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consensus

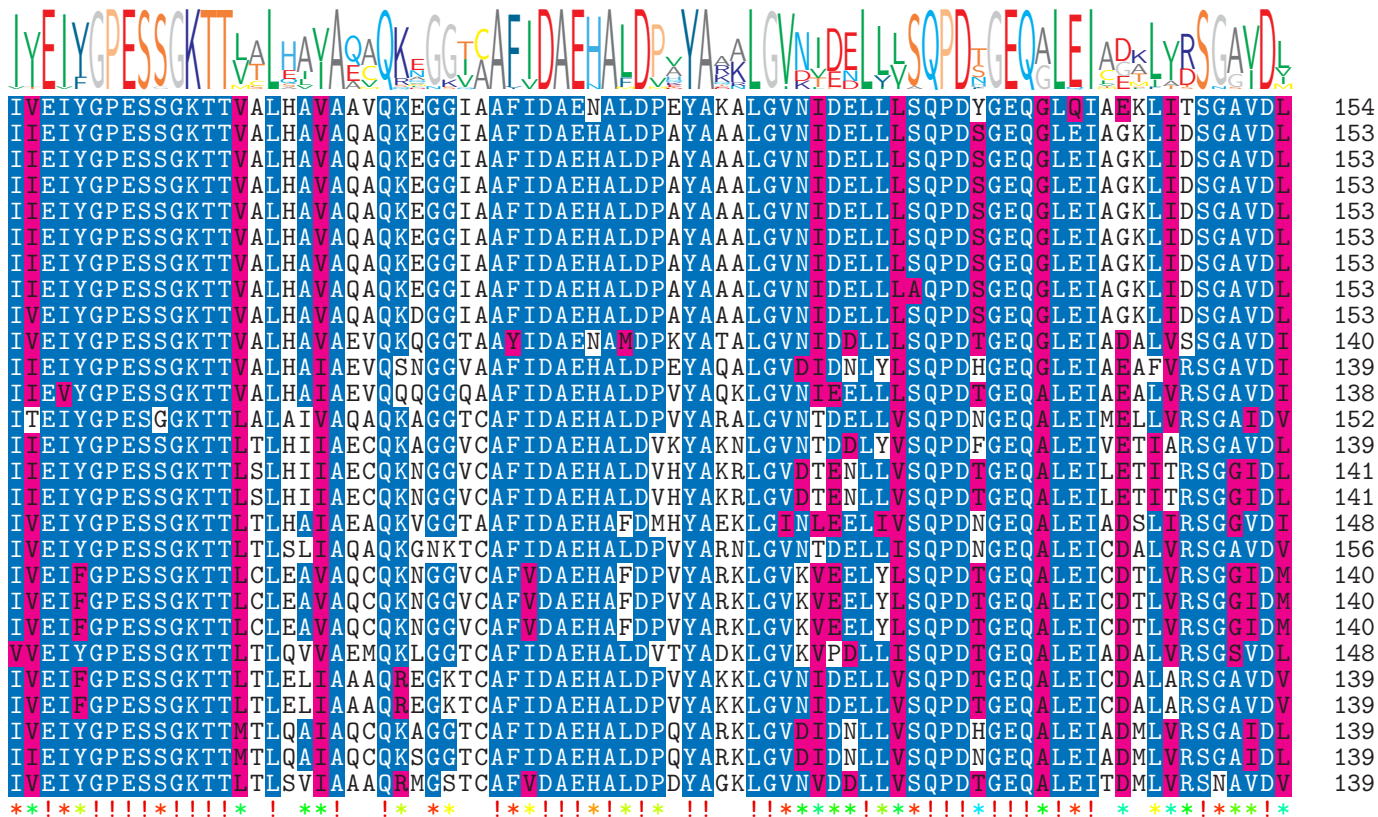
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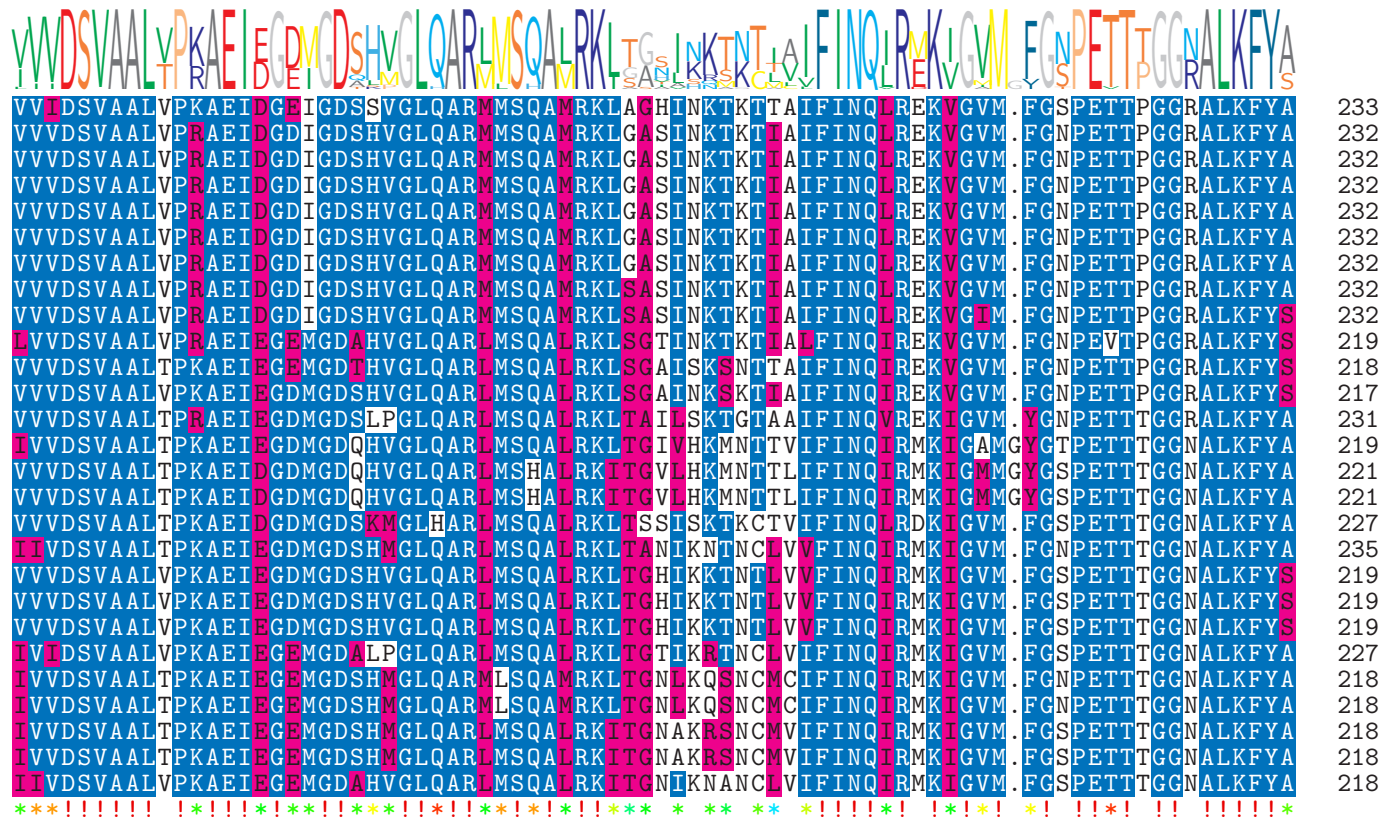
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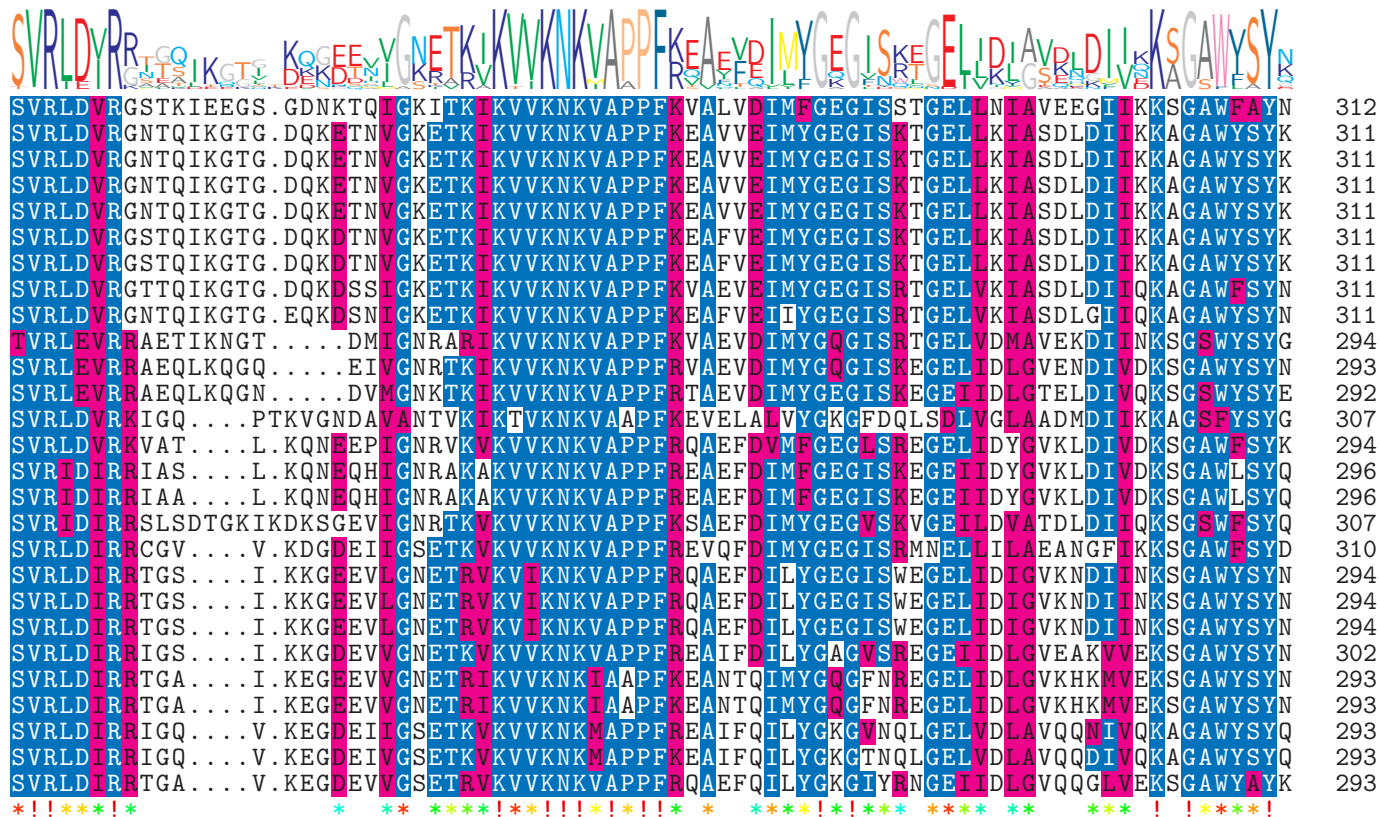
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Sequence	Score
DEKIGQGA ⁺ E ⁺ KA ⁺ KN ⁺ YL ⁺ KE ⁺ HQ ⁺ DV ⁺ FD ⁺ ED ⁺ DH ⁺ KV ⁺ RA ⁺ AH ⁺ GI ⁺ LDDSEVAETEETETASKTKAKAKKEEKAVETEEIELELED....	387
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYLA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ ID ⁺ KQ ⁺ VR ⁺ SK ⁺ FG ⁺ LIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYLA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ ID ⁺ KQ ⁺ VR ⁺ SK ⁺ FG ⁺ LIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYLA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ ID ⁺ KQ ⁺ VR ⁺ SK ⁺ FG ⁺ LIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYLA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ ID ⁺ HQ ⁺ VR ⁺ VQ ⁺ FG ⁺ LIDGEEIAES....KKDE....AAQVDS..VNEEVTLDLGDELEIE	381
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYLA ⁺ DN ⁺ PE ⁺ IF ⁺ DE ⁺ ID ⁺ HQ ⁺ VR ⁺ VQ ⁺ FG ⁺ LIDGEEAAS....KKDE....VAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGS ⁺ EN ⁺ AK ⁺ RYLA ⁺ DHP ⁺ QL ⁺ FD ⁺ ED ⁺ IR ⁺ KV ⁺ RV ⁺ KF ⁺ GL ⁺ LEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGS ⁺ EN ⁺ AK ⁺ KFLA ⁺ DN ⁺ PE ⁺ IF ⁺ DD ⁺ ID ⁺ HK ⁺ VR ⁺ VQ ⁺ YGL ⁺ IEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
SERIGQGR ⁺ EN ⁺ AK ⁺ NYLA ⁺ DH ⁺ ED ⁺ VE ⁺ EV ⁺ RL ⁺ KV ⁺ RA ⁺ AAY ⁺ GISDVPPEEDLPTTEDEQINILPDDSTEE.....	355
GERMGQG ⁺ KEN ⁺ V ⁺ KMYL ⁺ KEN ⁺ PQ ⁺ IK ⁺ EE ⁺ ID ⁺ RKL ⁺ REK ⁺ LG ⁺ ISDGDVEETEDA...PKSLFDEE.....	347
EERLGQGR ⁺ EN ⁺ AK ⁺ KQ ⁺ FL ⁺ KEN ⁺ DK ⁺ IM ⁺ LM ⁺ IQ ⁺ EQ ⁺ IR ⁺ EH ⁺ YGL ⁺ DNNGVVQQQAETQEELFEFE.....	348
DERIGQG ⁺ KE ⁺ KT ⁺ IA ⁺ Y ⁺ IA ⁺ ER ⁺ PE ⁺ ME ⁺ QE ⁺ IR ⁺ DR ⁺ VMAA ⁺ IRAGNAGEAPALAPAPAPEAEAE.....	363
DK ⁺ KL ⁺ GQGR ⁺ EN ⁺ SKA ⁺ FL ⁺ KEN ⁺ PE ⁺ IA ⁺ DE ⁺ IT ⁺ KA ⁺ IQ ⁺ NSM ⁺ GI ⁺ EGMI....SGSEDD..EGEE.....	343
DK ⁺ KL ⁺ GQGR ⁺ EN ⁺ AK ⁺ ALL ⁺ KE ⁺ DKA ⁺ LAD ⁺ EIT ⁺ LK ⁺ IK ⁺ ES ⁺ IGS ⁺ NEEI....MPLPDE..PLEEME.....	347
DK ⁺ KL ⁺ GQGR ⁺ EN ⁺ AK ⁺ ALL ⁺ KE ⁺ DKA ⁺ LAD ⁺ EIT ⁺ LK ⁺ IK ⁺ ES ⁺ IGS ⁺ NEEI....MPLPDE..PLEEME.....	347
DTKL ⁺ GQGRD ⁺ TV ⁺ KE ⁺ L ⁺ IK ⁺ DN ⁺ PE ⁺ LAE ⁺ LE ⁺ AK ⁺ IREK ⁺ LQAK.....	343
GTKIGQG ⁺ KNN ⁺ AV ⁺ KWL ⁺ KEN ⁺ PE ⁺ IA ⁺ DK ⁺ LE ⁺ QEI ⁺ IRNT ⁺ LASNPNS....VLKATASDSNDESD..VEEFSEEL.....	372
GAKIGQG ⁺ KDN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ ID ⁺ AK ⁺ IRAL ⁺ NCV ⁺ EMHI....TEGTQDET ⁺ DGER.....PEE.....	348
GAKIGQG ⁺ KDN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ ID ⁺ AK ⁺ IRAL ⁺ NCV ⁺ EMHI....TEGTQDET ⁺ DGER.....PEE.....	348
GAKIGQG ⁺ KDN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ ID ⁺ AK ⁺ IRAL ⁺ NCV ⁺ EMHI....TEGTQDET ⁺ DGER.....PEE.....	348
GE ⁺ RIGQRD ⁺ NC ⁺ REF ⁺ LRENA ⁺ E ⁺ LARE ⁺ IE ⁺ KN ⁺ VR ⁺ HL ⁺ GV ⁺ TPMG....AVTLA.EEEVED.....	352
GDKIGQG ⁺ KAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PE ⁺ IA ⁺ AK ⁺ TLD ⁺ KKL ⁺ REML ⁺ LN ⁺ PNEM....QLIAETSSAADDVE..FGAVPEEF.....	354
GD ⁺ KIGQG ⁺ KAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PE ⁺ IA ⁺ AK ⁺ TLD ⁺ KKL ⁺ REML ⁺ LN ⁺ PNEM....QLIAETSSAADDVE..FGAVPEEF.....	354
GN ⁺ KIGQG ⁺ KNN ⁺ VIR ⁺ Y ⁺ LEEN ⁺ PQ ⁺ ISTE ⁺ IE ⁺ AV ⁺ IREQ ⁺ LLTKASD....QTAA.HDETEEEP ⁺ D..LL..ES.....	349
GN ⁺ KIGQG ⁺ KNN ⁺ VIR ⁺ Y ⁺ FEEN ⁺ NQ ⁺ IA ⁺ E ⁺ EI ⁺ ERN ⁺ IREQ ⁺ LLTTGTN....GAVQ.I.EDEEEP ⁺ D..LL..LES.....	349
GS ⁺ KIGQG ⁺ KANA ⁺ AK ⁺ Y ⁺ LEEN ⁺ PE ⁺ IG ⁺ QE ⁺ IE ⁺ QQ ⁺ IRAK ⁺ LL ⁺ Y ⁺ TSA ⁺ N....TKATPVAEDLADAD..I.....	347

logo

		LEE	
NTDB id 600 KW2 RS01765 WP 011675413.1	...	387	
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE	388	
NTDB id 228 SPD RS09265 WP 001085462.1	IEE	388	
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consensus			

- non conserved
- similar
- ≥ 50% conserved