  ---SGPGSPF QLPADTPPPA YMPPDDQMGQ DNSQPMDTS- -NNMIPQIMP
gi_13959559_sp  ---SGPGSPF QLPADTPPPA YMPPDDQMAP DNSQPMDTS- -SNMIPQTMP
gi_13633872_sp  ---SDPGSPF QMPADTPPPA YLPPEDPMAQ DGSQPMDTNM TNMTAPTLPA
gi_13959539_sp  --PSEPESPY QHSVDTPPLP YHATEASETQ SG-QPVDA-- --TADRHVVL
gi_21264049_sp  ---SDPGSPF QMP-ETPPPA YMPPEEPMTQ DCPQPMDTN- -LLAPNLPLE
gi_66774168_sp  -----PSSPG HVFPQSPCPT SYPHSPGSPS ESDSPYQH-- ----------
gi_13959527_sp  -----PSSPG HVFPQSPCPT SYPQSPGSPS ESDSPYQH-- ----------
gi_51338669_sp  ---MDAGSPN -LSPNPMSPA HNN------- ---------- ----------
gi_60414603_sp  ---MDAGSPN -LSPNPMSPA HNN------- ---------- ----------
gi_117949830_sp ---MDTGSPA ELSPTTLSPV NHS------- ---------- ----------
gi_13633871_sp  ---MDTGSPA ELSPTTLSPV NHS------- ---------- ----------
gi_13633914_sp  ---MDTGSPA ELSPTTLSPV NHS------- ---------- ----------
gi_75041393_sp  ---MDTGSPA ELSPTTLSPV NHS------- ---------- ----------
gi_110826300_sp ---MDTGSPA ELSPTTLSPV NHS------- ---------- ----------
gi_21264050_sp  ---MDTGSPA ELSPSTLSPV NHG------- ---------- ----------
gi_341942043_sp QIASGPQPGQ QQNGFTAQPA TYHHNSTTTW TGSRTAPYTP NLPHHQNGHL
gi_13959528_sp  QIASGPQPGQ QQNGFTAQPA TYHHNSTTTW TGSRTAPYTP NLPHHQNGHL
gi_13959561_sp  QIASGPQPGQ QQNGFTGQPA TYHHNSTTTW TGSRTAPYTP NLPHHQNGHL
gi_116256078_sp QIASGPQPGQ QQNGFTGQPA TYHHNSTTTW TGGRTAPYTP NLPHHQNGHL
gi_13959531_sp  QIASGPQPGQ QQNGFTGQPA TYHHNSTTTW TGSRTAPYPP NLPHHQNGHL
gi_13959540_sp  -----ITAPG EFSDASMS-- ---------- ---------- ----------
gi_115502451_sp -----ITAPG EFSDASMS-- ---------- ---------- ----------
gi_13959573_sp  -----NVTPG EFSDASTS-- ---------- ---------- ----------
gi_13959541_sp  -----YLAPG GLSDSQLL-- ---------- ---------- ----------
gi_13959538_sp  -----YLAPG GLSDSQLL-- ---------- ---------- ----------
gi_13959529_sp  -----YLAPG GLSDSQLL-- ---------- ---------- ----------
Consistency     0004354773 5654474464 3331211111 2122211100 0111111000


..........510.........520.........530.........540.........550

gi_13633932_sp  D--------- -------IHR GDVQA--VAY EEPKHWCSIV YYELNNRVGE
gi_118573879_sp E--------- -------INR GDVQA--VAY EEPKHWCSIV YYELNNRVGE
gi_13633915_sp  E--------- -------INR GDVQA--VAY EEPKHWCSIV YYELNNRVGE
gi_341942042_sp E--------- -------ISR GDVQA--VAY EEPKHWCSIV YYELNNRVGE
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Results colour-coded for amino acid conservation

```
gi_82121811_sp_ N---------- --------IST RDVQP--VAY EEPKHWCSIV YYELNNRVGE
gi_21264062_sp_ N---------- --------MPR GDVQP--VEY QEPSHWCSIV YYELNNRVGE
gi_13959533_sp_ S---------- --------ISS RDVQP--VAY EEPKHWCSIV YYELNNRVGE
gi_13959566_sp_ S---------- --------ISS RDVQP--VAY EEPKHWCSIV YYELNNRVGE
gi_13959559_sp_ S---------- --------ISS RDVQP--VAY EEPKHWCSIV YYELNNRVGE
gi_13633872_sp_ E---------- --------INR GDVQA--VAY EEPKHWCSIV YYELNNRVGE
gi_13959539_sp_ S---------- --------IPN GDFRP--VCY EEPQHWCSVA YYELNNRVGE
gi_21264049_sp_ I---------- --------SNR TDVHP--VAY QEPKHWCSIV YYELNNRVGE
gi_66774168_sp_ ---------- ---------- SDFRP--VCY EEPQHWCSVA YYELNNRVGE
gi_13959527_sp_ ---------- ---------- SDFRP--VCY EEPLHWCSVA YYELNNRVGE
gi_51338669_sp_ ---------- ---------- LDLQP--VTY CEPAFWCSIS YYELNQRVGE
gi_60414603_sp_ ---------- ---------- LDLQP--VTY CEPAFWCSIS YYELNQRVGE
gi_117949830_sp ---------- ---------- LDLQP--VTY SEPAFWCSIA YYELNQRVGE
gi_13633871_sp_ ---------- ---------- LDLQP--VTY SEPAFWCSIA YYELNQRVGE
gi_13633914_sp_ ---------- ---------- LDLQP--VTY SEPAFWCSIA YYELNQRVGE
gi_75041393_sp_ ---------- ---------- LDLQP--VTY SEPAFWCSIA YYELNQRVGE
gi_110826300_sp ---------- ---------- LDLQP--VTY SEPAFWCSIA YYELNQRVGE
gi_21264050_sp_ ---------- ---------- MDLQP--VTY SEPAFWCSIA YYELNQRVGE
gi_341942043_sp QHHPPMPPHP GHYWPV-HNE LAFQPPISNH PAPEYWCSIA YFEMDVQVGE
gi_13959528_sp_ QHHPPMPPHP GHYWPV-HNE LAFQPPISNH PAPEYWCSIA YFEMDVQVGE
gi_13959561_sp_ QHHPPMPPHP GHYWPV-HNE LAFQPPISNH PAPEYWCSIA YFEMDVQVGE
gi_116256078_sp QHHPPMPPHP GHYWPPVHNE LAFQPPISNH PAPEYWCSIA YFEMDVQVGE
gi_13959531_sp_ QHHPPMPPHP GHYWPV-HNE LAFQPPISNH PAPEYWCSIA YFEMDVQVGE
gi_13959540_sp_ ---------- ---------- -------PDA TKPSHWCSVA YWEHRTRVGR
gi_115502451_sp ---------- ---------- -------PDA TKPSHWCSVA YWEHRTRVGR
gi_13959573_sp_ ---------- ---------- -------PDA VKRSHWCNVA YWEHRTRVGR
gi_13959541_sp_ ---------- ---------- -------LEP GDRSHWCVVA YWEEKTRVGR
gi_13959538_sp_ ---------- ---------- -------LEP GDRSHWCVVA YWEEKTRVGR
gi_13959529_sp_ ---------- ---------- -------LEP GDRSHWCVVA YWEEKTRVGR
Consistency     1000000000 0000000111 2545500646 47856**897 *7*6758**8


         .........560.........570.........580.........590.........600
gi_13633932_sp_ AFHASST--S ILVDGFTDPS NNKNRFCLGL LSNVNRNSTI ENTRRHIGKG
gi_118573879_sp AFHASST--S VLVDGFTDPS NNKNRFCLGL LSNVNRNSTI ENTRRHIGKG
gi_13633915_sp_ AFHASST--S VLVDGFTDPS NNKNRFCLGL LSNVNRNSTI ENTRRHIGKG
gi_341942042_sp AFHASST--S VLVDGFTDPS NNKNRFCLGL LSNVNRNSTI ENTRRHIGKG
gi_82121811_sp_ AFHASST--S VLVDGFTDPS NNKNRFCLGL LSNVNRNSTI ENTRRHIGKG
gi_21264062_sp_ AYHASST--S VLVDGFTDPS NNKNRFCLGL LSNVNRNSTI ENTRRHIGKG
gi_13959533_sp_ AFHASST--S VLVDGFTDPA NNKSRFCLGL LSNVNRNSTI ENTRRHIGKG
gi_13959566_sp_ AFHASST--S VLVDGFTDPS NNKSRFCLGL LSNVNRNSTI ENTRRHIGKG
gi_13959559_sp_ AFHASST--S VLVDGFTDPS NNKSRFCLGL LSNVNRNSTI ENTRRHIGKG
gi_13633872_sp_ RFHASST--S VLVDGFTDPS NNKNRFCLGL LSNVNRNSTI ENTRRHIGKG
gi_13959539_sp_ TFQASSR--S VLIDGFTDPS NNRNRFCLGL LSNVNRNSTI ENTRRHIGKG
gi_21264049_sp_ AFLASST--S VLVDGFTDPS NNRNRFCLGL LSNVNRNSTI ENTRRHIGKG
gi_66774168_sp_ TFQASSR--S VLIDGFTDPS NNRNRFCLGL LSNVNRNSTI ENTRRHIGKG
gi_13959527_sp_ TFQASSR--S VLIDGFTDPS NNRNRFCLGL LSNVNRNSTI ENTRRHIGKG
gi_51338669_sp_ TFHASQP--S MTVDGFTDPS NS-ERFCLGL LSNVNRNAAV ELTRRHIGRG
gi_60414603_sp_ TFHASQP--S MTVDGFTDPS NS-ERFCLGL LSNVNRNAAV ELTRRHIGRG
gi_117949830_sp TFHASQP--S LTVDGFTDPS NS-ERFCLGL LSNVNRNATV EMTRRHIGRG
gi_13633871_sp_ TFHASQP--S LTVDGFTDPS NS-ERFCLGL LSNVNRNATV EMTRRHIGRG
gi_13633914_sp_ TFHASQP--S LTVDGFTDPS NS-ERFCLGL LSNVNRNATV EMTRRHIGRG
gi_75041393_sp_ TFHASQP--S LTVDGFTDPS NS-ERFCLGL LSNVNRNATV EMTRRHIGRG
gi_110826300_sp TFHASQP--S LTVDGFTDPS NS-ERFCLGL LSNVNRNATV EMTRRHIGRG
gi_21264050_sp_ TFHASQP--S LTVDGFTDPS NS-ERFCLGL LSNVNRNATV EMTRRHIGRG
gi_341942043_sp TFKVPSSCPV VTVDGYVDPS GG-DRFCLGQ LSNVHRTEAI ERARLHIGKG
gi_13959528_sp_ TFKVPSSCPI VTVDGYVDPS GG-DRFCLGQ LSNVHRTEAI ERARLHIGKG
gi_13959561_sp_ TFKVPSSCPI VTVDGYVDPS GG-DRFCLGQ LSNVHRTEAI ERARLHIGKG
gi_116256078_sp TFKVPSSCPI VTVDGYVDPS GG-DRFCLGQ LSNVHRTEAI ERARLHIGKG
gi_13959531_sp_ TFKVPSSCPI VTVDGYVDPS GG-DRFCLGQ LSNVHRTEAI ERARLHIGKG
gi_13959540_sp_ LYAVY----D QAVSIFYDLP QG-SGFCLGQ LNLEQRSESV RRTRSKIGFG
gi_115502451_sp LYAVY----D QAVSIFYDLP QG-SGFCLGQ LNLEQRSESV RRTRSKIGFG
gi_13959573_sp_ LYTVY----E QSVSIFYDLP QG-NGFCLGQ LNLENRSETV RRTRSKIGYG
gi_13959541_sp_ LYCVQ----E PSLDIFYDLP QG-NGFCLGQ LNSDNKSQLV QKVRSKIGCG
gi_13959538_sp_ LYCVQ----E PSLDIFYDLP QG-NGFCLGQ LNSDNKSQLV QKVRSKIGCG
gi_13959529_sp_ LYCVQ----E PSLDIFYDLP QG-NGFCLGQ LNSDNKSQLV QKVRSKIGCG
Consistency     6847653006 6599696*77 66167****6 *877797669 857*67**6*


         .........610.........620.........630.........640.........650
gi_13633932_sp_ VHLYYVG-GE VYAECLSDSS IFVQSRNCNY HHGFHPT-TV CKIPSGCSLK
gi_118573879_sp VHLYYVG-GE VYAECLSDSS IFVQSRNCNY HHGFHPT-TV CKIPSGCSLK
gi_13633915_sp_ VHLYYVG-GE VYAECLSDSS IFVQSRNCNY HHGFHPT-TV CKIPSGCSLK
gi_341942042_sp VHLYYVG-GE VYAECLSDSS IFVQSRNCNY HHGFHPT-TV CKIPSGCSLK
gi_82121811_sp_ VHLYYVG-GE VYAECLSDSS IFVQSRNCNY HHGFHPT-TV CKIPSGCSLK
gi_21264062_sp_ VHLYYVG-GE VYAECLSDTS IFVQSRNCNY HHGFHPT-TV CKIPSGCSLK
gi_13959533_sp_ VHLYYVG-GE VYAECLSDSS IFVQSRNCNF HHGFHPT-TV CKIPSSCSLK
```

Results colour-coded for amino acid conservation   6

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gi_13959566_sp_VHLYYVG-GE VYAECLSDSS IFVQSRNCNF HHGFHPT-TV CKIPSSCSLK
gi_13959559_sp_VHLYYVG-GE VYAECLSDSS IFVQSRNCNF HHGFHPT-TV CKIPSSCSLK
gi_13633872_sp_VHLYYVG-GE VYAECLSDSS IFVQSRNCNY HHGFHPT-TV CKIPSGCSLK
gi_13959539_sp_VHLYYVG-GE VYAECVSDSS IFVQSRNCNY QHGFHPA-TV CKIPSGCSLK
gi_21264049_sp_VHLYYVG-GE VYAECLSDSS IFVQSRNCNY HHGFHPT-TV CKIPSRCSLK
gi_66774168_sp_VHLYYVG-GE VYAECVSDSS IFVQSRNCNY QHGFHPA-TV CKIPSGCSLK
gi_13959527_sp_VHLYYVG-GE VYAECVSDSS IFVQSRNCNY QHGFHPA-TV CKIPSGCSLK
gi_51338669_sp_VRLYYIG-GE VFAECLSDSA IFVQSPNCNQ RYGWHPA-TV CKIPPGCNLK
gi_60414603_sp_VRLYYIG-GE VFAECLSDSA IFVQSPNCNQ RYGWHPA-TV CKIPPGCNLK
gi_117949830_spVRLYYIG-GE VFAECLSDSA IFVQSPNCNQ RYGWHPA-TV CKIPPGCNLK
gi_13633871_sp_VRLYYIG-GE VFAECLSDSA IFVQSPNCNQ RYGWHPA-TV CKIPPGCNLK
gi_13633914_sp_VRLYYIG-GE VFAECLSDSA IFVQSPNCNQ RYGWHPA-TV CKIPPGCNLK
gi_75041393_sp_VRLYYIG-GE VFAECLSDSA IFVQSPNCNQ RYGWHPA-TV CKIPPGCNLK
gi_110826300_spVRLYYIG-GE VFAECLSDSA IFVQSPNCNQ RYGWHPA-TV CKIPPGCNLK
gi_21264050_sp_VRLYYIG-GE VFAECLSDSA IFVQSPNCNQ RYGWHPA-TV CKIPPGCNLK
gi_341942043_spVQLECKGEGD VWVRCLSDHA VFVQSYYLDR EAGRAPGDAV HKIYPSAYIK
gi_13959528_sp_VQLECKGEGD VWVRCLSDHA VFVQSYYLDR EAGRAPGDAV HKIYPSAYIK
gi_13959561_sp_VQLECKGEGD VWVRCLSDHA VFVQSYYLDR EAGRAPGDAV HKIYPSAYIK
gi_116256078_spVQLECKGEGD VWVRCLSDHA VFVQSYYLDR EAGRAPGDAV HKIYPSAYIK
gi_13959531_sp_VQLECKGEGD VWVRCLSDHA VFVQSYYLDR EAGRAPGDAV HKIYPSAYIK
gi_13959540_sp_ILLSKEP-DG VWAYNRGEHP IFVNSPTLDA PGG-RAL-VV RKVPPGYSIK
gi_115502451_spILLSKEP-DG VWAYNRGEHP IFVNSPTLDA PGG-RAL-VV RKVPPGYSIK
gi_13959573_sp_ILLSKEP-DG VWAYNRSEHP IFVNSPTLDI PNC-RTL-IV RKVMPGYSIK
gi_13959541_sp_IQLTREV-DG VWVYNRSSYP IFIKSATLDN PDS-RTL-LV HKVFPGFSIK
gi_13959538_sp_IQLTREV-DG VWVYNRSSYP IFIKSATLDN PDS-RTL-LV HKVFPGFSIK
gi_13959529_sp_IQLTREV-DG VWVYNRSSYP IFIKSATLDN PDS-RTL-LV HKVFPGFSIK
Consistency    95*5557076 *6867798669*9846674 4483675506* 5*9667668*
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```
          .........660.........670.........680.........690.........700
gi_13633932_sp_IFNNQEFAQL ----LAQSVN HGFET----- ---------- ----------
gi_118573879_spIFNNQEFAQL ----LAQSVN HGFET----- ---------- ----------
gi_13633915_sp_IFNNQEFAQL ----LAQSVN HGFET----- ---------- ----------
gi_341942042_spIFNNQEFAQL ----LAQSVN HGFET----- ---------- ----------
gi_82121811_sp_IFNNQEFAQL ----LAQSVN HGFEA----- ---------- ----------
gi_21264062_sp_IFNNQEFAQL ----LAQSVN HGFEA----- ---------- ----------
gi_13959533_sp_IFNNQEFAQL ----LAQSVN HGFEA----- ---------- ----------
gi_13959566_sp_IFNNQEFAQL ----LAQSVN HGFEA----- ---------- ----------
gi_13959559_sp_IFNNQEFAQL ----LAQSVN HGFEA----- ---------- ----------
gi_13633872_sp_IFNNQEFAQL ----LAQSVN HGFET----- ---------- ----------
gi_13959539_sp_VFNNQLFAQL ----LAQSVH HGFEV----- ---------- ----------
gi_21264049_sp_IFNNQEFAEL ----LAQSVN HGFEA----- ---------- ----------
gi_66774168_sp_VFNNQLFAQL ----LAQSVH HGFEV----- ---------- ----------
gi_13959527_sp_VFNNQLFAQL LAQLLAQSVH HGFEV----- ---------- ----------
gi_51338669_sp_IFNNQEFAAL ----LAQSVN QGFEA----- ---------- ----------
gi_60414603_sp_IFNNQEFAAL ----LAQSVN QGFEA----- ---------- ----------
gi_117949830_spIFNNQEFAAL ----LAQSVN QGFEA----- ---------- ----------
gi_13633871_sp_IFNNQEFAAL ----LAQSVN QGFEA----- ---------- ----------
gi_13633914_sp_IFNNQEFAAL ----LAQSVN QGFEA----- ---------- ----------
gi_75041393_sp_IFNNQEFAAL ----LAQSVN QGFEA----- ---------- ----------
gi_110826300_spIFNNQGFAAL ----LAQSVN QGFEA----- ---------- ----------
gi_21264050_sp_IFNNQEFAAL ----LAQSVN QGFEA----- ---------- ----------
gi_341942043_spVFDLRQCHRQ ----MQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI
gi_13959528_sp_VFDLRQCHRQ ----MQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI
gi_13959561_sp_VFDLRQCHRQ ----MQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI
gi_116256078_spVFDLRQCHRQ ----MQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI
gi_13959531_sp_VFDLRQCHRQ ----MQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI
gi_13959540_sp_VFDFERSGLL ----QHADAA HG-------- ---------- ----------
gi_115502451_spVF-DFERSGL ----QHAPEP DA-------- ---------- ----------
gi_13959573_sp_VFDYEKSCLL ----QHTAEL DY-------- ---------- ----------
gi_13959541_sp_AFDYEKAYSL ----QRPNDH EF-------- ---------- ----------
gi_13959538_sp_AFDYEKAYSL ----QRPNDH EF-------- ---------- ----------
gi_13959529_sp_AFDYEKAYSL ----QRPNDH EF-------- ---------- ----------
Consistency    8*75765657 0000767765 5645500000 0000000000 0000000000
```

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          .........710.........720.........730.........740.........750
gi_13633932_sp_---------V YELTKMCTLR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP
gi_118573879_sp---------V YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP
gi_13633915_sp_---------V YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP
gi_341942042_sp---------V YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP
gi_82121811_sp_---------V YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP
gi_21264062_sp_---------V YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEVHLHGP
gi_13959533_sp_---------V YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP
gi_13959566_sp_---------V YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP
gi_13959559_sp_---------V YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP
gi_13633872_sp_---------E YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP
```

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gi_13959539_sp_---------V  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
gi_21264049_sp_---------V  YELTKMCTIR  MSFVKGWGAK  YHRQDVTSTP  CWIEIHLHGP
gi_66774168_sp_---------V  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
gi_13959527_sp_---------V  YELTKMCTIR  MSFVKGWGAE  YHRQDVTSTP  CWIEIHLHGP
gi_51338669_sp_---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
gi_60414603_sp_---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
gi_117949830_sp---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
gi_13633871_sp_---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
gi_13633914_sp_---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
gi_75041393_sp_---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
gi_110826300_sp---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
gi_21264050_sp_---------V  YQLTRMCTIR  MSFVKGWGAE  YRRQTVTSTP  CWIELHLNGP
gi_341942043_spSLSAAAGIGV  DDLRRLCILR  MSFVKGWGPD  YPRQSIKETP  CWIEIHLHRA
gi_13959528_sp_SLSAAAGIGV  DDLRRLCILR  MSFVKGWGPD  YPRQSIKETP  CWIEIHLHRA
gi_13959561_sp_SLSAAAGIGV  DDLRRLCILR  MSFVKGWGPD  YPRQSIKETP  CWIEIHLHRA
gi_116256078_spSLSAAAGIGV  DDLRRLCILR  MSFVKGWGPD  YPRQSIKETP  CWIEIHLHRA
gi_13959531_sp_SLSAAAGIGV  DDLRRLCILR  MSFVKGWGPD  YPRQSIKETP  CWIEIHLHRA
gi_13959540_sp_---------P  ---YDPHSVR  ISFAKGWGPC  YSRQFITSCP  CWLEILLNNH
gi_115502451_sp---------A  DGPYDPNSVR  ISFAKGWGPC  YSRQFITSCP  CWLEILLNNP
gi_13959573_sp_---------A  DGPYDPNSVR  ISFAKGWGPC  YSRQFITSCP  CWLEILLSNN
gi_13959541_sp_---------M  QQPWTGFTVQ  ISFVKGWGQC  YTRQFISSCP  CWLEVIFNSR
gi_13959538_sp_---------M  QQPWTGFTVQ  ISFVKGWGQC  YTRQFISSCP  CWLEVIFNSR
gi_13959529_sp_---------M  QQPWTGFTVQ  ISFVKGWGQC  YTRQFISSCP  CWLEVIFNSR
Consistency    0000000007  5676667789  8**9****66  *4**49787*  **9*879766

                 . . . . . . . . . 760 . . . . . . . . 770 . .
gi_13633932_sp_LQWLDKVLTQ  MGSPHNPISS  VS
gi_118573879_spLQWLDKVLTQ  MGSPHNPISS  VS
gi_13633915_sp_LQWLDKVLTQ  MGSPHNPISS  VS
gi_341942042_spLQWLDKVLTQ  MGSPHNPISS  VS
gi_82121811_sp_LQWLDKVLTQ  MGSPLNPISS  VS
gi_21264062_sp_LQWLDKVLTQ  MGSPLNPISS  VS
gi_13959533_sp_LQWLDKVLTQ  MGSPLNPISS  VS
gi_13959566_sp_LQWLDKVLTQ  MGSPLNPISS  VS
gi_13959559_sp_LQWLDKVLTQ  MGSPLNPISS  VS
gi_13633872_sp_LQWLDKVLTQ  MGSPHNPISS  VS
gi_13959539_sp_LQWLDKVLTQ  MGSPHNPISS  VS
gi_21264049_sp_LQWLDKVLTQ  MGSPHNPISS  VS
gi_66774168_sp_LQWLDKVLTQ  MGSPHNPISS  VS
gi_13959527_sp_LQWLDKVLTQ  MGSPHNPISS  VS
gi_51338669_sp_LQWLDKVLTQ  MGSPSIRCSS  VS
gi_60414603_sp_LQWLDKVLTQ  MGSPSIRCSS  VS
gi_117949830_spLQWLDKVLTQ  MGSPSVRCSS  MS
gi_13633871_sp_LQWLDKVLTQ  MGSPSVRCSS  MS
gi_13633914_sp_LQWLDKVLTQ  MGSPSVRCSS  MS
gi_75041393_sp_LQWLDKVLTQ  MGSPSVRCSS  MS
gi_110826300_spLQWLDKVLTQ  MGSPSVRCSS  MS
gi_21264050_sp_LQWLDKVLTQ  MGSPSVRCSS  MS
gi_341942043_spLQLLDEVLHT  MPIA-DP-QP  LD
gi_13959528_sp_LQLLDEVLHT  MPIA-DP-QP  LD
gi_13959561_sp_LQLLDEVLHT  MPIA-DP-QP  LD
gi_116256078_spLQLLDEVLHT  MPIA-DP-QP  LD
gi_13959531_sp_LQLLDEVLHT  MPIA-DP-QP  LD
gi_13959540_sp_R---------  ----------  --
gi_115502451_spR---------  ----------  --
gi_13959573_sp_R---------  ----------  --
gi_13959541_sp_----------  ----------  --
gi_13959538_sp_----------  ----------  --
gi_13959529_sp_----------  ----------  --
Consistency    7646656645  6455234255  55
```

Results colour-coded for amino acid conservation