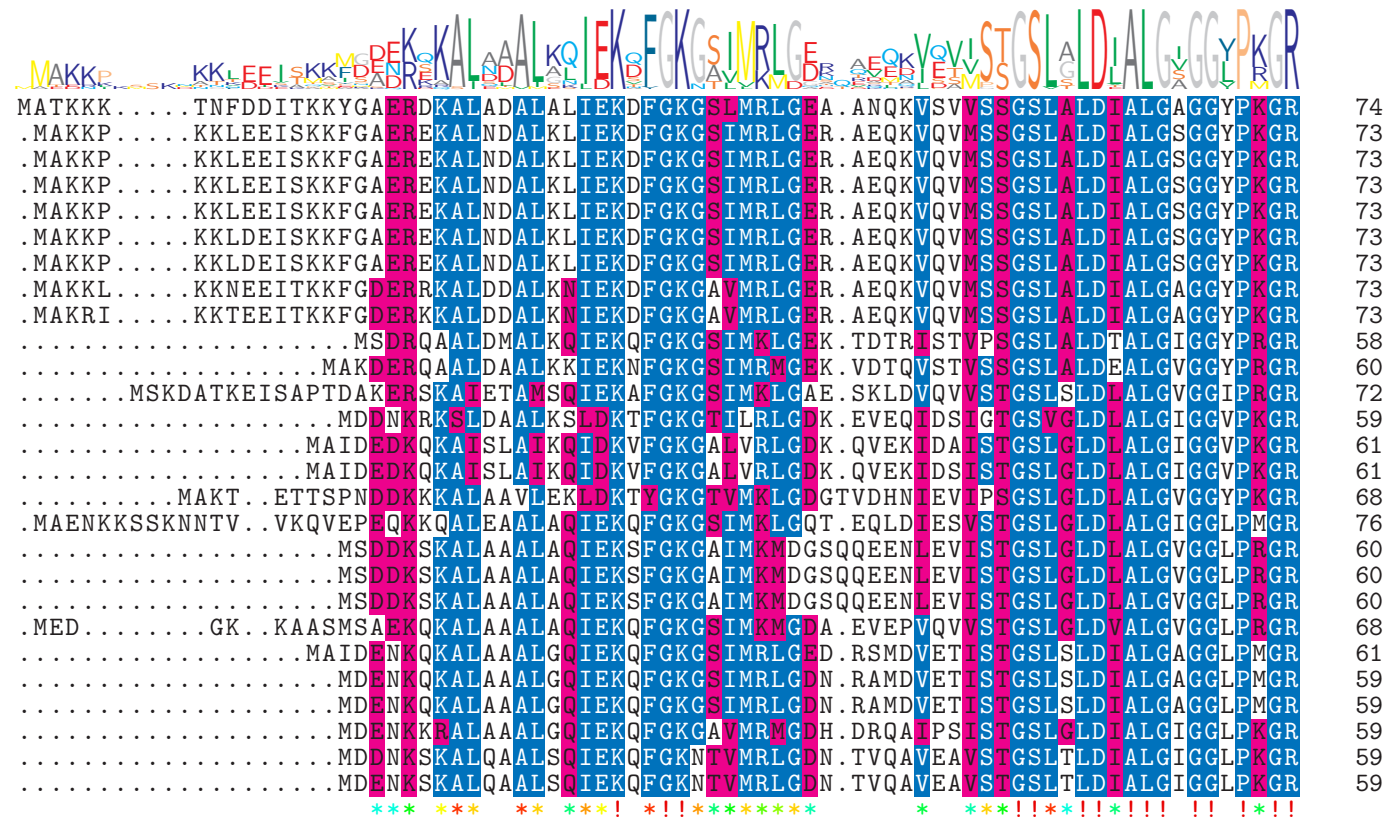


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consensus

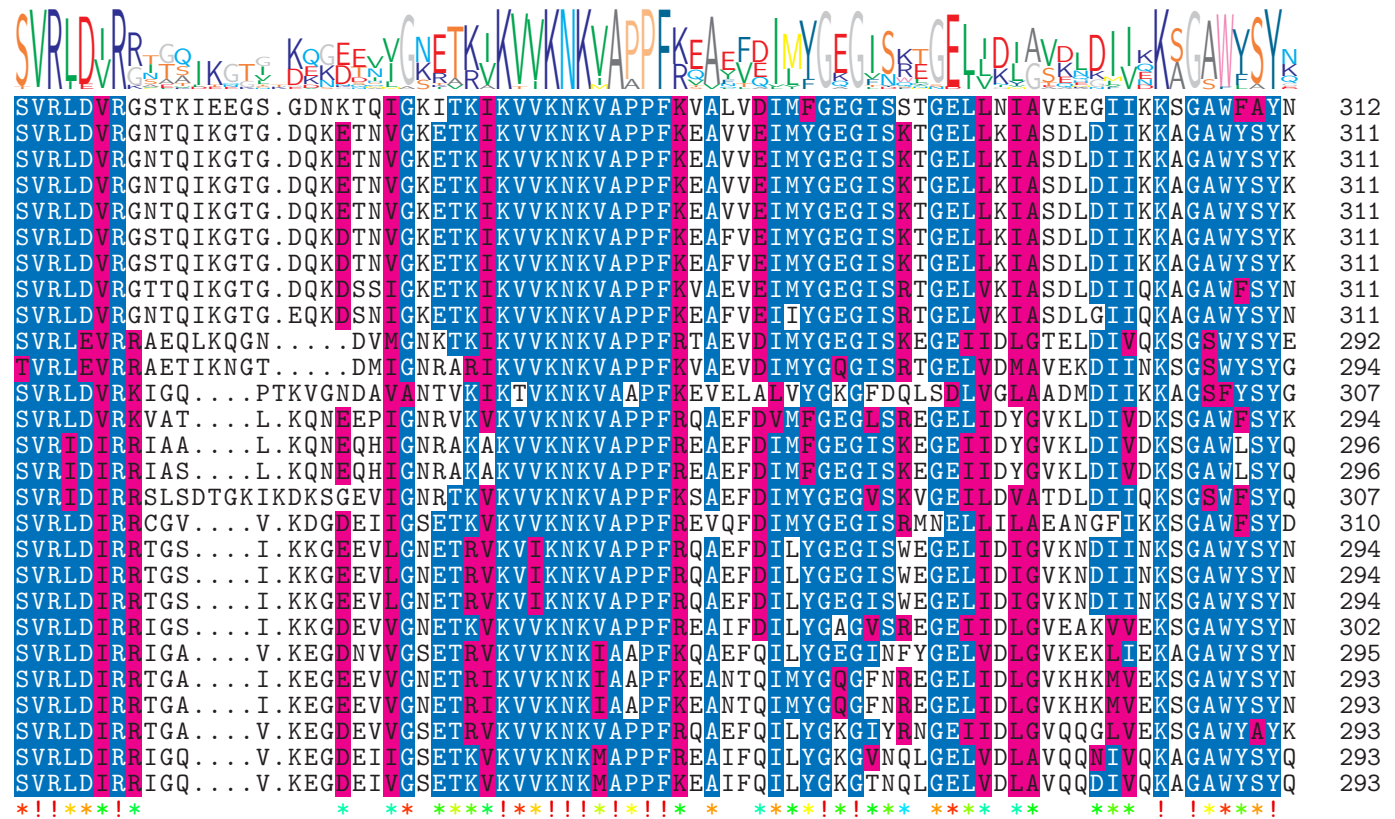
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
DEKIGGGA ¹ E ² KA ³ KN ⁴ YL ⁵ KE ⁶ HQ ⁷ DV ⁸ F ⁹ DE ¹⁰ ID ¹¹ HK ¹² VRAAH ¹³ GI ¹⁴ LDDSEVAETEEETTA...SKTKAKAKKEEKAVETEEIELELED.	387
DEKIGGGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SKF ¹² GI ¹³ LIDGEEVSEQD ¹⁴ TENK...DE...PKKEEA...VNEEVPLDLGDE	381
DEKIGGGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SKF ¹² GI ¹³ LIDGEEVSEQD ¹⁴ TENK...DE...PKKEEA...VNEEVPLDLGDE	381
DEKIGGGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SKF ¹² GI ¹³ LIDGEEVSEQD ¹⁴ TENK...DE...PKKEEA...VNEEVPLDLGDE	381
DEKIGGGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PE ⁶ VFA ⁷ DE ⁸ ID ⁹ HQ ¹⁰ VR ¹¹ VQF ¹² GI ¹³ LIDGEEAAE...SKK...DE...VAQVDS...VNEEVTLDLGD	377
DEKIGGGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ HQ ¹⁰ VR ¹¹ VQF ¹² GI ¹³ LIDGEEIAE...SKK...DE...AAQVDS...VNEEVTLDLGD	377
GEKIGGGS ¹ EN ² AK ³ RYLA ⁴ DHP ⁵ QL ⁶ FD ⁷ DE ⁸ ID ⁹ RK ¹⁰ VR ¹¹ VKF ¹² GL ¹³ LEESEESAMAVASE...E...TDDLALDLNG	373
GEKIGGGS ¹ EN ² AK ³ KFLA ⁴ DN ⁵ PE ⁶ IF ⁷ DD ⁸ ID ⁹ HK ¹⁰ VR ¹¹ VQY ¹² GL ¹³ IEEDNTEEKQSSKEK...ETDEK...ADKNLVLELDDT	378
EE ¹ RL ² GQ ³ GRE ⁴ NA ⁵ KQ ⁶ FL ⁷ KE ⁸ NK ⁹ DI ¹⁰ ML ¹¹ IQ ¹² EQ ¹³ IRE ¹⁴ HY ¹⁵ GL ¹⁶ DNNGVVQQAEETQE...EL ¹⁷ .EFE ¹⁸ .E...EE	348
SERIGGG ¹ RE ² NA ³ KNYLA ⁴ DH ⁵ ED ⁶ VE ⁷ DE ⁸ VR ⁹ LK ¹⁰ VRAAY ¹¹ GIS ¹² DVPEEDLPTTEDE...QI ¹³ .NILPDDST...EE	355
DERIGGG ¹ KE ² KTI ³ AY ⁴ IA ⁵ ERP ⁶ EME ⁷ QE ⁸ IT ⁹ DR ¹⁰ VMAA ¹¹ IRAGNAGEAPALAPAPAAPEAA ¹² EA	363
DKKLGGG ¹ RE ² NSKA ³ FL ⁴ KE ⁵ NP ⁶ IEA ⁷ DE ⁸ IT ⁹ KA ¹⁰ IQ ¹¹ NSM ¹² GI ¹³ EGMI...SGSEDD...EGEE	343
DKKLGGG ¹ RE ² NA ³ KALL ⁴ KED ⁵ KALA ⁶ DE ⁷ IT ⁸ TK ⁹ IK ¹⁰ ESIG ¹¹ SNEEI...MPLPDE...PLEEME	347
DKKLGGG ¹ RE ² NA ³ KALL ⁴ KED ⁵ KALA ⁶ DE ⁷ IT ⁸ TK ⁹ IK ¹⁰ ESIG ¹¹ SNEEI...MPLPDE...PLEEME	347
DTKLGGGR ¹ DT ² V ³ KEL ⁴ IK ⁵ DN ⁶ PELA ⁷ E ⁸ LE ⁹ AK ¹⁰ IREKLQAK	343
GTKIGGG ¹ KNN ² AVK ³ WL ⁴ KEN ⁵ PEIA ⁶ DK ⁷ LE ⁸ QE ⁹ IRNTLA ¹⁰ SNPNS...VLKATASDSN ¹¹ DES ¹² DVEEFS...EEEL	372
GAKIGGG ¹ KDN ² VR ³ VL ⁴ WLN ⁵ KEN ⁶ PEIS ⁷ DE ⁸ IDA ⁹ KIRALNG ¹⁰ VMHI...TEGTQDET...GERP...EE	348
GAKIGGG ¹ KDN ² VR ³ VL ⁴ WLN ⁵ KEN ⁶ PEIS ⁷ DE ⁸ IDA ⁹ KIRALNG ¹⁰ VMHI...TEGTQDET...GERP...EE	348
GAKIGGG ¹ KDN ² VR ³ VL ⁴ WLN ⁵ KEN ⁶ PEIS ⁷ DE ⁸ IDA ⁹ KIRALNG ¹⁰ VMHI...TEGTQDET...GERP...EE	348
GERIGGG ¹ RD ² NC ³ REFL ⁴ RENA ⁵ E ⁶ LARE ⁷ IE ⁸ ENK ⁹ VREHL ¹⁰ GVTPMG...AVTL ¹¹ .AAEEVE ¹² ED	352
GEKIGGG ¹ KANATN ² WL ³ KN ⁴ PEATA ⁵ IE ⁶ EKK ⁷ RELLLNQDS...TPDFSVDSDG ⁸ EDV...KETN...EDF	354
GDKIGGG ¹ KANACKY ² LKEN ³ PEIA ⁴ TK ⁵ LKK ⁶ REMLLN ⁷ PENM...QLIAETSSAAD ⁸ VEFGAVP...EEF	354
GDKIGGG ¹ KANACKY ² LKEN ³ PEIA ⁴ TK ⁵ LKK ⁶ REMLLN ⁷ PENM...QLIAETSSAAD ⁸ VEFGAVP...EEF	354
GSKIGGG ¹ KANA ² AKY ³ LEEN ⁴ PEIG ⁵ Q ⁶ EIE ⁷ QQ ⁸ IRAKLL ⁹ Y ¹⁰ TSAN...TKATPVAEDLADADI	347
GNKIGGG ¹ KNN ² VIRY ³ LEEN ⁴ PQ ⁵ ISTE ⁶ IE ⁷ EAV ⁸ IREQLLT ⁹ KASD...QTA ¹⁰ .HDETE ¹¹ EE ¹² PDLLES	349
GNKIGGG ¹ KNN ² VIRY ³ FEENN ⁴ QIA ⁵ EIE ⁶ ERN ⁷ IREQLLT ⁸ TGTN...GAVQ ⁹ .I ¹⁰ EDEE ¹¹ EE ¹² PDLLES	349

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NTDB id 600 KW2 RS01765 WP 011675413.1		387
NTDB id 269 KZH43 RS08665 WP 001085462.1	LEIEIEE	388
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consensus		

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