

## Results colour-coded for secondary structure

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

The 3-state (H, E C) secondary structure for each sequence is represented by a colour. If a sequence in the alignment has no colours assigned, this means that either there is no DSSP information available (if this was requested), or that no prediction was possible for that sequence (if this was requested).  
The colour assignments are:

**HELIX (H)** **STRAND (E)** You have selected to perform secondary structure prediction using **DSSP** ([Kabsch and Sander, 1983](#)).

		..... 10	..... 20	..... 30	..... 40	..... 50
(N/A )	gi_13633932_sp_	-----MNVT	SLFSFTSPAV	KRLLGWK---	-----	-QGDEEEKWA
(N/A )	gi_118573879_sp_	-----MNVT	SLFSFTSPAV	KRLLGWK---	-----	-QGDEEEKWA
(N/A )	gi_13633915_sp_	-----MNVT	SLFSFTSPAV	KRLLGWK---	-----	-QGDEEEKWA
(N/A )	gi_341942042_sp_	-----MNVT	SLFSFTSPAV	KRLLGWK---	-----	-QGDEEEKWA
(N/A )	gi_13633872_sp_	-----MNVT	SLFSFTSPAV	KRLLGWK---	-----	-QGDEEEKWA
(N/A )	gi_13959533_sp_	---M--TSMA	SLFSFTSPAV	KRLLGWK---	-----	-QGDEEEKWA
(N/A )	gi_13959566_sp_	---M--TSMA	SLFSFTSPAV	KRLLGWK---	-----	-QGDEEEKWA
(N/A )	gi_13959559_sp_	---M--TSMA	SLFSFTSPAV	KRLLGWK---	-----	-QGDEEEKWA
(N/A )	gi_82121811_sp_	---M--TSMA	SLFSFTSPAV	KRLLGWK---	-----	-QGDEEEKWA
(N/A )	gi_21264062_sp_	---M--TSMS	SLFSFTSPAV	KRLLGWK---	-----	-QGDEEEKWA
(N/A )	gi_21264049_sp_	-----MNVT	SLFSFTSPAV	KRLLGWK---	-----	-QGDEEEKWA
(N/A )	gi_13959539_sp_	MHST--TPIS	SLFSFTSPAV	KRLLGWK---	-----	-QGDEEEKWA
(N/A )	gi_66774168_sp_	MHPS--TPIS	SLFSFTSPAV	KRLLGWK---	-----	-QGDEEEKWA
(N/A )	gi_13959527_sp_	MHPS--TPIS	SLFSFTSPAV	KRLLGWK---	-----	-QGDEEEKWA
(N/A )	gi_51338669_sp_	-----MS	SILPFTPPIV	KRLLGWKK--	-----G	EQNGQEEKWC
(N/A )	gi_60414603_sp_	-----MS	SILPFTPPIV	KRLLGWKK--	-----G	EQNGQEEKWC
(N/A )	gi_117949830_sp_	-----MS	SILPFTPPVV	KRLLGWKKSA	GGSGGA-GGG	EQNGQEEKWC
(N/A )	gi_13633871_sp_	-----MS	SILPFTPPVV	KRLLGWKKSA	GGSGGA-GGG	EQNGQEEKWC
(N/A )	gi_13633914_sp_	-----MS	SILPFTPPVV	KRLLGWKKSA	GGSGGA-GGG	EQNGQEEKWC
(N/A )	gi_75041393_sp_	-----MS	SILPFTPPVV	KRLLGWKKSA	GGSGGA-GGG	EQNGQEEKWC
(N/A )	gi_110826300_sp_	-----MS	SILPFTPPVV	KRLLGWKKSA	GGSGGA-GGG	EQNGQEEKWC
(N/A )	gi_21264050_sp_	-----MS	SILPFTPPVV	KRLLGWKKSA	SGSSGAGGGG	EQNGQEEKWC
(N/A )	gi_341942043_sp_	MDNMSITNTP	TSNDACLSIV	HSLMCHR---	-----	-QGGESETFA
(N/A )	gi_13959528_sp_	MDNMSITNTP	TSNDACLSIV	HSLMCHR---	-----	-QGGESETFA
(N/A )	gi_13959561_sp_	MDNMSITNTP	TSNDACLSIV	HSLMCHR---	-----	-QGGESETFA
(N/A )	gi_13959531_sp_	MDNMSITNTP	TSNDACLSIV	HSLMCHR---	-----	-QGGESETFA
(N/A )	gi_116256078_sp_	MDNMSITNTP	TSNDACLSIV	HSLMCHR---	-----	-QGGESETFA
(N/A )	gi_13959540_sp_	MFRSKRSGLV	RRL-WRSRVV	P--DREE-GS	GGGGGVDEDG	SLGSRAEP-A
(N/A )	gi_115502451_sp_	MFRSKRSGLV	RRL-WRSRVV	P--DREEGGS	GGGGGGDEDG	SLGSRAEP-A
(N/A )	gi_13959573_sp_	MFRSKRSGLV	RRL-WRSRVI	P--ERD----	----GGDGNG	QSERNAT-A
(N/A )	gi_13959541_sp_	MFRTKRSALV	RRL-WRSRA-	PGGEDEEEGV	GGGGGG---G	EL--RGEG-A
(N/A )	gi_13959529_sp_	MFRTKRSALV	RRL-WRSRA-	PGGEDEEEGV	GGGGGG---G	GL--RGEG-A
(N/A )	gi_13959538_sp_	MFRTKRSALV	RRL-WRSRA-	PGGEDEEEGA	GGGGGG---G	EL--RGEG-A

  

		..... 60	..... 70	..... 80	..... 90	..... 100
(N/A )	gi_13633932_sp_	EKAVIDA----	----LVKKLK	KKKGAMEEELE	KALSCPGQ-P	SNCVTIP---
(N/A )	gi_118573879_sp_	EKAVIDA----	----LVKKLK	KKKGAMEEELE	KALSCPGQ-P	SNCVTIP---
(N/A )	gi_13633915_sp_	EKAVIDA----	----LVKKLK	KKKGAMEEELE	KALSCPGQ-P	SNCVTIP---
(N/A )	gi_341942042_sp_	EKAVIDA----	----LVKKLK	KKKGAMEEELE	KALSCPGQ-P	SNCVTIP---
(N/A )	gi_13633872_sp_	EKAVIDA----	----LVKKLK	KKKGAMEEELE	KALSCPGQ-P	SNCVTIP---
(N/A )	gi_13959533_sp_	EKAVIDA----	----LVKKLK	KKKGAMEEELE	KALSSPGQ-P	SKCVTIP---
(N/A )	gi_13959566_sp_	EKAVIDA----	----LVKKLK	KKKGAMEEELE	KALSSPGQ-P	SKCVTIP---
(N/A )	gi_13959559_sp_	EKAVIDA----	----LVKKLK	KKKGAMEEELE	KALSSPGQ-P	SKCVTIP---
(N/A )	gi_82121811_sp_	EKAVIDA----	----LVKKLK	KKKGAMEEELE	KALSSPGQ-P	SKCVTIP---
(N/A )	gi_21264062_sp_	EKAVIDA----	----LVKKLK	KKKGAMEDLE	KALSSPGQ-P	SKCVTIP---
(N/A )	gi_21264049_sp_	EKAVIDA----	----LVKKLK	KKKGAMEEELE	RALSCPGQ-P	SNCVTIP---
(N/A )	gi_13959539_sp_	EKAVIDS----	----LVKKLK	KKKGAMDELE	RALSCPGQ-P	SKCVTIP---
(N/A )	gi_66774168_sp_	EKAVIDS----	----LVKKLK	KKKGAMDELE	RALSCPGQ-P	SKCVTIP---
(N/A )	gi_13959527_sp_	EKAVIDS----	----LVKKLK	KKKGAMDELE	RALSCPGQ-P	SKCVTIP---
(N/A )	gi_51338669_sp_	EKAVKS----	----LVKKL-	KKTGQLDELE	KAITTQNV-N	TKCITIP---
(N/A )	gi_60414603_sp_	EKAVKS----	----LVKKL-	KKTGQLDELE	KAITTQNI-N	TKCITIP---
(N/A )	gi_117949830_sp_	EKAVKS----	----LVKKL-	KKTGRLDELE	KAITTQNC-N	TKCVTIPSTC
(N/A )	gi_13633871_sp_	EKAVKS----	----LVKKL-	KKTGRLDELE	KAITTQNC-N	TKCVTIPSTC
(N/A )	gi_13633914_sp_	EKAVKS----	----LVKKL-	KKTGRLDELE	KAITTQNC-N	TKCVTIPSTC
(N/A )	gi_75041393_sp_	EKAVKS----	----LVKKL-	KKTGRLDELE	KAITTQNC-N	TKCVTIPSTC
(N/A )	gi_110826300_sp_	EKAVKS----	----LVKKL-	KKTGRLDELE	KAITTQNC-N	TKCVTIPSTC
(N/A )	gi_21264050_sp_	EKAVKS----	----LVKKL-	KKTGQLDELE	KAITTQNR-N	TKCVTIPSN
(N/A )	gi_341942043_sp_	KRAIES----	----LVKKLK	EKKDELDSL	TAITTNGAHP	SKCVTIQ---
(N/A )	gi_13959528_sp_	KRAIES----	----LVKKLK	EKKDELDSL	TAITTNGAHP	SKCVTIQ---
(N/A )	gi_13959561_sp_	KRAIES----	----LVKKLK	EKKDELDSL	TAITTNGAHP	SKCVTIQ---
(N/A )	gi_13959531_sp_	KRAIES----	----LVKKLK	EKKDELDSL	TAITTNGAHP	SKCVTIQ---
(N/A )	gi_116256078_sp_	KRAIES----	----LVKKLK	EKKDELDSL	TAITTNGAHP	SKCVTIQ---
(N/A )	gi_13959540_sp_	PRAREGGGCS	RSEVRSVAPR	RPRDAVGPRG	AAIAGRRTT	GGLPRPVSES

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(N/A ) gi_115502451_sp PRAREGGGCG RSEVRPVAPR RPRDAVGQRG AQQAGRRRRA GGPPRPMSEP
(N/A ) gi_13959573_sp VTA-EG---- ---QRMAQPR RAQEGEG--- ----- ---RP----
(N/A ) gi_13959541_sp T---DG---- ----- RAYGAGG--- ----- GGAGR-----
(N/A ) gi_13959529_sp T---DG---- ----- RAYGAGG--- ----- GGAGR-----
(N/A ) gi_13959538_sp T---DS---- ----- RAHGAGG--- ----- GGPGR-----

          . . . . . 110. . . . . 120. . . . . 130. . . . . 140. . . . . 150
(N/A ) gi_13633932_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_118573879_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_13633915_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_341942042_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_13633872_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_13959533_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_13959566_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_13959559_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_82121811_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_21264062_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_21264049_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_13959539_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_66774168_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_13959527_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_51338669_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_60414603_sp ----- RSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_117949830_sp SEIWGLSTAN TVDQWDTTGL YSFSEQTRSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_13633871_sp SEIWGLSTAN TVDQWDTTGL YSFSEQTRSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_13633914_sp SEIWGLSTPN TIDQWDTTGL YSFSEQTRSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_75041393_sp SEIWGLSTPN TIDQWDTTGL YSFSEQTRSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_110826300_sp SEIWGLSTPN TIDQWDTTGL YSFSEQTRSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_21264050_sp SEIWGLSTPN TIEQWDTSG L YSPDQTRSL DGR LQVSHRK GLPHVIYCRV
(N/A ) gi_341942043_sp ----- RTL DGR LQVAGRK GFPHVIYARL
(N/A ) gi_13959528_sp ----- RTL DGR LQVAGRK GFPHVIYARL
(N/A ) gi_13959561_sp ----- RTL DGR LQVAGRK GFPHVIYARL
(N/A ) gi_13959531_sp ----- RTL DGR LQVAGRK GFPHVIYARL
(N/A ) gi_116256078_sp ----- RTL DGR LQVAGRK GFPHVIYARL
(N/A ) gi_13959540_sp GAGAGGSPLD VAEPGGPGWL PESDCETVTC CLFSE RDAAG APRDSGDPQA
(N/A ) gi_115502451_sp GAGAGSSLLD VAEPGGPGWL PESDCETVTC CLFSE RDAAG APRDASDPLA
(N/A ) gi_13959573_sp ----- VRC CLFAERPGE LPPPPPPPPP
(N/A ) gi_13959541_sp ----- AGC CLGKA VRGAK GHHPHPPTS
(N/A ) gi_13959529_sp ----- AGC CLGKA VRGAK GHHPHPSS
(N/A ) gi_13959538_sp ----- AGC CLGKA VRGAK GHHPHPAA

          . . . . . 160. . . . . 170. . . . . 180. . . . . 190. . . . . 200
(N/A ) gi_13633932_sp WRWPD LQSHH ELKPLECCEF PFGSKQKEVC INPYHYKRVE SPVL-----
(N/A ) gi_118573879_sp WRWPD LQSHH ELKPLECCEF PFGSKQKEVC INPYHYKRVE SPVL-----
(N/A ) gi_13633915_sp WRWPD LQSHH ELKPLECCEF PFGSKQKEVC INPYHYKRVE SPVL-----
(N/A ) gi_341942042_sp WRWPD LQSHH ELKPLECCEF PFGSKQKEVC INPYHYKRVE SPVL-----
(N/A ) gi_13633872_sp WRWPD LQSHH ELKPLECCEF PFGSKQKEVC INPYHYKRVE SPVL-----
(N/A ) gi_13959533_sp WRWPD LQSHH ELKPLDICEF PFGSKQKEVC INPYHYKRVE SPVL-----
(N/A ) gi_13959566_sp WRWPD LQSHH ELKPLDICEF PFGSKQKEVC INPYHYKRVE SPVL-----
(N/A ) gi_13959559_sp WRWPD LQSHH ELKPLDICEF PFGSKQKEVC INPYHYKRVE SPVL-----
(N/A ) gi_82121811_sp WRWPD LQSHH ELKPLDICEF PFGSKQKEVC INPYHYKRVE SPVL-----
(N/A ) gi_21264062_sp WRWPD LQSHH ELKPLEVCEY PFGSKQKEVC INPYHYKRVE SPVL-----
(N/A ) gi_21264049_sp WRWPD LQSHH ELKALECCEF PFGSKQK DVC INPYHYKRVD SPVL-----
(N/A ) gi_13959539_sp WRWPD LQSHH ELKPLECCEF PFGSKQKEVC INPYHYRRVE TPVL-----
(N/A ) gi_66774168_sp WRWPD LQSHH ELKPLECCEF PFGSKQKEVC INPYHYRRVE TPVL-----
(N/A ) gi_13959527_sp WRWPD LQSHH ELKPLECCEF PFGSKQKEVC INPYHYRRVE TPVL-----
(N/A ) gi_51338669_sp WRWPD LQSHH ELRAMELC EF AFNMKKDEVC VNPYHYQRVE TPVL-----
(N/A ) gi_60414603_sp WRWPD LQSHH ELRAMEMCEY AFNMKKDEVC VNPYHYQRVE TPVL-----
(N/A ) gi_117949830_sp WRWPD LQSHH ELKAIENCEY AFNLKKDEVC VNPYHYQRVE TPVL-----
(N/A ) gi_13633871_sp WRWPD LQSHH ELKAIENCEY AFSLKKDEVC VNPYHYQRVE TPVL-----
(N/A ) gi_13633914_sp WRWPD LQSHH ELKAIENCEY AFNLKKDEVC VNPYHYQRVE TPVL-----
(N/A ) gi_75041393_sp WRWPD LQSHH ELKAIENCEY AFNLKEDEVC VNPYHYQRVE TPVL-----
(N/A ) gi_110826300_sp WRWPD LQSHH ELKAIENCEY AFNLKKDEVC VNPYHYQRVE TPVL-----
(N/A ) gi_21264050_sp WRWPD LQSHH ELRAIETCEY AFNLKKDEVC VNPYHYQRVE TPVL-----
(N/A ) gi_341942043_sp WRWPD LQSHH ELKHVKYCQY AFDLKCDSVC VNPYHYERVV SPGIDLSGLT
(N/A ) gi_13959528_sp WRWPD LQSHH ELKHVKYCQY AFDLKCDSVC VNPYHYERVV SPGIDLSGLT
(N/A ) gi_13959561_sp WRWPD LQSHH ELKHVKYCQY AFDLKCDSVC VNPYHYERVV SPGIDLSGLT
(N/A ) gi_13959531_sp WRWPD LQSHH ELKHVKYCQY AFDLKCDSVC VNPYHYERVV SPGIDLSGLT
(N/A ) gi_116256078_sp WRWPD LQSHH ELKHVKYCQY AFDLKCDSVC VNPYHYERVV SPGIDLSGLT
(N/A ) gi_13959540_sp RQSPEPEEGG GPRSREARSR LLLLEQELKT VTYSLLKRLK ERS L-----
(N/A ) gi_115502451_sp GAAL EP-AGG G-RSREARSR LLLLEQELKT VTYSLLKRLK ERS L-----
(N/A ) gi_13959573_sp GGASPPGPGG G----EARSR LVLLERELKA VTYSLLKRLK ERS L-----
(N/A ) gi_13959541_sp GAGA---AGG A----- ---EADLKA LTHSVLKKLK ERQL-----
(N/A ) gi_13959529_sp GAGA---AGG A----- ---EADLKA LTHSVLKKLK ERQL-----
(N/A ) gi_13959538_sp GAGA---AGG A----- ---EADLKA LTHSVLKKLK ERQL-----

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..... 210..... 220..... 230..... 240..... 250
(N/A ) gi_13633932_sp_ -----PPVLV PRHS---EYN PQHSLLAQFR N-LGQNEPHM PHNATFPDSF
(N/A ) gi_118573879_sp_ -----PPVLV PRHS---EYN PQHSLLAQFR N-LGQNEPHM PLNATFPDSF
(N/A ) gi_13633915_sp_ -----PPVLV PRHS---EYN PQHSLLAQFR N-LGQNEPHM PLNATFPDSF
(N/A ) gi_341942042_sp_ -----PPVLV PRHS---EYN PQHSLLAQFR N-LGQNEPHM PLNATFPDSF
(N/A ) gi_13633872_sp_ -----PPVLV PRHS---EYN PQHSLLAQFR N-LGQNEPHM PLNATFPDSF
(N/A ) gi_13959533_sp_ -----PPVLV PRHN---EFN PQHSLLVQFR N-LSHNEPHM PQNATFPDSF
(N/A ) gi_13959566_sp_ -----PPVLV PRHN---EFN PQHSLLVQFR N-LSHNEPHM PQNATFPDSF
(N/A ) gi_13959559_sp_ -----PPVLV PRHN---EFN PQHSLLVQFR N-LSHNEPHM PQNATFPDSF
(N/A ) gi_82121811_sp_ -----PPVLV PRHS---EFN PQHSLLVQFR N-LSHNEPHM PHNATFPDSF
(N/A ) gi_21264062_sp_ -----PPVLV PRHS---EFN PQHSLLVQFR N-LSHNEPHM PLNATFPDSF
(N/A ) gi_21264049_sp_ -----PPVLV PRNS---EFN AKLSMLPRFR NPLHQTEPPM PQNATFPDSF
(N/A ) gi_13959539_sp_ -----PPVLV PRHS---EYN PQLSLLAKFR SASLHSEPLM PHNATYPDSF
(N/A ) gi_66774168_sp_ -----PPVLV PRHS---EYN PQLSLLAKFR SASLHSEPLM PHNATYPDSF
(N/A ) gi_13959527_sp_ -----PPVLV PRHS---EYN PQLSLLAKFR SASLHSEPLM PHNATYPDSF
(N/A ) gi_51338669_sp_ -----PPVLV PRHT---EIP AEFPPLLDDY- ---SHS---I PENTNFPAGI
(N/A ) gi_60414603_sp_ -----PPVLV PRHT---EIP AEFPPLLDDY- ---SHS---I PENTNFPAGI
(N/A ) gi_117949830_sp_ -----PPVLV PRHT---EIL TELPPLDDY- ---THS---I PENTNFPAGI
(N/A ) gi_13633871_sp_ -----PPVLV PRHT---EIL TELPPLDDY- ---THS---I PENTNFPAGI
(N/A ) gi_13633914_sp_ -----PPVLV PRHT---EIL TELPPLDDY- ---THS---I PENTNFPAGI
(N/A ) gi_75041393_sp_ -----PPVLV PRHT---EIL TELPPLDDY- ---THS---I PENTNFPAGI
(N/A ) gi_110826300_sp_ -----PPVLV PRHT---EIL TELPPLDDY- ---THS---I PENTNFPAGI
(N/A ) gi_21264050_sp_ -----PPVLV PRHT---EIL TELPPLDDY- ---TNS---I PENTNFPAGI
(N/A ) gi_341942043_sp_ LQSNAPPSML VKDEYVHDFE GQPSLPTEGH S--IQTIQHP PSNRASTETY
(N/A ) gi_13959528_sp_ LQSNAPPSML VKDEYVHDFE GQPSLPTEGH S--IQTIQHP PSNRASTETY
(N/A ) gi_13959561_sp_ LQSNAPSSMM VKDEYVHDFE GQPSLPTEGH S--IQTIQHP PSNRASTETY
(N/A ) gi_13959531_sp_ LQSNAPSGML VKDEYVHDFE GQPSLPTEGH S--IQTIQHP PSNRASTETY
(N/A ) gi_116256078_sp_ LQSNAPPSML VKDEYVHDFE GQPSLPTEGH S--IQTIQHP PSNRASTETY
(N/A ) gi_13959540_sp_ -----DTLLE AVESRGGVPG GCVLVP-RAD LRLG-GQPA- -----PPQ--
(N/A ) gi_115502451_sp_ -----DTLLE AVESRGGVPG GCVLVP-RAD LRLG-GQPA- -----PPQ--
(N/A ) gi_13959573_sp_ -----HSLLO AVESRGGTPG GCVLVA-RGE LRLGAARRP- -----PPH--
(N/A ) gi_13959541_sp_ -----ELLLQ AVESRGGTRT ACLLLPGRD CRLGPGAPAS AQPAQPPSSY
(N/A ) gi_13959529_sp_ -----ELLLQ AVESRGGTRT ACLLLPGRD CRLGPGAPAS AQPAQPPSSY
(N/A ) gi_13959538_sp_ -----ELLLQ AVESRGGTRT ACLLLPGRD CRLGPGAPAG AQPAQPPSSY

..... 260..... 270..... 280..... 290..... 300
(N/A ) gi_13633932_sp_ QQ-P-NSHPF -PHSPNSSYP NSPGS---SS STY---PHSP A---S-SDPG
(N/A ) gi_118573879_sp_ QQ-P-NSHPF -PHSPNSSYP NSPGS---SS STY---PHSP T---S-SDPG
(N/A ) gi_13633915_sp_ QQ-P-NSHPF -PHSPNSSYP NSPGS---SS STY---PHSP T---S-SDPG
(N/A ) gi_341942042_sp_ QQ-P-NSHPF -PHSPNSSYP NSPGG---SS STY---PHSP T---S-SDPG
(N/A ) gi_13633872_sp_ QQ-P-HSHPF -AQYPNSSYP NSPGS---SS STY---PHSP T---S-SDPG
(N/A ) gi_13959533_sp_ HQ-P-NSTPF -PLSPNSPYP PSP-A---SS -TY---PNSP A---S-SGPG
(N/A ) gi_13959566_sp_ HQ-P-NSTPF -PLSPNSPYP PSP-A---SS -TY---PNSP A---S-SGPG
(N/A ) gi_13959559_sp_ HQ-P-NNAPF -PLSPNSPYP PSP-A---SS -TY---PNSP A---S-SGPG
(N/A ) gi_82121811_sp_ QQ-P-NSTPF -SISPNSPYP PSP-A---SS -TY---PSSP A---S-SGPS
(N/A ) gi_21264062_sp_ QQHS-GGSSF -PISPNSPYP PSP-A---SS GTY---PNSP A---S-SGPS
(N/A ) gi_21264049_sp_ PQQPANALPF TPNSPTNSYP SSPNSGTGST ATF---PHSP S---S-SDPG
(N/A ) gi_13959539_sp_ QQ---PPCSA LPPSPSHAFS QSP-----CT ASY---PHSP G---SPSEPE
(N/A ) gi_66774168_sp_ QQ---SLCPA PPSSPGHVFP QSP-----CP TSY---PHSP G---SPSESD
(N/A ) gi_13959527_sp_ QQ---SLGPA PPSSPGHVFP QSP-----CP TSY---PQSP G---SPSESD
(N/A ) gi_51338669_sp_ E-----PQSN-- -----I---P---
(N/A ) gi_60414603_sp_ E-----PQSNY- -----I---P---
(N/A ) gi_117949830_sp_ E-----PQSNY- -----I---P---
(N/A ) gi_13633871_sp_ E-----PQSNY- -----I---P---
(N/A ) gi_13633914_sp_ E-----PQSNY- -----I---P---
(N/A ) gi_75041393_sp_ E-----PQSNY- -----I---P---
(N/A ) gi_110826300_sp_ E-----PQSNY- -----I---P---
(N/A ) gi_21264050_sp_ E-----PPNNY- -----I---P---
(N/A ) gi_341942043_sp_ SAPALLAPAE SNATSTTNFP NIPVASTSQP ASILAGSHSE GLLQIASGPQ
(N/A ) gi_13959528_sp_ SAPALLAPSE SNATSTTNFP NIPVASTSQP ASILAGSHSE GLLQIASGPQ
(N/A ) gi_13959561_sp_ STPALLAPSE SNATSTTNFP NIPVASTSQP ASILAGSHSE GLLQIASGPQ
(N/A ) gi_13959531_sp_ STPALLAPSE SNATSTTNFP NIPVASTSQP ASILAGSHSE GLLQIASGPQ
(N/A ) gi_116256078_sp_ STPALLAPSE SNATSTTNFP NIPVASTSQP ASILAGSHSE GLLQIASGPQ
(N/A ) gi_13959540_sp_ ---LLLGRLF --RWPDLQHA -VELKPLCGC HSFTAAADGP TVCCNPYHFS
(N/A ) gi_115502451_sp_ ---LLLGRLF --RWPDLQHA -VELKPLCGC HSFAAAADGP TVCCNPYHFS
(N/A ) gi_13959573_sp_ ---LLLGRLF --RWPDLQHA -VELKPLCGC HSFAAAADGP TVCCNPYHFS
(N/A ) gi_13959541_sp_ SLPLLLCKVF --RWPDLRHS -SEVKRLCCC ESY-GKINPE LVCCNPHHLS
(N/A ) gi_13959529_sp_ SLPLLLCKVF --RWPDLRHS -SEVKRLCCC ESY-GKINPE LVCCNPHHLS
(N/A ) gi_13959538_sp_ SLPLLLCKVF --RWPDLRHS -SEVKRLCCC ESY-GKINPE LVCCNPHHLS

..... 310..... 320..... 330..... 340..... 350
(N/A ) gi_13633932_sp_ SPFQMPADTP PPA-YLPPE- DQMTHTDSQP MD---TNMMA -----PGIH
(N/A ) gi_118573879_sp_ SPFQMPADTP PPA-YLPPE- DPMTQDGSQP MD---TNMMA -----PSLP
(N/A ) gi_13633915_sp_ SPFQMPADTP PPA-YLPPE- DPMTQDGSQP MD---TNMMA -----PPLP

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(N/A ) gi_341942042_sp SPFQMPADTP PPA-YLPPE- DPMAQDGSQP MD---TNMMA -----PPLP
(N/A ) gi_13633872_sp SPFQMPADTP PPA-YLPPE- DPMAQDGSQP MDTNMTNMTA -----PTLP
(N/A ) gi_13959533_sp SPFQLPADTP PPA-YMPPD- DQMGQDNSQP MDT--SNNMI -----PQIM
(N/A ) gi_13959566_sp SPFQLPADTP PPA-YMPPD- DQMGQDNSQP MDT--SNNMI -----PQIM
(N/A ) gi_13959559_sp SPFQLPADTP PPA-YMPPD- DQMAPDNSQP MDT--SSNMI -----PQTM
(N/A ) gi_82121811_sp SPFQLPADTP PPA-YMPPD- DQMGQDNSQS MDT--SNTMI -----PQIM
(N/A ) gi_21264062_sp SPFQLPADTP PPA-YMPPD- EQMGQDGSQS MET--GSSLA -----PQNM
(N/A ) gi_21264049_sp SPFQMP-ETP PPA-YMPPE- EPMTQDCPQP MD---TNLLA -----PNLP
(N/A ) gi_13959539_sp SPYQHSVDTP PLP-YHATE- ASETQSG-QP VDATADRHVV -----LSIP
(N/A ) gi_66774168_sp SPYQHS-----
(N/A ) gi_13959527_sp SPYQHS-----
(N/A ) gi_51338669_sp -----ETP PPG-YLSEDG ETS DHQMNHS MDAGSP-NLS -----PNPM
(N/A ) gi_60414603_sp -----ETP PPG-YLSEDG ETS DHQMNPS MDAGSP-NLS -----PNPM
(N/A ) gi_117949830_sp -----ETP PPG-YISEDG ETS DQQLNQS MDTGSPAELS -----PTTL
(N/A ) gi_13633871_sp -----ETP PPG-YISEDG ETS DQQLNQS MDTGSPAELS -----PTTL
(N/A ) gi_13633914_sp -----ETP PPG-YISEDG ETS DQQLNQS MDTGSPAELS -----PTTL
(N/A ) gi_75041393_sp -----ETP PPG-YISEDG ETS DQQLNQS MDTGSPAELS -----PTTL
(N/A ) gi_110826300_sp -----ETP PPG-YISEDG ETS DQQLNQS MDTGSPAELS -----PTTL
(N/A ) gi_21264050_sp -----ETP PPG-YISEDG EAS DQQMNS MDTGSPAELS -----PSTL
(N/A ) gi_341942043_sp PGQQQNGFTA QPATYHHNST TTWTGSRTAP YTPNLP HHQN GH LQHHPMP
(N/A ) gi_13959528_sp PGQQQNGFTA QPATYHHNST TTWTGSRTAP YTPNLP HHQN GH LQHHPMP
(N/A ) gi_13959561_sp PGQQQNGFTG QPATYHHNST TTWTGSRTAP YTPNLP HHQN GH LQHHPMP
(N/A ) gi_13959531_sp PGQQQNGFTG QPATYHHNST TTWTGSRTAP YPPNLP HHQN GH LQHHPMP
(N/A ) gi_116256078_sp PGQQQNGFTG QPATYHHNST TTWTGGR TAP YTPNLP HHQN GH LQHHPMP
(N/A ) gi_13959540_sp RLCGPESPPP PYSRLSPDQ YKP-LDLSDS T LSYTETEAT NSLITAPGEF
(N/A ) gi_115502451_sp RLCGPESPPP PYSRLSPRDE YKP-LDLSDS T LSYTETEAT NSLITAPGEF
(N/A ) gi_13959573_sp RLCGPESPPP PYSRLSPNDE QKP-LDLSDS T LSYTETEAT NSPNVTPGEF
(N/A ) gi_13959541_sp RLCELESPPP PYSRY-PMDF LKPTAGCPDA VPSSAETGGT NYL--APGGL
(N/A ) gi_13959529_sp RLCELESPPP PYSRY-PMDF LKPTADCPDA VPSSDETGGT NYL--APGGL
(N/A ) gi_13959538_sp RLCELESPPP PYSRY-PMDF LKPTADCPDA VPSSAETGGT NYL--APGGL

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..... 360..... 370..... 380..... 390..... 400

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(N/A ) gi_13633932_sp P-----DI HRG-DVQ-AV A-YEEP KHC SIVYYELNNR VGEAFH--AS
(N/A ) gi_118573879_sp S-----EI NRG-DVQ-AV A-YEEP KHC SIVYYELNNR VGEAFH--AS
(N/A ) gi_13633915_sp S-----EI NRG-DVQ-AV A-YEEP KHC SIVYYELNNR VGEAFH--AS
(N/A ) gi_341942042_sp A-----EI SRG-DVQ-AV A-YEEP KHC SIVYYELNNR VGEAFH--AS
(N/A ) gi_13633872_sp A-----EI NRG-DVQ-AV A-YEEP KHC SIVYYELNNR VGERFH--AS
(N/A ) gi_13959533_sp P-----SI SSR-DVQ-PV A-YEEP KHC SIVYYELNNR VGEAFH--AS
(N/A ) gi_13959566_sp P-----SI SSR-DVQ-PV A-YEEP KHC SIVYYELNNR VGEAFH--AS
(N/A ) gi_13959559_sp P-----SI SSR-DVQ-PV A-YEEP KHC SIVYYELNNR VGEAFH--AS
(N/A ) gi_82121811_sp P-----NI STR-DVQ-PV A-YEEP KHC SIVYYELNNR VGEAFH--AS
(N/A ) gi_21264062_sp P-----R --G-DVQ-PV E-YQEP SHWC SIVYYELNNR VGEAYH--AS
(N/A ) gi_21264049_sp L-----EI SNRTDVH-PV A-YQEP KHC SIVYYELNNR VGEAFL--AS
(N/A ) gi_13959539_sp N-----G ---DFR-PV C-YEEP QHC SVAYYELNNR VGETFQ--AS
(N/A ) gi_66774168_sp ----- ----DFR-PV C-YEEP QHC SVAYYELNNR VGETFQ--AS
(N/A ) gi_13959527_sp ----- ----DFR-PV C-YEEP LHC SVAYYELNNR VGETFQ--AS
(N/A ) gi_51338669_sp S-----PA HNNLDLQ-PV T-YCEPAFWC SISYYELNQR VGETFH--AS
(N/A ) gi_60414603_sp S-----PA HNNLDLQ-PV T-YCEPAFWC SISYYELNQR VGETFH--AS
(N/A ) gi_117949830_sp S-----PV NHSLDLQ-PV T-YSEPAFWC SIAYYELNQR VGETFH--AS
(N/A ) gi_13633871_sp S-----PV NHSLDLQ-PV T-YSEPAFWC SIAYYELNQR VGETFH--AS
(N/A ) gi_13633914_sp S-----PV NHSLDLQ-PV T-YSEPAFWC SIAYYELNQR VGETFH--AS
(N/A ) gi_75041393_sp S-----PV NHSLDLQ-PV T-YSEPAFWC SIAYYELNQR VGETFH--AS
(N/A ) gi_110826300_sp S-----PV NHSLDLQ-PV T-YSEPAFWC SIAYYELNQR VGETFH--AS
(N/A ) gi_21264050_sp S-----PV NHGMDLQ-PV T-YSEPAFWC SIAYYELNQR VGETFH--AS
(N/A ) gi_341942043_sp PHPGHYW-PV HNELAFQ PPI SNHPAPEYWC SIAYFEMDVQ VGETFKVPSS
(N/A ) gi_13959528_sp PHPGHYW-PV HNELAFQ PPI SNHPAPEYWC SIAYFEMDVQ VGETFKVPSS
(N/A ) gi_13959561_sp PHPGHYW-PV HNELAFQ PPI SNHPAPEYWC SIAYFEMDVQ VGETFKVPSS
(N/A ) gi_13959531_sp PHPGHYW-PV HNELAFQ PPI SNHPAPEYWC SIAYFEMDVQ VGETFKVPSS
(N/A ) gi_116256078_sp PHPGHYWPPV HNELAFQ PPI SNHPAPEYWC SIAYFEMDVQ VGETFKVPSS
(N/A ) gi_13959540_sp S----- --DAS-MS PDA TKPSHC SVAYWEHRTR VGRLYA--VY
(N/A ) gi_115502451_sp S----- --DAS-MS PDA TKPSHC SVAYWEHRTR VGRLYA--VY
(N/A ) gi_13959573_sp S----- --DAS-TS PDA VKRSHWC NVAYWEHRTR VGRLYT--VY
(N/A ) gi_13959541_sp S----- --DSQ-LL LEPGDRSHWC VVAYWEEKTR VGRLYC--VQ
(N/A ) gi_13959529_sp S----- --DSQ-LL LEPGDRSHWC VVAYWEEKTR VGRLYC--VQ
(N/A ) gi_13959538_sp S----- --DSQ-LL LEPGDRSHWC VVAYWEEKTR VGRLYC--VQ

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..... 410..... 420..... 430..... 440..... 450

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(N/A ) gi_13633932_sp STSVLVDGFT D-PSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_118573879_sp STSVLVDGFT D-PSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_13633915_sp STSVLVDGFT D-PSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_341942042_sp STSVLVDGFT D-PSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_13633872_sp STSVLVDGFT D-PSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_13959533_sp STSVLVDGFT D-PANNKSRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_13959566_sp STSVLVDGFT D-PSNNKSRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_13959559_sp STSVLVDGFT D-PSNNKSRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV

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(N/A ) gi_82121811_sp STSVLVDGFT D-PSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_21264062_sp STSVLVDGFT D-PSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_21264049_sp STSVLVDGFT D-PSNNRNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_13959539_sp SRSVLIDGFT D-PSNNRNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_66774168_sp SRSVLIDGFT D-PSNNRNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_13959527_sp SRSVLIDGFT D-PSNNRNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_51338669_sp QPSMTVDGFT D-PSNSE-RF CLGLLSNVNR NAAVELTRRH IGRGVRLLYYI
(N/A ) gi_60414603_sp QPSMTVDGFT D-PSNSE-RF CLGLLSNVNR NAAVELTRRH IGRGVRLLYYI
(N/A ) gi_117949830_sp QPSLTVDGFT D-PSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLLYYI
(N/A ) gi_13633871_sp QPSLTVDGFT D-PSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLLYYI
(N/A ) gi_13633914_sp QPSLTVDGFT D-PSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLLYYI
(N/A ) gi_75041393_sp QPSLTVDGFT D-PSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLLYYI
(N/A ) gi_110826300_sp QPSLTVDGFT D-PSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLLYYI
(N/A ) gi_21264050_sp QPSLTVDGFT D-PSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLLYYI
(N/A ) gi_341942043_sp CPVVTVDGYV D-PSGGD-RF CLGQLSNVHR TEAIERARLH IGKGVQLECK
(N/A ) gi_13959528_sp CPIVTVVDGYV D-PSGGD-RF CLGQLSNVHR TEAIERARLH IGKGVQLECK
(N/A ) gi_13959561_sp CPIVTVVDGYV D-PSGGD-RF CLGQLSNVHR TEAIERARLH IGKGVQLECK
(N/A ) gi_13959531_sp CPIVTVVDGYV D-PSGGD-RF CLGQLSNVHR TEAIERARLH IGKGVQLECK
(N/A ) gi_116256078_sp CPIVTVVDGYV D-PSGGD-RF CLGQLSNVHR TEAIERARLH IGKGVQLECK
(N/A ) gi_13959540_sp DQAVSI--FY DLPQGS--F CLGQLNLEQR SESVRRTRSK IGF GILLSKE
(N/A ) gi_115502451_sp DQAVSI--FY DLPQGS--F CLGQLNLEQR SESVRRTRSK IGF GILLSKE
(N/A ) gi_13959573_sp EQSVSI--FY DLPQNG--F CLGQLNLENR SETVRRTRSK IGY GILLSKE
(N/A ) gi_13959541_sp EPSLDI--FY DLPQNG--F CLGQLNSDNK SQLVQKVRSK IGC GIQLTRE
(N/A ) gi_13959529_sp EPSLDI--FY DLPQNG--F CLGQLNSDNK SQLVQKVRSK IGC GIQLTRE
(N/A ) gi_13959538_sp EPSLDI--FY DLPQNG--F CLGQLNSDNK SQLVQKVRSK IGC GIQLTRE

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. . . . . 460 . . . . . 470 . . . . . 480 . . . . . 490 . . . . . 500
(N/A ) gi_13633932_sp G-GEVYAECL SDSSIFVQSR NCNYHHGFHP T-TVCKIPSG CSLKIFN---
(N/A ) gi_118573879_sp G-GEVYAECL SDSSIFVQSR NCNYHHGFHP T-TVCKIPSG CSLKIFN---
(N/A ) gi_13633915_sp G-GEVYAECL SDSSIFVQSR NCNYHHGFHP T-TVCKIPSG CSLKIFN---
(N/A ) gi_341942042_sp G-GEVYAECL SDSSIFVQSR NCNYHHGFHP T-TVCKIPSG CSLKIFN---
(N/A ) gi_13633872_sp G-GEVYAECL SDSSIFVQSR NCNYHHGFHP T-TVCKIPSG CSLKIFN---
(N/A ) gi_13959533_sp G-GEVYAECL SDSSIFVQSR NCNFHHGFHP T-TVCKIPSS CSLKIFN---
(N/A ) gi_13959566_sp G-GEVYAECL SDSSIFVQSR NCNFHHGFHP T-TVCKIPSS CSLKIFN---
(N/A ) gi_13959559_sp G-GEVYAECL SDSSIFVQSR NCNFHHGFHP T-TVCKIPSS CSLKIFN---
(N/A ) gi_82121811_sp G-GEVYAECL SDSSIFVQSR NCNYHHGFHP T-TVCKIPSG CSLKIFN---
(N/A ) gi_21264062_sp G-GEVYAECL SDTSIFVQSR NCNYHHGFHP T-TVCKIPSG CSLKIFN---
(N/A ) gi_21264049_sp G-GEVYAECL SDSSIFVQSR NCNYHHGFHP T-TVCKIPSR CSLKIFN---
(N/A ) gi_13959539_sp G-GEVYAECL SDSSIFVQSR NCNYQHGFHP A-TVCKIPSG CSLKVFN---
(N/A ) gi_66774168_sp G-GEVYAECL SDSSIFVQSR NCNYQHGFHP A-TVCKIPSG CSLKVFN---
(N/A ) gi_13959527_sp G-GEVYAECL SDSSIFVQSR NCNYQHGFHP A-TVCKIPSG CSLKVFN---
(N/A ) gi_51338669_sp G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
(N/A ) gi_60414603_sp G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
(N/A ) gi_117949830_sp G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
(N/A ) gi_13633871_sp G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
(N/A ) gi_13633914_sp G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
(N/A ) gi_75041393_sp G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
(N/A ) gi_110826300_sp G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
(N/A ) gi_21264050_sp G-GEVFAECL SDSAIFVQSP NCNQRYGWHP A-TVCKIPPG CNLKIFN---
(N/A ) gi_341942043_sp GEGDVWVRCL SDHAVFVQSY YLDREAGRAB GDAVHKIYPS AYIKVFDLRQ
(N/A ) gi_13959528_sp GEGDVWVRCL SDHAVFVQSY YLDREAGRAB GDAVHKIYPS AYIKVFDLRQ
(N/A ) gi_13959561_sp GEGDVWVRCL SDHAVFVQSY YLDREAGRAB GDAVHKIYPS AYIKVFDLRQ
(N/A ) gi_13959531_sp GEGDVWVRCL SDHAVFVQSY YLDREAGRAB GDAVHKIYPS AYIKVFDLRQ
(N/A ) gi_116256078_sp GEGDVWVRCL SDHAVFVQSY YLDREAGRAB GDAVHKIYPS AYIKVFDLRQ
(N/A ) gi_13959540_sp PDG-VWAYNR GEHPIFVNSP TLDAPGGR-- ALVVRKVPPG YSIKVFD---
(N/A ) gi_115502451_sp PDG-VWAYNR GEHPIFVNSP TLDAPGGR-- ALVVRKVPPG YSIKVFD---
(N/A ) gi_13959573_sp PDG-VWAYNR SEHPIFVNSP TLDIPNCR-- TLIVRKVMPG YSIKVFD---
(N/A ) gi_13959541_sp VDG-VWVYNR SSYPFIKSA TLDNPDSR-- TLLVHKVFPF FSIKAFD---
(N/A ) gi_13959529_sp VDG-VWVYNR SSYPFIKSA TLDNPDSR-- TLLVHKVFPF FSIKAFD---
(N/A ) gi_13959538_sp VDG-VWVYNR SSYPFIKSA TLDNPDSR-- TLLVHKVFPF FSIKAFD---

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. . . . . 510 . . . . . 520 . . . . . 530 . . . . . 540 . . . . . 550
(N/A ) gi_13633932_sp -----NQEF- ---AQLLAQS V----N---- ---HGFE--- -----TV
(N/A ) gi_118573879_sp -----NQEF- ---AQLLAQS V----N---- ---HGFE--- -----TV
(N/A ) gi_13633915_sp -----NQEF- ---AQLLAQS V----N---- ---HGFE--- -----TV
(N/A ) gi_341942042_sp -----NQEF- ---AQLLAQS V----N---- ---HGFE--- -----TV
(N/A ) gi_13633872_sp -----NQEF- ---AQLLAQS V----N---- ---HGFE--- -----TE
(N/A ) gi_13959533_sp -----NQEF- ---AQLLAQS V----N---- ---HGFE--- -----AV
(N/A ) gi_13959566_sp -----NQEF- ---AQLLAQS V----N---- ---HGFE--- -----AV
(N/A ) gi_13959559_sp -----NQEF- ---AQLLAQS V----N---- ---HGFE--- -----AV
(N/A ) gi_82121811_sp -----NQEF- ---AQLLAQS V----N---- ---HGFE--- -----AV
(N/A ) gi_21264062_sp -----NQEF- ---AQLLAQS V----N---- ---HGFE--- -----AV
(N/A ) gi_21264049_sp -----NQEF- ---AQLLAQS V----N---- ---HGFE--- -----AV
(N/A ) gi_13959539_sp -----NQLF- ---AQLLAQS V----H---- ---HGFE--- -----VV
(N/A ) gi_66774168_sp -----NQLF- ---AQLLAQS V----H---- ---HGFE--- -----VV

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(N/A ) gi_13959527_sp_ -----NQLFA QLLAQLLAQS V-----H----- ---HGFE--- -----VV
(N/A ) gi_51338669_sp_ -----NQEF- ---AALLAQS V-----N----- ---QGFE--- -----AV
(N/A ) gi_60414603_sp_ -----NQEF- ---AALLAQS V-----N----- ---QGFE--- -----AV
(N/A ) gi_117949830_sp_ -----NQEF- ---AALLAQS V-----N----- ---QGFE--- -----AV
(N/A ) gi_13633871_sp_ -----NQEF- ---AALLAQS V-----N----- ---QGFE--- -----AV
(N/A ) gi_13633914_sp_ -----NQEF- ---AALLAQS V-----N----- ---QGFE--- -----AV
(N/A ) gi_75041393_sp_ -----NQEF- ---AALLAQS V-----N----- ---QGFE--- -----AV
(N/A ) gi_110826300_sp_ -----NQGF- ---AALLAQS V-----N----- ---QGFE--- -----AV
(N/A ) gi_21264050_sp_ -----NQEF- ---AALLAQS V-----N----- ---QGFE--- -----AV
(N/A ) gi_341942043_sp_ CHRQMQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI SLSAAAGIGV
(N/A ) gi_13959528_sp_ CHRQMQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI SLSAAAGIGV
(N/A ) gi_13959561_sp_ CHRQMQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI SLSAAAGIGV
(N/A ) gi_13959531_sp_ CHRQMQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI SLSAAAGIGV
(N/A ) gi_116256078_sp_ CHRQMQQQAA TAQAAAAAQA AAVAGNIPGP GSVGGIAPAI SLSAAAGIGV
(N/A ) gi_13959540_sp_ -----FER-- ---SGLLQHA -----D--- -----AA
(N/A ) gi_115502451_sp_ -----FER-- ---SG-LQHA -----PEPD--- -----AA
(N/A ) gi_13959573_sp_ -----YEK-- ---SCLLQHT -----AELD--- -----YA
(N/A ) gi_13959541_sp_ -----YEK-- ---AYSLQRP -----NDHE--- -----FM
(N/A ) gi_13959529_sp_ -----YEK-- ---AYSLQRP -----NDHE--- -----FM
(N/A ) gi_13959538_sp_ -----YEK-- ---AYSLQRP -----NDHE--- -----FM

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

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(N/A ) gi_13633932_sp_ YELTKMCTLR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTO
(N/A ) gi_118573879_sp_ YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTO
(N/A ) gi_13633915_sp_ YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTO
(N/A ) gi_341942042_sp_ YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTO
(N/A ) gi_13633872_sp_ YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTO
(N/A ) gi_13959533_sp_ YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTO
(N/A ) gi_13959566_sp_ YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTO
(N/A ) gi_13959559_sp_ YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTO
(N/A ) gi_82121811_sp_ YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTO
(N/A ) gi_21264062_sp_ YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEVHLHGP LQWLDKVLTO
(N/A ) gi_21264049_sp_ YELTKMCTIR MSFVKGWGAK YHRQDVTSTP CWIEIHLHGP LQWLDKVLTO
(N/A ) gi_13959539_sp_ YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTO
(N/A ) gi_66774168_sp_ YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTO
(N/A ) gi_13959527_sp_ YELTKMCTIR MSFVKGWGAE YHRQDVTSTP CWIEIHLHGP LQWLDKVLTO
(N/A ) gi_51338669_sp_ YQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTO
(N/A ) gi_60414603_sp_ YQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTO
(N/A ) gi_117949830_sp_ YQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTO
(N/A ) gi_13633871_sp_ YQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTO
(N/A ) gi_13633914_sp_ YQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTO
(N/A ) gi_75041393_sp_ YQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTO
(N/A ) gi_110826300_sp_ YQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTO
(N/A ) gi_21264050_sp_ YQLTRMCTIR MSFVKGWGAE YRRQTVTSTP CWIELHLNGP LQWLDKVLTO
(N/A ) gi_341942043_sp_ DDLRRLCILR MSFVKGWGPD YPRQSIKETP CWIEIHLHRA LQLLDEVLHT
(N/A ) gi_13959528_sp_ DDLRRLCILR MSFVKGWGPD YPRQSIKETP CWIEIHLHRA LQLLDEVLHT
(N/A ) gi_13959561_sp_ DDLRRLCILR MSFVKGWGPD YPRQSIKETP CWIEIHLHRA LQLLDEVLHT
(N/A ) gi_13959531_sp_ DDLRRLCILR MSFVKGWGPD YPRQSIKETP CWIEIHLHRA LQLLDEVLHT
(N/A ) gi_116256078_sp_ DDLRRLCILR MSFVKGWGPD YPRQSIKETP CWIEIHLHRA LQLLDEVLHT
(N/A ) gi_13959540_sp_ HGPYDPHSVR ISFAKGWGPC YSRQFITSCP CWLEILLNNH R-----
(N/A ) gi_115502451_sp_ DGPYDPNSVR ISFAKGWGPC YSRQFITSCP CWLEILLNNP R-----
(N/A ) gi_13959573_sp_ DGPYDPNSVR ISFAKGWGPC YSRQFITSCP CWLEILLSNN R-----
(N/A ) gi_13959541_sp_ QQPWTGFTVQ ISFVKGWGQC YTRQFISSCP CWLEVIFNSR -----
(N/A ) gi_13959529_sp_ QQPWTGFTVQ ISFVKGWGQC YTRQFISSCP CWLEVIFNSR -----
(N/A ) gi_13959538_sp_ QQPWTGFTVQ ISFVKGWGQC YTRQFISSCP CWLEVIFNSR -----

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(N/A ) gi_13633932_sp_ MGSPHNPISS VS
(N/A ) gi_118573879_sp_ MGSPHNPISS VS
(N/A ) gi_13633915_sp_ MGSPHNPISS VS
(N/A ) gi_341942042_sp_ MGSPHNPISS VS
(N/A ) gi_13633872_sp_ MGSPHNPISS VS
(N/A ) gi_13959533_sp_ MGSPHNPISS VS
(N/A ) gi_13959566_sp_ MGSPHNPISS VS
(N/A ) gi_13959559_sp_ MGSPHNPISS VS
(N/A ) gi_82121811_sp_ MGSPHNPISS VS
(N/A ) gi_21264062_sp_ MGSPHNPISS VS
(N/A ) gi_21264049_sp_ MGSPHNPISS VS
(N/A ) gi_13959539_sp_ MGSPHNPISS VS
(N/A ) gi_66774168_sp_ MGSPHNPISS VS
(N/A ) gi_13959527_sp_ MGSPHNPISS VS
(N/A ) gi_51338669_sp_ MGSPSIRCSS VS
(N/A ) gi_60414603_sp_ MGSPSIRCSS VS
(N/A ) gi_117949830_sp_ MGSPSVRCSS MS
(N/A ) gi_13633871_sp_ MGSPSVRCSS MS

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(N/A ) gi_13633914_sp_ MGSPSVRCSS MS
(N/A ) gi_75041393_sp_ MGSPSVRCSS MS
(N/A ) gi_110826300_sp MGSPSVRCSS MS
(N/A ) gi_21264050_sp_ MGSPSVRCSS MS
(N/A ) gi_341942043_sp M--PIADPQP LD
(N/A ) gi_13959528_sp_ M--PIADPQP LD
(N/A ) gi_13959561_sp_ M--PIADPQP LD
(N/A ) gi_13959531_sp_ M--PIADPQP LD
(N/A ) gi_116256078_sp M--PIADPQP LD
(N/A ) gi_13959540_sp_ ----- --
(N/A ) gi_115502451_sp ----- --
(N/A ) gi_13959573_sp_ ----- --
(N/A ) gi_13959541_sp_ ----- --
(N/A ) gi_13959529_sp_ ----- --
(N/A ) gi_13959538_sp_ ----- --

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