

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
NP_115893_1_pro	MVKRKSSSEQ	EQDGGRGIP	PIQTFLWRQT	SAFLRPKLGK	QYEASCVSFE
XP_003309496_1	MVKRKSSSEQ	EQDGGRGIP	PIQTFLWRQT	SAFLRPKLGK	QYEASCVSFE
NP_001193492_1	MVKRKSSSEQ	EQDSGRGIP	PIQTFLWRQT	SAFLRPKLGK	QYEASCVSFE
NP_780719_2_pro	MVKRKSSSEQ	EQDGGRGIP	PIQTFLWRQT	SAFLRPKLGK	QYEASCVSFE
Consistency	*****	***7*****	*****	*****	*****
	..... 60 .....	..... 70 .....	..... 80 .....	..... 90 .....	..... 100
NP_115893_1_pro	RVLVENKLHG	LSPALSEAIQ	SISRWELVQA	ALPHVLHCTA	TLLSNRNKLG
XP_003309496_1	RVLVENKLHG	LSPALSEAIQ	SISRWELVQA	ALPHVLHCTA	TLLSNRNKLG
NP_001193492_1	RVLVENKLHG	LSPALSEAIQ	SISRWELVQA	ALPHVLHCTA	TLLSNRNKLG
NP_780719_2_pro	RVLVENKLHG	LSPALSEAIQ	SISRWELVQA	ALPHVLHCTA	TLLSNRNKLG
Consistency	*****	*****	*****	*****	*****
	..... 110 .....	..... 120 .....	..... 130 .....	..... 140 .....	..... 150
NP_115893_1_pro	HQDKLGVAET	KLLHTLHWML	LEAPQDCNNE	RFGGTDRGSS	WGGSSSAFIH
XP_003309496_1	HQDKLGVAET	KLLHTLHWML	LEAPQDCNNE	RFGGTDRGSS	WGGSSSAFIH
NP_001193492_1	HQDKLGVAET	KLLHTLHWML	LEAPQDCNSE	RFGGTDRGSS	WAGSSSAFVH
NP_780719_2_pro	HQDKLGVAET	KLLHTLHWML	LEAPQDCNND	QFGGTDRGSS	WGGSSSAFIH
Consistency	*****	*****	*****78	7*****	*7*****9*
	..... 160 .....	..... 170 .....	..... 180 .....	..... 190 .....	..... 200
NP_115893_1_pro	QVENQGSPGQ	PCQSSSNDEE	ENNRRKIFQN	SMATVELFVF	LFAPLVHRIK
XP_003309496_1	QVENQGSPGQ	PCQSSSNDEE	ENNRRKIFQN	SMATVELFVF	LFAPLVHRIK
NP_001193492_1	QVENQGSPGQ	PCQSTAHDEE	ENNRRKIFQN	SMATVELFVF	LFAPLVHRIK
NP_780719_2_pro	QIENQGSPGQ	PCRSSSHDEE	ENNRRKTFQN	SMATVELFVF	LFAPLVHRIK
Consistency	*9*****	**7*786***	*****6***	*****	*****
	..... 210 .....	..... 220 .....	..... 230 .....	..... 240 .....	..... 250
NP_115893_1_pro	ESDLTFRLAS	GLVIWQPMWE	HRQPGVSGFT	ALVKPIRNII	TAKRSSPINS
XP_003309496_1	ESDLTFRLAS	GLVIWQPMWE	HRQPEVSGFT	ALVKPIRNII	TAKRSSPINS
NP_001193492_1	ESDLTFRLAS	GLVIWQPMWE	HRQPEVSGFT	ALVKPIRNII	TAKRSSPINS
NP_780719_2_pro	ESDLTFRLAS	GLVIWQPMWE	HRQPEVSGFT	ALVKPIRNII	TAKRSSPINS
Consistency	*****	*****	***6****	*****	*****
	..... 260 .....	..... 270 .....	..... 280 .....	..... 290 .....	..... 300
NP_115893_1_pro	QSRTCESPNQ	DARHL-EG	VVCETFQSDS	ISPKATISGC	HRGNSFDGSL
XP_003309496_1	QSQTCESPNQ	DARHL-EG	VVCETFQSDS	ISPKATISGC	HRGNSFDGSL
NP_001193492_1	QSQTCESPNQ	DTRHR-EG	VVCETFQSDS	ISPKATISGC	HRGNSLDGSL
NP_780719_2_pro	QSQTCESPNQ	DTRQQGEG	VVSEALQSDS	ISPKATISGC	HQGNSFDGSL
Consistency	**7*****	*6*640****	**6*77****	*****	*7***7****
	..... 310 .....	..... 320 .....	..... 330 .....	..... 340 .....	..... 350
NP_115893_1_pro	SSQTSQERGP	SHSRASLVIP	PCQRSRYATY	FDVAVLRCLL	QPHWSEEGTQ
XP_003309496_1	SSQTSQERGP	SHSRASLVIP	PCQRSRYATY	FDVAVLRCLL	QPHWSEEGTQ
NP_001193492_1	SSQTSQERGP	SHSRVSLVIP	PCQRSRYATY	FDVAVLRCLL	QPHWSEEGTQ
NP_780719_2_pro	SSQTSQERGP	SHSRASLVIP	PCQRSRYATY	FDVAVLRCLL	QPHWSEEGTQ
Consistency	*****	***7*****	*****	*****	*****
	..... 360 .....	..... 370 .....	..... 380 .....	..... 390 .....	..... 400
NP_115893_1_pro	WSLMYYLQRL	RHMLEEKPEK	PPEPDIPLLP	RPRSSSMVAA	APSLVNTHKT
XP_003309496_1	WSLMYYLQRL	RHMLEEKPEK	PPEPDIPLLP	RPRSSSMVAA	APSLVNTHKT
NP_001193492_1	WSLMYYLQRL	RHMLEEKPEK	PPEPDIPLLP	RPRSSSMVAA	APSLVNTHKT
NP_780719_2_pro	WSLMYYLQRL	RHMLEEKPEK	TPDPDIPLLP	RPRSSSMVAA	APSLVNTHKT
Consistency	*****	*****	6*8*****	*****	*****
	..... 410 .....	..... 420 .....	..... 430 .....	..... 440 .....	..... 450
NP_115893_1_pro	QDLTMKCNEE	EKSLSSEAFS	KVSLTNLRRS	AVPDLSSDLG	MNIFKKFKSR
XP_003309496_1	QDLTMKCNEE	EKSLSSEAFS	KVSLTNLRRS	AVPDLSSDLG	MNIFKKFKSR
NP_001193492_1	QDLTMKCNEE	EKSLSPEAFS	KVSLTNLRRS	AIPDLSSDLG	MNIFKKFKSR
NP_780719_2_pro	QDLTMKCNEE	EKSLSPEAFS	KVSLTNLRRS	AVPDLSSDLG	MNIFKKFKSR
Consistency	*****	*****5****	*****	*9*****	*****
	..... 460 .....	..... 470 .....	..... 480 .....	..... 490 .....	..... 500
NP_115893_1_pro	KEDRERKGS	PFHHTGKRRP	RRMGVPFLLH	EDHLDVSPTR	STFSFGSFSG

XP_003309496_1	KEDRERKGS I	PFHHTGKRRP	RRMGVPFLLH	EDHLDVSPTR	STFSFGSFSG
NP_001193492_1	KEDRERKGS I	PFHHTGKRRP	RRMGVPFLLH	EDHLDVSPTR	STFSFGSFSG
NP_780719_2_pro	KEDRERKGS I	PFHHTGKRRP	RRMGVPFLLH	EDHLDVSPTR	STFSFGSFSG
Consistency	*****	*****	*****	*****	*****
	..... 510	..... 520	..... 530	..... 540	..... 550
NP_115893_1_pro	LGEDRRG I E K	GGWQTTILGK	L TRRGSSDAA	TEMESLSARH	SHSHHTLVSD
XP_003309496_1	LGEDRRG I E K	GGWQTTILGK	L TRRGSSDAA	TEMESLSARH	SHSHHTLVSD
NP_001193492_1	LGEDRRG M E K	GGWQTTILGK	F TRRGSSDAA	TEMESLSARH	SHSHHTLVSD
NP_780719_2_pro	LGEDRRG I E K	GGWQTTILGK	L TRRGSSDAA	TEMESLSARH	SHSHHTLVSD
Consistency	***** 7 *	*****	7 *****	*****	*****
	..... 560	..... 570	..... 580	..... 590	..... 600
NP_115893_1_pro	LPDP SN SHGE	NTVKEVRSQ I	STITVATFNT	TLASFNVGYA	DDF NEHMRKL
XP_003309496_1	LPDP SN SHGE	NTVKEVRSQ I	STITVATFNT	TLASFNVGYA	DDF NEHMRKL
NP_001193492_1	PPDHSN SHGE	NIVKEVRSQ I	STITVATFNT	TLASFNVGYA	DDF SEHMRKL
NP_780719_2_pro	LPDHSN SHGE	NTVKEVRSQ I	STITVATFNT	TLASFNVGYA	DDF SEHMRKL
Consistency	5 ** 4 *****	* 6 *****	*****	*****	*** 7 *****
	..... 610	..... 620	..... 630	..... 640	..... 650
NP_115893_1_pro	CNQVPIPEMP	HEPLACANLP	RSLTDSCIN Y	SYLEDTEHID	GTNNFVHKNG
XP_003309496_1	CNQVPIPEMP	HEPLACANLP	RSLTDSCIN Y	SYLEDTEHID	GTNNFVHKNG
NP_001193492_1	CNQVPIPEMP	HEPLACANLP	RSLTDSCIN Y	SYLEDTEHID	GTNNFVHKNG
NP_780719_2_pro	CSQVPIPEMP	HEPLACANLP	RSLTDSCIN Y	SYLEDTEHID	GTNNFVHKNG
Consistency	* 7 *****	*****	*****	*****	*****
	..... 660	..... 670	..... 680	..... 690	..... 700
NP_115893_1_pro	MLDLSVVLKA	VYLVLNHDIS	SRICDVALNI	VECLLQLGVV	PCVEKNRKK S
XP_003309496_1	MLDLSVVLKA	VYLVLNHDIS	SRICDVALNI	VECLLQLGVV	PCVEKNRKK S
NP_001193492_1	MLDLSVVLKA	VYLVLNHDIS	SRICDVALNI	VECLLQLGVV	PCVEKNRKK S
NP_780719_2_pro	MLDLSVVLKA	VYLVLNHDIS	SRICDVALNI	VECLLQLGVV	PCVEKNRKK S
Consistency	*****	*****	*****	*****	*****
	..... 710	..... 720	..... 730	..... 740	..... 750
NP_115893_1_pro	ENKENETLEK	RPSEGAFQFK	GVSGSSTCGF	GGPAVSGAGD	GGGEEGGGGD
XP_003309496_1	ENKENETLEK	RPSEGAFQFK	GVSGSSTCGF	GGPAVSGAGD	GGGEEGGGGD
NP_001193492_1	ENKENGTV EK	RPSEGTFQFK	GVSGSSTCGF	GGPTVSGAGD	GGGDEGGGGD
NP_780719_2_pro	ENKENESVEK	RPSEGAFQFK	GVSSSSTS GF	GAP SASGAGD	GGGEEGGGGD
Consistency	***** 6 7 7 *	***** 7 *****	*** 7 *** 6 *	* 7 * 6 7 *****	*** 8 *****
	..... 760	..... 770	..... 780	..... 790	..... 800
NP_115893_1_pro	GG--GGGGDG	GGGGGGGGGP	YEKNDKNQ EK	DESTPVS NHR	LALTMLIKIV
XP_003309496_1	GG--GGGGDG	GGGGGGGGGP	YEKNDKNQ EK	DESTPVS NHR	LALTMLIKIV
NP_001193492_1	GG--GGGGDG	GGGGGGGGGP	YEKNDKNQ DK	DESIPVS NHR	LALTMLIKIV
NP_780719_2_pro	GGGGGGGGDG	GGGGGGGGGP	YEKNEKNQ EK	DDNIPVS NHR	LALTMLIKIV
Consistency	** 0 0 *****	*****	*** * 8 *** 8 *	* 8 7 5 *****	*****
	..... 810	..... 820	..... 830	..... 840	..... 850
NP_115893_1_pro	KSLGCAYGCG	EGHRGLSGDR	LRHQVFRENA	QNCLTKLYKL	DKMQFRQTMR
XP_003309496_1	KSLGCAYGCG	EGHRGLSGDR	LRHQVFRENA	QNCLTKLYKL	DKMQFRQTMR
NP_001193492_1	KSLGCAYGCG	EGHRGLSGDR	LRHQVFRENA	QNCLTKLYKL	DKMQFRQTMR
NP_780719_2_pro	KSLGCAYGCG	EGHRGLSGDR	LRHQVFRENA	QNCLTKLYKL	DKIQFRQTMR
Consistency	*****	*****	*****	*****	** 7 *****
	..... 860	..... 870	..... 880	..... 890	..... 900
NP_115893_1_pro	DYVNKDSLNN	VVDFLHALLG	FCMEPVTDNK	AGFGNNFTTV	DNKSTAQNVE
XP_003309496_1	DYVNKDSLNN	VVDFLHALLG	FCMEPVTDNK	AGFGNNFTTV	DNKSTAQNVE
NP_001193492_1	DYVNKDSLNN	VVDFLHALLG	FCMEPVTDNK	AGFGNNFTTV	DNKSTAQNVE
NP_780719_2_pro	DYVNKDSLNN	VVDFLHALLG	FCMEPVTDNK	AGFGNNFTTV	DNKSTAQNVE
Consistency	*****	*****	*****	*****	*****
	..... 910	..... 920	..... 930	..... 940	..... 950
NP_115893_1_pro	GIIVSAMFKS	LITRCASTTH	ELHSPENLGL	YCDIRQLVQF	IKEAHGNVFR
XP_003309496_1	GIIVSAMFKS	LITRCASTTH	ELHSPENLGL	YCDIRQLVQF	IKEAHGNVFR
NP_001193492_1	GIVVSAMFKS	LITRCASTTH	ELHSPENLGL	YCDIRQLVQF	IKEANGNVFR
NP_780719_2_pro	GIIVGAMFKS	LITRCASTTH	ELHSPENLGL	YCDIRQLVQF	IKEAHGNVFR
Consistency	** 9 * 7 *****	*****	*****	*****	*** * 7 *****
	..... 960	..... 970	..... 980	..... 990	..... 1000
NP_115893_1_pro	RVALSALLDS	AEKLAPGKKV	EENEQESKPA	GSKRSEAGSI	VDKGQVSSAP
XP_003309496_1	RVALSALLDS	AEKLAPGKKV	EENEQESKPA	GSKRSEAGSI	VDKGQVSSAP
NP_001193492_1	RVALSALLDS	AEKLAPGKKV	EENEPESKPG	RGKRSEAGSV	VDKGPVTAAP
NP_780719_2_pro	RVALSALLDS	AEKLAPGKKV	EENGQESKPV	GSKRSEAGSI	ADKGQVSSAP
Consistency	*****	*****	*** 6 6 *** * 5	6 7 ***** 9	7 *** 6 * 7 8 *

	..... 1010..... 1020..... 1030..... 1040..... 1050
NP_115893_1_pro	EECRSFMSGR PSQTPEHDEQ MQGANLGRKD FWRKMFKSQS AASDTSSQSE
XP_003309496_1	EECRSFMSGR PSQTPEHDEQ MQGANLGRKD FWRKMFKSQS AASDTSSQSE
NP_001193492_1	EECRSFMSGR PSQTPEHDEQ MQGGNLGRKD FWRKMFKSQS AASDTSSQSE
NP_780719_2_pro	EECRSFMSGR PSQTPEHDEP MQGGNLGRKD FWRKMFKSQS AASDTSSQSE
Consistency	***** 6 ***6*****
	..... 1060..... 1070..... 1080..... 1090..... 1100
NP_115893_1_pro	QDTSECTTAH SGTTSDDRRAR SRSRRISLRK KLKLPIGKRN WLKRSSLGL
XP_003309496_1	QDTSECTTAH SGTTSDDRRAR SRSRRISLRK KLKLPIGKRN WLKRSSLGL
NP_001193492_1	QDTSECTTAH SGTTSDDRRAR SRSRRISLRK KLKLPIGKRN WLKRSSLGL
NP_780719_2_pro	QDTSECTTAH SGNTSDDRRAR SRSRRISLRK KLKLPI--GN WLKRSSLGL
Consistency	***** **7***** *****556* *****
	..... 1110..... 1120..... 1130..... 1140..... 1150
NP_115893_1_pro	ADGVEDLLDI SSVDRLSFIR QSSKVKFTSA VKLSEGGPGS GMENGRDEEE
XP_003309496_1	ADGVEDLLDI SSVDRLSFIR QSSKVKFTSA VKLSEGGPGS GMENGRDEEE
NP_001193492_1	ADGVEDLLDI SSVDRLSFIR QSSKVKFTSA VKLSEGGPGS GIENGRDEEE
NP_780719_2_pro	ADGVEDLLDI SSVDRLSFIR QSSKVKFTSA VKLSEGGPGS GMENGREEEE
Consistency	***** ***** ***** *****7*****8***
	..... 1160..... 1170..... 1180..... 1190..... 1200
NP_115893_1_pro	NFFKRLGCHS FDDHLSNPD GSKSKNVVNL GAIRQGMKRF QFLLNCCEPG
XP_003309496_1	NFFKRLGCHS FDDHLSNPD GSKSKNVVNL GAIRQGMKRF QFLLNCCEPG
NP_001193492_1	NFFKRLGCHS FDDHLSNPD GSKSKNVVNL GAIRQGMKRF QFLLNCCEPG
NP_780719_2_pro	NFFKRLGCHS FDDHLSNPD GSKSKNVVNL GAIRQGMKRF QFLLNCCEPG
Consistency	***** *****66*** ***** *****
	..... 1210..... 1220..... 1230..... 1240..... 1250
NP_115893_1_pro	TIPDASILAA ALDLEAPVVA RAALFLECAR FVHRCNRGNW PEWMKGHHVN
XP_003309496_1	TIPDASILAA ALDLEAPVVA RAALFLECAR FVHRCNRGNW PEWMKGHHVN
NP_001193492_1	TIPDASILAA ALDLEAPVVA RAALFLECAR FVHRCNRGNW PEWMKGHHVN
NP_780719_2_pro	TIPDASILAA ALDLEAPVVA RAALFLECAR FVHRCNRGNW PEWMKGHHVN
Consistency	***** ***** ***** ***** *****
	..... 1260..... 1270..... 1280..... 1290..... 1300
NP_115893_1_pro	ITKKGLSRGR SPIVGNKRNQ KLQWNAAKLF YQWGDAIGVR LNELCHGESE
XP_003309496_1	ITKKGLSRGR SPIVGNKRNQ KLQWNAAKLF YQWGDAIGVR LNELCHGESE
NP_001193492_1	ITKKGLSRGR SPIVGNKRNQ KLQWNAAKLF YQWGDAIGVR LNELCHGESE
NP_780719_2_pro	ITKKGLSRGR SPTVGNKRNQ KLQWSAAKLF YQWGDAIGIR LNELCHGESE
Consistency	***** **6***** *****7*****9* *****
	..... 1310..... 1320..... 1330..... 1340..... 1350
NP_115893_1_pro	SPANLLGLIY DEETKRRLRK EDEEEDFLDD STVNPSKCGC PFALKMAACQ
XP_003309496_1	SPANLLGLIY DEETKRRLRK EDEEEDFLDD STVNPSKCGC PFALKMAACQ
NP_001193492_1	SPANLLGLIY DEETKRRLRK EDEEEDFLDD STVNPSKCGC PFALKMAACQ
NP_780719_2_pro	SPANLLGLIY DEETKRRLRK EDEEEDFLDD STVNPSKCGC PFALKMAACQ
Consistency	*****8** ***** ***** ***** *****
	..... 1360..... 1370..... 1380..... 1390..... 1400
NP_115893_1_pro	LLLEITTFLR ETFSCLPRPR TEPLVDLESC RLRLDPELDR HRYERKISFA
XP_003309496_1	LLLEITTFLR ETFSCLPRPR TEPLVDLESC RLRLDPELDR HRYERKISFA
NP_001193492_1	LLLEITTFLR ETFSCLPRPR TEPLMDLESC RLRLDPELDR HRYERKISFA
NP_780719_2_pro	LLLEITTFLR ETFSCLPRPR TEPLVDLESC RLRLDPELDR HRYERKISFA
Consistency	***** ***** *****7***** ***** *****
	..... 1410..... 1420..... 1430..... 1440..... 1450
NP_115893_1_pro	GVLDENEDSK DSLHSSSHTL KSDAGVE--- ---
XP_003309496_1	GVLDENEDSK DSLHSSSHTL KSDAGVE--- ---
NP_001193492_1	GVLDENEDSK DSLHSSSHTL KSDAGVE--- ---
NP_780719_2_pro	GVLDENEDSK DSLHSSSHTI KSDAGAEKK VPSRKIRIGG SRLLOIKGTR
Consistency	***** *****8 *****7*000 0000000000 0000000000
	..... 1460..... 1470..... 1480..... 1490..... 1500
NP_115893_1_pro	----- EKKEG-----
XP_003309496_1	----- EKKEG-----
NP_001193492_1	----- EKKE-----G
NP_780719_2_pro	SFQVKKGGSLS SSIRRVGSLK SSKLSRQDSE SEAEELQLSQ SRDVTVDLEG
Consistency	0000000000 0000000000 0000000000 0*67*10000 0000000001
	..... 1510..... 1520..... 1530..... 1540..... 1550
NP_115893_1_pro	SPWSASEPSI EPEGMSNAGA EENYHRNMSW LHMILLCNQ QSFICTHVDY
XP_003309496_1	SPWSASEPSI EPEGMSNAGA EENYHRNMSW LHMILLCNQ QSFICTHVDY
NP_001193492_1	SPWSASEPSI EPEGMSTAGV EENYHRNMSW LHMILLCNQ QSFICTHIDY
NP_780719_2_pro	SPWSASEPSI EPEGLSNAGT EENYHRNMSW LHMILLCNQ QSFICTHVDY

Consistency	*****	****8*7**5	*****	*****	*****9**
	..... 1560..... 1570..... 1580..... 1590..... 1600				
NP_115893_1_pro	CHPHCYLHHS	RSCARLVRAI	KLLYGDSVDS	LRESSNISSV	ALRGKKQKEC
XP_003309496_1	CHPHCYLHHS	RSCARLVRAI	KLLYGDSVDS	LRESSNISSV	ALRGKKQKEC
NP_001193492_1	CHPHCYLHHS	RSCARLVRAI	KLLYGDTVDS	LRESNSISNV	ALRGKKQKEC
NP_780719_2_pro	CHPHCYLHHS	RSCARLVRAI	KLLYGDSVDS	LRESNHISNV	ALRGKKQKEC
Consistency	*****	*****	*****7**	****75**7*	*****
	..... 1610..... 1620..... 1630..... 1640..... 1650				
NP_115893_1_pro	SDKSCLRTPS	LKKRVSDANL	EGKKDSGMLK	YIRLQVMSLS	PAPLSLLIKA
XP_003309496_1	SDKSCLRTPS	LKKRVSDANL	EGKKDSGMLK	YIRLQVMSLS	PAPLSLLIKA
NP_001193492_1	SDKSCLRTPS	LKKRVSDANL	EGKKDSGMLK	YIRLQVMSLS	PAPLSLLIKA
NP_780719_2_pro	SDKSCLRTPS	LKKRVSDVNL	EGKKDSGMLK	YIRFQVMSLS	PAPLSLLIKA
Consistency	*****	*****7**	*****	***7*****	*****
	..... 1660..... 1670..... 1680..... 1690..... 1700				
NP_115893_1_pro	APILTEEMYG	DIQPAAWELL	LSMDEHMAGA	AAAMFLLCAV	KVPEAVSDML
XP_003309496_1	APILTEEMYG	DIQPAAWELL	LSMDEHMAGA	AAAMFLLCAV	KVPEAVSDML
NP_001193492_1	APILTEEMYG	DIQPAAWELL	LSMDEHMAGA	AAAMFLLCAV	KVPEAVSDML
NP_780719_2_pro	APILTEEMYG	DIQPAAWELL	LSMDEHMAGA	AAAMFLLCAV	KVPDAVSDML
Consistency	*****	*****	*****	*****	***8*****
	..... 1710..... 1720..... 1730..... 1740..... 1750				
NP_115893_1_pro	MSEFHHPETV	QRLNAVLKFH	TLWRFRYQVW	PRMEEGAQQI	FKIPPPSINF
XP_003309496_1	MSEFHHPETV	QRLNAVLKFH	TLWRFRYQVW	PRMEEGAQQI	FKIPPPSINF
NP_001193492_1	TSEFHHPETV	QRLNAVLKFH	TLWRFRYQVW	PRMEEGAQQI	FKIPPPSINF
NP_780719_2_pro	MSEFHHAETV	QRLNAVLKFH	TLWRFRYQVW	PRMEEGAQQI	FKIPPPSINF
Consistency	6*****6***	*****	*****	*****	*****
	..... 1760..... 1770..... 1780..... 1790..... 1800				
NP_115893_1_pro	TLPSPVLGMP	SVPMFDPPWV	PQCSGSVQDP	INEDQSKSFS	ARAVSRSHQR
XP_003309496_1	TLPSPVLGMP	SVPMFDPPWV	PQCSGSVQDP	INEDQSKSFS	ARAVSRSHQR
NP_001193492_1	TLPSPVLGMP	SVPMFDPPWV	PQCSGSVQDP	INEDQSKSFS	ARAVSRSHQR
NP_780719_2_pro	TLPSPVLGMP	SVPMFDPPWV	PQCSGSVQDP	INEDQSKSFS	ARAVSRSHQR
Consistency	*****	*****	*****	*****	*****
	..... 1810..... 1820..... 1830..... 1840..... 1850				
NP_115893_1_pro	AEHILKNLQQ	EEEKKRLGRE	ASLITAIPIT	QEACYEPTCT	PNSEPEEEVE
XP_003309496_1	AEHILKNLQQ	EEEKKRLGRE	ASLITAIPIT	QEACYEPTCT	PNSEPEEEVE
NP_001193492_1	AEHILKNLQQ	EEEKKRLGRE	ASLITAIPIT	QEACYEPTCT	PNSEPEEEVE
NP_780719_2_pro	AEHILKNLQQ	EEEKKRLGRE	ASLITAIPIT	QEACYEPTCT	PNSEPEEEEE
Consistency	*****	*****	*****	*****	*****6*
	..... 1860..... 1870..... 1880..... 1890..... 1900				
NP_115893_1_pro	EVTNLA SRRL	SVSPSCTSST	SHRNYSFRRG	SVWSVRS AVS	AEDEEHTTEH
XP_003309496_1	EVTNLA SRRL	SVSPSCTSST	SHRNYSFRRG	SVWSVRS AVS	AEDEEHTTEH
NP_001193492_1	EVTNLA SRRL	SVSPSCTSST	SHRNYSFRRG	SVWSVRS AVS	AEDEEHTTEH
NP_780719_2_pro	VA-NLTSRRL	SVSPSCTSST	SHRNYSFRRG	SVWSVRS AVS	AEDEEHATEH
Consistency	675**7****	*****	*****	*****	*****7***
	..... 1910..... 1920..... 1930..... 1940..... 1950				
NP_115893_1_pro	TPNHHVPQPP	QAVFPACICA	AVLPIVHLME	DGEVREDGVA	VSAVAQQVLW
XP_003309496_1	TPNHHVPQPP	QAVFPACICA	AVLPIVHLME	DGEVREDGVA	VSAVAQQVLW
NP_001193492_1	TPNHHVPQPP	QAVFPACICA	AVLPIVHLME	DGEVREDGVA	VSAVAQQVLW
NP_780719_2_pro	TPNHHVPQPP	QAVFPACICA	AVLPIVHLME	DGEVREDGVA	VSAVAQQVLW
Consistency	*****	*****	*****	*****	*****
	..... 1960..... 1970..... 1980..... 1990..... 2000				
NP_115893_1_pro	NCLIEDPSTV	LRHFLEKLT I	SNRQDELMYM	LRKLLLNIGD	FPAQTSHILF
XP_003309496_1	NCLIEDPSTV	LRHFLEKLT I	SNRQDELMYM	LRKLLLNIGD	FPAQTSHILF
NP_001193492_1	NCLIEDPSTV	LRHFLEKLT I	SNRQDELMYM	LRKLLLNIGD	FPAQTSHILF
NP_780719_2_pro	NCLIEDPSTV	LRHFLEKLT I	SNRQDELMYM	LRKLLLNIGD	FPAQTSHILF
Consistency	*****	*****	*****	*****	*****
	..... 2010..... 2020..... 2030..... 2040..... 2050				
NP_115893_1_pro	NYLVGLIMYF	VRTPCEWGMD	AISATLTFLW	EVVG YVEGLF	FKDLKQTMKK
XP_003309496_1	NYLVGLIMYF	VRTPCEWGMD	AISATLTFLW	EVVG YVEGLF	FKDLKQTMKK
NP_001193492_1	NYLVGLIMYF	VRTPCEWGMD	AISATLTFLW	EVVG YVEGLF	FKDLKQTMKK
NP_780719_2_pro	NYLVGLIMYF	VRTPCEWGMD	AISATLTFLW	EVVG YVEGLF	FKDLKQTMKK
Consistency	*****	*****	*****	*****	*****
	..... 2060..... 2070..... 2080..... 2090..... 2100				
NP_115893_1_pro	EQCEVKLLVT	ASMPGTKTLV	VHGQNECDIP	TQLPVHEDTQ	FEALLKECLE
XP_003309496_1	EQCEVKLLVT	ASMPGTKTLV	VHGQNECDIP	TQLPVHEDTQ	FEALLKECLE



NP_001193492_1	EQCEVKLLVT	ASMPGTKTLV	VHGQNECDIP	TQLPVHEDTQ	FEALLKECLE
NP_780719_2_pro	EQCEVKLLVT	ASMPGTKTLV	VHGQNECDIP	TQLPVHEDTQ	FEALLKECLE
Consistency	*****	*****	*****	*****	*****
..... 2110..... 2120..... 2130..... 2140..... 2150					
NP_115893_1_pro	FFNIPESQST	HYFLMDKRWN	LIHYNKTYVR	DIYPFRRSVS	PQLNLVHMHP
XP_003309496_1	FFNIPESQST	HYFLMDKRWN	LIHYNKTYVR	DIYPFRRSVS	PQLNLVHMHP
NP_001193492_1	FFNIPESQST	HYFLMDKRWN	LIHYNKTYVR	DIYPFRRSVS	PQLNLVHMHP
NP_780719_2_pro	FFNIPESQST	HYFLMDKRWN	LIHYNKTYVR	DIYPFRRSVS	PQLNLVHMHP
Consistency	*****	*****	*****	*****	*****
..... 2160..... 2170..... 2180..... 2190..... 2200					
NP_115893_1_pro	EKGQELIQKQ	VFTRKLEEVG	RVLFLISLTQ	KIPTAHKQSH	VSMLQEDLLR
XP_003309496_1	EKGQELIQKQ	VFTRKLEEVG	RVLFLISLTQ	KIPTAHKQSH	VSMLQEDLLR
NP_001193492_1	EKGQELIQKQ	VFTRKLEEVG	RVLFLISLTQ	KIPTAHKQSH	VSMLQEDLLR
NP_780719_2_pro	EKGQELIQKQ	VFTRKLEEVG	RVLFLISLTQ	KIPTAHKQSH	VSMLQEDLLR
Consistency	*****	*****	*****	*****	*****
..... 2210..... 2220..... 2230..... 2240..... 2250					
NP_115893_1_pro	LPSFPRSAID	AEFSLFSDPQ	AGKELFGLDT	LQKSLWIQLL	EEMFLGMPSE
XP_003309496_1	LPSFPRSAID	AEFSLFSDPQ	AGKELFGLDT	LQKSLWIQLL	EEMFLGMPSE
NP_001193492_1	LPSFPRSAID	AEFSLFSDPQ	AGKELFGLDT	LQKSLWIQLL	EEMFLGMPSE
NP_780719_2_pro	LPSFPRSAID	AEFSLFSDPQ	AGKELFGLDT	LQKSLWIQLL	EEMFLGMPSE
Consistency	*****	*****	*****	*****	*****
..... 2260..... 2270..... 2280..... 2290..... 2300					
NP_115893_1_pro	FPWGDEIMLF	LNVFNGALIL	HPEDSALLRQ	YAATVINTAV	HFNHLFSLSG
XP_003309496_1	FPWGDEIMLF	LNVFNGALIL	HPEDSALLRQ	YAATVINTAV	HFNHLFSLSG
NP_001193492_1	FPWGDEIMLF	LNVFNGALIL	HPEDSALLRQ	YAATVINSAV	HFNHLFSLSG
NP_780719_2_pro	FPWGDEIMLF	LNVFNGALIL	HPEDSALLRQ	YAATVINTAV	HFNHLFSLSG
Consistency	*****	*****	*****	*****7**	*****
..... 2310..... 2320..... 2330..... 2340..... 2350					
NP_115893_1_pro	YQWILPTMLQ	VYSDYESNPQ	LRQAIEFACH	QFYILHRKPF	VLQLFASVAP
XP_003309496_1	YQWILPTMLQ	VYSDYESNPQ	LRQAIEFACH	QFYILHRKPF	VLQLFASVAP
NP_001193492_1	YQWILPTMLQ	VYSDYESNPQ	LRQAIEFACH	QFYILHRKPF	VLQLFASVAP
NP_780719_2_pro	YQWILPTMLQ	VYSDYESNPQ	LRRAIEFACH	QFYILHRKPF	VLQLFASVAP
Consistency	*****	*****	**7*****	*****	*****
..... 2360..... 2370..... 2380..... 2390..... 2400					
NP_115893_1_pro	LLEFPDAANN	GPSKGVSAQC	LFDLLQSLEG	ETTDILDILE	LVKAEKPLKS
XP_003309496_1	LLEFPDAANN	GPSKGVSAQC	LFDLLQSLEG	ETTDILDILE	LVKAEKPLKS
NP_001193492_1	LLEFPDAANT	GSSKGVSAQC	LFDLLQSLEG	ETTDILDILE	LVKAEKPLKS
NP_780719_2_pro	LLEFPDAANT	GSSKGVSAQC	LFDLLQSLEG	ETTDILDILE	LVKAEKPLKS
Consistency	*****6	*5*****	*****	*****	*****
..... 2410..... 2420..... 2430..... 2440..... 2450					
NP_115893_1_pro	LDFCYGNEDL	TFSISEAIKL	CVTVVAYAPE	SFRSLQMLMV	LEALVPCYLQ
XP_003309496_1	LDFCYGNEDL	TFSISEAIKL	CVTVVAYAPE	SFRSLQMLMV	LEALVPCYLQ
NP_001193492_1	LDFCYGNEDL	TFSISEAIKL	CVTVVAYAPE	SFRSLQMLMV	LEALVPCYLQ
NP_780719_2_pro	LDFCYGNEDL	TFSISEAIKL	CVTVVAYAPE	SFRSLQMLMV	LEALVPCYLQ
Consistency	*****	*****	*****	*****	*****
..... 2460..... 2470..... 2480..... 2490..... 2500					
NP_115893_1_pro	KLKRQTSQVE	TVPAAREEIA	ATAALATSLO	ALLYSVEVLT	RPMTAPQMSR
XP_003309496_1	KLKRQTSQVE	TVPAAREEIA	ATAALATSLO	ALLYSVEVLT	RPMTAPQMSR
NP_001193492_1	KLKRQTSQVE	TVPAAREEIA	AMAALATSLO	ALLYSVEVLT	RPMTAPQMSR
NP_780719_2_pro	KMKRQTSQVE	TVPAAREEIA	ATAALATSLO	ALLYSVEVLT	RPMTAPQMSR
Consistency	*8*****	*****	*6*****	*****	*****
..... 2510..... 2520..... 2530..... 2540..... 2550					
NP_115893_1_pro	CDQGHKGTTT	ANHTMSSGVN	TRYQEQGAKL	HFIRENLHLL	EEGQGIPREE
XP_003309496_1	CDQGHKGTTT	ANHTMSSGVN	TRYQEQGAKL	HFIRENLHLL	EEGQGIPREE
NP_001193492_1	CDQGHKGATT	ANHTMSSGVN	TRYQEQGTKL	HFIRENLHLL	EEGQGLPREE
NP_780719_2_pro	SDQGHKGTTT	ANHTMSSGVN	TRYPEQGAKL	HFIRENLHLL	EEGQGLPREE
Consistency	6*****7**	*****	***6***7**	*****	*****8****
..... 2560..... 2570..... 2580..... 2590..... 2600					
NP_115893_1_pro	LDERIAREEF	RRPRESLLNI	CTEFYKHCGP	RLKILQNLAG	EPRVIALELL
XP_003309496_1	LDERIAREEF	RRPRESLLNI	CTEFYKHCGP	RLKILQNLAG	EPRVTALELL
NP_001193492_1	LDERIAREEF	RRPRESLLNI	CTEFYKHCGP	RLKILQNLAG	EPRVTALELL
NP_780719_2_pro	LDERISREEF	RRPRESLLNI	CTEFYKHCGP	RLKILQNLAG	EPRVTALELL
Consistency	*****8****	*****	*****	*****	*****6*****
..... 2610..... 2620..... 2630..... 2640..... 2650					

NP_115893_1_pro	DVKSHMRLAE	IAHSLLKLAP	YDTQTMESRG	LRRYIMEMPL	ITDWT	TAEAVR
XP_003309496_1	DVKSHMRLAE	IAHSLLKLAP	YDTQTMESRG	LRRYIMEMPL	ITDWT	TAEAVR
NP_001193492_1	DVKSHMRLAE	IAHSLLKLAP	YDTQTMESRG	LRRYIMEMPL	ITDWS	AEAVR
NP_780719_2_pro	DVKSHMRLAE	IAHSLLKLAP	YDTQTMESRG	LRRYIMEMPL	ITDWS	AEAVR
Consistency	*****	*****	*****	*****	****7	*****
..... 2660..... 2670..... 2680..... 2690..... 2700						
NP_115893_1_pro	PALILILKRL	DRMFNKIHKM	PTLRRQVEWE	PAS	N	LIIEGVC
XP_003309496_1	PALILILKRL	DRMFNKIHKM	PTLRRQVEWE	PAS	N	LIIEGVC
NP_001193492_1	PALILILKRL	DRMFNKIHKM	PTLRRQVEWE	PAS	N	LIIEGVC
NP_780719_2_pro	PALILILKRL	DRMFNKIHKM	PTLRRQVEWE	PAS	S	LIIEGVC
Consistency	*****	*****	*****	***7	*****	*****
..... 2710..... 2720..... 2730..... 2740..... 2750						
NP_115893_1_pro	FLPHLRSLIN	VCVNLMGVV	GPSSVADGLP	LLHLSPYLS	P	LPFSTAVVR
XP_003309496_1	FLPHLRSLIN	VCVNLMGVV	GPSSVADGLP	LLHLSPYLS	P	LPFSTAVVR
NP_001193492_1	FLPHLRSLIN	VCVNLMGVV	GPSSVADGLP	LLHLSPYLS	P	LPFSTAVVR
NP_780719_2_pro	FLPHLRSLIN	VCVNLMGVV	GPSSVADGLP	LLHLSPYLS	P	LPFSTAVVR
Consistency	*****	*****	*****	*****	*****	*****
..... 2760..... 2770..... 2780..... 2790..... 2800						
NP_115893_1_pro	LVALQIQALK	EDFPLSHVIS	PFTNQERREG	MLNLNLLIPFV	L	TVGSGSKDS
XP_003309496_1	LVALQIQALK	EDFPLSHVIS	PFTNQERREG	MLNLNLLIPFV	L	TVGSGSKDS
NP_001193492_1	LVALQIQALK	EDFPLSHVIS	PFTNQERREG	MLNLNLLIPFV	L	TVGSGSKDS
NP_780719_2_pro	LVALQIQALK	EDFPLSHVIS	PFTNQERREG	MLNLNLLIPFV	L	TVGSGSKDS
Consistency	*****	*****	*****	*****	*****	*****
..... 2810..... 2820..... 2830..... 2840..... 2850						
NP_115893_1_pro	PWLEQPEVQL	LLQTVINVLL	PPRIISTSR	KNFMLESSPA	H	CSTPGDAGK
XP_003309496_1	PWLEQPEVQL	LLQTVINVLL	PPRIISTSR	KNFMLESSPA	H	CSTPGDAGK
NP_001193492_1	PWLEQPEVQL	LLQTVINVLL	PPRIISTSR	KNFMLESSPA	H	CSTPGDASK
NP_780719_2_pro	PWLEQPEVQL	LLQTVINVLL	PPRIISTSR	KNFMLESSPA	H	CSTPGDAGK
Consistency	*****	*****	*****	*****	*****	***7*
..... 2860..... 2870..... 2880..... 2890..... 2900						
NP_115893_1_pro	DLRREGLAES	TSQAAYLALK	VILVCFERQL	GSQWYWLSLQ	V	KEMALRKVG
XP_003309496_1	DLRREGLAES	TSQAAYLALK	VILVCFERQL	GSQWYWLSLQ	V	KEMALRKVG
NP_001193492_1	DLRKEGLAES	TSQAAYLALK	VILVCFERQL	GSQWYWLSLQ	V	KEMALRKVG
NP_780719_2_pro	DLRKEGLAES	TSQAAYLALK	VILVCFERQL	GSQWYWLSLQ	V	KEMALRKVG
Consistency	***7	*****	*****	*****	*****	*****
..... 2910..... 2920..... 2930..... 2940..... 2950						
NP_115893_1_pro	GLALWDFLDF	IVRTRIPFV	LLRPFIQCKL	LAQPAENHEE	L	SARQHIADQ
XP_003309496_1	GLALWDFLDF	IVRTRIPFV	LLRPFIQCKL	LAQPAENHEE	L	SARQHIADQ
NP_001193492_1	GLALWDFLDF	IVRTRIPFV	LLRPFIQCKL	LAQPAENHEE	L	SARQHIADQ
NP_780719_2_pro	GLALWDFLDF	IVRTRIPFV	LLRPFIQCKL	LAQPAENHEE	L	SARQHISDQ
Consistency	*****	*****	*****	*****	*****	***8**
..... 2960..... 2970..... 2980..... 2990..... 3000						
NP_115893_1_pro	LERRFIPRPL	CKSSLIAEFN	SELKILKEAV	HSGSAYQGKT	S	ISTVGTSTS
XP_003309496_1	LERRFIPRPL	CKSSLIAEFN	SELKILKEAV	HSGSAYQGKT	S	ISTVGTSTS
NP_001193492_1	LERRFIPRPL	CKSSLIAEFN	SELKILKEAV	HSGSAYQGKT	S	ISTVGTSTS
NP_780719_2_pro	LERRFIPRPL	CKSSLIAEFN	SELKILKEAV	HSGSAYQGKT	S	ISTVGTSTS
Consistency	*****	*****	*****	*****	*****	*****
..... 3010..... 3020..... 3030..... 3040..... 3050						
NP_115893_1_pro	AYRLSLATMS	RSNTGTGTW	EQDSEPSQQA	SQDTLSRTDE	E	DEENDSISM
XP_003309496_1	AYRLSLATMS	RSNTGTGTW	EQDSEPSQQA	SQDTLSRTDE	E	DEENDSISM
NP_001193492_1	AYRLSLATMS	RSNTGTGTW	EQDSEPSQQA	SQDTLSRTDE	E	DEENDSVSM
NP_780719_2_pro	AYRLSLATMS	RSNTGTGTW	EQDSEPSQQA	SQDTLSRTDE	E	DEENDSVSM
Consistency	*****	*****	*****	*****	*****	***9**
..... 3060..... 3070..... 3080..... 3090..... 3100						
NP_115893_1_pro	PSVVSEQEAY	LLSA	IGRRRF	SSHVSSMSVP	QAEVGMLPSQ	SEPNVLDDSQ
XP_003309496_1	PSVVSEQEAY	LLSA	IGRRRF	SSHVSSMSAP	QAEVGMLPSQ	SEPNVLDDSQ
NP_001193492_1	PSVVSEQEAY	LLST	IGRRRF	SSHVSSMSAP	QAEVGMLPSQ	SEPNVLDDSQ
NP_780719_2_pro	PSVVSEQEAC	LLST	IGRRRF	SSHVSSMSAP	QAEVGMLPSQ	SEPNVLDDSQ
Consistency	*****5	***6	*****	*****7*	*****	*****
..... 3110..... 3120..... 3130..... 3140..... 3150						
NP_115893_1_pro	GLAAEGSLSR	VASI	QSEPGQ	QNLLV	QQPLG	RKRGLRQLRR
XP_003309496_1	GLAAEGSLSR	VASI	QSEPGQ	QNLLV	QQPLG	RKRGLRQLRR
NP_001193492_1	GLAAEGSLSR	VASV	QSEPGQ	QNLLI	QQPLG	RKRGLRQLRR
NP_780719_2_pro	GLAAEGSLSR	VASI	QSEPGQ	QNVLL	QQPLG	RKRGLRQLRR
Consistency	*****	***9	*****	**8*7	*****	*****

	..... 3160..... 3170..... 3180..... 3190..... 3200
NP_115893_1_pro	EPRNRQGARLSTTRRSIQPKTKPSADQKRSVTFIEAQPEPAAAPTDALPA
XP_003309496_1	EPRNRQGARLSTTRRSIQPKTKPSADQKRSVTFIEAQPEPAAAPTDALPA
NP_001193492_1	EPRNRHGARLSTTRRSIQPKTKPSADQKRSVTFIEAQPEPAGAPTDTLA
NP_780719_2_pro	EPRNRHGARLSTTRRSIQPKTKPSVDQKRSVTFIEAQPEPTAAPTDIFPA
Consistency	*****5**********7*****77*****575*

	..... 3210..... 3220..... 3230..... 3240..... 3250
NP_115893_1_pro	TGQLQGCSPA PSRKPEAMDE PVLTSSPAIV VADLHSVSPK QSENFPTTEEG
XP_003309496_1	TGQLQGCSPA PSRKPEAMDE PVLTSSPAIV VADLHSVSPK QSENFPTTEEG
NP_001193492_1	TGQPQGCSPA PSRKPEGMDK PVLTSSPAIV VADLHSLSPK QGENFLAEEG
NP_780719_2_pro	TGQPQSCSPG RARKPEGTEK PVLTSSPAII IADLHSLSPK QSEPLLAEEG
Consistency	***4*7***768*****6687*****99*****7****7*5746***

	..... 3260..... 3270..... 3280..... 3290..... 3300
NP_115893_1_pro	EKEEDTEAQQ ATAHSPLSAQ LSDPDDFTGL ETSSLLQHGD TVLHISEENG
XP_003309496_1	EKEEDTEAQQ ATAHSPNSTQ LSDPDDFTGL ETSSLLQHGD TVLHISEENG
NP_001193492_1	ERKEDTEVQG ATAHSPNSTQ LSDPDDFTGL ETSILLQHGD TVLHISEENG
NP_780719_2_pro	EKKEDDEIQG ATAHCPNSTQ LSDPDDFTGL ETSSLLQHGD TVLHISEENG
Consistency	*87**6*6*******6***7******6*****

	..... 3310..... 3320.....
NP_115893_1_pro	MENPLLS SQF TFTPTELGKT DAVLDESHV
XP_003309496_1	MENPLLS SQF TFTPTELGKT DAVLDESHV
NP_001193492_1	MENPLLASQF PFTPTEGET DVDLDESHV
NP_780719_2_pro	TENPLLS SQF TFTPPELGDT DSALDESHV
Consistency	6*****8***6***6*6*5* *54*****