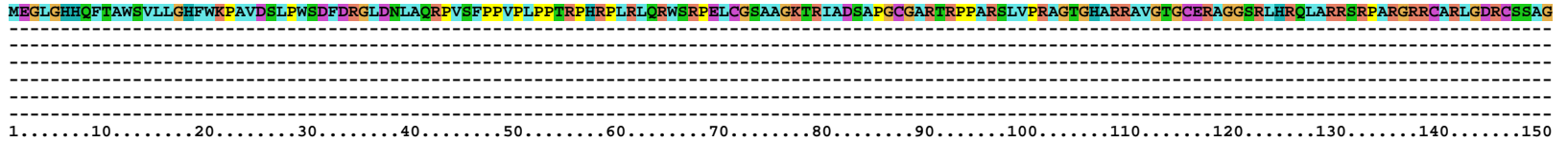
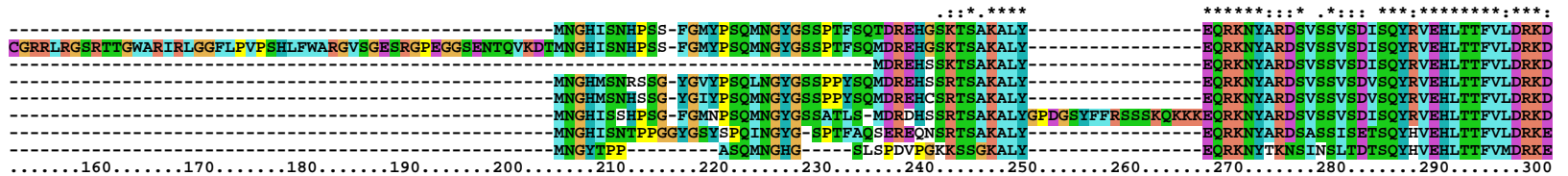


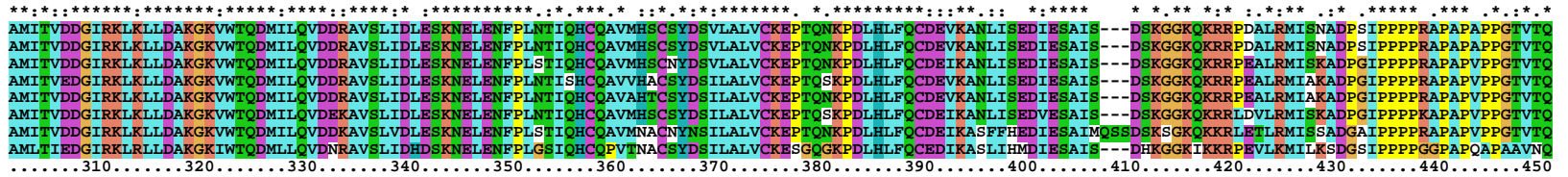
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gi | 114643723 | ref | XP\_528750.2 |  
gi | 73997126 | ref | XP\_534881.2 |  
gi | 75677397 | ref | NP\_031971.2 |  
gi | 109472736 | ref | XP\_232499.4 |  
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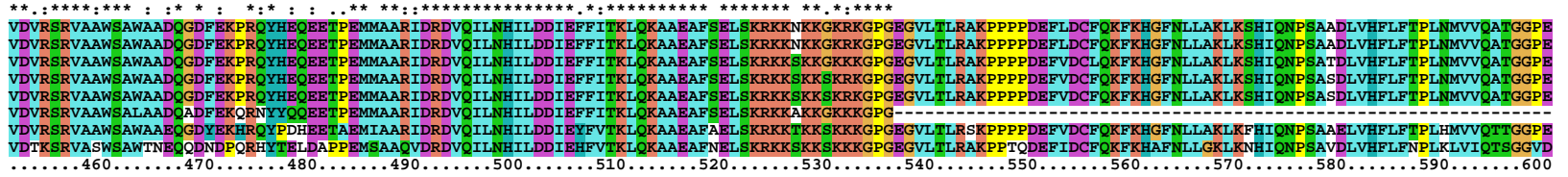
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gi | 73997126 | ref | XP\_534881.2 |  
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gi | 109472736 | ref | XP\_232499.4 |  
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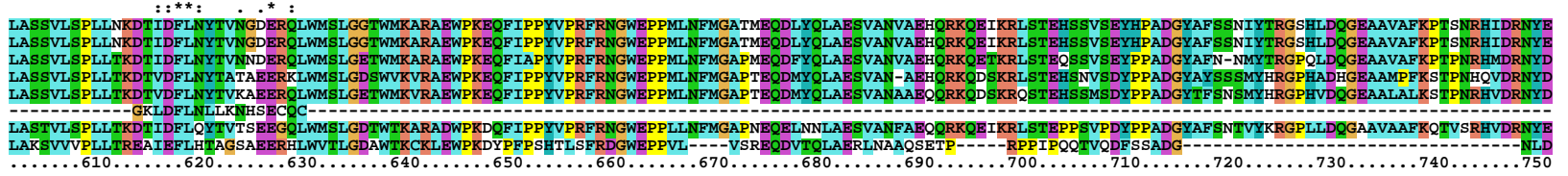
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gi | 114643723 | ref | XP\_528750.2 |  
gi | 73997126 | ref | XP\_534881.2 |  
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gi | 109472736 | ref | XP\_232499.4 |  
gi | 115497926 | ref | NP\_001069570.1 |  
gi | 118083068 | ref | XP\_416405.2 |  
gi | 41053845 | ref | NP\_956536.1 |



gi	56682953	ref	NP_004438.3	PI-KTQPKKYAKSKYDFVARNNS	ELSVLKDDILEILDDRQWVKVRNASGDSGFVPNNILDIVRPPESGLGRADPPYTHTIQKORMEYGPR-PAD-TPPAPSPPTPAPVP-----VFLPPSTPA--PVPVSKVPANITRON	658
gi	114643723	ref	XP_528750.2	PI-KTQPKKYAKSKYDFVARNNS	ELSVLKDDILEILDDRQWVKVRNASGDSGFVPNNILDIVRPPESGLGRADPPYTHTIQKORMEYGPR-PAD-TPPAPSPPTPAPVP-----VFLPPSTPA--PVPVSKVPANITRON	861
gi	73997126	ref	XP_534881.2	PI-KGQPKKYAKSKYDFVARNNS	ELSVLKDDILEILDDRQWVKVRNASGDSGFVPNNILDIVRPPESGLGRADPPYTHTIQKORMEYGPR-PTD-TPSAPSPPTPAPVP-----VFLPPSTPA--PVSVPKVPANVTRON	627
gi	75677397	ref	NP_031971.2	AV-KTQPKKYAKSKYDFVARNS	SELSVMKDDVLEILDDRQWVKVRNASGDSGFVPNNILDIMRTPESGVGRADPPYTHTIQKORTEYGLR-SAD-TPSAPSPPTPAPVP-----VFLPPSVPA--PVSVPKVPANVTRON	657
gi	109472736	ref	XP_232499.4	PV-KTQPKKYAKSKYDFVARNS	SELSVMKDDVLEILDDRQWVKVRNASGDSGFVPNNILDMRTPESGVGRADPPYTHTIQKORTEYGLR-SAD-TPSAPSPPTPAPVP-----VFLPPSAPA--PVPVSKVPANVTRON	658
gi	115497926	ref	NP_001069570.1		-----	345
gi	118083068	ref	XP_416405.2	AHNKIQSKKYAKCKYEFMARNNS	ELSVLKEEIVEILDDRQWVKVRNKSNTGFVPNNILDLRNYEGGLGLPEPVYTRAIQKQIDYVAK-QPDEVPATPSPPMPAPVPA-----AVLPPSTPAIPVFPKAPATVRRS	667
gi	41053845	ref	NP_956536.1	AHSRTAQRNFAKSKYDFVARNT	ELSVLKDEVEVLEILDDRQWVKVRNAGASGYVPNNILEISR-AVDMTGRGEPIYSHTIQKQIDYVPRPTVTEAPFTPPPPPPAPLLPTASPAHQSAAAIIPANQSIGATSPANQRAVATSPANQS	620
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gi	56682953	ref	NP_004438.3	SSSSDSGGG	-----IVRDSQRHKQLPVDRRKSQMEEVQDELIHRLTIGRSAAQKKFHVPRONVVPVINITYDSTPEDVKTWLSKGFNPVTVNSLGVNLGAQLFSLNKDELRTVCPE-GARVYSQITVOKAALEDSS	788
gi	114643723	ref	XP_528750.2	SSSSDSGGG	-----IVRDSQRHKQLPVDRRKSQMEEVQDELIHRLTIGRSAAQKKFHVPRONVVPVINITYDSTPEDVKTWLSKGFNPVTVNSLGVNLGAQLFSLNKDELRTVCPE-GARVYSQITVOKAALEDSS	988
gi	73997126	ref	XP_534881.2	SSSSDSGGG	-----IVRDNQRHKQLPVDRRKSQMEEVQDELIHRLTIGRSAAQKKFHVPRONVVPVINITYDSTPEDVKTWLSKGFNPVTVNSLGVNLGAQLFSLNKDELRTVCPE-GSRVFSQITVOKAALEDNS	757
gi	75677397	ref	NP_031971.2	SSSSDSGGG	-----IVRDSQRHKQLPVDRRKSQMEEVQDELFQRLTIGRSAAQKKFHVPRONVVPVINITYDSSPEEVKTWLSKGFNPVTVNSLGVNLGAQLFSLNKDELRTVCPE-GARVFNQITVOKAALEDNS	787
gi	109472736	ref	XP_232499.4	SSSSDSGGG	-----IARDSQRYKQLPVDRRKSQMEEVQDELFQRLTIGRSAAQKKFHVPRONVVPVINITYDSSPEEVKTWLSKGFNPVTVNSLGVNLGAQLFSLNKDELRTVCPE-GARVFSQITVOKAALEDSS	788
gi	115497926	ref	NP_001069570.1		-----	345
gi	118083068	ref	XP_416405.2	STSSDSGGG	-----VARDSQKHKQLPVDRRKSQMEEVQDELVHRLTIGRSNAQRKFHVPRNIPVVPVINITYDSSPEDVKAQLSKGFNPVTVNSLGVNLGAQLFSLNKDELRTVCPE-GSRVYSQITVOKSALEAN	797
gi	41053845	ref	NP_956536.1	AAADQANQSENSGEQDDIVSES	DSVNMREQQRERAAPARRKSNMEEVQDELMYRLTIGRSAAQKRIQTPSRSSQPALSISYDSTPQOVKDWLMLKGFSAATVSLGVNLGAQLFSLNKDELRTVCPEDDGARVFSQITVOKAALERS	770
				.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050		



gi	56682953	ref	NP_004438.3	GSSSELQEIIMRRROEKISAAAS	-DSGVESFDEGSSH	822
gi	114643723	ref	XP_528750.2	-----	VRLVNLRWCFSAN-----	1001
gi	73997126	ref	XP_534881.2	GSSSELQEIIMRRROEKISAAAS	-DSGVESFDEGSSH	791
gi	75677397	ref	NP_031971.2	GSSSELQEIIMRRROEKISAAAS	-DSGVESFDEGSSH	821
gi	109472736	ref	XP_232499.4	GSSSELQEIIMRRROEKISAAAS	-DSGVESFDEGSSH	822
gi	115497926	ref	NP_001069570.1		-----	345
gi	118083068	ref	XP_416405.2	GSSSELQEIIMRRROEKISAAAS	-DSGVESFDEGSSH	831
gi	41053845	ref	NP_956536.1	GS-ELMEVMRRROEKLAAT	ATSDSGVESFDEASSH	804
				.....1060.....1070.....1080.....		

