

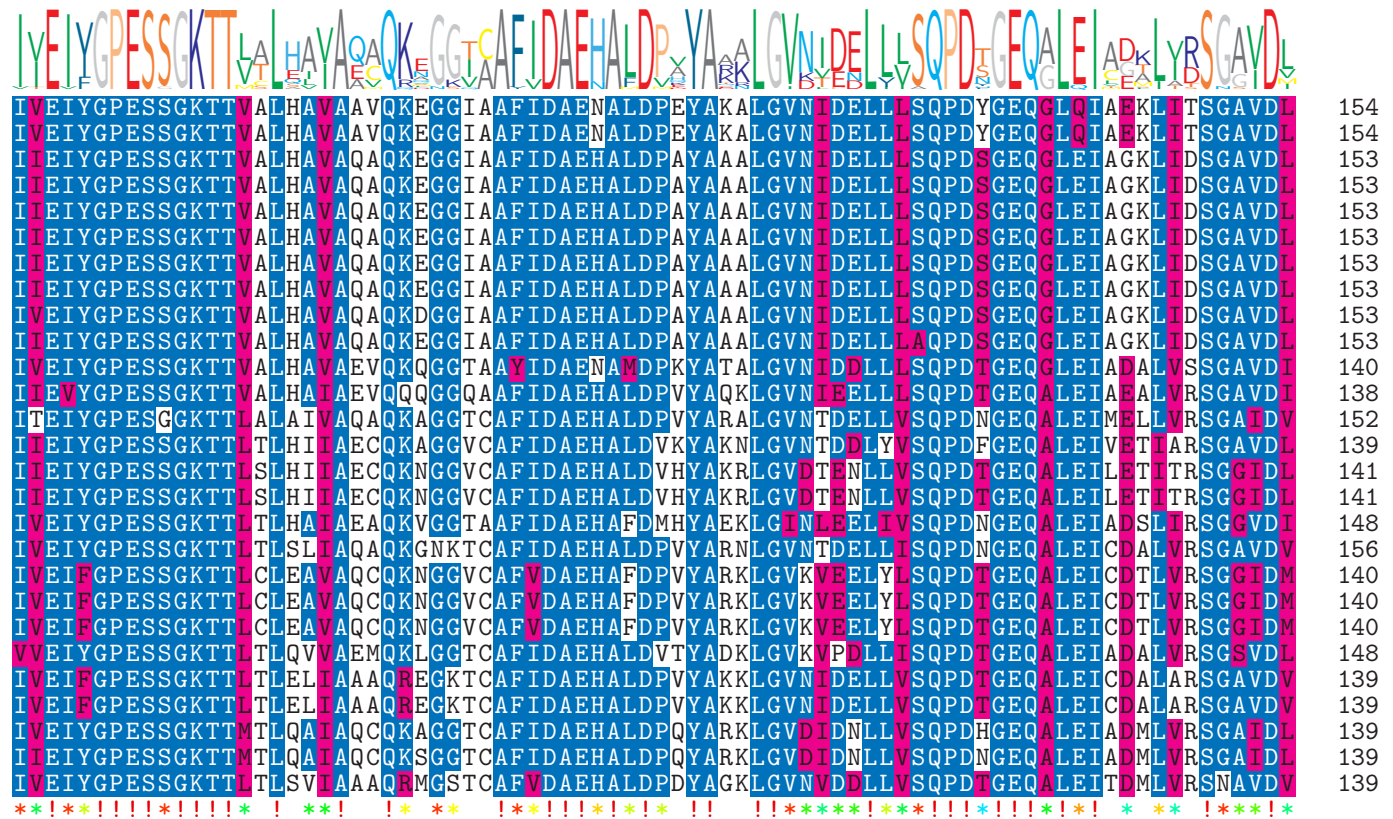
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NTDB id 600 KW2 RS01765 WP 011675413.1	MATKK....KTNFDDITKKYGAERDKALADALALIEKDFGKCSIMRLCEA.ANQKVSVVSSGSLALDIALGAGGYPKGR	74
NTDB id 269 KZH43 RS08665 WP 001085462.1	.MAKK....PKKLEEISKKFGAERBKALNDALKLIEKDFGKCSIMRLCEA.AEQKVQVMSSGSLALDIALCSGGYPKGR	73
NTDB id 228 SPD RS09265 WP 001085462.1	.MAKK....PKKLEEISKKFGAERBKALNDALKLIEKDFGKCSIMRLCEA.AEQKVQVMSSGSLALDIALCSGGYPKGR	73
NTDB id 194 SPR RS08825 WP 001085462.1	.MAKK....PKKLEEISKKFGAERBKALNDALKLIEKDFGKCSIMRLCEA.AEQKVQVMSSGSLALDIALCSGGYPKGR	73
NTDB id 159 SP RS09750 WP 001085462.1	.MAKK....PKKLEEISKKFGAERBKALNDALKLIEKDFGKCSIMRLCEA.AEQKVQVMSSGSLALDIALCSGGYPKGR	73
NTDB id 499 SM12261 RS08315 WP 078228268.1	.MAKK....PKKLEEISKKFGAERBKALNDALKLIEKDFGKCSIMRLCEA.AEQKVQVMSSGSLALDIALCSGGYPKGR	73
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NTDB id 408 SMU RS09530 WP 002262392.1	.MAKR....IKKTEEITKKFGDERKKALDDALKNIEKDFGKGAVMRLCEA.AEQKVQVMSSGSLALDIALGAGGYPKGR	73
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NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALKQIEKQFGKCSIMKLCEK.TDTRISTVPSGSLALDTALCTGGYPGR	58
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTDAKERSKATETAMSQIEKAFGKCSIMKLGAESKLDVQVVSTGSLSLDLALCVGGTIPGR	72
NTDB id 1245 Cj1673c YP 002345041.1	MDDNKRKSLDAALKSLDKTFGKCTILRLCK.EVEQIDSIGTGSVGLDLALCTGGVPKGR	59
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDEDKQKATSLATKQIDKVFVGKCALVRLCDK.QVEKIDAISTGSLGLDLALCTGGVPKGR	61
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NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTV..VKQVEPEQKKQALEAALAQIEKQFGKCSIMKLGGT.EQLDIESVSTGSLGLDLALCTGGLPGR	76
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NTDB id 1427 RS RS02760 WP 011000510.1	.MEDG.....K..KAASMSAEKQKALAAALAQIEKQFGKCSIMKMGDA.EVEPVQVVSTGSLGLDVALCVGGLPGR	68
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NTDB id 1142 GTF74 RS11550 WP 000344154.1	MDENKQKALAAALGQIEKQFGKCSIMRLCDN.RAMDVETISTGSLSLDLALCAGGLPMGR	59
NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDDNKSALQAALSQIEKQFGKNTVMRLCDN.TVQAVEAVSTGSLTLDIALCTGGLPKGR	59
NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSALQAALSQIEKQFGKNTVMRLCDN.TVQAVEAVSTGSLTLDIALCTGGLPKGR	59
NTDB id 1205 PSJM300 05545 AFN77183.1	MDENKKFALAAALGQIEKQFGKGAVMRMGDH.DRQAIPSIISTGSLGLDLALCTGGLPKGR	59
consensus	* ** * * ! * ! ! * * * * * * * * * * * * * * ! * ! !	

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NTDB id 600 KW2 RS01765 WP 011675413.1
NTDB id 269 KZH43 RS08665 WP 001085462.1
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NTDB id 194 SPR RS08825 WP 001085462.1
NTDB id 159 SP RS09750 WP 001085462.1
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NTDB id 527 SMSK321 RS11065 WP 001085454.1
NTDB id 408 SMU RS09530 WP 002262392.1
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NTDB id 1142 GTF74 RS11550 WP 000344154.1
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

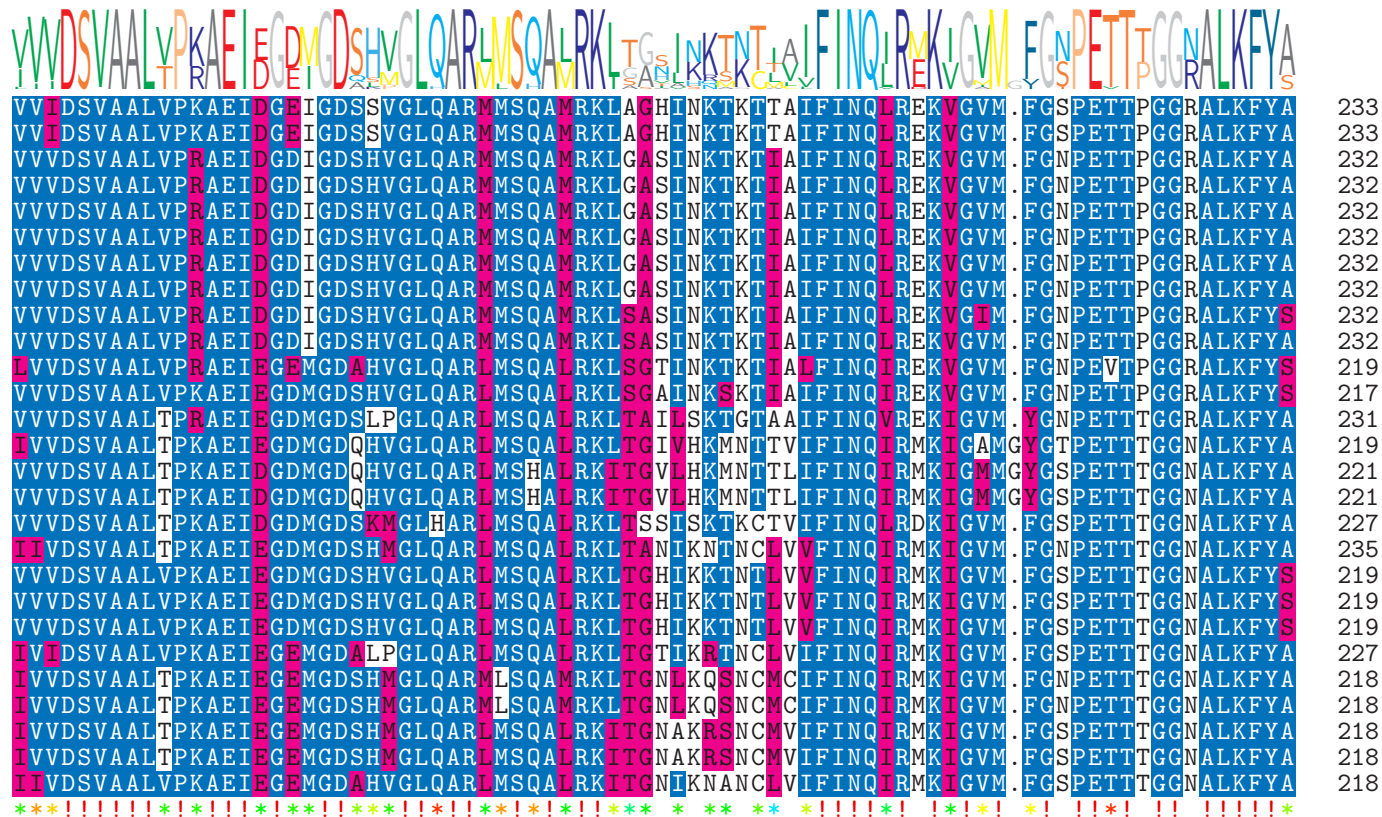
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consensus

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NTDB id 988175 AAEU35 RS05430 WP 058221214.1	SVRLDVRG	STKIEEGS	.GDNKTQ	IGKITK	KVVKNKVAPP	FKVALVD	IMFGEGIS	STGELLN	IAVDEGI	TIKKS	SGAWFAYN	312
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consensus	*!!	*****!	*	*	*	*	*****!*	*****!*	*****!*	*****!	*****!	

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NTDB id 988175 AAEU35 RS05430 WP 058221214.1
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NTDB id 269 KZH43 RS08665 WP 001085462.1
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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Sequence	Score
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DEKIGGGA ⁺ E ⁺ KA ⁺ KN ⁺ YL ⁺ KE ⁺ HQ ⁺ DV ⁺ FDE ⁺ ID ⁺ HK ⁺ VR ⁺ AA ⁺ HLDDSEVAETE....EETTASKTKAKAKKEEKAVETEEIELELED	387
DEKIGGGS ⁺ EN ⁺ AK ⁺ KN ⁺ YL ⁺ AE ⁺ HP ⁺ E ⁺ IF ⁺ DE ⁺ ID ⁺ DK ⁺ VR ⁺ SK ⁺ FGLIDGEEVSEQD....TENKK ⁺ DE ⁺KKEEAV ⁺ ..NEEVPLDLGD	380
DEKIGGGS ⁺ EN ⁺ AK ⁺ KN ⁺ YL ⁺ AE ⁺ HP ⁺ E ⁺ IF ⁺ DE ⁺ ID ⁺ DK ⁺ VR ⁺ SK ⁺ FGLIDGEEVSEQD....TENKK ⁺ DE ⁺KKEEAV ⁺ ..NEEVPLDLGD	380
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GEKIGGGS ⁺ EN ⁺ AK ⁺ KN ⁺ FL ⁺ AD ⁺ NPE ⁺ IF ⁺ DD ⁺ ID ⁺ DH ⁺ KV ⁺ RV ⁺ QY ⁺ GLIEEDNTEEKQ....SSKEK.....ETDEKA ⁺ ..DKNLVLELDD	377
GEKIGGGS ⁺ EN ⁺ AK ⁺ KN ⁺ RY ⁺ LAD ⁺ HP ⁺ QL ⁺ FDE ⁺ ID ⁺ DR ⁺ KV ⁺ RV ⁺ KF ⁺ GLEESEEEESAM....AVASE.....E.....TDDLALDLN	372
SERIGGGS ⁺ REN ⁺ AK ⁺ KN ⁺ YL ⁺ AD ⁺ HDE ⁺ VE ⁺ DEV ⁺ RL ⁺ QV ⁺ IR ⁺ AA ⁺ YGISDVPEEDLPT....TEDE.QINIL.....PDD	351
EERLGGGREN ⁺ AK ⁺ KN ⁺ FL ⁺ EN ⁺ KD ⁺ I ⁺ MLM ⁺ I ⁺ QK ⁺ IR ⁺ EH ⁺ YGLDNNGVVQQQA....EETQE ⁺ LEFE.....E.	348
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DKKLGGGREN ⁺ SK ⁺ AF ⁺ LKEN ⁺ PE ⁺ IA ⁺ DE ⁺ IT ⁺ KA ⁺ IQ ⁺ NSM ⁺ CTEGMI....SGSEDD..EGE ⁺	343
DKKLGGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ IT ⁺ LK ⁺ IK ⁺ ESIGSNEEI....MPLPDE..PLE ⁺ EME.....	347
DKKLGGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ IT ⁺ LK ⁺ IK ⁺ ESIGSNEEI....MPLPDE..PLE ⁺ EME.....	347
DTKLGGGRD ⁺ TV ⁺ KE ⁺ L ⁺ IK ⁺ DN ⁺ PE ⁺ LAE ⁺ LE ⁺ AK ⁺ IREKLQAK.....	343
GTKIGGKKN ⁺ NAV ⁺ KL ⁺ KN ⁺ PE ⁺ IA ⁺ DK ⁺ LE ⁺ QE ⁺ IRNTLASNPNS....VLKATASDSND ⁺ SDVEEF.....SEE	370
GAKIGGQK ⁺ DN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KIR ⁺ ALN ⁺ GVEMHI....TEGTQDET ⁺ DGER.....PEE	348
GAKIGGQK ⁺ DN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KIR ⁺ ALN ⁺ GVEMHI....TEGTQDET ⁺ DGER.....PEE	348
GAKIGGQK ⁺ DN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KIR ⁺ ALN ⁺ GVEMHI....TEGTQDET ⁺ DGER.....PEE	348
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GDKIGGQKAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PE ⁺ IA ⁺ KT ⁺ LD ⁺ KK ⁺ LREMLLN ⁺ PENM....QLIAETSSAAD ⁺ VEFGAV.....PEE	353
GDKIGGQKAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PE ⁺ IA ⁺ KT ⁺ LD ⁺ KK ⁺ LREMLLN ⁺ PENM....QLIAETSSAAD ⁺ VEFGAV.....PEE	353
GNKIGGQK ⁺ NN ⁺ VIR ⁺ YLE ⁺ EN ⁺ PQ ⁺ ISTE ⁺ IE ⁺ AV ⁺ IREQLLTKASD....QTAA.HDETEE ⁺ PDLL.....ES.	349
GNKIGGQK ⁺ NN ⁺ VIR ⁺ YFE ⁺ EN ⁺ NQ ⁺ IA ⁺ EI ⁺ ERN ⁺ IREQLLTGTN....GAVQ.I.EDEE ⁺ PDLL.....LES	349
GSKIGGQKAN ⁺ AA ⁺ KYLE ⁺ EN ⁺ PE ⁺ IA ⁺ GQ ⁺ IE ⁺ QQ ⁺ IRAKLLVTSAN....TKATPVAEDLAD ⁺ ADI.....	347

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		EELEE	
NTDB id 988175 AAEU35 RS05430 WP 058221214.1			387
NTDB id 600 KW2 RS01765 WP 011675413.1			387
NTDB id 269 KZH43 RS08665 WP 001085462.1	ELEIEIEE		388
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NTDB id 159 SP RS09750 WP 001085462.1	ELEIEIEE		388
NTDB id 499 SM12261 RS08315 WP 078228268.1	ELEIEIEE		384
NTDB id 527 SMSK321 RS11065 WP 001085454.1	ELEIEIEE		384
NTDB id 408 SMU RS09530 WP 002262392.1	TIELED..		383
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NTDB id 1074 ABD1 RS10195 WP 000344167.1			349
NTDB id 1205 PSJM300 05545 AFN77183.1			347
consensus			

- non conserved
- similar
- ≥ 50% conserved