

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](#)).

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          . . . . . 10 . . . . . 20 . . . . . 30 . . . . . 40 . . . . . 50
(N/A ) gi_13633932_sp_ ----MNVTS L FSFTSPAVKR LLGWK----- Q GDEEEKWAEK
(N/A ) gi_118573879_sp ----MNVTS L FSFTSPAVKR LLGWK----- Q GDEEEKWAEK
(N/A ) gi_13633915_sp_ ----MNVTS L FSFTSPAVKR LLGWK----- Q GDEEEKWAEK
(N/A ) gi_341942042_sp ----MNVTS L FSFTSPAVKR LLGWK----- Q GDEEEKWAEK
(N/A ) gi_13633872_sp_ ----MNVTS L FSFTSPAVKR LLGWK----- Q GDEEEKWAEK
(N/A ) gi_13959533_sp_ ---MTSMAS L FSFTSPAVKR LLGWK----- Q GDEEEKWAEK
(N/A ) gi_13959566_sp_ ---MTSMAS L FSFTSPAVKR LLGWK----- Q GDEEEKWAEK
(N/A ) gi_13959559_sp_ ---MTSMAS L FSFTSPAVKR LLGWK----- Q GDEEEKWAEK
(N/A ) gi_82121811_sp_ ---MTSMAS L FSFTSPAVKR LLGWK----- Q GDEEEKWAEK
(N/A ) gi_21264062_sp_ ---MTSMSS L FSFTSPAVKR LLGWK----- Q GDEEEKWAEK
(N/A ) gi_21264049_sp_ ----MNVTS L FSFTSPAVKR LLGWK----- Q GDEEEKWAEK
(N/A ) gi_13959539_sp_ MHSTTP ISSL FSFTSPAVKR LLGWK----- Q GDEEEKWAEK
(N/A ) gi_66774168_sp_ MHPSTP ISSL FSFTSPAVKR LLGWK----- Q GDEEEKWAEK
(N/A ) gi_13959527_sp_ MHPSTP ISSL FSFTSPAVKR LLGWK----- Q GDEEEKWAEK
(N/A ) gi_51338669_sp_ -----MSSI LPFTPP IVKR LLGWKK----- GEQ NGQEEKWCEK
(N/A ) gi_60414603_sp_ -----MSSI LPFTPP IVKR LLGWKK----- GEQ NGQEEKWCEK
(N/A ) gi_117949830_sp -----MSSI LPFTPP VVKR LLGWKK SAGG SGGA-GGGEQ NGQEEKWCEK
(N/A ) gi_13633871_sp_ -----MSSI LPFTPP VVKR LLGWKK SAGG SGGA-GGGEQ NGQEEKWCEK
(N/A ) gi_13633914_sp_ -----MSSI LPFTPP VVKR LLGWKK SAGG SGGA-GGGEQ NGQEEKWCEK
(N/A ) gi_75041393_sp_ -----MSSI LPFTPP VVKR LLGWKK SAGG SGGA-GGGEQ NGQEEKWCEK
(N/A ) gi_110826300_sp -----MSSI LPFTPP VVKR LLGWKK SAGG SGGA-GGGEQ NGQEEKWCEK
(N/A ) gi_21264050_sp -----MSSI LPFTPP VVKR LLGWKK SASG SSGAGGGGEQ NGQEEKWCEK

          . . . . . 60 . . . . . 70 . . . . . 80 . . . . . 90 . . . . . 100
(N/A ) gi_13633932_sp_ AVDALVKKLK KKKGAMEELE KALSCPGQPS NCVTIP---- -----
(N/A ) gi_118573879_sp AVDALVKKLK KKKGAMEELE KALSCPGQPS NCVTIP---- -----
(N/A ) gi_13633915_sp_ AVDALVKKLK KKKGAMEELE KALSCPGQPS NCVTIP---- -----
(N/A ) gi_341942042_sp AVDALVKKLK KKKGAMEELE KALSCPGQPS NCVTIP---- -----
(N/A ) gi_13633872_sp_ AVDALVKKLK KKKGAMEELE KALSCPGQPS NCVTIP---- -----
(N/A ) gi_13959533_sp_ AVDALVKKLK KKKGAMEELE KALSSPGQPS KCVTIP---- -----
(N/A ) gi_13959566_sp_ AVDALVKKLK KKKGAMEELE KALSSPGQPS KCVTIP---- -----
(N/A ) gi_13959559_sp_ AVDALVKKLK KKKGAMEELE KALSSPGQPS KCVTIP---- -----
(N/A ) gi_82121811_sp_ AVDALVKKLK KKKGAMEELE KALSSPGQPS KCVTIP---- -----
(N/A ) gi_21264062_sp_ AVDALVKKLK KKKGAMEDLE KALSSPGQPS KCVTIP---- -----
(N/A ) gi_21264049_sp_ AVDALVKKLK KKKGAMEELE RALSCPGQPS NCVTIP---- -----
(N/A ) gi_13959539_sp_ AVDSL VKKLK KKKGAMDELE RALSCPGQPS KCVTIP---- -----
(N/A ) gi_66774168_sp_ AVDSL VKKLK KKKGAMDELE RALSCPGQPS KCVTIP---- -----
(N/A ) gi_13959527_sp_ AVDSL VKKLK KKKGAMDELE RALSCPGQPS KCVTIP---- -----
(N/A ) gi_51338669_sp_ AVKSLVKKL- KKTGQLDELE KAITTQNVNT KCITIP---- -----
(N/A ) gi_60414603_sp_ AVKSLVKKL- KKTGQLDELE KAITTQNINT KCITIP---- -----
(N/A ) gi_117949830_sp AVKSLVKKL- KKTGRLDELE KAITTQNCNT KCVTIPSTCS EIWGLSTANT
(N/A ) gi_13633871_sp_ AVKSLVKKL- KKTGRLDELE KAITTQNCNT KCVTIPSTCS EIWGLSTANT
(N/A ) gi_13633914_sp_ AVKSLVKKL- KKTGRLDELE KAITTQNCNT KCVTIPSTCS EIWGLSTPNT
(N/A ) gi_75041393_sp_ AVKSLVKKL- KKTGRLDELE KAITTQNCNT KCVTIPSTCS EIWGLSTPNT
(N/A ) gi_110826300_sp AVKSLVKKL- KKTGRLDELE KAITTQNCNT KCVTIPSTCS EIWGLSTPNT
(N/A ) gi_21264050_sp_ AVKSLVKKL- KKTGQLDELE KAITTQNRNT KCVTIPSNCS EIWGLSTPNT

          . . . . . 110 . . . . . 120 . . . . . 130 . . . . . 140 . . . . . 150
(N/A ) gi_13633932_sp_ ----- RSLD GRLQVSHRKG LPHVIYCRVW RWPDLQSHHE
(N/A ) gi_118573879_sp ----- RSLD GRLQVSHRKG LPHVIYCRVW RWPDLQSHHE
(N/A ) gi_13633915_sp_ ----- RSLD GRLQVSHRKG LPHVIYCRVW RWPDLQSHHE
(N/A ) gi_341942042_sp ----- RSLD GRLQVSHRKG LPHVIYCRVW RWPDLQSHHE
(N/A ) gi_13633872_sp_ ----- RSLD GRLQVSHRKG LPHVIYCRVW RWPDLQSHHE
(N/A ) gi_13959533_sp_ ----- RSLD GRLQVSHRKG LPHVIYCRVW RWPDLQSHHE
(N/A ) gi_13959566_sp_ ----- RSLD GRLQVSHRKG LPHVIYCRVW RWPDLQSHHE
(N/A ) gi_13959559_sp_ ----- RSLD GRLQVSHRKG LPHVIYCRVW RWPDLQSHHE
(N/A ) gi_82121811_sp_ ----- RSLD GRLQVSHRKG LPHVIYCRVW RWPDLQSHHE
(N/A ) gi_21264062_sp_ ----- RSLD GRLQVSHRKG LPHVIYCRVW RWPDLQSHHE
(N/A ) gi_21264049_sp_ ----- RSLD GRLQVSHRKG LPHVIYCRVW RWPDLQSHHE
(N/A ) gi_13959539_sp_ ----- RSLD GRLQVSHRKG LPHVIYCRVW RWPDLQSHHE
(N/A ) gi_66774168_sp_ ----- RSLD GRLQVSHRKG LPHVIYCRVW RWPDLQSHHE
(N/A ) gi_13959527_sp_ ----- RSLD GRLQVSHRKG LPHVIYCRVW RWPDLQSHHE
(N/A ) gi_51338669_sp_ ----- RSLD GRLQVSHRKG LPHVIYCRLW RWPDLHSHHE

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(N/A ) gi_60414603_sp_ -----RSLD GRLQVSHRKG LPHVIYCRLW RWPDLHSHHE
(N/A ) gi_117949830_sp VDQWDTTGLY SFSEQTRSLD GRLQVSHRKG LPHVIYCRLW RWPDLHSHHE
(N/A ) gi_13633871_sp_ VDQWDTTGLY SFSEQTRSLD GRLQVSHRKG LPHVIYCRLW RWPDLHSHHE
(N/A ) gi_13633914_sp_ IDQWDTTGLY SFSEQTRSLD GRLQVSHRKG LPHVIYCRLW RWPDLHSHHE
(N/A ) gi_75041393_sp_ IDQWDTTGLY SFSEQTRSLD GRLQVSHRKG LPHVIYCRLW RWPDLHSHHE
(N/A ) gi_110826300_sp IDQWDTTGLY SFSEQTRSLD GRLQVSHRKG LPHVIYCRLW RWPDLHSHHE
(N/A ) gi_21264050_sp_ IEQWDTSGLY SYPDQTRSLD GRLQVSHRKG LPHVIYCRLW RWPDLHSHHE

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..... 160..... 170..... 180..... 190..... 200
(N/A ) gi_13633932_sp_ LKPLECCEFP FGSKQKEVCI NPYHYKRVES PVLPPVLVPR HSEYNPQHSL
(N/A ) gi_118573879_sp LKPLECCEFP FGSKQKEVCI NPYHYKRVES PVLPPVLVPR HSEYNPQHSL
(N/A ) gi_13633915_sp_ LKPLECCEFP FGSKQKEVCI NPYHYKRVES PVLPPVLVPR HSEYNPQHSL
(N/A ) gi_341942042_sp LKPLECCEFP FGSKQKEVCI NPYHYKRVES PVLPPVLVPR HSEYNPQHSL
(N/A ) gi_13633872_sp_ LKPLECCEFP FGSKQKEVCI NPYHYKRVES PVLPPVLVPR HSEYNPQHSL
(N/A ) gi_13959533_sp_ LKPLDICEFP FGSKQKEVCI NPYHYKRVES PVLPPVLVPR HNEFNPQHSL
(N/A ) gi_13959566_sp_ LKPLDICEFP FGSKQKEVCI NPYHYKRVES PVLPPVLVPR HNEFNPQHSL
(N/A ) gi_13959559_sp_ LKPLDICEFP FGSKQKEVCI NPYHYKRVES PVLPPVLVPR HNEFNPQHSL
(N/A ) gi_82121811_sp_ LKPLDICEFP FGSKQKEVCI NPYHYKRVES PVLPPVLVPR HSEFNPQHSL
(N/A ) gi_21264062_sp_ LKPLEVCEYP FGSKQKEVCI NPYHYKRVES PVLPPVLVPR HSEFNPQHSL
(N/A ) gi_21264049_sp_ LKALECCEFP FGSKQKDVCI NPYHYKRVDS PVLPPVLVPR NSEFNAKLSM
(N/A ) gi_13959539_sp_ LKPLECCEFP FGSKQKEVCI NPYHYRRVET PVLPPVLVPR HSEYNPQLSL
(N/A ) gi_66774168_sp_ LKPLECCEFP FGSKQKEVCI NPYHYRRVET PVLPPVLVPR HSEYNPQLSL
(N/A ) gi_13959527_sp_ LKPLECCEFP FGSKQKEVCI NPYHYRRVET PVLPPVLVPR HSEYNPQLSL
(N/A ) gi_51338669_sp_ LRAMELCEFA FNMKKDEVCV NPYHYQRVET PVLPPVLVPR HTEIPAEFFP
(N/A ) gi_60414603_sp_ LRAMEMCEYA FNMKKDEVCV NPYHYQRVET PVLPPVLVPR HTEIPAEFFP
(N/A ) gi_117949830_sp LKAIENCEYA FNLKKDEVCV NPYHYQRVET PVLPPVLVPR HTEILTELPP
(N/A ) gi_13633871_sp_ LKAIENCEYA FSLKKDEVCV NPYHYQRVET PVLPPVLVPR HTEILTELPP
(N/A ) gi_13633914_sp_ LKAIENCEYA FNLKKDEVCV NPYHYQRVET PVLPPVLVPR HTEILTELPP
(N/A ) gi_75041393_sp_ LKAIENCEYA FNLKEDEVCV NPYHYQRVET PVLPPVLVPR HTEILTELPP
(N/A ) gi_110826300_sp LKAIENCEYA FNLKKDEVCV NPYHYQRVET PVLPPVLVPR HTEILTELPP
(N/A ) gi_21264050_sp_ LRAIETCEYA FNLKKDEVCV NPYHYQRVET PVLPPVLVPR HTEILTELPP

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..... 210..... 220..... 230..... 240..... 250
(N/A ) gi_13633932_sp_ LAQFRN-LGQ NEPHMPHNAT FPDSFQQ-P- NSHPF-PHSP NSSYPNSPGS
(N/A ) gi_118573879_sp LAQFRN-LGQ NEPHMPLNAT FPDSFQQ-P- NSHPF-PHSP NSSYPNSPGS
(N/A ) gi_13633915_sp_ LAQFRN-LGQ NEPHMPLNAT FPDSFQQ-P- NSHPF-PHSP NSSYPNSPGS
(N/A ) gi_341942042_sp LAQFRN-LGQ NEPHMPLNAT FPDSFQQ-P- NSHPF-PHSP NSSYPNSPGG
(N/A ) gi_13633872_sp_ LAQFRN-LGQ NEPHMPLNAT FPDSFQQ-P- HSHPF-AQYP NSSYPNSPGS
(N/A ) gi_13959533_sp_ LVQFRN-LSH NEPHMPQONAT FPDSFHQ-P- NSTPF-PLSP NSPYPPSP-A
(N/A ) gi_13959566_sp_ LVQFRN-LSH NEPHMPQONAT FPDSFHQ-P- NNTPF-PLSP NSPYPPSP-A
(N/A ) gi_13959559_sp_ LVQFRN-LSH NEPHMPQONAT FPDSFHQ-P- NNAPF-PLSP NSPYPPSP-A
(N/A ) gi_82121811_sp_ LVQFRN-LSH NEPHMPHNAT FPDSFQQ-P- NSTPF-SISP NSPYPPSP-A
(N/A ) gi_21264062_sp_ LVQFRN-LSH NEPHMPLNAT FPESFQQHS- GGSSF-PISP NSPYPPSP-A
(N/A ) gi_21264049_sp_ LPRFRNPLHQ TEPPMPQONAT FPDSFPQQPA NALPFTPNSP TNSYPSSPNS
(N/A ) gi_13959539_sp_ LAKFRSASLH SEPLMPHNAT YPDSFQQ--- PPCSALPPSP SHAFSQSP--
(N/A ) gi_66774168_sp_ LAKFRSASLH SEPLMPHNAT YPDSFQQ--- SLCPAPPSSP GHVFPQSP--
(N/A ) gi_13959527_sp_ LAKFRSASLH SEPLMPHNAT YPDSFQQ--- SLGPAPPSSP GHVFPQSP--
(N/A ) gi_51338669_sp_ LDDY----SH S---IPENTN FPAGIE----P QSN-----
(N/A ) gi_60414603_sp_ LDDY----SH S---IPENTN FPAGIE----P QSNY-----
(N/A ) gi_117949830_sp LDDY----TH S---IPENTN FPAGIE----P QSNY-----
(N/A ) gi_13633871_sp_ LDDY----TH S---IPENTN FPAGIE----P QSNY-----
(N/A ) gi_13633914_sp_ LDDY----TH S---IPENTN FPAGIE----P QSNY-----
(N/A ) gi_75041393_sp_ LDDY----TH S---IPENTN FPAGIE----P QSNY-----
(N/A ) gi_110826300_sp LDDY----TH S---IPENTN FPAGIE----P QSNY-----
(N/A ) gi_21264050_sp_ LDDY----TN S---IPENTN FPTGIE----P PNNY-----

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..... 260..... 270..... 280..... 290..... 300
(N/A ) gi_13633932_sp_ ---SSSTYPH SPAS-SDPGS PFQMPADTPP PAYLPPE-DQ MTHDTSQPM
(N/A ) gi_118573879_sp ---SSSTYPH SPTS-SDPGS PFQMPADTPP PAYLPPE-DP MTQDGSQPM
(N/A ) gi_13633915_sp_ ---SSSTYPH SPTS-SDPGS PFQMPADTPP PAYLPPE-DP MTQDGSQPM
(N/A ) gi_341942042_sp ---SSSTYPH SPTS-SDPGS PFQMPADTPP PAYLPPE-DP MAQDGSQPM
(N/A ) gi_13633872_sp_ ---SSSTYPH SPTS-SDPGS PFQMPADTPP PAYLPPE-DP MAQDGSQPM
(N/A ) gi_13959533_sp_ ---SS-TYPN SPAS-SGPGS PFQLPADTPP PAYMPPD-DQ MGQDNSQPM
(N/A ) gi_13959566_sp_ ---SS-TYPN SPAS-SGPGS PFQLPADTPP PAYMPPD-DQ MGQDNSQPM
(N/A ) gi_13959559_sp_ ---SS-TYPN SPAS-SGPGS PFQLPADTPP PAYMPPD-DQ MAPDNSQPM
(N/A ) gi_82121811_sp_ ---SS-TYPS SPAS-SGPSS PFQLPADTPP PAYMPPD-DQ MGQDNSQSMD
(N/A ) gi_21264062_sp_ ---SSGTYPN SPAS-SGPSS PFQLPADTPP PAYMPPD-EQ MGQDGSQSME
(N/A ) gi_21264049_sp_ GTGSTATFPH SPSS-SDPGS PFQMP-ETPP PAYMPPE-EP MTQDCQPM
(N/A ) gi_13959539_sp_ ---CTASYPH SPGSPSEPES PYQHSVDTPP LPYHATE-AS ETQSG-QPVD
(N/A ) gi_66774168_sp_ ---CPTSYPH SPGSPSESDS PYQHS-----
(N/A ) gi_13959527_sp_ ---CPTSYPQ SPGSPSESDS PYQHS-----
(N/A ) gi_51338669_sp_ -----IP- -----ETPP PGYLSGEDGET SDHQMNHSM
(N/A ) gi_60414603_sp_ -----IP- -----ETPP PGYLSGEDGET SDHQMNPMS
(N/A ) gi_117949830_sp -----IP- -----ETPP PGYISEDGET SDQQLNQSM
(N/A ) gi_13633871_sp_ -----IP- -----ETPP PGYISEDGET SDQQLNQSM

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(N/A ) gi_13633914_sp_ -----IP- -----ETPP PGYISEDGET SDQQLNQSMDS
(N/A ) gi_75041393_sp_ -----IP- -----ETPP PGYISEDGET SDQQLNQSMDS
(N/A ) gi_110826300_sp_ -----IP- -----ETPP PGYISEDGET SDQQLNQSMDS
(N/A ) gi_21264050_sp_ -----IP- -----ETPP PGYISEDGEA SDQQMNQSMDS

..... 310..... 320..... 330..... 340..... 350
(N/A ) gi_13633932_sp_ ---TNMMAPG IHPDIHRG-D VQAVAYEEPK HWCSIVYYEL NNRVGEAFHA
(N/A ) gi_118573879_sp_ ---TNMMAPS LPSEINRG-D VQAVAYEEPK HWCSIVYYEL NNRVGEAFHA
(N/A ) gi_13633915_sp_ ---TNMMAPP LPSEINRG-D VQAVAYEEPK HWCSIVYYEL NNRVGEAFHA
(N/A ) gi_341942042_sp_ ---TNMMAPP LPAEISRG-D VQAVAYEEPK HWCSIVYYEL NNRVGEAFHA
(N/A ) gi_13633872_sp_ TNMTNMTAPT LPAEINRG-D VQAVAYEEPK HWCSIVYYEL NNRVGERFHA
(N/A ) gi_13959533_sp_ T--SNNMIPQ IMPSISSR-D VQPVAYEEPK HWCSIVYYEL NNRVGEAFHA
(N/A ) gi_13959566_sp_ T--SNNMIPQ IMPSISSR-D VQPVAYEEPK HWCSIVYYEL NNRVGEAFHA
(N/A ) gi_13959559_sp_ T--SSNMIPQ TMPSISSR-D VQPVAYEEPK HWCSIVYYEL NNRVGEAFHA
(N/A ) gi_82121811_sp_ T--SNTMIPQ IMPNISTR-D VQPVAYEEPK HWCSIVYYEL NNRVGEAFHA
(N/A ) gi_21264062_sp_ T--GSSLAPQ NMPR---G-D VQPVVEYQEPS HWCSIVYYEL NNRVGEAYHA
(N/A ) gi_21264049_sp_ ---TNLLAPN LPLEISNRTD VHPVAYQEPK HWCSIVYYEL NNRVGEAFHA
(N/A ) gi_13959539_sp_ ATADRHVVL IPNG-----D FRPVCYEEPQ HWCSVAYYEL NNRVGETFQA
(N/A ) gi_66774168_sp_ -----D FRPVCYEEPQ HWCSVAYYEL NNRVGETFQA
(N/A ) gi_13959527_sp_ -----D FRPVCYEEPL HWCSVAYYEL NNRVGETFQA
(N/A ) gi_51338669_sp_ AGSP-NLSPN PMSPAHHNLD LQPVITYCEPA FWCSISYYEL NQRVGETFHA
(N/A ) gi_60414603_sp_ AGSP-NLSPN PMSPAHHNLD LQPVITYCEPA FWCSISYYEL NQRVGETFHA
(N/A ) gi_117949830_sp_ TGSPAELSPT TLSPVNHSLD LQPVITYSEPA FWCSIAYYEL NQRVGETFHA
(N/A ) gi_13633871_sp_ TGSPAELSPT TLSPVNHSLD LQPVITYSEPA FWCSIAYYEL NQRVGETFHA
(N/A ) gi_13633914_sp_ TGSPAELSPT TLSPVNHSLD LQPVITYSEPA FWCSIAYYEL NQRVGETFHA
(N/A ) gi_75041393_sp_ TGSPAELSPT TLSPVNHSLD LQPVITYSEPA FWCSIAYYEL NQRVGETFHA
(N/A ) gi_110826300_sp_ TGSPAELSPT TLSPVNHSLD LQPVITYSEPA FWCSIAYYEL NQRVGETFHA
(N/A ) gi_21264050_sp_ TGSPAELSPTS TLSPVNHGMD LQPVITYSEPA FWCSIAYYEL NQRVGETFHA

..... 360..... 370..... 380..... 390..... 400
(N/A ) gi_13633932_sp_ SSTSILVDGF TDPSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_118573879_sp_ SSTSILVDGF TDPSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_13633915_sp_ SSTSILVDGF TDPSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_341942042_sp_ SSTSILVDGF TDPSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_13633872_sp_ SSTSILVDGF TDPSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_13959533_sp_ SSTSILVDGF TDPANNKSRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_13959566_sp_ SSTSILVDGF TDPSNNKSRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_13959559_sp_ SSTSILVDGF TDPSNNKSRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_82121811_sp_ SSTSILVDGF TDPSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_21264062_sp_ SSTSILVDGF TDPSNNKNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_21264049_sp_ SSTSILVDGF TDPSNNRNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_13959539_sp_ SSRSVLIDGF TDPSNNRNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_66774168_sp_ SSRSVLIDGF TDPSNNRNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_13959527_sp_ SSRSVLIDGF TDPSNNRNRF CLGLLSNVNR NSTIENTRRH IGKGVHLYYV
(N/A ) gi_51338669_sp_ SQPSMTVDGF TDPSNSE-RF CLGLLSNVNR NAAVELTRRH IGRGVRLYYI
(N/A ) gi_60414603_sp_ SQPSMTVDGF TDPSNSE-RF CLGLLSNVNR NAAVELTRRH IGRGVRLYYI
(N/A ) gi_117949830_sp_ SQPSLTVDGF TDPSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLYYI
(N/A ) gi_13633871_sp_ SQPSLTVDGF TDPSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLYYI
(N/A ) gi_13633914_sp_ SQPSLTVDGF TDPSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLYYI
(N/A ) gi_75041393_sp_ SQPSLTVDGF TDPSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLYYI
(N/A ) gi_110826300_sp_ SQPSLTVDGF TDPSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLYYI
(N/A ) gi_21264050_sp_ SQPSLTVDGF TDPSNSE-RF CLGLLSNVNR NATVEMTRRH IGRGVRLYYI

..... 410..... 420..... 430..... 440..... 450
(N/A ) gi_13633932_sp_ GGEVYAECLS DSSIFVQSRN CNYHHGFHPT TVCKIPSGCS LKIFNNQEF-
(N/A ) gi_118573879_sp_ GGEVYAECLS DSSIFVQSRN CNYHHGFHPT TVCKIPSGCS LKIFNNQEF-
(N/A ) gi_13633915_sp_ GGEVYAECLS DSSIFVQSRN CNYHHGFHPT TVCKIPSGCS LKIFNNQEF-
(N/A ) gi_341942042_sp_ GGEVYAECLS DSSIFVQSRN CNYHHGFHPT TVCKIPSGCS LKIFNNQEF-
(N/A ) gi_13633872_sp_ GGEVYAECLS DSSIFVQSRN CNYHHGFHPT TVCKIPSGCS LKIFNNQEF-
(N/A ) gi_13959533_sp_ GGEVYAECLS DSSIFVQSRN CNFHHGFHPT TVCKIPSSCS LKIFNNQEF-
(N/A ) gi_13959566_sp_ GGEVYAECLS DSSIFVQSRN CNFHHGFHPT TVCKIPSSCS LKIFNNQEF-
(N/A ) gi_13959559_sp_ GGEVYAECLS DSSIFVQSRN CNFHHGFHPT TVCKIPSSCS LKIFNNQEF-
(N/A ) gi_82121811_sp_ GGEVYAECLS DSSIFVQSRN CNYHHGFHPT TVCKIPSGCS LKIFNNQEF-
(N/A ) gi_21264062_sp_ GGEVYAECLS DTSIFVQSRN CNYHHGFHPT TVCKIPSGCS LKIFNNQEF-
(N/A ) gi_21264049_sp_ GGEVYAECLS DSSIFVQSRN CNYHHGFHPT TVCKIPSRCS LKIFNNQEF-
(N/A ) gi_13959539_sp_ GGEVYAECVS DSSIFVQSRN CNYQHGFHPTA TVCKIPSGCS LKVFNNQLF-
(N/A ) gi_66774168_sp_ GGEVYAECVS DSSIFVQSRN CNYQHGFHPTA TVCKIPSGCS LKVFNNQLF-
(N/A ) gi_13959527_sp_ GGEVYAECVS DSSIFVQSRN CNYQHGFHPTA TVCKIPSGCS LKVFNNQLFA
(N/A ) gi_51338669_sp_ GGEVFAECLS DSAIFVQSPN CNQRYGWHPTA TVCKIPPGCN LKIFNNQEF-
(N/A ) gi_60414603_sp_ GGEVFAECLS DSAIFVQSPN CNQRYGWHPTA TVCKIPPGCN LKIFNNQEF-
(N/A ) gi_117949830_sp_ GGEVFAECLS DSAIFVQSPN CNQRYGWHPTA TVCKIPPGCN LKIFNNQEF-
(N/A ) gi_13633871_sp_ GGEVFAECLS DSAIFVQSPN CNQRYGWHPTA TVCKIPPGCN LKIFNNQEF-
(N/A ) gi_13633914_sp_ GGEVFAECLS DSAIFVQSPN CNQRYGWHPTA TVCKIPPGCN LKIFNNQEF-
(N/A ) gi_75041393_sp_ GGEVFAECLS DSAIFVQSPN CNQRYGWHPTA TVCKIPPGCN LKIFNNQEF-
(N/A ) gi_110826300_sp_ GGEVFAECLS DSAIFVQSPN CNQRYGWHPTA TVCKIPPGCN LKIFNNQGF-

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(N/A) gi_21264050_sp_ GGEVFAECLS DSAIFVQSPN CNQRYGWHPA TVCKIPPGCN LKIFNNQEF-

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

(N/A) gi_13633932_sp_ ---AQLLAQS VNHGFETVYE LTKMCTLRMS FVKGWGAHEYH RQDVTSTPCW
 (N/A) gi_118573879_sp_ ---AQLLAQS VNHGFETVYE LTKMCTIRMS FVKGWGAHEYH RQDVTSTPCW
 (N/A) gi_13633915_sp_ ---AQLLAQS VNHGFETVYE LTKMCTIRMS FVKGWGAHEYH RQDVTSTPCW
 (N/A) gi_341942042_sp_ ---AQLLAQS VNHGFETVYE LTKMCTIRMS FVKGWGAHEYH RQDVTSTPCW
 (N/A) gi_13633872_sp_ ---AQLLAQS VNHGFETEYE LTKMCTIRMS FVKGWGAHEYH RQDVTSTPCW
 (N/A) gi_13959533_sp_ ---AQLLAQS VNHGFEAVYE LTKMCTIRMS FVKGWGAHEYH RQDVTSTPCW
 (N/A) gi_13959566_sp_ ---AQLLAQS VNHGFEAVYE LTKMCTIRMS FVKGWGAHEYH RQDVTSTPCW
 (N/A) gi_13959559_sp_ ---AQLLAQS VNHGFEAVYE LTKMCTIRMS FVKGWGAHEYH RQDVTSTPCW
 (N/A) gi_82121811_sp_ ---AQLLAQS VNHGFEAVYE LTKMCTIRMS FVKGWGAHEYH RQDVTSTPCW
 (N/A) gi_21264062_sp_ ---AQLLAQS VNHGFEAVYE LTKMCTIRMS FVKGWGAHEYH RQDVTSTPCW
 (N/A) gi_21264049_sp_ ---AELLAQS VNHGFEAVYE LTKMCTIRMS FVKGWGAKYH RQDVTSTPCW
 (N/A) gi_13959539_sp_ ---AQLLAQS VHHGFEVVYE LTKMCTIRMS FVKGWGAHEYH RQDVTSTPCW
 (N/A) gi_66774168_sp_ ---AQLLAQS VHHGFEVVYE LTKMCTIRMS FVKGWGAHEYH RQDVTSTPCW
 (N/A) gi_13959527_sp_ QLLAQLLAQS VHHGFEVVYE LTKMCTIRMS FVKGWGAHEYH RQDVTSTPCW
 (N/A) gi_51338669_sp_ ---AALLAQS VNQGFEAVYQ LTRMCTIRMS FVKGWGAHEYR RQTVTSTPCW
 (N/A) gi_60414603_sp_ ---AALLAQS VNQGFEAVYQ LTRMCTIRMS FVKGWGAHEYR RQTVTSTPCW
 (N/A) gi_117949830_sp_ ---AALLAQS VNQGFEAVYQ LTRMCTIRMS FVKGWGAHEYR RQTVTSTPCW
 (N/A) gi_13633871_sp_ ---AALLAQS VNQGFEAVYQ LTRMCTIRMS FVKGWGAHEYR RQTVTSTPCW
 (N/A) gi_13633914_sp_ ---AALLAQS VNQGFEAVYQ LTRMCTIRMS FVKGWGAHEYR RQTVTSTPCW
 (N/A) gi_75041393_sp_ ---AALLAQS VNQGFEAVYQ LTRMCTIRMS FVKGWGAHEYR RQTVTSTPCW
 (N/A) gi_110826300_sp_ ---AALLAQS VNQGFEAVYQ LTRMCTIRMS FVKGWGAHEYR RQTVTSTPCW
 (N/A) gi_21264050_sp_ ---AALLAQS VNQGFEAVYQ LTRMCTIRMS FVKGWGAHEYR RQTVTSTPCW

..... 510..... 520..... 530

(N/A) gi_13633932_sp_ IEIHLHGPLQ WLDKVLTMG SPHNPISSVS
 (N/A) gi_118573879_sp_ IEIHLHGPLQ WLDKVLTMG SPHNPISSVS
 (N/A) gi_13633915_sp_ IEIHLHGPLQ WLDKVLTMG SPHNPISSVS
 (N/A) gi_341942042_sp_ IEIHLHGPLQ WLDKVLTMG SPHNPISSVS
 (N/A) gi_13633872_sp_ IEIHLHGPLQ WLDKVLTMG SPHNPISSVS
 (N/A) gi_13959533_sp_ IEIHLHGPLQ WLDKVLTMG SPLNPISSVS
 (N/A) gi_13959566_sp_ IEIHLHGPLQ WLDKVLTMG SPLNPISSVS
 (N/A) gi_13959559_sp_ IEIHLHGPLQ WLDKVLTMG SPLNPISSVS
 (N/A) gi_82121811_sp_ IEIHLHGPLQ WLDKVLTMG SPLNPISSVS
 (N/A) gi_21264062_sp_ IEVHLHGPLQ WLDKVLTMG SPLNPISSVS
 (N/A) gi_21264049_sp_ IEIHLHGPLQ WLDKVLTMG SPHNPISSVS
 (N/A) gi_13959539_sp_ IEIHLHGPLQ WLDKVLTMG SPHNPISSVS
 (N/A) gi_66774168_sp_ IEIHLHGPLQ WLDKVLTMG SPHNPISSVS
 (N/A) gi_13959527_sp_ IEIHLHGPLQ WLDKVLTMG SPHNPISSVS
 (N/A) gi_51338669_sp_ IELHLNGPLQ WLDKVLTMG SPSIRCSSVS
 (N/A) gi_60414603_sp_ IELHLNGPLQ WLDKVLTMG SPSIRCSSVS
 (N/A) gi_117949830_sp_ IELHLNGPLQ WLDKVLTMG SPSVRCSSMS
 (N/A) gi_13633871_sp_ IELHLNGPLQ WLDKVLTMG SPSVRCSSMS
 (N/A) gi_13633914_sp_ IELHLNGPLQ WLDKVLTMG SPSVRCSSMS
 (N/A) gi_75041393_sp_ IELHLNGPLQ WLDKVLTMG SPSVRCSSMS
 (N/A) gi_110826300_sp_ IELHLNGPLQ WLDKVLTMG SPSVRCSSMS
 (N/A) gi_21264050_sp_ IELHLNGPLQ WLDKVLTMG SPSVRCSSMS