

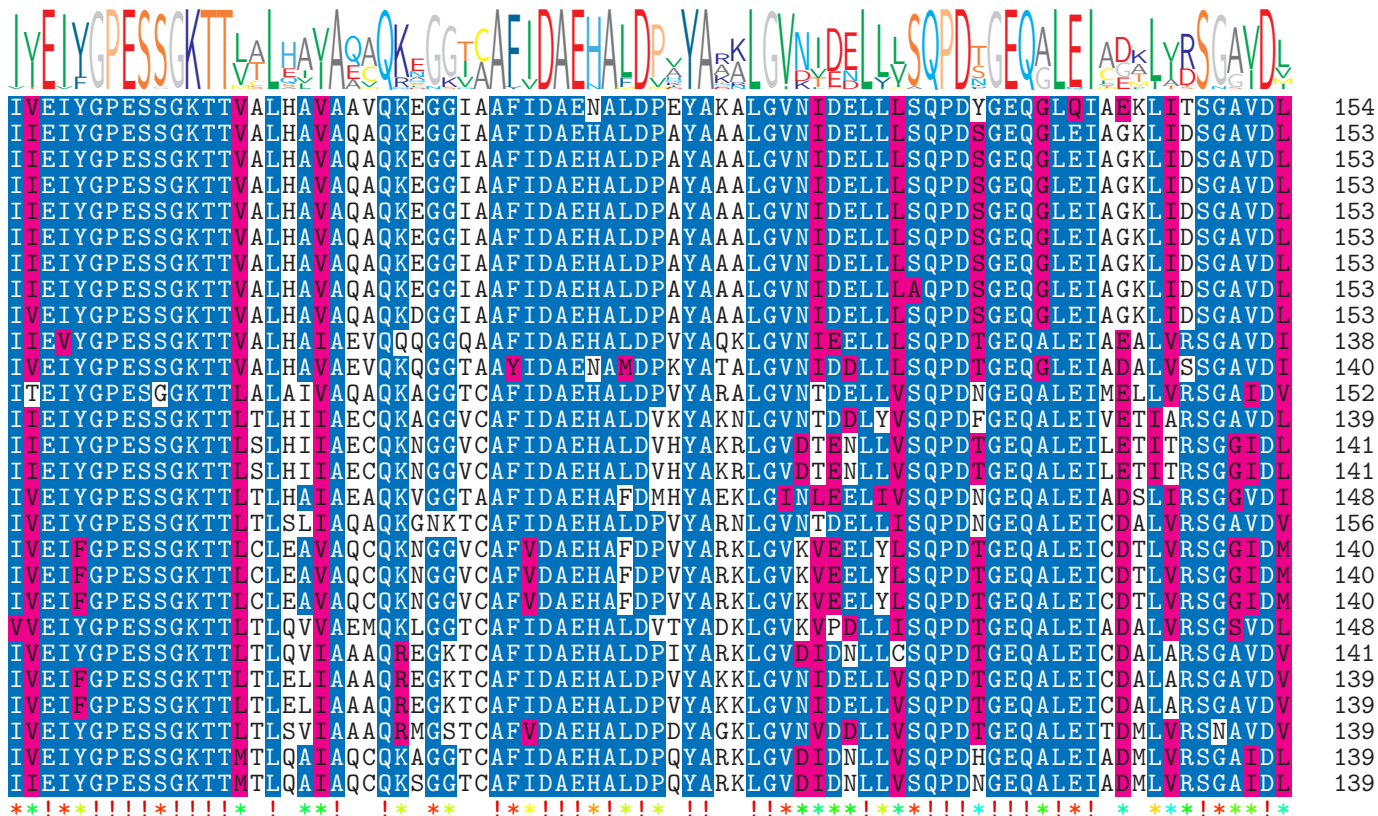
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NTDB id 625 LCA RS02525 WP 011374196.1	MAKDERQAALDAALKKIEKNFGKCSIMRMGER.VDTQVSTVSSGSLALDEALGVGGYPGR	60
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NTDB id 1124 NGFG RS03960 WP 003688695.1	MSDDKSKALAAALAQIEKSFGKGAIMKMDGSQQEENLEVIISTGSLGLDIALGVGGLPGR	60
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NTDB id 1142 GTF74 RS11550 WP 000344154.1	MDENKQKALAAALGQIEKQFGKCSIMRLCDN.RAMDVETISTGSLSLDIALGAGGLPMGR	59
NTDB id 1205 PSJM300 05545 AFN77183.1	MDENKRALAAALGQIEKQFGKCAVMRLCDH.DRQALPSISTGSLGLDIALGIGGLPKGR	59
NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDENKSKALQAALSQIEKQFGKNTVMRLCDN.TVQAVEAVSTGSLTLDIALGIGGLPKGR	59
NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSKALQAALSQIEKQFGKNTVMRLCDN.TVQAVEAVSTGSLTLDIALGIGGLPKGR	59
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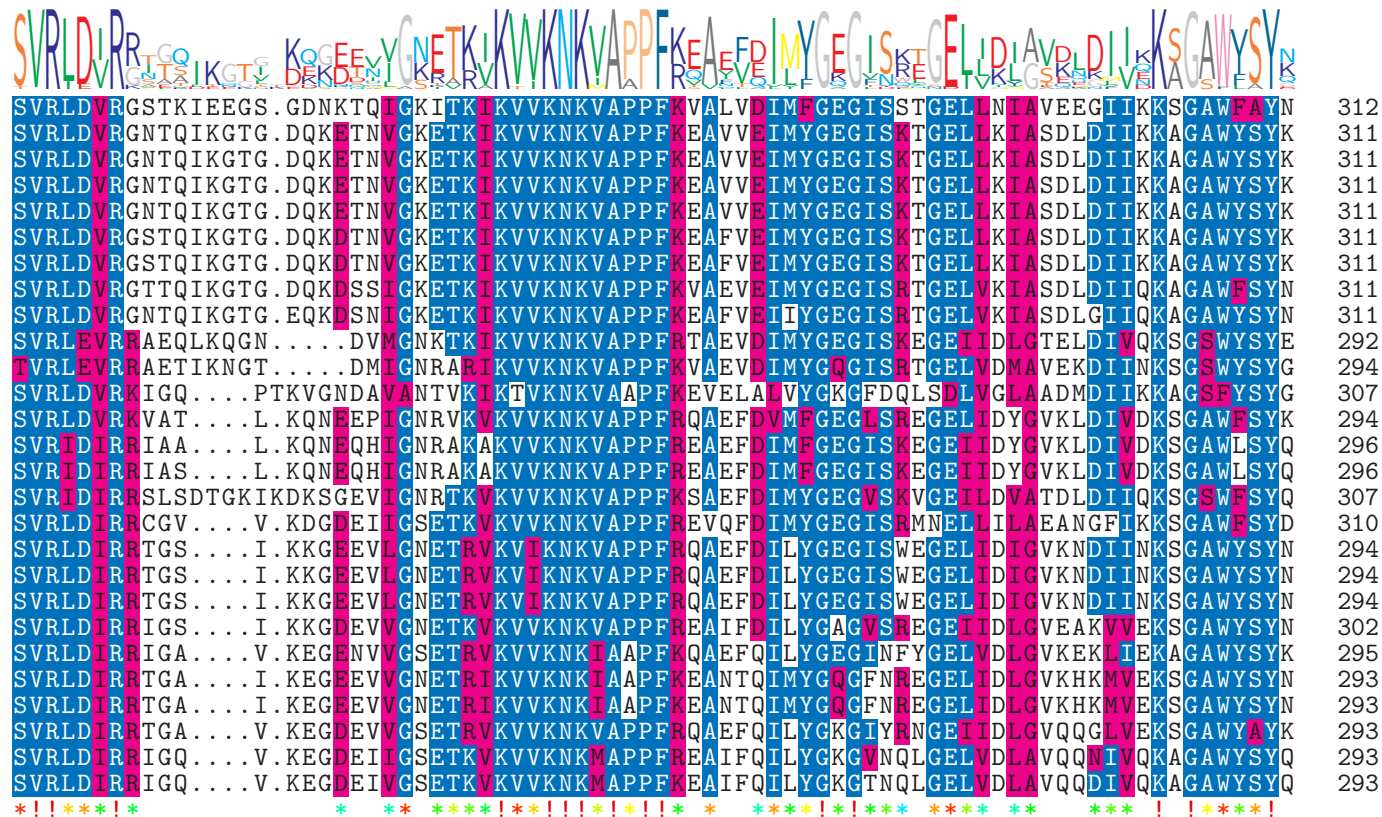
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Sequence	Score
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DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ ID ⁺ DK ⁺ QV ⁺ RS ⁺ KF ⁺ GLIDGEEVSEQD ⁺ TEN ⁺ KK ⁺ DE....PK ⁺ KE ⁺ EA ⁺ ..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DE ⁺ ID ⁺ DK ⁺ QV ⁺ RS ⁺ KF ⁺ GLIDGEEVSEQD ⁺ TEN ⁺ KK ⁺ DE....PK ⁺ KE ⁺ EA ⁺ ..VNEEVPLDLGDELEIE	385
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SERIGQGS ⁺ RE ⁺ NA ⁺ KNY ⁺ LAD ⁺ HED ⁺ VE ⁺ DEV ⁺ RL ⁺ KV ⁺ RA ⁺ AY ⁺ GISDVPPEEDLPTTEDE..QI ⁺ .NILPDDST.....EE.....	355
DERIGQG ⁺ KE ⁺ KT ⁺ IAY ⁺ IA ⁺ ER ⁺ PE ⁺ ME ⁺ QE ⁺ IRDRV ⁺ AA ⁺ IRAGNAGEAPALAPAPAAPEAA...EA.....	363
DKKL ⁺ GQGS ⁺ RE ⁺ NA ⁺ SK ⁺ AL ⁺ FL ⁺ KE ⁺ NPE ⁺ IA ⁺ DE ⁺ IT ⁺ KA ⁺ IQ ⁺ NSM ⁺ CTEGM.....ISGSEDDEG.....EE.....	343
DKKL ⁺ GQGS ⁺ RE ⁺ NA ⁺ KALL ⁺ KE ⁺ DK ⁺ AL ⁺ ADE ⁺ IT ⁺ LK ⁺ IK ⁺ ES ⁺ IG ⁺ SNEE....IMPLPDEPL.....EEME.....	347
DKKL ⁺ GQGS ⁺ RE ⁺ NA ⁺ KALL ⁺ KE ⁺ DK ⁺ AL ⁺ ADE ⁺ IT ⁺ LK ⁺ IK ⁺ ES ⁺ IG ⁺ SNEE....IMPLPDEPL.....EEME.....	347
DTKL ⁺ GQGRD ⁺ TV ⁺ KE ⁺ L ⁺ IK ⁺ DN ⁺ PE ⁺ LAE ⁺ ELE ⁺ AK ⁺ IRE ⁺ KLQAK.....	343
GTKIGQG ⁺ KNN ⁺ AV ⁺ KL ⁺ KE ⁺ NPE ⁺ IA ⁺ DK ⁺ LE ⁺ QEI ⁺ RNTL ⁺ AS ⁺ NP ⁺ N....SVLKATASDSN...DES ⁺ DVEEFSEEEEL.....	372
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GAKIGQG ⁺ KDN ⁺ VR ⁺ VWL ⁺ KE ⁺ NPE ⁺ IS ⁺ DE ⁺ IDA ⁺ KI ⁺ RAL ⁺ NCV ⁺ EMH....ITEG.....T...QDET ⁺ DGER ⁺ PEE.....	348
GAKIGQG ⁺ KDN ⁺ VR ⁺ VWL ⁺ KE ⁺ NPE ⁺ IS ⁺ DE ⁺ IDA ⁺ KI ⁺ RAL ⁺ NCV ⁺ EMH....ITEG.....T...QDET ⁺ DGER ⁺ PEE.....	348
GERIGQGRD ⁺ NC ⁺ REF ⁺ LR ⁺ EN ⁺ AE ⁺ LARE ⁺ IE ⁺ NK ⁺ VRE ⁺ HLGV ⁺ TPM.....GAVTLAE ⁺ EE ⁺ .VE...ED.....	352
GEKIGQG ⁺ KAN ⁺ ATA ⁺ WL ⁺ KN ⁺ PETA ⁺ KE ⁺ IE ⁺ KK ⁺ VRE ⁺ LLSN ⁺ PN....STPDFSV...D...DSEGVAETNEDF.....	353
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GDKIGQG ⁺ KAN ⁺ ACK ⁺ YL ⁺ KE ⁺ NPE ⁺ IA ⁺ KT ⁺ LD ⁺ KK ⁺ LRE ⁺ MLLN ⁺ PEN....MQLIAETSSAA...DDVE ⁺ F ⁺ GAV ⁺ PEEF.....	354
GSKIGQG ⁺ KANA ⁺ AK ⁺ YLE ⁺ EN ⁺ PE ⁺ IG ⁺ QIE ⁺ QQI ⁺ RA ⁺ KLLV ⁺ TSA....NTKATPVAEDL...ADAD ⁺ I.....	347
GNKIGQG ⁺ KNN ⁺ VIR ⁺ YLE ⁺ EN ⁺ PC ⁺ ISTE ⁺ IE ⁺ AV ⁺ IRE ⁺ QLLT ⁺ TKAS....DQTAA ⁺ .HDETE...EEP ⁺ DLLES.....	349
GNKIGQG ⁺ KNN ⁺ VIR ⁺ YLE ⁺ EN ⁺ NC ⁺ IA ⁺ EIE ⁺ ERN ⁺ IRE ⁺ QLLT ⁺ TGT....NGAV ⁺ Q ⁺ .I ⁺ .EDE...EEP ⁺ DLLES.....	349

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consensus			

- non conserved
- similar
- ≥ 50% conserved