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NTDB id 115 BSU 16940 NP 389576.2	MS	DRQAALDMALKQIEKQ	FGKGSIMKLGEK	.TDTRIST	VPSGSLALD	T	ALGIGGY	PRGR	58	
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTD	AKERSKATETAMSQIEK	AFGKGSIMKLGA	E.SKLDVQV	VSTGSLSLD	L	ALGVGGI	PRGR	72	
NTDB id 1245 Cj1673c YP 002345041.1	MDDN	KRKSLDAALKSLDKT	FGKGTILRLGDK	.EVEQIDS	IGTGSVGLD	L	ALGIGGV	PKGR	59	
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NTDB id 1205 PSJM300 05545 AFN77183.1	MDEN	KKRALAAALGQIEKQ	FGKGAVMRMGDH	.DRQAIPS	ISTGSLGLD	I	ALGIGGL	PKGR	59	
consensus		*** **	***	***!	***!	*****	*	***!!*!!*!!*!!*!!*!!*!!		

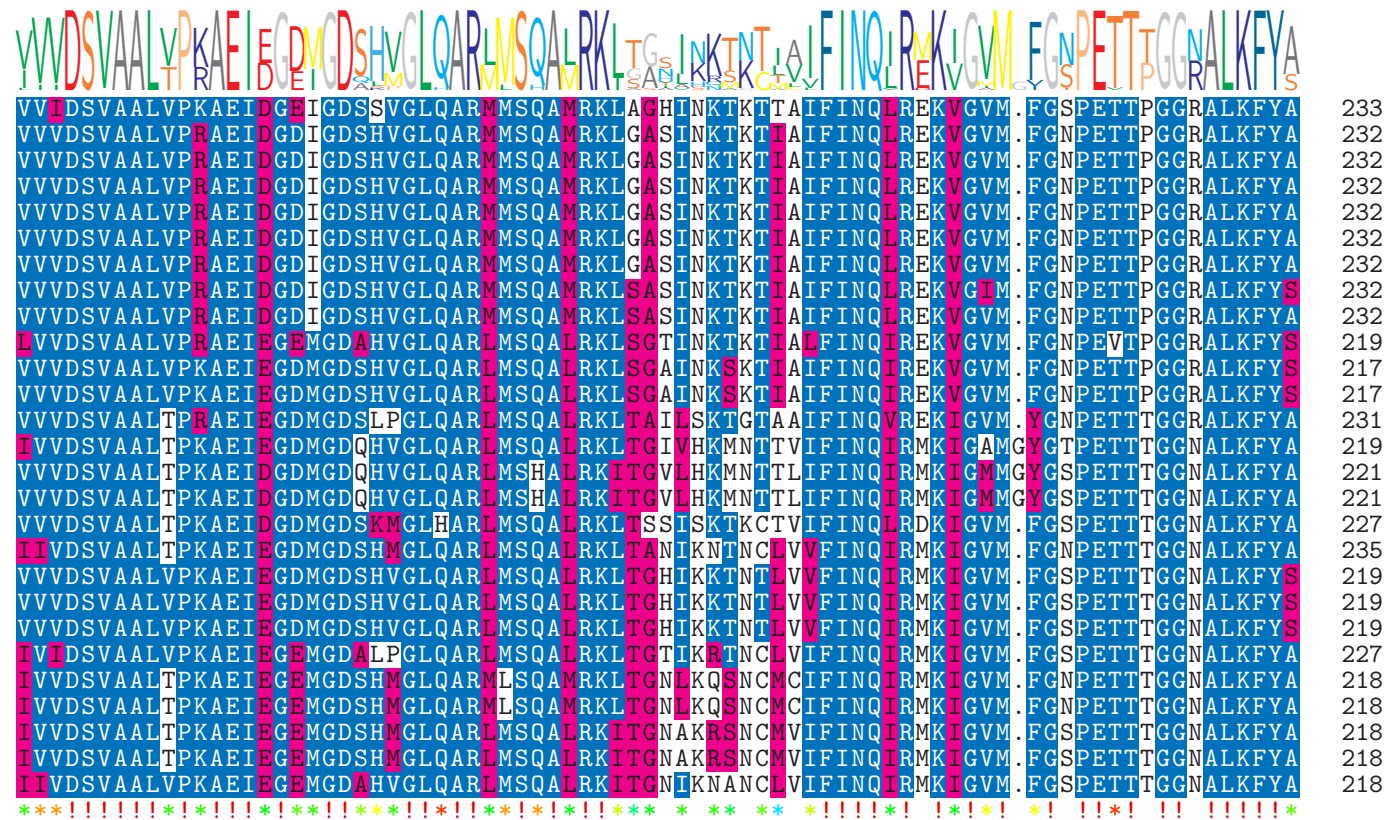
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NTDB id 269 KZH43 RS08665 WP 001085462.1	I	I	E	I	Y	G	P	E	S	S	G	K	T	T	V	A	L	H	A	V	A	Q	A	Q	K	E	G	G	I	A	A	F	I	D	A	E	H	A	L	D	P	A	Y	A	A	A	L	G	V	N	I	D	E	L	L	S	Q	P	D	S	G	E	Q	G	L	E	I	A	G	K	L	I	D	S	G	A	V	D	L	153	
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NTDB id 499 SM12261 RS08315 WP 078228268.1	I	I	E	I	Y	G	P	E	S	S	G	K	T	T	V	A	L	H	A	V	A	Q	A	Q	K	E	G	G	I	A	A	F	I	D	A	E	H	A	L	D	P	A	Y	A	A	A	L	G	V	N	I	D	E	L	L	S	Q	P	D	S	G	E	Q	G	L	E	I	A	G	K	L	I	D	S	G	A	V	D	L	153	
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consensus	*	*	!	*	*	!	!	!	!	!	!	*	!	*	!	*	*	!	*	*	!	*	*	!	*	*	!	*	*	!	*	*	!	!	*	*	!	!	*	*	!																																								

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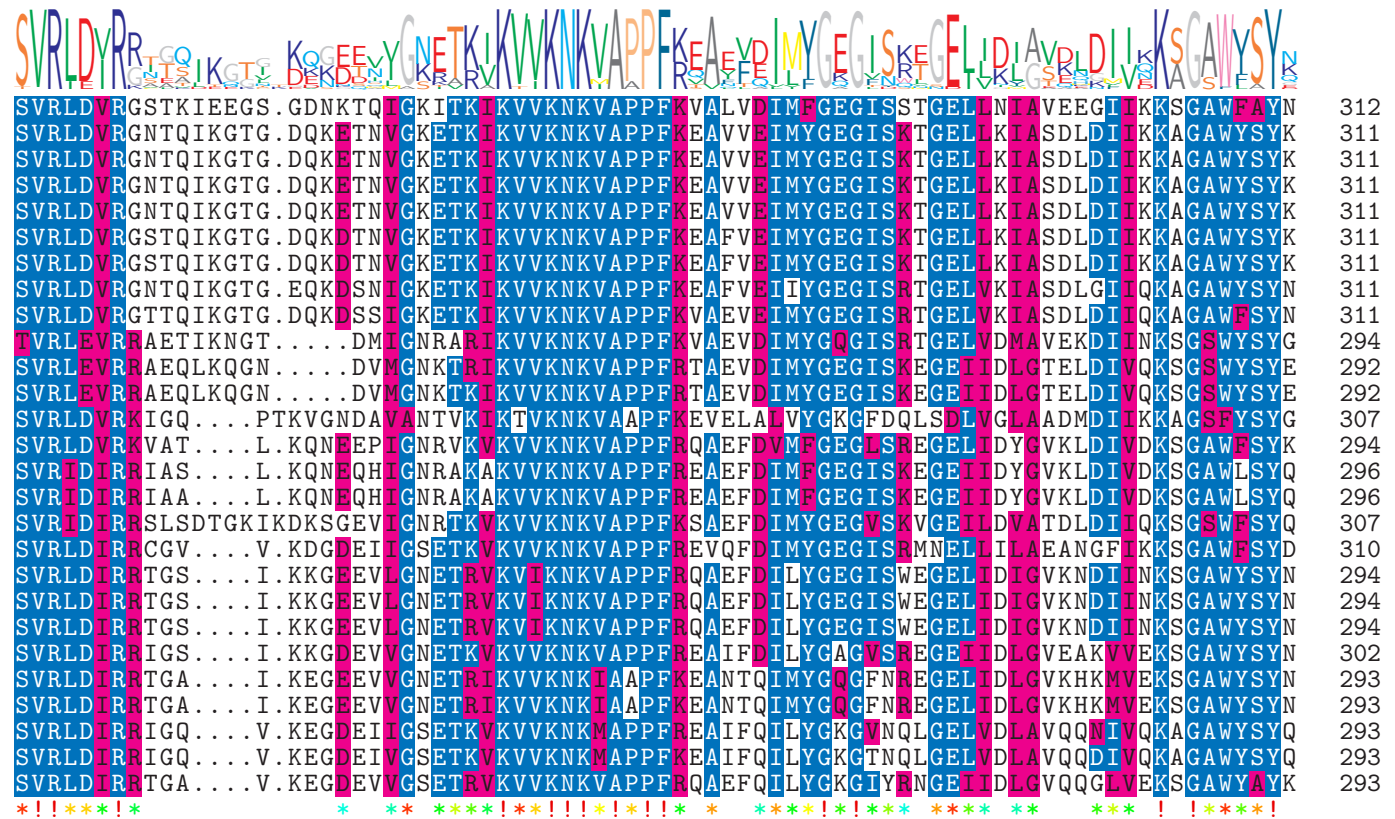
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
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consensus

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Sequence	Score
DEKIGGGA ⁺ EA ⁺ KA ⁺ KN ⁺ YL ⁺ KE ⁺ HQ ⁺ DV ⁺ FD ⁺ EID ⁺ HK ⁺ V ⁺ RAAH ⁺ CL ⁺ LD ⁺ DEVAETEET ⁺ TASK ⁺ TKAKAKKEEK ⁺ AVETEEIELE ⁺ ED ⁺	387
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DEID ⁺ DK ⁺ QV ⁺ RSKF ⁺ CL ⁺ ID ⁺ GEEVSEQD ⁺ TENKKDE ⁺PKKEEA ⁺ ..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DEID ⁺ DK ⁺ QV ⁺ RSKF ⁺ CL ⁺ ID ⁺ GEEVSEQD ⁺ TENKKDE ⁺PKKEEA ⁺ ..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DEID ⁺ DK ⁺ QV ⁺ RSKF ⁺ CL ⁺ ID ⁺ GEEVSEQD ⁺ TENKKDE ⁺PKKEEA ⁺ ..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DEID ⁺ DK ⁺ QV ⁺ RSKF ⁺ CL ⁺ ID ⁺ GEEVSEQD ⁺ TENKKDE ⁺PKKEEA ⁺ ..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AD ⁺ NPE ⁺ VFAE ⁺ ID ⁺ HQ ⁺ VR ⁺ VQF ⁺ CL ⁺ ID ⁺ GEEAAE ⁺SKKDE ⁺VAQVDS ⁺ ..VNEEVPLDLGDELEIE	381
DEKIGGGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AD ⁺ NPE ⁺ IF ⁺ DEID ⁺ HQ ⁺ VR ⁺ VQF ⁺ CL ⁺ ID ⁺ GEEIAE ⁺SKKDE ⁺AAQVDS ⁺ ..VNEEVPLDLGDELEIE	381
GEKIGGGS ⁺ EN ⁺ AK ⁺ KFL ⁺ AD ⁺ NPE ⁺ IF ⁺ DD ⁺ ID ⁺ HK ⁺ VR ⁺ VQY ⁺ CL ⁺ IEED ⁺ NTLEEK ⁺ QSSKE ⁺ETDEK ⁺ ..ADKNLVLELDDTIEIE	382
GEKIGGGS ⁺ EN ⁺ AK ⁺ KRYL ⁺ AD ⁺ HQP ⁺ LF ⁺ DEID ⁺ DR ⁺ KV ⁺ RVKF ⁺ CL ⁺ LEESEEEESAMAVASE ⁺E.....TDDLALDLDN ⁺ GIIEIE	377
SE ⁺ RIGGG ⁺ RE ⁺ NA ⁺ KN ⁺ YL ⁺ AD ⁺ HED ⁺ VE ⁺ DE ⁺ VR ⁺ LKV ⁺ RAAY ⁺ GIS ⁺ SDVPEEDLP ⁺ TTEDEQINILPDDSTEE ⁺	355
EER ⁺ LGQGR ⁺ EN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IM ⁺ LM ⁺ IQE ⁺ QIREHY ⁺ CL ⁺ DNNGVTDK ⁺ ..AE ⁺ EVQEEMELEE ⁺	347
EER ⁺ LGQGR ⁺ EN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IM ⁺ LM ⁺ IQE ⁺ QIREHY ⁺ CL ⁺ DNNGVVQQQAEETQEELEFEE ⁺	348
DER ⁺ IGQGK ⁺ EKT ⁺ IAY ⁺ IA ⁺ ERP ⁺ EME ⁺ QE ⁺ IR ⁺ DRV ⁺ MAA ⁺ IRAGNAGEAPALAPAPAAPEAAEA ⁺	363
DK ⁺ KLGGG ⁺ RE ⁺ NS ⁺ KA ⁺ FL ⁺ KEN ⁺ PEI ⁺ AD ⁺ EIT ⁺ KA ⁺ IQNSM ⁺ CT ⁺ EGMI ⁺SGSEDD ⁺ ..EGEE ⁺	343
DK ⁺ KLGGG ⁺ RE ⁺ NA ⁺ KAL ⁺ LKED ⁺ KALADE ⁺ EIT ⁺ LK ⁺ IKES ⁺ GSNEEI ⁺MPLPDE ⁺ ..PLEEME ⁺	347
DK ⁺ KLGGG ⁺ RE ⁺ NA ⁺ KAL ⁺ LKED ⁺ KALADE ⁺ EIT ⁺ LK ⁺ IKES ⁺ GSNEEI ⁺MPLPDE ⁺ ..PLEEME ⁺	347
DT ⁺ KLGGGRD ⁺ TV ⁺ KE ⁺ L ⁺ IKDN ⁺ PE ⁺ LA ⁺ EEL ⁺ AK ⁺ IREKLQAK ⁺	343
GT ⁺ KIGGK ⁺ NN ⁺ AV ⁺ KWL ⁺ KEN ⁺ PEI ⁺ AD ⁺ KL ⁺ EQ ⁺ IRNTLA ⁺ SNPNS ⁺VLKATASDSNDESDV ⁺ ..EEFSEEEEL ⁺	372
GAKIGGQK ⁺ DN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SDE ⁺ ID ⁺ AK ⁺ IRALN ⁺ GVEMHI ⁺TEGTQDET ⁺ DGER ⁺PEE ⁺	348
GAKIGGQK ⁺ DN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SDE ⁺ ID ⁺ AK ⁺ IRALN ⁺ GVEMHI ⁺TEGTQDET ⁺ DGER ⁺PEE ⁺	348
GAKIGGQK ⁺ DN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SDE ⁺ ID ⁺ AK ⁺ IRALN ⁺ GVEMHI ⁺TEGTQDET ⁺ DGER ⁺PEE ⁺	348
GE ⁺ RIGGGRD ⁺ NC ⁺ REF ⁺ LRE ⁺ NA ⁺ EL ⁺ LARE ⁺ EN ⁺ KV ⁺ REHL ⁺ CVTPMG ⁺AVTLA ⁺ ..EEVEED ⁺	352
GD ⁺ KIGGK ⁺ KAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PEI ⁺ AK ⁺ TL ⁺ DK ⁺ KL ⁺ REMLLN ⁺ PNEM ⁺QLIAETSSAADDVEF ⁺ ..GAVPEEF ⁺	354
GD ⁺ KIGGK ⁺ KAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PEI ⁺ AK ⁺ TL ⁺ DK ⁺ KL ⁺ REMLLN ⁺ PNEM ⁺QLIAETSSAADDVEF ⁺ ..GAVPEEF ⁺	354
GN ⁺ KIGGK ⁺ KNN ⁺ VIR ⁺ YL ⁺ EEN ⁺ PQ ⁺ IST ⁺ EIE ⁺ AVI ⁺ REQLLT ⁺ TKASD ⁺QTAA ⁺ ..HDETEEEPDL ⁺ ..L ⁺ ..ES ⁺	349
GN ⁺ KIGGK ⁺ KNN ⁺ VIR ⁺ YL ⁺ EEN ⁺ PQ ⁺ IA ⁺ EIE ⁺ ERN ⁺ IREQLLT ⁺ TGTN ⁺GAVQ ⁺ ..I ⁺ ..EDEEEPDL ⁺ ..L ⁺ ..LES ⁺	349
GS ⁺ KIGGK ⁺ KANA ⁺ AK ⁺ YL ⁺ EEN ⁺ PEI ⁺ GQ ⁺ EIE ⁺ QQ ⁺ IRAK ⁺ LL ⁺ YTSAN ⁺TKATPVAEDLADADI ⁺	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	...	387
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NTDB id 194 SPR RS08825 WP 001085462.1	IEE	388
NTDB id 159 SP RS09750 WP 001085462.1	IEE	388
NTDB id 527 SMSK321 RS11065 WP 001085454.1	IEE	384
NTDB id 499 SM12261 RS08315 WP 078228268.1	IEE	384
NTDB id 408 SMU RS09530 WP 002262392.1	D..	383
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NTDB id 1165 A1552VC RS01565 WP 000344154.1	...	354
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	...	349
NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349
NTDB id 1205 PSJM300 05545 AFN77183.1	...	347

consensus

 non conserved
 similar
 ≥ 50% conserved