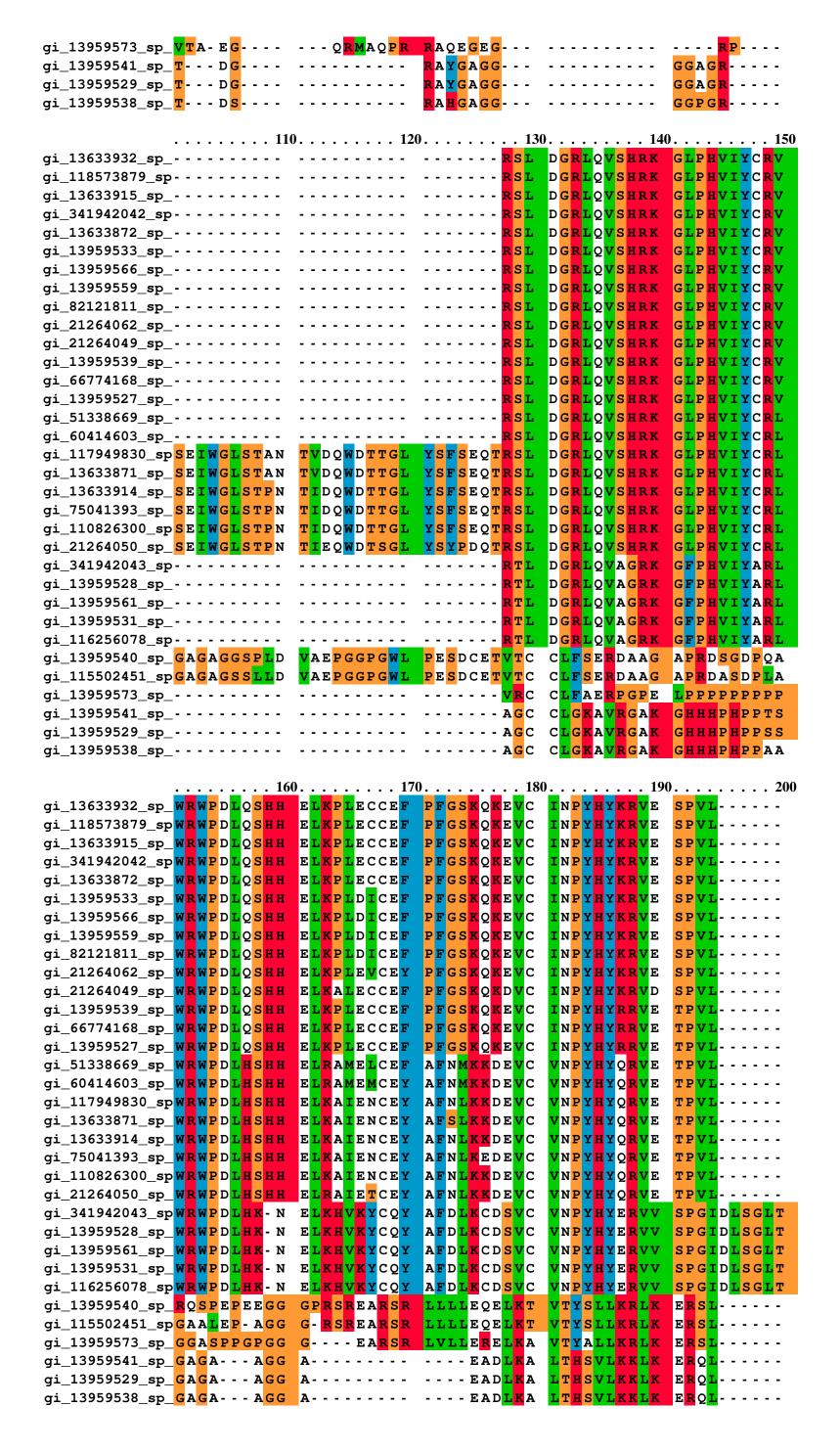# Results colour-coded according to the CLUSTALX residue colour scheme

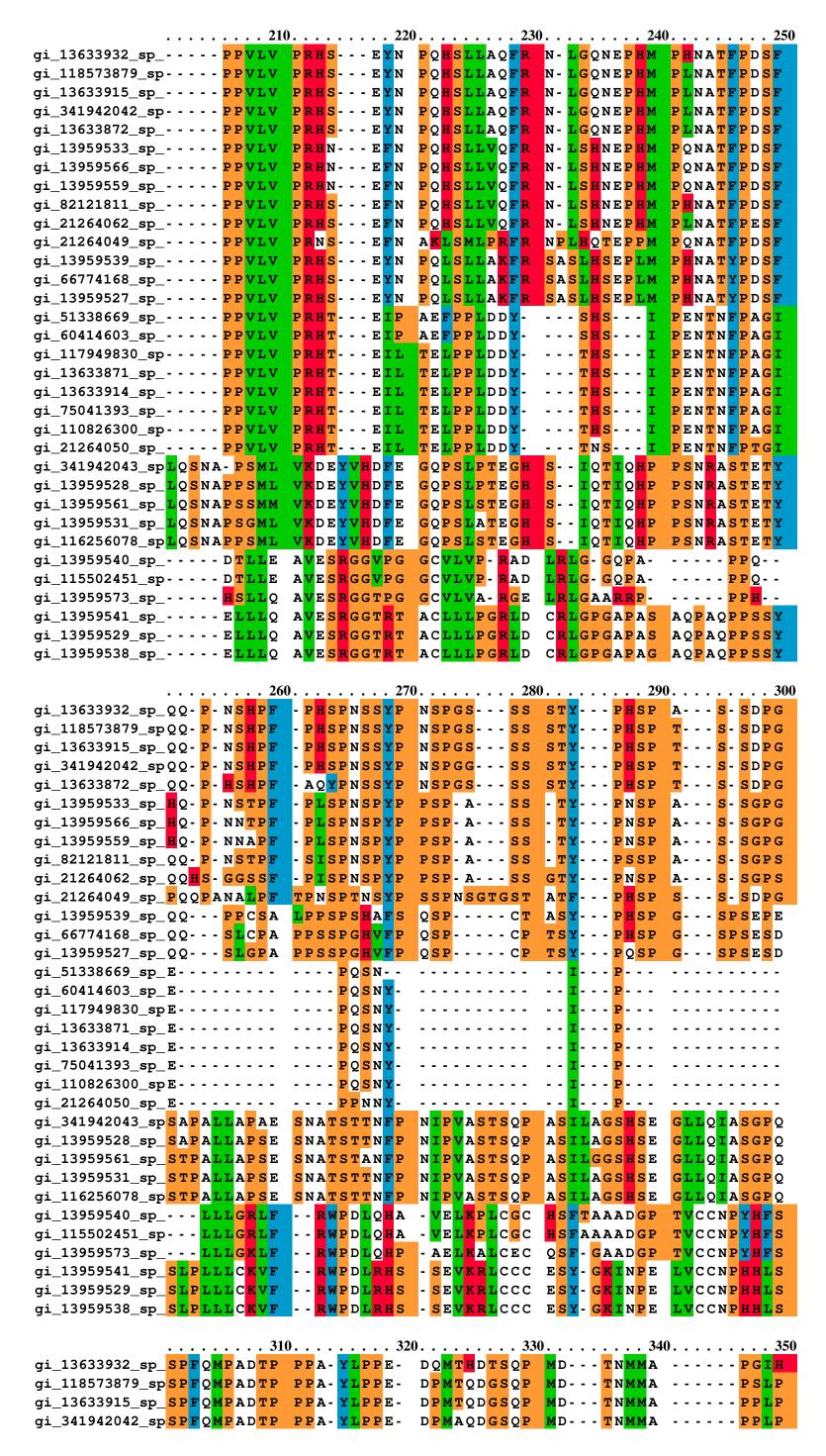The current colourscheme of the alignment is by **residue**.
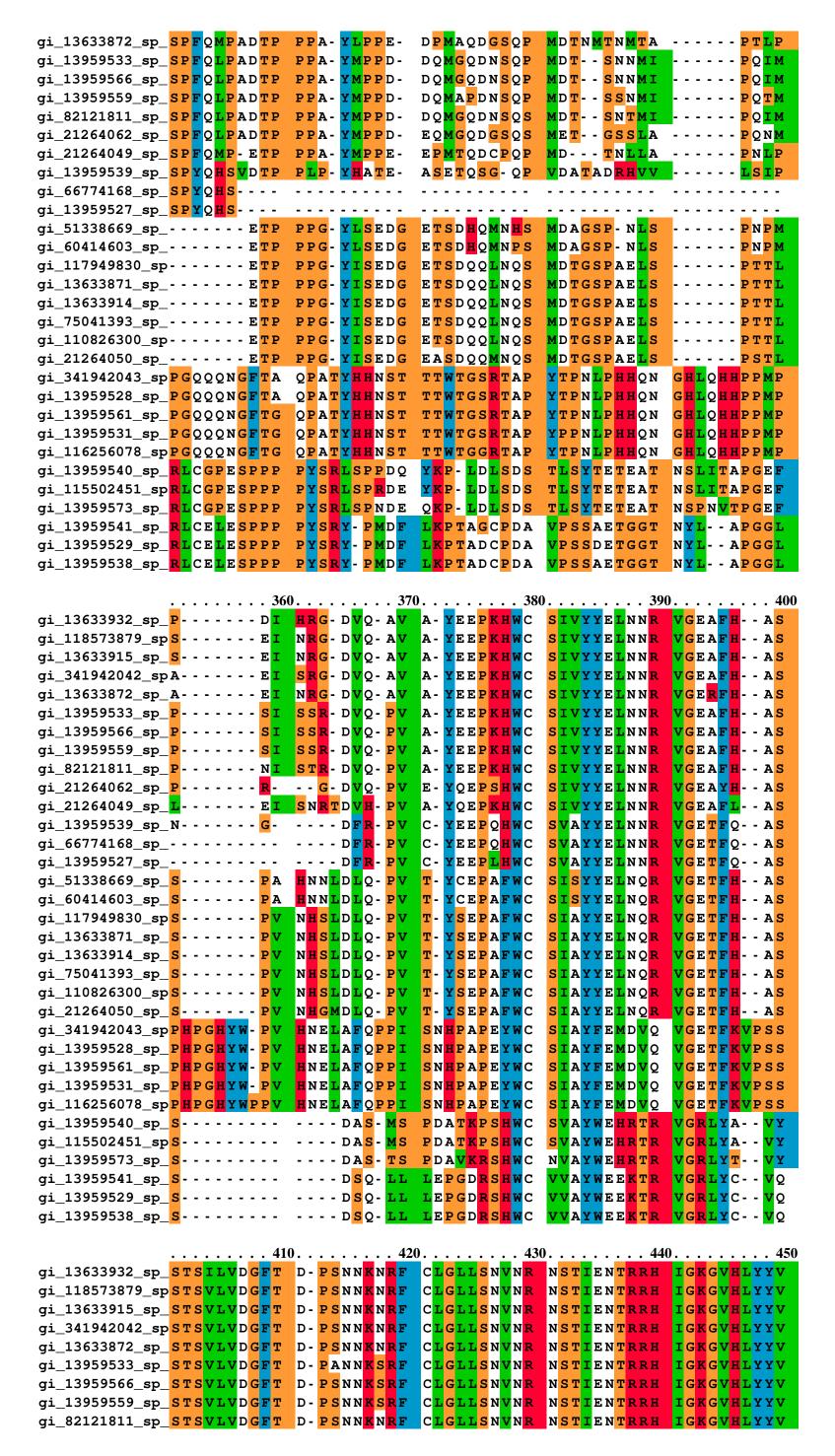
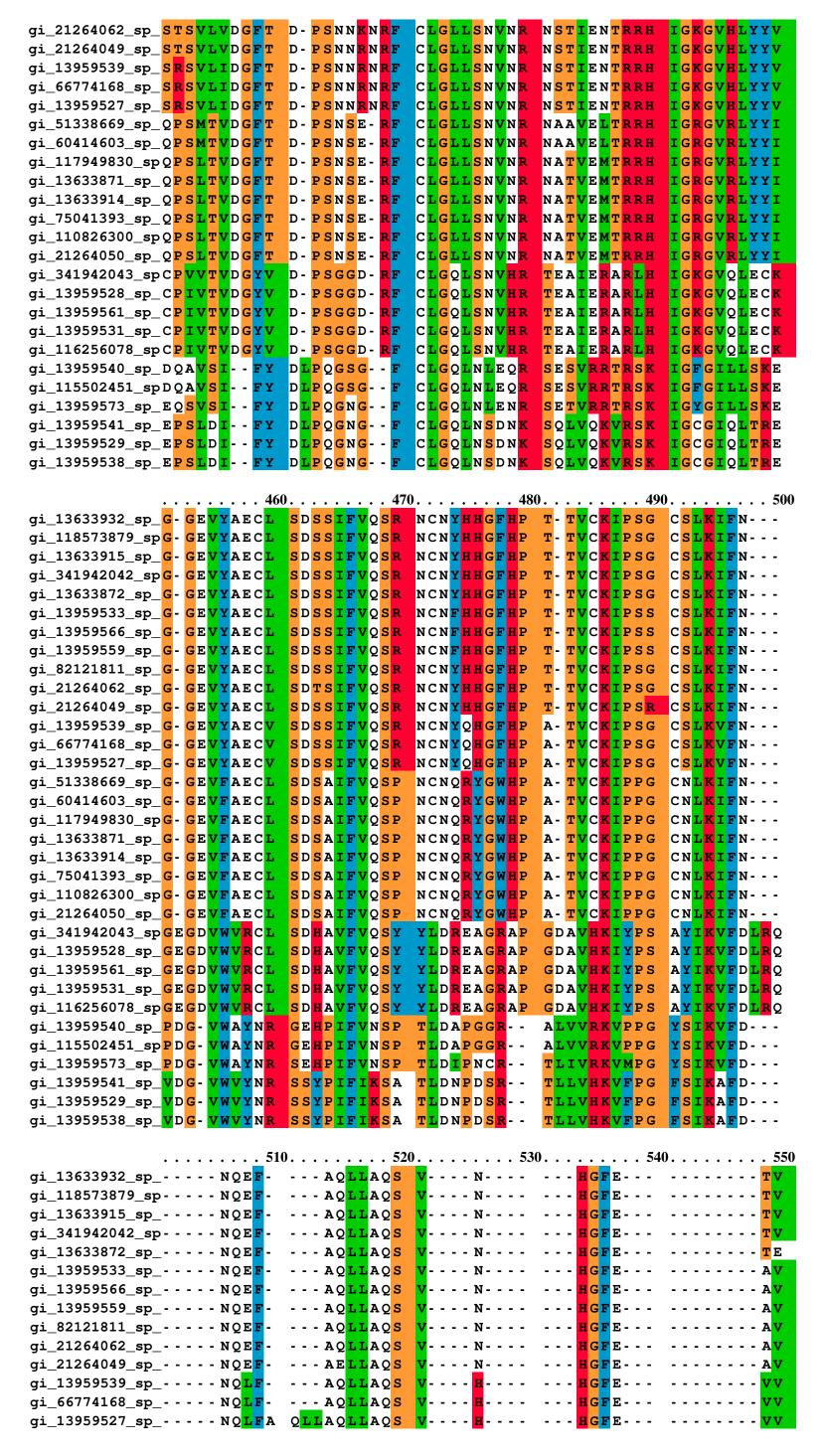The colour assignments have been adapted from the defaults in CLUSTALX (Thompson *et al*, 1997) Abstract :
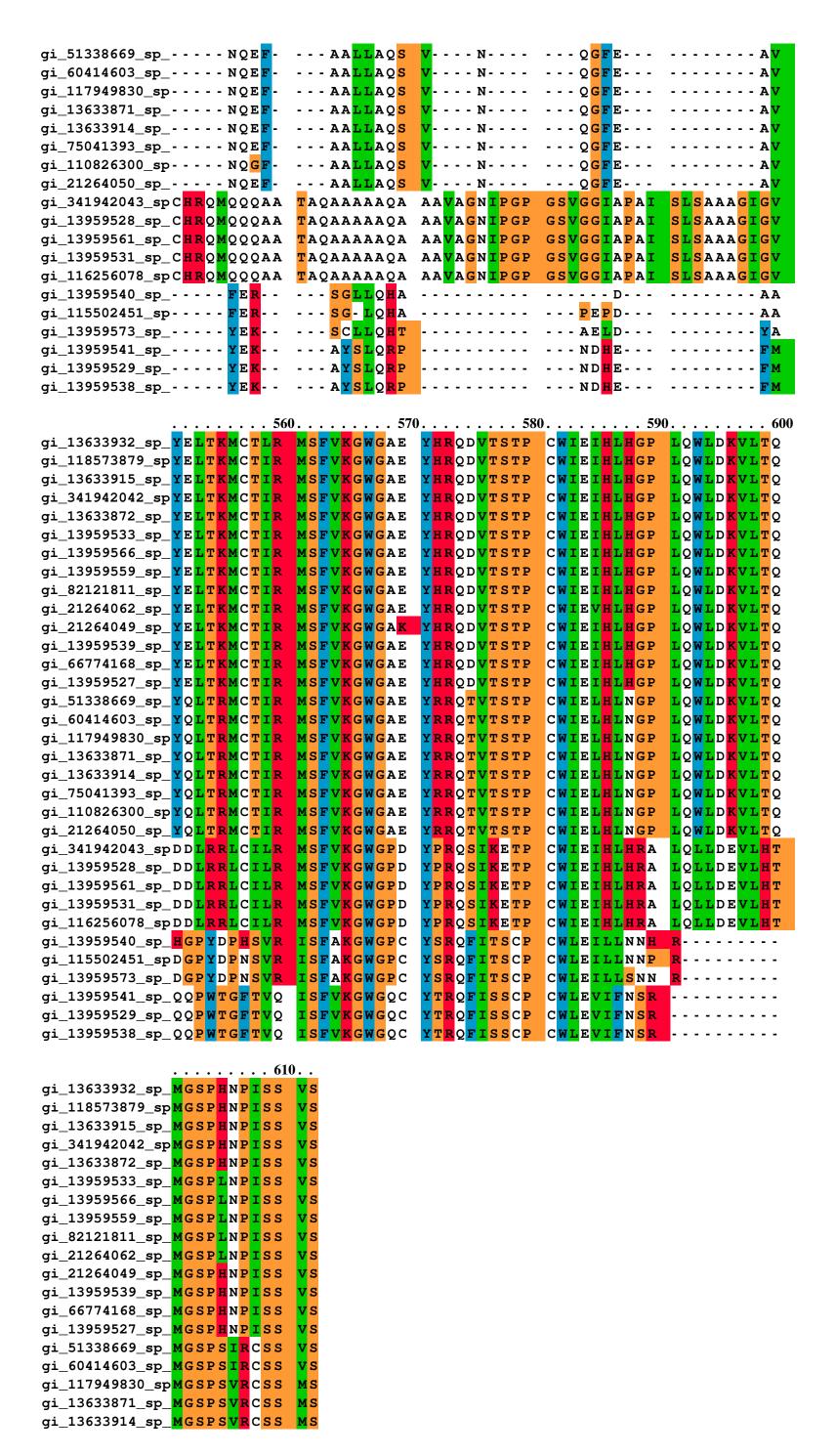
G, P, S, T   H, K, R   F, W, Y   I, L, M, V

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. . . . . . . . . . 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_spMDNMSITNTP 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_spMDNMSITNTP TSNDACLSIV HSLMCHR--- ---------- -QGGESETFA
gi_13959540_sp_MFRSKRSGLV RRL-WRSRVV P--DREE-GS GGGGGVDEDG SLGSRAEP-A
gi_115502451_spMFRSKRSGLV 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

. . . . . . . . . . 60 . . . . . . . . . 70 . . . . . . . . . 80 . . . . . . . . . 90 . . . . . . . . . 100
gi_13633932_sp_EKAVDA---- ----LVKKLK KKKGAMEELE KALSCPGQ-P SNCVTIP---
gi_118573879_spEKAVDA---- ----LVKKLK KKKGAMEELE KALSCPGQ-P SNCVTIP---
gi_13633915_sp_EKAVDA---- ----LVKKLK KKKGAMEELE KALSCPGQ-P SNCVTIP---
gi_341942042_spEKAVDA---- ----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_spEKAVKS---- ----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_spEKAVKS---- ----LVKKL- KKTGRLDELE KAITTQNC-N TKCVTIPSTC
gi_21264050_sp_EKAVKS---- ----LVKKL- KKTGQLDELE KAITTQNR-N TKCVTIPSNC
gi_341942043_spKRAIES---- ----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_spKRAIES---- ----LVKKLK EKKDELDSLI TAITTNGAHP SKCVTIQ---
gi_13959540_sp_PRAREGGCS RSEVRSVAPR RPRDAVGPRG AAIAGRRRRT GGLPRPVSES
gi_115502451_spPRAREGGCG RSEVRPVAPR RPRDAVGQRG AQGAGRRRRA GGPPRPMSEP
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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-----
```

```
          .........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_spSEIWGLSTAN 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_spSEIWGLSTPN 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_spGAGAGSSLLD 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
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          .........160.........170.........180.........190.........200
gi_13633932_sp_WRWPDLQSHH ELKPLECCEF PFGSKQKEVC INPYHYKRVE SPVL------
gi_118573879_spWRWPDLQSHH ELKPLECCEF PFGSKQKEVC INPYHYKRVE SPVL------
gi_13633915_sp_WRWPDLQSHH ELKPLECCEF PFGSKQKEVC INPYHYKRVE SPVL------
gi_341942042_spWRWPDLQSHH 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_spWRWPDLHSHH 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_spWRWPDLHSHH ELKAIENCEY AFNLKKDEVC VNPYHYQRVE TPVL------
gi_21264050_sp_WRWPDLHSHH ELRAIETCEY AFNLKKDEVC VNPYHYQRVE TPVL------
gi_341942043_spWRWPDLHK-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_spWRWPDLHK-N ELKHVKYCQY AFDLKCDSVC VNPYHYERVV SPGIDLSGLT
gi_13959540_sp_RQSPEPEEGG GPRSREARSR LLLLEQELKT VTYSLLKRLK ERSL------
gi_115502451_spGAALEP-AGG G-RSREARSR LLLLEQELKT VTYSLLKRLK ERSL------
gi_13959573_sp_GGASPPGPGG G----EARSR LVLLERELKA VTYALLKRLK ERSL------
gi_13959541_sp_GAGA---AGG A--------- ----EADLKA LTHSVLKKLK ERQL------
gi_13959529_sp_GAGA---AGG A--------- ----EADLKA LTHSVLKKLK ERQL------
gi_13959538_sp_GAGA---AGG A--------- ----EADLKA LTHSVLKKLK ERQL------
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Results colour-coded according to the CLUSTALX residue colour scheme

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                  .........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

                  .........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

                  .........310.........320.........330.........340.........350
gi_13633932_sp_SPFQMPADTP PPA-YLPPE- DQMTHDTSQP MD---TNMMA ------PGIH
gi_118573879_spSPFQMPADTP PPA-YLPPE- DPMTQDGSQP MD---TNMMA ------PSLP
gi_13633915_sp_SPFQMPADTP PPA-YLPPE- DPMTQDGSQP MD---TNMMA ------PPLP
gi_341942042_spSPFQMPADTP PPA-YLPPE- DPMAQDGSQP MD---TNMMA ------PPLP
```

Results colour-coded according to the CLUSTALX residue colour scheme

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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

         . . . . . . . . . 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

         . . . . . . . . . 410 . . . . . . . . 420 . . . . . . . . 430 . . . . . . . . . 440 . . . . . . . . 450
gi_13633932_sp_ STSILVDGFT D-PSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
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
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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_spQPSLTVDGFT  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_spQPSLTVDGFT  D- PSNSE- RF  CLGLLSNVNR  NATVEMTRRH  IGRGVRLYYI
gi_21264050_sp_QPSLTVDGFT  D- PSNSE- RF  CLGLLSNVNR  NATVEMTRRH  IGRGVRLYYI
gi_341942043_spCPVVTVDGYV  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_spCPIVTVDGYV  D- PSGGD- RF  CLGQLSNVHR  TEAIERARLH  IGKGVQLECK
gi_13959540_sp_DQAVSI- - FY  DLPQGSG- - F  CLGQLNLEQR  SESVRRTRSK  IGFGILLSKE
gi_115502451_spDQAVSI- - 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
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          . . . . . . . . . 460 . . . . . . . . 470 . . . . . . . . . 480 . . . . . . . . . 490 . . . . . . . . 500
gi_13633932_sp_G- GEVYAECL  SDSSIFVQSR  NCNYHHGFHP  T- TVCKIPSG  CSLKIFN- - -
gi_118573879_spG- GEVYAECL  SDSSIFVQSR  NCNYHHGFHP  T- TVCKIPSG  CSLKIFN- - -
gi_13633915_sp_G- GEVYAECL  SDSSIFVQSR  NCNYHHGFHP  T- TVCKIPSG  CSLKIFN- - -
gi_341942042_spG- 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_spG- 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_spG- GEVFAECL  SDSAIFVQSP  NCNQRYGWHP  A- TVCKIPPG  CNLKIFN- - -
gi_21264050_sp_G- GEVFAECL  SDSAIFVQSP  NCNQRYGWHP  A- TVCKIPPG  CNLKIFN- - -
gi_341942043_spGEGDVWVRCL  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_spGEGDVWVRCL  SDHAVFVQSY  YLDREAGRAP  GDAVHKIYPS  AYIKVFDLRQ
gi_13959540_sp_PDG- VWAYNR  GEHPIFVNSP  TLDAPGGR- -  ALVVRKVPPG  YSIKVFD- - -
gi_115502451_spPDG- 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- - -
```

```
          . . . . . . . . . 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
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
```

Results colour-coded according to the CLUSTALX residue colour scheme   5

```
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
```

```
         .........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 ----------
```

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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
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_spMGSPSVRCSS MS
gi_13633871_sp_MGSPSVRCSS MS
gi_13633914_sp_MGSPSVRCSS MS
```

Results colour-coded according to the CLUSTALX residue colour scheme

```
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_   ----------  --
```