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NTDB id 115 BSU 16940 NP 389576.2	MS	DRQAALDMALKQIEKQ	FGKGSIMKLG	EK.TDTRIST	VP	SGSLALD	TALG	IGGYPRGR	58	
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NTDB id 1123 OK783 RS03845 WP 003688695.1	MSD	DKSKALAAALAQIEKS	FGKGAIMKMDGSQ	QENLEVIST	GSLGLD	L	ALGV	GGLPGR	60	
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDDN	KSKALQAALSQIEKQ	FGKNTVMRLGDN	.TVQAVEA	VSTGSLTLD	I	ALGIGGL	PKGR	59	
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NTDB id 1205 PSJM300 05545 AFN77183.1	MDEN	KKRALAAALGQIEKQ	FGKGAVMRMGDH	.DRQAIPS	ISTGSLGLD	I	ALGIGGL	PKGR	59	
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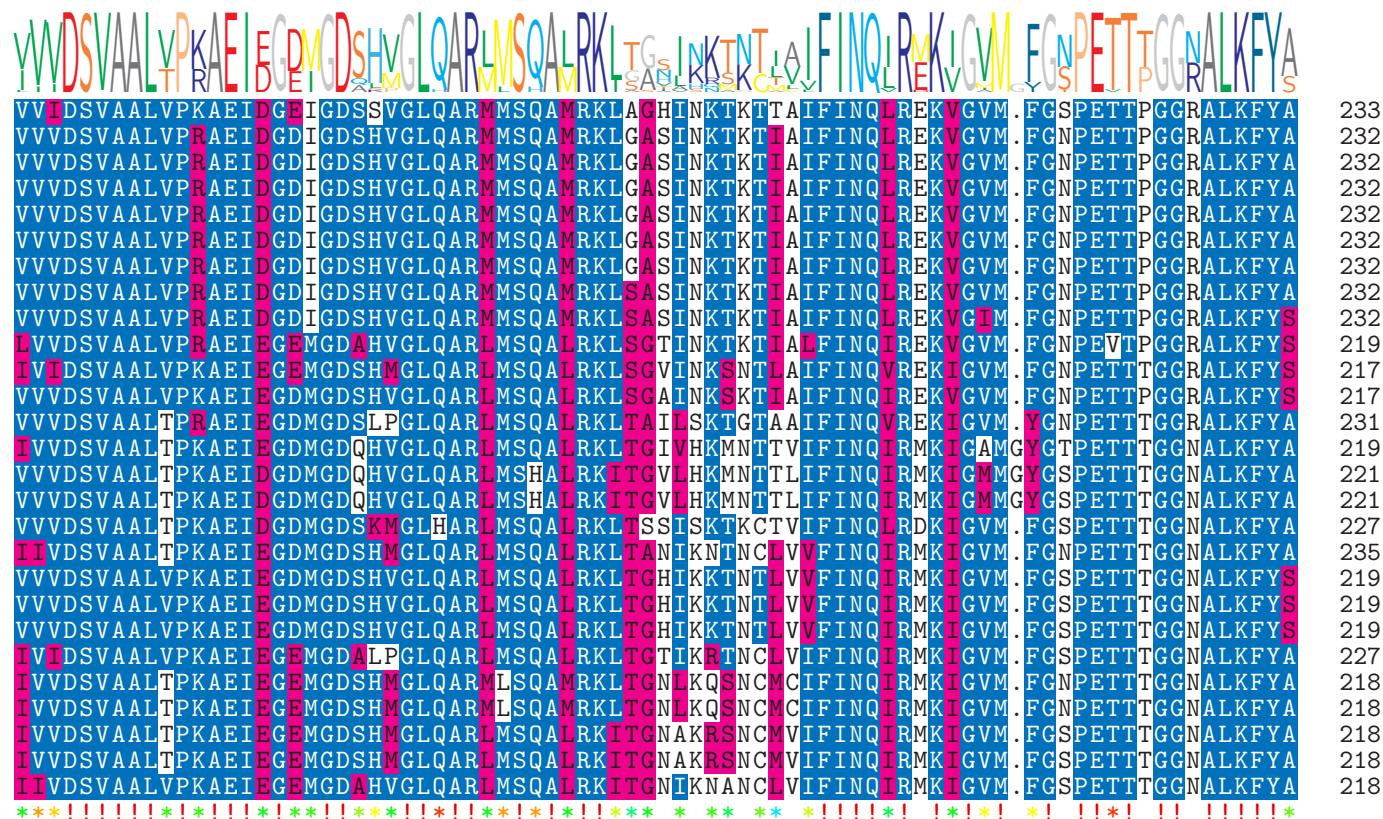
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consensus

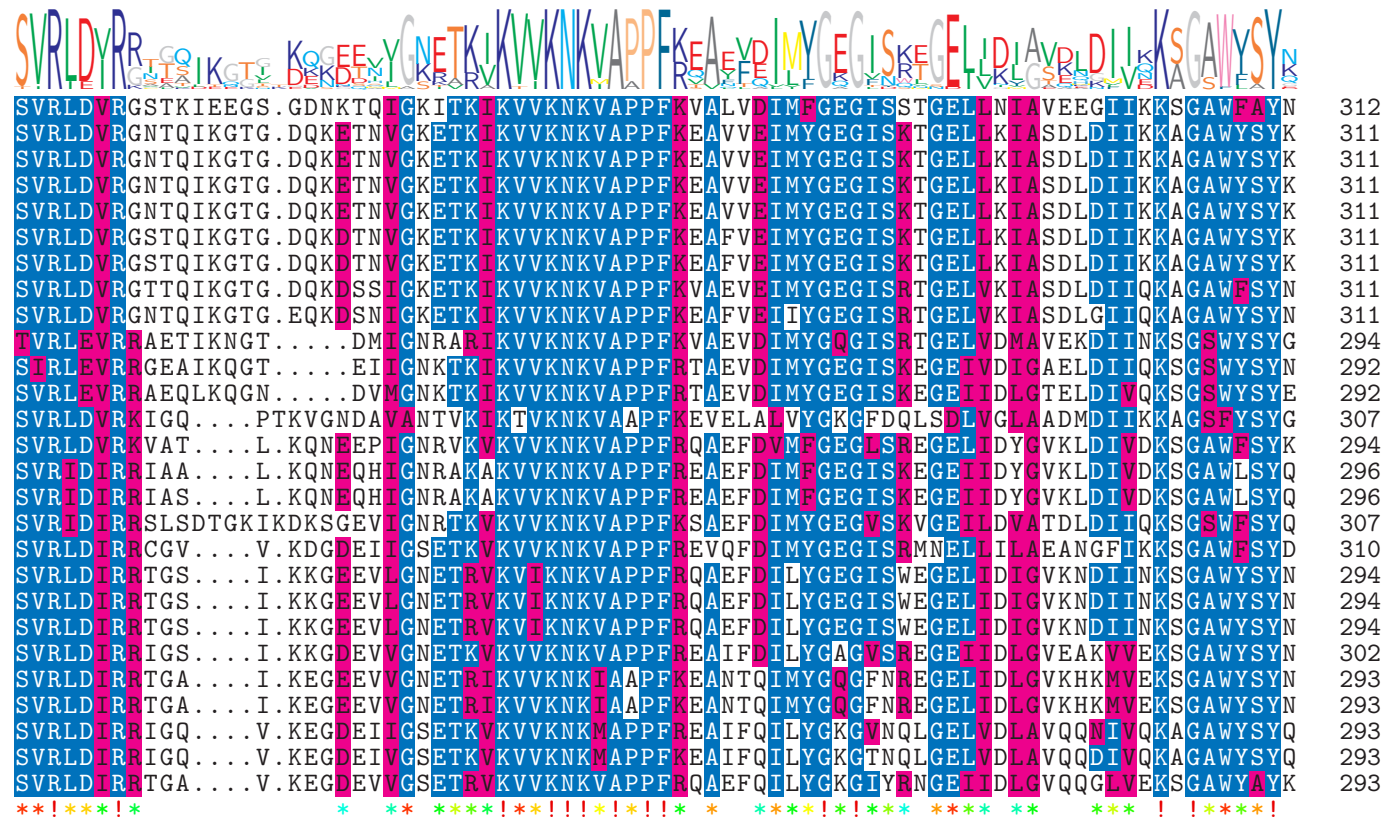
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consensus

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NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

Sequence	Score
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DEKIGQGS ⁺ EN ⁺ AK ⁺ KY ⁺ LA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ DK ⁺ QV ⁺ RS ⁺ KF ⁺ CL ⁺ ID ⁺ GE ⁺ EV ⁺ SEQD ⁺ TEN ⁺ KK ⁺ DE ⁺PK ⁺ KEEA ⁺ ..VNE ⁺ EV ⁺ PLD ⁺ LG ⁺ DE ⁺ LE ⁺ IE ⁺	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KY ⁺ LA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ DK ⁺ QV ⁺ RS ⁺ KF ⁺ CL ⁺ ID ⁺ GE ⁺ EV ⁺ SEQD ⁺ TEN ⁺ KK ⁺ DE ⁺PK ⁺ KEEA ⁺ ..VNE ⁺ EV ⁺ PLD ⁺ LG ⁺ DE ⁺ LE ⁺ IE ⁺	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KY ⁺ LA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ DK ⁺ QV ⁺ RS ⁺ KF ⁺ CL ⁺ ID ⁺ GE ⁺ EV ⁺ SEQD ⁺ TEN ⁺ KK ⁺ DE ⁺PK ⁺ KEEA ⁺ ..VNE ⁺ EV ⁺ PLD ⁺ LG ⁺ DE ⁺ LE ⁺ IE ⁺	385
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DEKIGQGS ⁺ EN ⁺ AK ⁺ KY ⁺ LAD ⁺ NPE ⁺ VF ⁺ AE ⁺ ID ⁺ HQ ⁺ VR ⁺ VQ ⁺ FL ⁺ ID ⁺ GE ⁺ EA ⁺ ES ⁺KK ⁺ DE ⁺VA ⁺ QV ⁺ DS ⁺ ..VNE ⁺ EV ⁺ TLD ⁺ LG ⁺ DE ⁺ LE ⁺ IE ⁺	381
GEKIGQGS ⁺ EN ⁺ AK ⁺ RY ⁺ LAD ⁺ HP ⁺ QL ⁺ FD ⁺ DR ⁺ KV ⁺ VK ⁺ FL ⁺ LE ⁺ EE ⁺ SE ⁺ ES ⁺ AM ⁺ VA ⁺ SE ⁺E ⁺TDD ⁺ LALD ⁺ LD ⁺ NG ⁺ IE ⁺ IE ⁺	377
GEKIGQGS ⁺ EN ⁺ AK ⁺ KFL ⁺ AD ⁺ NPE ⁺ IF ⁺ DD ⁺ ID ⁺ HK ⁺ VR ⁺ VQ ⁺ CL ⁺ IE ⁺ ED ⁺ NTE ⁺ EK ⁺ QSS ⁺ KE ⁺ K ⁺ET ⁺ DE ⁺ K ⁺ ..AD ⁺ KN ⁺ LV ⁺ LE ⁺ LD ⁺ DT ⁺ IE ⁺ LE ⁺	382
SERIGQGS ⁺ REN ⁺ AK ⁺ NY ⁺ LAD ⁺ HED ⁺ VE ⁺ EV ⁺ RL ⁺ KV ⁺ RAAY ⁺ CI ⁺ IS ⁺ DV ⁺ PE ⁺ ED ⁺ LP ⁺ ..TTE ⁺ DE ⁺ EQ ⁺ I ⁺NIL ⁺ PDD ⁺ STEE ⁺ ..	355
SERIGQGS ⁺ REN ⁺ VK ⁺ QFF ⁺ FK ⁺ EN ⁺ PAI ⁺ KE ⁺ EV ⁺ TE ⁺ KI ⁺ RQH ⁺ FI ⁺ GEL ⁺ GY ⁺ TIG ⁺ AND ⁺ TT ⁺ DEE ⁺ EL ⁺DE ⁺ LE ⁺ LF ⁺ FE ⁺ DE ⁺ KE ⁺ ...	356
EERLGGGREN ⁺ AK ⁺ FL ⁺ KEN ⁺ KD ⁺ IM ⁺ LI ⁺ QE ⁺ QI ⁺ RE ⁺ HY ⁺ CL ⁺ DN ⁺ NG ⁺ VV ⁺ QQ ⁺ QA ⁺ ET ⁺ QE ⁺E ⁺ LE ⁺ FE ⁺ E ⁺	348
DERIGQGE ⁺ KTI ⁺ AI ⁺ YI ⁺ AER ⁺ PE ⁺ ME ⁺ QE ⁺ IR ⁺ DRV ⁺ MAA ⁺ IRAG ⁺ EAP ⁺ ALAP ⁺ APAA ⁺ PEAA ⁺ E ⁺A ⁺	363
DKKLGGGREN ⁺ SKA ⁺ FL ⁺ KEN ⁺ PEI ⁺ ADE ⁺ IT ⁺ KAI ⁺ QNS ⁺ MC ⁺ IE ⁺ GM ⁺ I ⁺SG ⁺ SEDD ⁺ ..EGE ⁺E ⁺	343
DKKLGGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ IT ⁺ LK ⁺ IK ⁺ ES ⁺ IG ⁺ SNEE ⁺ I ⁺MPL ⁺ PDE ⁺ ..PLE ⁺EME ⁺	347
DKKLGGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ IT ⁺ LK ⁺ IK ⁺ ES ⁺ IG ⁺ SNEE ⁺ I ⁺MPL ⁺ PDE ⁺ ..PLE ⁺EME ⁺	347
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GAKIGGKGD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SDE ⁺ IDA ⁺ KI ⁺ RAL ⁺ NC ⁺ VM ⁺ HI ⁺TEG ⁺ TQ ⁺ DET ⁺ DGE ⁺R ⁺PEE ⁺	348
GAKIGGKGD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SDE ⁺ IDA ⁺ KI ⁺ RAL ⁺ NC ⁺ VM ⁺ HI ⁺TEG ⁺ TQ ⁺ DET ⁺ DGE ⁺R ⁺PEE ⁺	348
GAKIGGKGD ⁺ NVR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SDE ⁺ IDA ⁺ KI ⁺ RAL ⁺ NC ⁺ VM ⁺ HI ⁺TEG ⁺ TQ ⁺ DET ⁺ DGE ⁺R ⁺PEE ⁺	348
GERIGGGRD ⁺ NCRE ⁺ FL ⁺ REN ⁺ AE ⁺ LARE ⁺ IE ⁺ EN ⁺ KV ⁺ RE ⁺ HL ⁺ CV ⁺ TPM ⁺ G ⁺AV ⁺ TLA ⁺ ..EE ⁺ VE ⁺ E ⁺D ⁺	3

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consensus			

- X non conserved
- X similar
- X ≥ 50% conserved