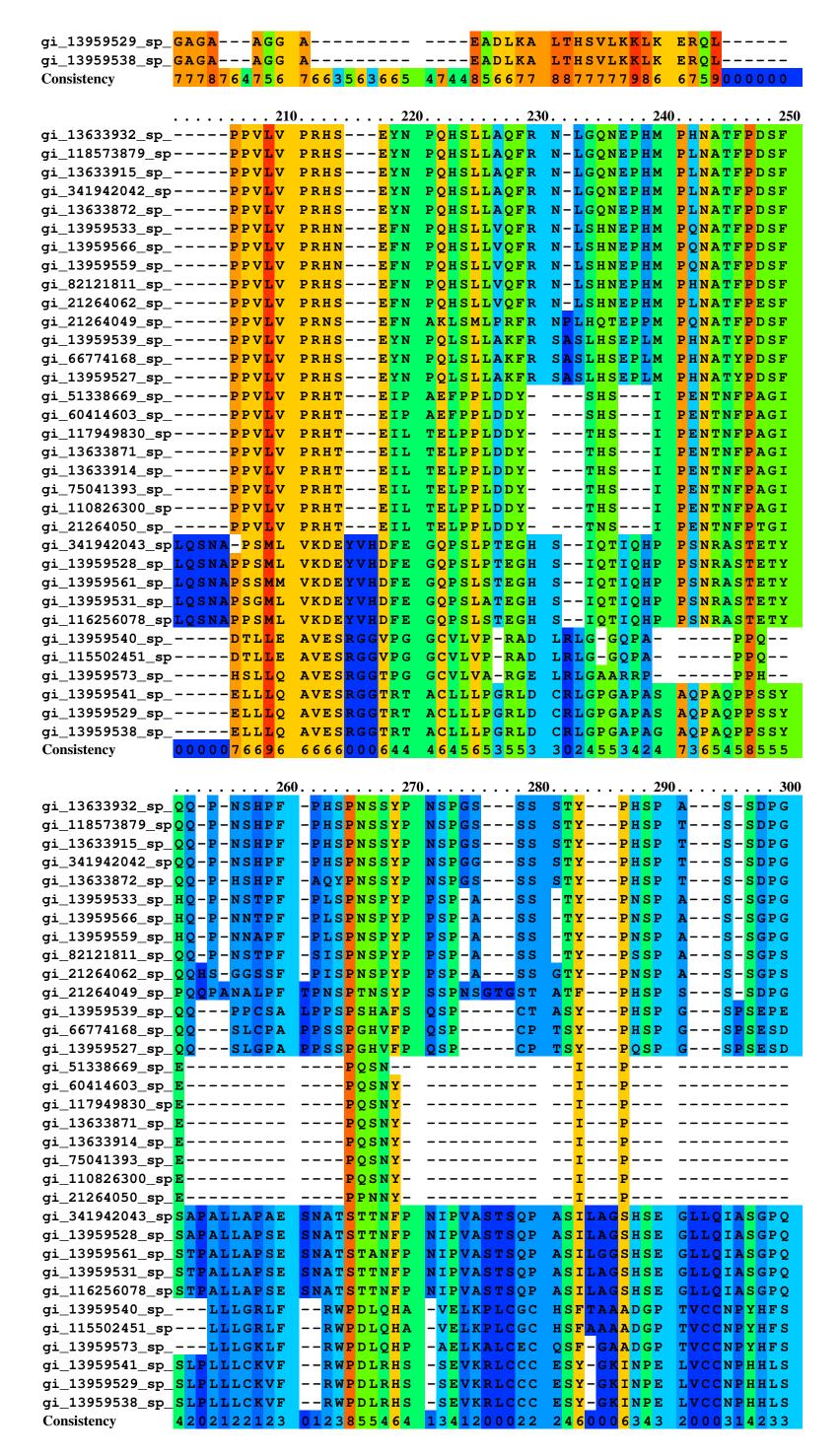# Results colour-coded for amino acid conservation

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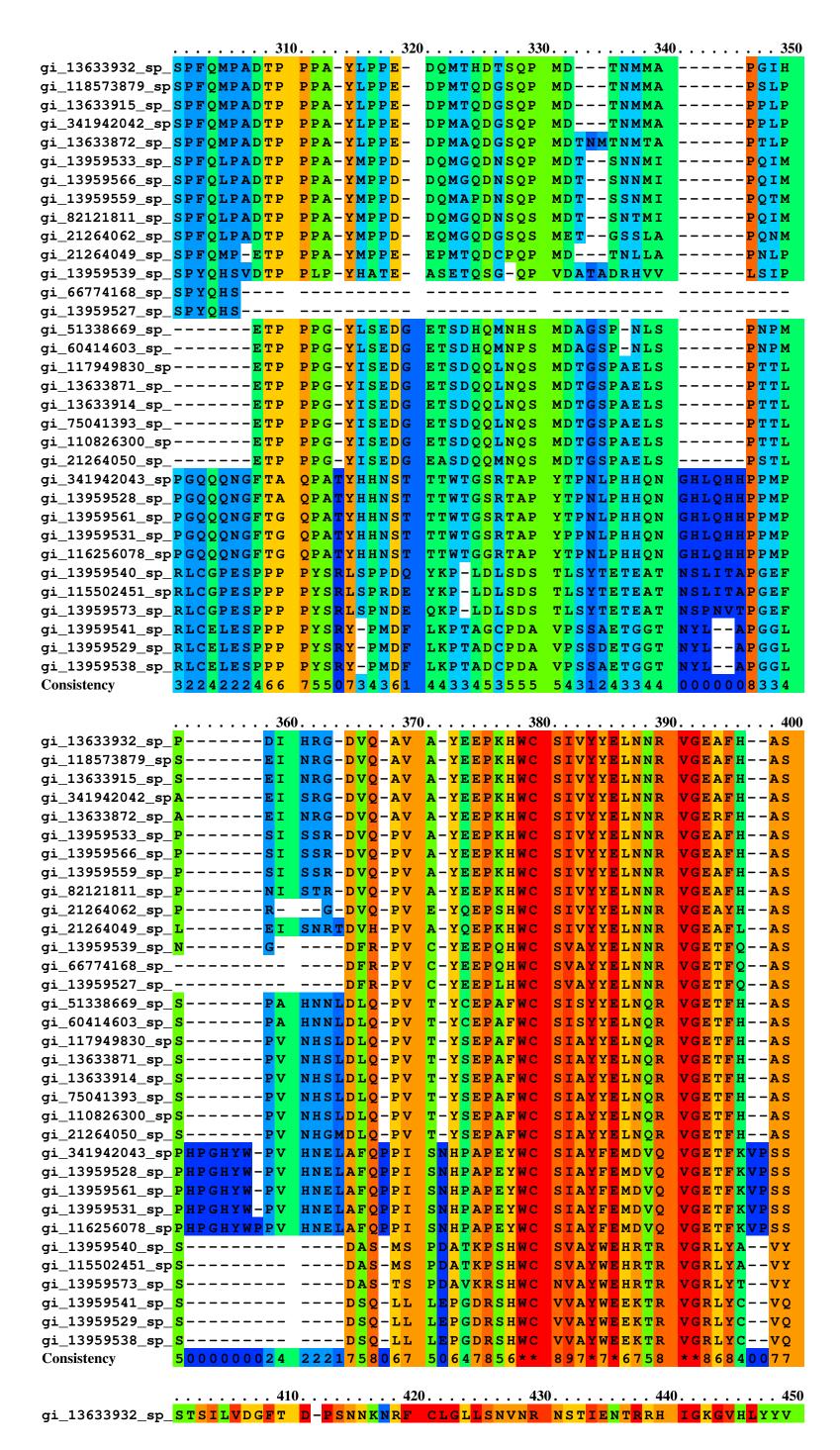
The conservation scoring is performed by PRALINE. The scoring scheme works from 0 for the least conserved alignment position, up to 10 for the most conserved alignment position. The colour assignments are:

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

```
                    . . . . . . . . . 10 . . . . . . . . . 20 . . . . . . . . . 30 . . . . . . . . . 40 . . . . . . . . . 50
gi_13633932_sp_  ------MNVT SLFSFTSPAV KRLLGWK--- ---------- -QGDEEEKWA
gi_118573879_sp  ------MNVT SLFSFTSPAV KRLLGWK--- ---------- -QGDEEEKWA
gi_13633915_sp_  ------MNVT SLFSFTSPAV KRLLGWK--- ---------- -QGDEEEKWA
gi_341942042_sp  ------MNVT SLFSFTSPAV KRLLGWK--- ---------- -QGDEEEKWA
gi_13633872_sp_  ------MNVT SLFSFTSPAV KRLLGWK--- ---------- -QGDEEEKWA
gi_13959533_sp_  ---M--TSMA SLFSFTSPAV KRLLGWK--- ---------- -QGDEEEKWA
gi_13959566_sp_  ---M--TSMA SLFSFTSPAV KRLLGWK--- ---------- -QGDEEEKWA
gi_13959559_sp_  ---M--TSMA SLFSFTSPAV KRLLGWK--- ---------- -QGDEEEKWA
gi_82121811_sp_  ---M--TSMA SLFSFTSPAV KRLLGWK--- ---------- -QGDEEEKWA
gi_21264062_sp_  ---M--TSMS SLFSFTSPAV KRLLGWK--- ---------- -QGDEEEKWA
gi_21264049_sp_  ------MNVT SLFSFTSPAV KRLLGWK--- ---------- -QGDEEEKWA
gi_13959539_sp_  MHST--TPIS SLFSFTSPAV KRLLGWK--- ---------- -QGDEEEKWA
gi_66774168_sp_  MHPS--TPIS SLFSFTSPAV KRLLGWK--- ---------- -QGDEEEKWA
gi_13959527_sp_  MHPS--TPIS SLFSFTSPAV KRLLGWK--- ---------- -QGDEEEKWA
gi_51338669_sp_  ---------MS SILPFTPPIV KRLLGWKK-- ---------G EQNGQEEKWC
gi_60414603_sp_  ---------MS SILPFTPPIV KRLLGWKK-- ---------G EQNGQEEKWC
gi_117949830_sp ---------MS SILPFTPPVV KRLLGWKKSA GGSGGA-GGG EQNGQEEKWC
gi_13633871_sp_  ---------MS SILPFTPPVV KRLLGWKKSA GGSGGA-GGG EQNGQEEKWC
gi_13633914_sp_  ---------MS SILPFTPPVV KRLLGWKKSA GGSGGA-GGG EQNGQEEKWC
gi_75041393_sp_  ---------MS SILPFTPPVV KRLLGWKKSA GGSGGA-GGG EQNGQEEKWC
gi_110826300_sp ---------MS SILPFTPPVV KRLLGWKKSA GGSGGA-GGG EQNGQEEKWC
gi_21264050_sp_  ---------MS SILPFTPPVV KRLLGWKKSA SGSSGAGGGG EQNGQEEKWC
gi_341942043_sp MDNMSITNTP TSNDACLSIV HSLMCHR--- ---------- -QGGESETFA
gi_13959528_sp_  MDNMSITNTP TSNDACLSIV HSLMCHR--- ---------- -QGGESETFA
gi_13959561_sp_  MDNMSITNTP TSNDACLSIV HSLMCHR--- ---------- -QGGESETFA
gi_13959531_sp_  MDNMSITNTP TSNDACLSIV HSLMCHR--- ---------- -QGGESETFA
gi_116256078_sp MDNMSITNTP TSNDACLSIV HSLMCHR--- ---------- -QGGESETFA
gi_13959540_sp_  MFRSKRSGLV RRL-WRSRVV P--DREE-GS GGGGVDEDG SLGSRAEP-A
gi_115502451_sp MFRSKRSGLV RRL-WRSRVV P--DREEGGS GGGGGGDEDG SLGSRAEP-A
gi_13959573_sp_  MFRSKRSGLV RRL-WRSRVI P--ERD---- ----GGDGNG QSSERNAT-A
gi_13959541_sp_  MFRTKRSALV RRL-WRSRA- PGGEDEEEGV GGGGGG---G EL--RGEG-A
gi_13959529_sp_  MFRTKRSALV RRL-WRSRA- PGGEDEEEGV GGGGGG---G GL--RGEG-A
gi_13959538_sp_  MFRTKRSALV RRL-WRSRA- PGGEDEEEGA GGGGGG---G EL--RGEG-A
Consistency      1001003365 7553665668 6566557000 0100100001 1764769657

                    . . . . . . . . . 60 . . . . . . . . . 70 . . . . . . . . . 80 . . . . . . . . . 90 . . . . . . . . . 100
gi_13633932_sp_  EKAVDA---- ----LVKKLK KKKGAMEELE KALSCPGQ-P SNCVTIP---
gi_118573879_sp EKAVDA---- ----LVKKLK KKKGAMEELE KALSCPGQ-P SNCVTIP---
gi_13633915_sp_  EKAVDA---- ----LVKKLK KKKGAMEELE KALSCPGQ-P SNCVTIP---
gi_341942042_sp EKAVDA---- ----LVKKLK KKKGAMEELE KALSCPGQ-P SNCVTIP---
gi_13633872_sp_  EKAVDA---- ----LVKKLK KKKGAMEELE KALSCPGQ-P SNCVTIP---
gi_13959533_sp_  EKAVDA---- ----LVKKLK KKKGAMEELE KALSSPGQ-P SKCVTIP---
gi_13959566_sp_  EKAVDA---- ----LVKKLK KKKGAMEELE KALSSPGQ-P SKCVTIP---
gi_13959559_sp_  EKAVDA---- ----LVKKLK KKKGAMEELE KALSSPGQ-P SKCVTIP---
gi_82121811_sp_  EKAVDA---- ----LVKKLK KKKGAMEELE KALSSPGQ-P SKCVTIP---
gi_21264062_sp_  EKAVDA---- ----LVKKLK KKKGAMEDLE KALSSPGQ-P SKCVTIP---
gi_21264049_sp_  EKAVDA---- ----LVKKLK KKKGAMEELE RALSCPGQ-P SNCVTIP---
gi_13959539_sp_  EKAVDS---- ----LVKKLK KKKGAMDELE RALSCPGQ-P SKCVTIP---
gi_66774168_sp_  EKAVDS---- ----LVKKLK KKKGAMDELE RALSCPGQ-P SKCVTIP---
gi_13959527_sp_  EKAVDS---- ----LVKKLK KKKGAMDELE RALSCPGQ-P SKCVTIP---
gi_51338669_sp_  EKAVKS---- ----LVKKL- KKTGQLDELE KAITTQNV-N TKCITIP---
gi_60414603_sp_  EKAVKS---- ----LVKKL- KKTGQLDELE KAITTQNI-N TKCITIP---
gi_117949830_sp EKAVKS---- ----LVKKL- KKTGRLDELE KAITTQNC-N TKCVTIPSTC
gi_13633871_sp_  EKAVKS---- ----LVKKL- KKTGRLDELE KAITTQNC-N TKCVTIPSTC
gi_13633914_sp_  EKAVKS---- ----LVKKL- KKTGRLDELE KAITTQNC-N TKCVTIPSTC
gi_75041393_sp_  EKAVKS---- ----LVKKL- KKTGRLDELE KAITTQNC-N TKCVTIPSTC
gi_110826300_sp EKAVKS---- ----LVKKL- KKTGRLDELE KAITTQNC-N TKCVTIPSTC
gi_21264050_sp_  EKAVKS---- ----LVKKL- KKTGQLDELE KAITTQNR-N TKCVTIPSNC
gi_341942043_sp KRAIES---- ----LVKKLK EKKDELDSLI TAITTNGAHP SKCVTIQ---
gi_13959528_sp_  KRAIES---- ----LVKKLK EKKDELDSLI TAITTNGAHP SKCVTIQ---
gi_13959561_sp_  KRAIES---- ----LVKKLK EKKDELDSLI TAITTNGAHP SKCVTIQ---
gi_13959531_sp_  KRAIES---- ----LVKKLK EKKDELDSLI TAITTNGAHP SKCVTIQ---
gi_116256078_sp KRAIES---- ----LVKKLK EKKDELDSLI TAITTNGAHP SKCVTIQ---
gi_13959540_sp_  PRAREGGGCS RSEVRSVAPR RPRDAVGPRG AAIAGRRRRT GGLPRPVSES
```

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gi_115502451_sp PRAREGGGCG RSEVRPVAPR RPRDAVGQRG AQGAGRRRA GGPPRPMSEP
gi_13959573_sp_ VTA-EG---- ---QRMAQPR RAQEGEG--- ---------- -----RP----
gi_13959541_sp_ T---DG---- ---------- RAYGAGG--- ---------- GGAGR-----
gi_13959529_sp_ T---DG---- ---------- RAYGAGG--- ---------- GGAGR-----
gi_13959538_sp_ T---DS---- ---------- RAHGAGG--- ---------- GGPGR-----
Consistency     6686670000 0000777764 7767666565 5765445304 6676765000
```

```
.......... 110 .......... 120 .......... 130 .......... 140 .......... 150
gi_13633932_sp_ ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRV
gi_118573879_sp ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRV
gi_13633915_sp_ ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRV
gi_341942042_sp ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRV
gi_13633872_sp_ ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRV
gi_13959533_sp_ ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRV
gi_13959566_sp_ ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRV
gi_13959559_sp_ ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRV
gi_82121811_sp_ ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRV
gi_21264062_sp_ ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRV
gi_21264049_sp_ ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRV
gi_13959539_sp_ ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRV
gi_66774168_sp_ ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRV
gi_13959527_sp_ ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRV
gi_51338669_sp_ ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRL
gi_60414603_sp_ ---------- ---------- -------RSL DGRLQVSHRK GLPHVIYCRL
gi_117949830_sp SEIWGLSTAN TVDQWDTTGL YSFSEQTRSL DGRLQVSHRK GLPHVIYCRL
gi_13633871_sp_ SEIWGLSTAN TVDQWDTTGL YSFSEQTRSL DGRLQVSHRK GLPHVIYCRL
gi_13633914_sp_ SEIWGLSTPN TIDQWDTTGL YSFSEQTRSL DGRLQVSHRK GLPHVIYCRL
gi_75041393_sp_ SEIWGLSTPN TIDQWDTTGL YSFSEQTRSL DGRLQVSHRK GLPHVIYCRL
gi_110826300_sp SEIWGLSTPN TIDQWDTTGL YSFSEQTRSL DGRLQVSHRK GLPHVIYCRL
gi_21264050_sp_ SEIWGLSTPN TIEQWDTSGL YSYPDQTRSL DGRLQVSHRK GLPHVIYCRL
gi_341942043_sp ---------- ---------- -------RTL DGRLQVAGRK GFPHVIYARL
gi_13959528_sp_ ---------- ---------- -------RTL DGRLQVAGRK GFPHVIYARL
gi_13959561_sp_ ---------- ---------- -------RTL DGRLQVAGRK GFPHVIYARL
gi_13959531_sp_ ---------- ---------- -------RTL DGRLQVAGRK GFPHVIYARL
gi_116256078_sp ---------- ---------- -------RTL DGRLQVAGRK GFPHVIYARL
gi_13959540_sp_ GAGAGGSPLD VAEPGGPGWL PESDCETVTC CLFSERDAAG APRDSGDPQA
gi_115502451_sp GAGAGSSLLD VAEPGGPGWL PESDCETVTC CLFSERDAAG APRDASDPLA
gi_13959573_sp_ ---------- ---------- -------VRC CLFAERPGPE LPPPPPPPPP
gi_13959541_sp_ ---------- ---------- -------AGC CLGKAVRGAK GHHHPHPPTS
gi_13959529_sp_ ---------- ---------- -------AGC CLGKAVRGAK GHHHPHPPSS
gi_13959538_sp_ ---------- ---------- -------AGC CLGKAVRGAK GHHHPHPPAA
Consistency     0000000000 0000000000 0000000777 7677887678 8578777676
```

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.......... 160 .......... 170 .......... 180 .......... 190 .......... 200
gi_13633932_sp_ WRWPDLQSHH ELKPLECCEF PFGSKQKEVC INPYHYKRVE SPVL------
gi_118573879_sp WRWPDLQSHH ELKPLECCEF PFGSKQKEVC INPYHYKRVE SPVL------
gi_13633915_sp_ WRWPDLQSHH ELKPLECCEF PFGSKQKEVC INPYHYKRVE SPVL------
gi_341942042_sp WRWPDLQSHH ELKPLECCEF PFGSKQKEVC INPYHYKRVE SPVL------
gi_13633872_sp_ WRWPDLQSHH ELKPLECCEF PFGSKQKEVC INPYHYKRVE SPVL------
gi_13959533_sp_ WRWPDLQSHH ELKPLDICEF PFGSKQKEVC INPYHYKRVE SPVL------
gi_13959566_sp_ WRWPDLQSHH ELKPLDICEF PFGSKQKEVC INPYHYKRVE SPVL------
gi_13959559_sp_ WRWPDLQSHH ELKPLDICEF PFGSKQKEVC INPYHYKRVE SPVL------
gi_82121811_sp_ WRWPDLQSHH ELKPLDICEF PFGSKQKEVC INPYHYKRVE SPVL------
gi_21264062_sp_ WRWPDLQSHH ELKPLEVCEY PFGSKQKEVC INPYHYKRVE SPVL------
gi_21264049_sp_ WRWPDLQSHH ELKALECCEF PFGSKQKDVC INPYHYKRVD SPVL------
gi_13959539_sp_ WRWPDLQSHH ELKPLECCEF PFGSKQKEVC INPYHYRRVE TPVL------
gi_66774168_sp_ WRWPDLQSHH ELKPLECCEF PFGSKQKEVC INPYHYRRVE TPVL------
gi_13959527_sp_ WRWPDLQSHH ELKPLECCEF PFGSKQKEVC INPYHYRRVE TPVL------
gi_51338669_sp_ WRWPDLHSHH ELRAMELCEF AFNMKKDEVC VNPYHYQRVE TPVL------
gi_60414603_sp_ WRWPDLHSHH ELRAMEMCEY AFNMKKDEVC VNPYHYQRVE TPVL------
gi_117949830_sp WRWPDLHSHH ELKAIENCEY AFNLKKDEVC VNPYHYQRVE TPVL------
gi_13633871_sp_ WRWPDLHSHH ELKAIENCEY AFSLKKDEVC VNPYHYQRVE TPVL------
gi_13633914_sp_ WRWPDLHSHH ELKAIENCEY AFNLKKDEVC VNPYHYQRVE TPVL------
gi_75041393_sp_ WRWPDLHSHH ELKAIENCEY AFNLKEDEVC VNPYHYQRVE TPVL------
gi_110826300_sp WRWPDLHSHH ELKAIENCEY AFNLKKDEVC VNPYHYQRVE TPVL------
gi_21264050_sp_ WRWPDLHSHH ELRAIETCEY AFNLKKDEVC VNPYHYQRVE TPVL------
gi_341942043_sp WRWPDLHK-N ELKHVKYCQY AFDLKCDSVC VNPYHYERVV SPGIDLSGLT
gi_13959528_sp_ WRWPDLHK-N ELKHVKYCQY AFDLKCDSVC VNPYHYERVV SPGIDLSGLT
gi_13959561_sp_ WRWPDLHK-N ELKHVKYCQY AFDLKCDSVC VNPYHYERVV SPGIDLSGLT
gi_13959531_sp_ WRWPDLHK-N ELKHVKYCQY AFDLKCDSVC VNPYHYERVV SPGIDLSGLT
gi_116256078_sp WRWPDLHK-N ELKHVKYCQY AFDLKCDSVC VNPYHYERVV SPGIDLSGLT
gi_13959540_sp_ RQSPEPEEGG GPRSREARSR LLLLEQELKT VTYSLLKRLK ERSL------
gi_115502451_sp GAALEP-AGG G-RSREARSR LLLLEQELKT VTYSLLKRLK ERSL------
gi_13959573_sp_ GGASPPGPGG G----EARSR LVLLERELKA VTYALLKRLK ERSL------
gi_13959541_sp_ GAGA---AGG A--------- ----EADLKA LTHSVLKKLK ERQL------
```

Results colour-coded for amino acid conservation

```
gi_13959529_sp_GAGA---AGG A--------- ----EADLKA LTHSVLKKLK ERQL------
gi_13959538_sp_GAGA---AGG A--------- ----EADLKA LTHSVLKKLK ERQL------
Consistency    7778764756 7663563665 4744856677 8877777986 6759000000
```

```
                    . . . . . . . . . 210 . . . . . . . . . 220 . . . . . . . . . 230 . . . . . . . . . 240 . . . . . . . . . 250
gi_13633932_sp_-----PPVLV PRHS---EYN PQHSLLAQFR N-LGQNEPHM PHNATFPDSF
gi_118573879_sp-----PPVLV PRHS---EYN PQHSLLAQFR N-LGQNEPHM PLNATFPDSF
gi_13633915_sp_-----PPVLV PRHS---EYN PQHSLLAQFR N-LGQNEPHM PLNATFPDSF
gi_341942042_sp-----PPVLV PRHS---EYN PQHSLLAQFR N-LGQNEPHM PLNATFPDSF
gi_13633872_sp_-----PPVLV PRHS---EYN PQHSLLAQFR N-LGQNEPHM PLNATFPDSF
gi_13959533_sp_-----PPVLV PRHN---EFN PQHSLLVQFR N-LSHNEPHM PQNATFPDSF
gi_13959566_sp_-----PPVLV PRHN---EFN PQHSLLVQFR N-LSHNEPHM PQNATFPDSF
gi_13959559_sp_-----PPVLV PRHN---EFN PQHSLLVQFR N-LSHNEPHM PQNATFPDSF
gi_82121811_sp_-----PPVLV PRHS---EFN PQHSLLVQFR N-LSHNEPHM PHNATFPDSF
gi_21264062_sp_-----PPVLV PRHS---EFN PQHSLLVQFR N-LSHNEPHM PLNATFPESF
gi_21264049_sp_-----PPVLV PRNS---EFN AKLSMLPRFR NPLHQTEPPM PQNATFPDSF
gi_13959539_sp_-----PPVLV PRHS---EYN PQLSLLAKFR SASLHSEPLM PHNATYPDSF
gi_66774168_sp_-----PPVLV PRHS---EYN PQLSLLAKFR SASLHSEPLM PHNATYPDSF
gi_13959527_sp_-----PPVLV PRHS---EYN PQLSLLAKFR SASLHSEPLM PHNATYPDSF
gi_51338669_sp_-----PPVLV PRHT---EIP AEFPPLDDY- ---SHS---I PENTNFPAGI
gi_60414603_sp_-----PPVLV PRHT---EIP AEFPPLDDY- ---SHS---I PENTNFPAGI
gi_117949830_sp-----PPVLV PRHT---EIL TELPPLDDY- ---THS---I PENTNFPAGI
gi_13633871_sp_-----PPVLV PRHT---EIL TELPPLDDY- ---THS---I PENTNFPAGI
gi_13633914_sp_-----PPVLV PRHT---EIL TELPPLDDY- ---THS---I PENTNFPAGI
gi_75041393_sp_-----PPVLV PRHT---EIL TELPPLDDY- ---THS---I PENTNFPAGI
gi_110826300_sp-----PPVLV PRHT---EIL TELPPLDDY- ---THS---I PENTNFPAGI
gi_21264050_sp_-----PPVLV PRHT---EIL TELPPLDDY- ---TNS---I PENTNFPTGI
gi_341942043_spLQSNA-PSML VKDEYVHDFE GQPSLPTEGH S--IQTIQHP PSNRASTETY
gi_13959528_sp_LQSNAPPSML VKDEYVHDFE GQPSLPTEGH S--IQTIQHP PSNRASTETY
gi_13959561_sp_LQSNAPSSMM VKDEYVHDFE GQPSLSTEGH S--IQTIQHP PSNRASTETY
gi_13959531_sp_LQSNAPSGML VKDEYVHDFE GQPSLATEGH S--IQTIQHP PSNRASTETY
gi_116256078_spLQSNAPPSML VKDEYVHDFE GQPSLSTEGH S--IQTIQHP PSNRASTETY
gi_13959540_sp_-----DTLLE AVESRGGVPG GCVLVP-RAD LRLG-GQPA- -----PPQ--
gi_115502451_sp-----DTLLE AVESRGGVPG GCVLVP-RAD LRLG-GQPA- -----PPQ--
gi_13959573_sp_-----HSLLQ AVESRGGTPG GCVLVA-RGE LRLGAARRP- -----PPH--
gi_13959541_sp_-----ELLLQ AVESRGGTRT ACLLLPGRLD CRLGPGAPAS AQPAQPPSSY
gi_13959529_sp_-----ELLLQ AVESRGGTRT ACLLLPGRLD CRLGPGAPAS AQPAQPPSSY
gi_13959538_sp_-----ELLLQ AVESRGGTRT ACLLLPGRLD CRLGPGAPAG AQPAQPPSSY
Consistency    0000076696 6666000644 4645653553 3024553424 7365458555
```

```
                    . . . . . . . . . 260 . . . . . . . . . 270 . . . . . . . . . 280 . . . . . . . . . 290 . . . . . . . . . 300
gi_13633932_sp_QQ-P-NSHPF -PHSPNSSYP NSPGS---SS STY---PHSP A---S-SDPG
gi_118573879_spQQ-P-NSHPF -PHSPNSSYP NSPGS---SS STY---PHSP T---S-SDPG
gi_13633915_sp_QQ-P-NSHPF -PHSPNSSYP NSPGS---SS STY---PHSP T---S-SDPG
gi_341942042_spQQ-P-NSHPF -PHSPNSSYP NSPGG---SS STY---PHSP T---S-SDPG
gi_13633872_sp_QQ-P-HSHPF -AQYPNSSYP NSPGS---SS STY---PHSP T---S-SDPG
gi_13959533_sp_HQ-P-NSTPF -PLSPNSPYP PSP-A---SS -TY---PNSP A---S-SGPG
gi_13959566_sp_HQ-P-NNTPF -PLSPNSPYP PSP-A---SS -TY---PNSP A---S-SGPG
gi_13959559_sp_HQ-P-NNAPF -PLSPNSPYP PSP-A---SS -TY---PNSP A---S-SGPG
gi_82121811_sp_QQ-P-NSTPF -SISPNSPYP PSP-A---SS -TY---PSSP A---S-SGPS
gi_21264062_sp_QQHS-GGSSF -PISPNSPYP PSP-A---SS GTY---PNSP A---S-SGPS
gi_21264049_sp_PQQPANALPF TPNSPTNSYP SSPNSGTGST ATF---PHSP S---S-SDPG
gi_13959539_sp_QQ---PPCSA LPPSPSHAFS QSP-----CT ASY---PHSP G---SPSEPE
gi_66774168_sp_QQ---SLCPA PPSSPGHVFP QSP-----CP TSY---PHSP G---SPSESD
gi_13959527_sp_QQ---SLGPA PPSSPGHVFP QSP-----CP TSY---PQSP G---SPSESD
gi_51338669_sp_E--------- ----PQSN-- ---------- --I---P--- ----------
gi_60414603_sp_E--------- ----PQSNY- ---------- --I---P--- ----------
gi_117949830_spE--------- ----PQSNY- ---------- --I---P--- ----------
gi_13633871_sp_E--------- ----PQSNY- ---------- --I---P--- ----------
gi_13633914_sp_E--------- ----PQSNY- ---------- --I---P--- ----------
gi_75041393_sp_E--------- ----PQSNY- ---------- --I---P--- ----------
gi_110826300_spE--------- ----PQSNY- ---------- --I---P--- ----------
gi_21264050_sp_E--------- ----PPNNY- ---------- --I---P--- ----------
gi_341942043_spSAPALLAPAE SNATSTTNFP NIPVASTSQP ASILAGSHSE GLLQIASGPQ
gi_13959528_sp_SAPALLAPSE SNATSTTNFP NIPVASTSQP ASILAGSHSE GLLQIASGPQ
gi_13959561_sp_STPALLAPSE SNATSTANFP NIPVASTSQP ASILGGSHSE GLLQIASGPQ
gi_13959531_sp_STPALLAPSE SNATSTTNFP NIPVASTSQP ASILAGSHSE GLLQIASGPQ
gi_116256078_spSTPALLAPSE SNATSTTNFP NIPVASTSQP ASILAGSHSE GLLQIASGPQ
gi_13959540_sp_---LLLGRLF --RWPDLQHA -VELKPLCGC HSFTAAADGP TVCCNPYHFS
gi_115502451_sp---LLLGRLF --RWPDLQHA -VELKPLCGC HSFAAAADGP TVCCNPYHFS
gi_13959573_sp_---LLLGKLF --RWPDLQHP -AELKALCEC QSF-GAADGP TVCCNPYHFS
gi_13959541_sp_SLPLLLCKVF --RWPDLRHS -SEVKRLCCC ESY-GKINPE LVCCNPHHLS
gi_13959529_sp_SLPLLLCKVF --RWPDLRHS -SEVKRLCCC ESY-GKINPE LVCCNPHHLS
gi_13959538_sp_SLPLLLCKVF --RWPDLRHS -SEVKRLCCC ESY-GKINPE LVCCNPHHLS
Consistency    4202122123 0123855464 1341200022 2460006343 2000314233
```

Results colour-coded for amino acid conservation

```
                    . . . . . . . . . 310 . . . . . . . . . 320 . . . . . . . . . 330 . . . . . . . . . 340 . . . . . . . . . 350
gi_13633932_sp_     SPFQMPADTP  PPA-YLPPE-  DQMTHDTSQP  MD---TNMMA  ------PGIH
gi_118573879_sp     SPFQMPADTP  PPA-YLPPE-  DPMTQDGSQP  MD---TNMMA  ------PSLP
gi_13633915_sp_     SPFQMPADTP  PPA-YLPPE-  DPMTQDGSQP  MD---TNMMA  ------PPLP
gi_341942042_sp     SPFQMPADTP  PPA-YLPPE-  DPMAQDGSQP  MD---TNMMA  ------PPLP
gi_13633872_sp_     SPFQMPADTP  PPA-YLPPE-  DPMAQDGSQP  MDTNMTNMTA  ------PTLP
gi_13959533_sp_     SPFQLPADTP  PPA-YMPPD-  DQMGQDNSQP  MDT--SNNMI  ------PQIM
gi_13959566_sp_     SPFQLPADTP  PPA-YMPPD-  DQMGQDNSQP  MDT--SNNMI  ------PQIM
gi_13959559_sp_     SPFQLPADTP  PPA-YMPPD-  DQMAPDNSQP  MDT--SSNMI  ------PQTM
gi_82121811_sp_     SPFQLPADTP  PPA-YMPPD-  DQMGQDNSQS  MDT--SNTMI  ------PQIM
gi_21264062_sp_     SPFQLPADTP  PPA-YMPPD-  EQMGQDGSQS  MET--GSSLA  ------PQNM
gi_21264049_sp_     SPFQMP-ETP  PPA-YMPPE-  EPMTQDCPQP  MD---TNLLA  ------PNLP
gi_13959539_sp_     SPYQHSVDTP  PLP-YHATE-  ASETQSG-QP  VDATADRHVV  ------LSIP
gi_66774168_sp_     SPYQHS----  ----------  ----------  ----------  ----------
gi_13959527_sp_     SPYQHS----  ----------  ----------  ----------  ----------
gi_51338669_sp_     -------ETP  PPG-YLSEDG  ETSDHQMNHS  MDAGSP-NLS  ------PNPM
gi_60414603_sp_     -------ETP  PPG-YLSEDG  ETSDHQMNPS  MDAGSP-NLS  ------PNPM
gi_117949830_sp     -------ETP  PPG-YISEDG  ETSDQQLNQS  MDTGSPAELS  ------PTTL
gi_13633871_sp_     -------ETP  PPG-YISEDG  ETSDQQLNQS  MDTGSPAELS  ------PTTL
gi_13633914_sp_     -------ETP  PPG-YISEDG  ETSDQQLNQS  MDTGSPAELS  ------PTTL
gi_75041393_sp_     -------ETP  PPG-YISEDG  ETSDQQLNQS  MDTGSPAELS  ------PTTL
gi_110826300_sp     -------ETP  PPG-YISEDG  ETSDQQLNQS  MDTGSPAELS  ------PTTL
gi_21264050_sp_     -------ETP  PPG-YISEDG  EASDQQMNQS  MDTGSPAELS  ------PSTL
gi_341942043_sp     PGQQQNGFTA  QPATYHHNST  TTWTGSRTAP  YTPNLPHHQN  GHLQHHPPMP
gi_13959528_sp_     PGQQQNGFTA  QPATYHHNST  TTWTGSRTAP  YTPNLPHHQN  GHLQHHPPMP
gi_13959561_sp_     PGQQQNGFTG  QPATYHHNST  TTWTGSRTAP  YTPNLPHHQN  GHLQHHPPMP
gi_13959531_sp_     PGQQQNGFTG  QPATYHHNST  TTWTGSRTAP  YPPNLPHHQN  GHLQHHPPMP
gi_116256078_sp     PGQQQNGFTG  QPATYHHNST  TTWTGGRTAP  YTPNLPHHQN  GHLQHHPPMP
gi_13959540_sp_     RLCGPESPPP  PYSRLSPPDQ  YKP-LDLSDS  TLSYTETEAT  NSLITAPGEF
gi_115502451_sp     RLCGPESPPP  PYSRLSPRDE  YKP-LDLSDS  TLSYTETEAT  NSLITAPGEF
gi_13959573_sp_     RLCGPESPPP  PYSRLSPNDE  QKP-LDLSDS  TLSYTETEAT  NSPNVTPGEF
gi_13959541_sp_     RLCELESPPP  PYSRY-PMDF  LKPTAGCPDA  VPSSAETGGT  NYL--APGGL
gi_13959529_sp_     RLCELESPPP  PYSRY-PMDF  LKPTADCPDA  VPSSDETGGT  NYL--APGGL
gi_13959538_sp_     RLCELESPPP  PYSRY-PMDF  LKPTADCPDA  VPSSAETGGT  NYL--APGGL
Consistency         3224222466  7550734361  4433453555  5431243344  0000008334

                    . . . . . . . . . 360 . . . . . . . . . 370 . . . . . . . . . 380 . . . . . . . . . 390 . . . . . . . . . 400
gi_13633932_sp_     P-------DI  HRG-DVQ-AV  A-YEEPKHWC  SIVYYELNNR  VGEAFH--AS
gi_118573879_sp     S-------EI  NRG-DVQ-AV  A-YEEPKHWC  SIVYYELNNR  VGEAFH--AS
gi_13633915_sp_     S-------EI  NRG-DVQ-AV  A-YEEPKHWC  SIVYYELNNR  VGEAFH--AS
gi_341942042_sp     A-------EI  SRG-DVQ-AV  A-YEEPKHWC  SIVYYELNNR  VGEAFH--AS
gi_13633872_sp_     A-------EI  NRG-DVQ-AV  A-YEEPKHWC  SIVYYELNNR  VGERFH--AS
gi_13959533_sp_     P-------SI  SSR-DVQ-PV  A-YEEPKHWC  SIVYYELNNR  VGEAFH--AS
gi_13959566_sp_     P-------SI  SSR-DVQ-PV  A-YEEPKHWC  SIVYYELNNR  VGEAFH--AS
gi_13959559_sp_     P-------SI  SSR-DVQ-PV  A-YEEPKHWC  SIVYYELNNR  VGEAFH--AS
gi_82121811_sp_     P-------NI  STR-DVQ-PV  A-YEEPKHWC  SIVYYELNNR  VGEAFH--AS
gi_21264062_sp_     P-------R-  --G-DVQ-PV  E-YQEPSHWC  SIVYYELNNR  VGEAYH--AS
gi_21264049_sp_     L-------EI  SNRTDVH-PV  A-YQEPKHWC  SIVYYELNNR  VGEAFL--AS
gi_13959539_sp_     N-------G-  ----DFR-PV  C-YEEPQHWC  SVAYYELNNR  VGETFQ--AS
gi_66774168_sp_     ----------  ----DFR-PV  C-YEEPQHWC  SVAYYELNNR  VGETFQ--AS
gi_13959527_sp_     ----------  ----DFR-PV  C-YEEPLHWC  SVAYYELNNR  VGETFQ--AS
gi_51338669_sp_     S-------PA  HNNLDLQ-PV  T-YCEPAFWC  SISYYELNQR  VGETFH--AS
gi_60414603_sp_     S-------PA  HNNLDLQ-PV  T-YCEPAFWC  SISYYELNQR  VGETFH--AS
gi_117949830_sp     S-------PV  NHSLDLQ-PV  T-YSEPAFWC  SIAYYELNQR  VGETFH--AS
gi_13633871_sp_     S-------PV  NHSLDLQ-PV  T-YSEPAFWC  SIAYYELNQR  VGETFH--AS
gi_13633914_sp_     S-------PV  NHSLDLQ-PV  T-YSEPAFWC  SIAYYELNQR  VGETFH--AS
gi_75041393_sp_     S-------PV  NHSLDLQ-PV  T-YSEPAFWC  SIAYYELNQR  VGETFH--AS
gi_110826300_sp     S-------PV  NHSLDLQ-PV  T-YSEPAFWC  SIAYYELNQR  VGETFH--AS
gi_21264050_sp_     S-------PV  NHGMDLQ-PV  T-YSEPAFWC  SIAYYELNQR  VGETFH--AS
gi_341942043_sp     PHPGHYW-PV  HNELAFQPPI  SNHPAPEYWC  SIAYFEMDVQ  VGETFKVPSS
gi_13959528_sp_     PHPGHYW-PV  HNELAFQPPI  SNHPAPEYWC  SIAYFEMDVQ  VGETFKVPSS
gi_13959561_sp_     PHPGHYW-PV  HNELAFQPPI  SNHPAPEYWC  SIAYFEMDVQ  VGETFKVPSS
gi_13959531_sp_     PHPGHYW-PV  HNELAFQPPI  SNHPAPEYWC  SIAYFEMDVQ  VGETFKVPSS
gi_116256078_sp     PHPGHYWPPV  HNELAFQPPI  SNHPAPEYWC  SIAYFEMDVQ  VGETFKVPSS
gi_13959540_sp_     S---------  ----DAS-MS  PDATKPSHWC  SVAYWEHRTR  VGRLYA--VY
gi_115502451_sp     S---------  ----DAS-MS  PDATKPSHWC  SVAYWEHRTR  VGRLYA--VY
gi_13959573_sp_     S---------  ----DAS-TS  PDAVKRSHWC  NVAYWEHRTR  VGRLYT--VY
gi_13959541_sp_     S---------  ----DSQ-LL  LEPGDRSHWC  VVAYWEEKTR  VGRLYC--VQ
gi_13959529_sp_     S---------  ----DSQ-LL  LEPGDRSHWC  VVAYWEEKTR  VGRLYC--VQ
gi_13959538_sp_     S---------  ----DSQ-LL  LEPGDRSHWC  VVAYWEEKTR  VGRLYC--VQ
Consistency         5000000024  2221758067  5064785 6**  897*7*6758  **868400 77

                    . . . . . . . . . 410 . . . . . . . . . 420 . . . . . . . . . 430 . . . . . . . . . 440 . . . . . . . . . 450
gi_13633932_sp_     STSILVDGFT  D-PSNNKNRF  CLGLLSNVNR  NSTIENTRRH  IGKGVHLYYV
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Results colour-coded for amino acid conservation

```
gi_118573879_sp STSVLVDGFT D-PSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
gi_13633915_sp_ STSVLVDGFT D-PSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
gi_341942042_sp STSVLVDGFT D-PSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
gi_13633872_sp_ STSVLVDGFT D-PSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
gi_13959533_sp_ STSVLVDGFT D-PANNKSRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
gi_13959566_sp_ STSVLVDGFT D-PSNNKSRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
gi_13959559_sp_ STSVLVDGFT D-PSNNKSRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
gi_82121811_sp_ STSVLVDGFT D-PSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
gi_21264062_sp_ STSVLVDGFT D-PSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
gi_21264049_sp_ STSVLVDGFT D-PSNNRNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
gi_13959539_sp_ SRSVLIDGFT D-PSNNRNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
gi_66774168_sp_ SRSVLIDGFT D-PSNNRNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
gi_13959527_sp_ SRSVLIDGFT D-PSNNRNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
gi_51338669_sp_ QPSMTVDGFT D-PSNSE-RF CLGLLSNVNR NAAVELTRRH IGRGVRLYYI
gi_60414603_sp_ QPSMTVDGFT D-PSNSE-RF CLGLLSNVNR NAAVELTRRH IGRGVRLYYI
gi_117949830_sp QPSLTVDGFT D-PSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLYYI
gi_13633871_sp_ QPSLTVDGFT D-PSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLYYI
gi_13633914_sp_ QPSLTVDGFT D-PSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLYYI
gi_75041393_sp_ QPSLTVDGFT D-PSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLYYI
gi_110826300_sp QPSLTVDGFT D-PSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLYYI
gi_21264050_sp_ QPSLTVDGFT D-PSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLYYI
gi_341942043_sp CPVVTVDGYV D-PSGGD-RF CLGQLSNVHR TEAIERARLH IGKGVQLECK
gi_13959528_sp_ CPIVTVDGYV D-PSGGD-RF CLGQLSNVHR TEAIERARLH IGKGVQLECK
gi_13959561_sp_ CPIVTVDGYV D-PSGGD-RF CLGQLSNVHR TEAIERARLH IGKGVQLECK
gi_13959531_sp_ CPIVTVDGYV D-PSGGD-RF CLGQLSNVHR TEAIERARLH IGKGVQLECK
gi_116256078_sp CPIVTVDGYV D-PSGGD-RF CLGQLSNVHR TEAIERARLH IGKGVQLECK
gi_13959540_sp_ DQAVSI--FY DLPQGSG--F CLGQLNLEQR SESVRRTRSK IGFGILLSKE
gi_115502451_sp DQAVSI--FY DLPQGSG--F CLGQLNLEQR SESVRRTRSK IGFGILLSKE
gi_13959573_sp_ EQSVSI--FY DLPQGNG--F CLGQLNLENR SETVRRTRSK IGYGILLSKE
gi_13959541_sp_ EPSLDI--FY DLPQGNG--F CLGQLNSDNK SQLVQKVRSK IGCGIQLTRE
gi_13959529_sp_ EPSLDI--FY DLPQGNG--F CLGQLNSDNK SQLVQKVRSK IGCGIQLTRE
gi_13959538_sp_ EPSLDI--FY DLPQGNG--F CLGQLNSDNK SQLVQKVRSK IGCGIQLTRE
Consistency     5578596696 *0*876516* ***6*87779 7669857*67 **6*95*555
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          .........460.........470.........480.........490.........500
gi_13633932_sp_ G-GEVYAECL SDSSIFVQSR NCNYHHGFHP T-TVCKIPSG CSLKIFN---
gi_118573879_sp G-GEVYAECL SDSSIFVQSR NCNYHHGFHP T-TVCKIPSG CSLKIFN---
gi_13633915_sp_ G-GEVYAECL SDSSIFVQSR NCNYHHGFHP T-TVCKIPSG CSLKIFN---
gi_341942042_sp G-GEVYAECL SDSSIFVQSR NCNYHHGFHP T-TVCKIPSG CSLKIFN---
gi_13633872_sp_ G-GEVYAECL SDSSIFVQSR NCNYHHGFHP T-TVCKIPSG CSLKIFN---
gi_13959533_sp_ G-GEVYAECL SDSSIFVQSR NCNFHHGFHP T-TVCKIPSS CSLKIFN---
gi_13959566_sp_ G-GEVYAECL SDSSIFVQSR NCNFHHGFHP T-TVCKIPSS CSLKIFN---
gi_13959559_sp_ G-GEVYAECL SDSSIFVQSR NCNFHHGFHP T-TVCKIPSS CSLKIFN---
gi_82121811_sp_ G-GEVYAECL SDSSIFVQSR NCNYHHGFHP T-TVCKIPSG CSLKIFN---
gi_21264062_sp_ G-GEVYAECL SDTSIFVQSR NCNYHHGFHP T-TVCKIPSG CSLKIFN---
gi_21264049_sp_ G-GEVYAECL SDSSIFVQSR NCNYHHGFHP T-TVCKIPSR CSLKIFN---
gi_13959539_sp_ G-GEVYAECV SDSSIFVQSR NCNYQHGFHP A-TVCKIPSG CSLKVFN---
gi_66774168_sp_ G-GEVYAECV SDSSIFVQSR NCNYQHGFHP A-TVCKIPSG CSLKVFN---
gi_13959527_sp_ G-GEVYAECV SDSSIFVQSR NCNYQHGFHP A-TVCKIPSG CSLKVFN---
gi_51338669_sp_ G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
gi_60414603_sp_ G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
gi_117949830_sp G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
gi_13633871_sp_ G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
gi_13633914_sp_ G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
gi_75041393_sp_ G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
gi_110826300_sp G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
gi_21264050_sp_ G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
gi_341942043_sp GEGDVWVRCL SDHAVFVQSY YLDREAGRAP GDAVHKIYPS AYIKVFDLRQ
gi_13959528_sp_ GEGDVWVRCL SDHAVFVQSY YLDREAGRAP GDAVHKIYPS AYIKVFDLRQ
gi_13959561_sp_ GEGDVWVRCL SDHAVFVQSY YLDREAGRAP GDAVHKIYPS AYIKVFDLRQ
gi_13959531_sp_ GEGDVWVRCL SDHAVFVQSY YLDREAGRAP GDAVHKIYPS AYIKVFDLRQ
gi_116256078_sp GEGDVWVRCL SDHAVFVQSY YLDREAGRAP GDAVHKIYPS AYIKVFDLRQ
gi_13959540_sp_ PDG-VWAYNR GEHPIFVNSP TLDAPGGR-- ALVVRKVPPG YSIKVFD---
gi_115502451_sp PDG-VWAYNR GEHPIFVNSP TLDAPGGR-- ALVVRKVPPG YSIKVFD---
gi_13959573_sp_ PDG-VWAYNR SEHPIFVNSP TLDIPNCR-- TLIVRKVMPG YSIKVFD---
gi_13959541_sp_ VDG-VWVYNR SSYPIFIKSA TLDNPDSR-- TLLVHKVFPG FSIKAFD---
gi_13959529_sp_ VDG-VWVYNR SSYPIFIKSA TLDNPDSR-- TLLVHKVFPG FSIKAFD---
gi_13959538_sp_ VDG-VWVYNR SSYPIFIKSA TLDNPDSR-- TLLVHKVFPG FSIKAFD---
Consistency     70*5*68677 98669*98*4 6674448446 606*5*9667 668*8*7000
```

```
          .........510.........520.........530.........540.........550
gi_13633932_sp_ -----NQEF- ---AQLLAQS V----N---- ---HGFE--- --------TV
gi_118573879_sp -----NQEF- ---AQLLAQS V----N---- ---HGFE--- --------TV
gi_13633915_sp_ -----NQEF- ---AQLLAQS V----N---- ---HGFE--- --------TV
gi_341942042_sp -----NQEF- ---AQLLAQS V----N---- ---HGFE--- --------TV
```

Results colour-coded for amino acid conservation

```
gi_13633872_sp_-----NQEF-   ---AQLLAQS V----N----   ---HGFE--- --------TE
gi_13959533_sp_-----NQEF-   ---AQLLAQS V----N----   ---HGFE--- --------AV
gi_13959566_sp_-----NQEF-   ---AQLLAQS V----N----   ---HGFE--- --------AV
gi_13959559_sp_-----NQEF-   ---AQLLAQS V----N----   ---HGFE--- --------AV
gi_82121811_sp_-----NQEF-   ---AQLLAQS V----N----   ---HGFE--- --------AV
gi_21264062_sp_-----NQEF-   ---AQLLAQS V----N----   ---HGFE--- --------AV
gi_21264049_sp_-----NQEF-   ---AELLAQS V----N----   ---HGFE--- --------AV
gi_13959539_sp_-----NQLF-   ---AQLLAQS V----H----   ---HGFE--- --------VV
gi_66774168_sp_-----NQLF-   ---AQLLAQS V----H----   ---HGFE--- --------VV
gi_13959527_sp_-----NQLFA QLLAQLLAQS V----H----   ---HGFE--- --------VV
gi_51338669_sp_-----NQEF-   ---AALLAQS V----N----   ---QGFE--- --------AV
gi_60414603_sp_-----NQEF-   ---AALLAQS V----N----   ---QGFE--- --------AV
gi_117949830_sp-----NQEF-   ---AALLAQS V----N----   ---QGFE--- --------AV
gi_13633871_sp_-----NQEF-   ---AALLAQS V----N----   ---QGFE--- --------AV
gi_13633914_sp_-----NQEF-   ---AALLAQS V----N----   ---QGFE--- --------AV
gi_75041393_sp_-----NQEF-   ---AALLAQS V----N----   ---QGFE--- --------AV
gi_110826300_sp-----NQGF-   ---AALLAQS V----N----   ---QGFE--- --------AV
gi_21264050_sp_-----NQEF-   ---AALLAQS V----N----   ---QGFE--- --------AV
gi_341942043_spCHRQMQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI SLSAAAGIGV
gi_13959528_sp_CHRQMQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI SLSAAAGIGV
gi_13959561_sp_CHRQMQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI SLSAAAGIGV
gi_13959531_sp_CHRQMQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI SLSAAAGIGV
gi_116256078_spCHRQMQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI SLSAAAGIGV
gi_13959540_sp_-----FER--   ---SGLLQHA ----------   -------D--- --------AA
gi_115502451_sp-----FER--   ---SG-LQHA ----------   ---PEPD--- --------AA
gi_13959573_sp_-----YEK--   ---SCLLQHT ----------   ---AELD--- --------YA
gi_13959541_sp_-----YEK--   ---AYSLQRP ----------   ---NDHE--- -------FM
gi_13959529_sp_-----YEK--   ---AYSLQRP ----------   ---NDHE--- -------FM
gi_13959538_sp_-----YEK--   ---AYSLQRP ----------   ---NDHE--- -------FM
Consistency    00000 68650 0009 568887 5000050000 0004767000 0000000058
```

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. . . . . . . . . . 560. . . . . . . . . 570. . . . . . . . . 580. . . . . . . . . 590. . . . . . . . . 600

gi_13633932_sp_YELTKMCTLR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTQ
gi_118573879_spYELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTQ
gi_13633915_sp_YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTQ
gi_341942042_spYELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTQ
gi_13633872_sp_YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTQ
gi_13959533_sp_YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTQ
gi_13959566_sp_YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTQ
gi_13959559_sp_YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTQ
gi_82121811_sp_YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTQ
gi_21264062_sp_YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEVHLHGP LQWLDKVLTQ
gi_21264049_sp_YELTKMCTIR MSFVKGWGAK YHRQDVTSTP CWIEIHLHGP LQWLDKVLTQ
gi_13959539_sp_YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTQ
gi_66774168_sp_YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTQ
gi_13959527_sp_YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTQ
gi_51338669_sp_YQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTQ
gi_60414603_sp_YQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTQ
gi_117949830_spYQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTQ
gi_13633871_sp_YQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTQ
gi_13633914_sp_YQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTQ
gi_75041393_sp_YQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTQ
gi_110826300_spYQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTQ
gi_21264050_sp_YQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTQ
gi_341942043_spDDLRRLCILR MSFVKGWGPD YPRQSIKETP CWIEIHLHRA LQLLDEVLHT
gi_13959528_sp_DDLRRLCILR MSFVKGWGPD YPRQSIKETP CWIEIHLHRA LQLLDEVLHT
gi_13959561_sp_DDLRRLCILR MSFVKGWGPD YPRQSIKETP CWIEIHLHRA LQLLDEVLHT
gi_13959531_sp_DDLRRLCILR MSFVKGWGPD YPRQSIKETP CWIEIHLHRA LQLLDEVLHT
gi_116256078_spDDLRRLCILR MSFVKGWGPD YPRQSIKETP CWIEIHLHRA LQLLDEVLHT
gi_13959540_sp_HGPYDPHSVR ISFAKGWGPC YSRQFITSCP CWLEILLNNH R---------
gi_115502451_spDGPYDPNSVR ISFAKGWGPC YSRQFITSCP CWLEILLNNP R---------
gi_13959573_sp_DGPYDPNSVR ISFAKGWGPC YSRQFITSCP CWLEILLSNN R---------
gi_13959541_sp_QQPWTGFTVQ ISFVKGWGQC YTRQFISSCP CWLEVIFNSR ----------
gi_13959529_sp_QQPWTGFTVQ ISFVKGWGQC YTRQFISSCP CWLEVIFNSR ----------
gi_13959538_sp_QQPWTGFTVQ ISFVKGWGQC YTRQFISSCP CWLEVIFNSR ----------
Consistency    5676667789 8**9****66 *4**49787* **9*879766 7646656645
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. . . . . . . . . . 610. .

gi_13633932_sp_MGSPHNPISS VS
gi_118573879_spMGSPHNPISS VS
gi_13633915_sp_MGSPHNPISS VS
gi_341942042_spMGSPHNPISS VS
gi_13633872_sp_MGSPHNPISS VS
gi_13959533_sp_MGSPLNPISS VS
gi_13959566_sp_MGSPLNPISS VS
```

Results colour-coded for amino acid conservation

```
gi_13959559_sp_  MGSPLNPISS  VS
gi_82121811_sp_  MGSPLNPISS  VS
gi_21264062_sp_  MGSPLNPISS  VS
gi_21264049_sp_  MGSPHNPISS  VS
gi_13959539_sp_  MGSPHNPISS  VS
gi_66774168_sp_  MGSPHNPISS  VS
gi_13959527_sp_  MGSPHNPISS  VS
gi_51338669_sp_  MGSPSIRCSS  VS
gi_60414603_sp_  MGSPSIRCSS  VS
gi_117949830_sp  MGSPSVRCSS  MS
gi_13633871_sp_  MGSPSVRCSS  MS
gi_13633914_sp_  MGSPSVRCSS  MS
gi_75041393_sp_  MGSPSVRCSS  MS
gi_110826300_sp  MGSPSVRCSS  MS
gi_21264050_sp_  MGSPSVRCSS  MS
gi_341942043_sp  M--PIADPQP  LD
gi_13959528_sp_  M--PIADPQP  LD
gi_13959561_sp_  M--PIADPQP  LD
gi_13959531_sp_  M--PIADPQP  LD
gi_116256078_sp  M--PIADPQP  LD
gi_13959540_sp_  ----------  --
gi_115502451_sp  ----------  --
gi_13959573_sp_  ----------  --
gi_13959541_sp_  ----------  --
gi_13959529_sp_  ----------  --
gi_13959538_sp_  ----------  --
Consistency      6446233355  55
```