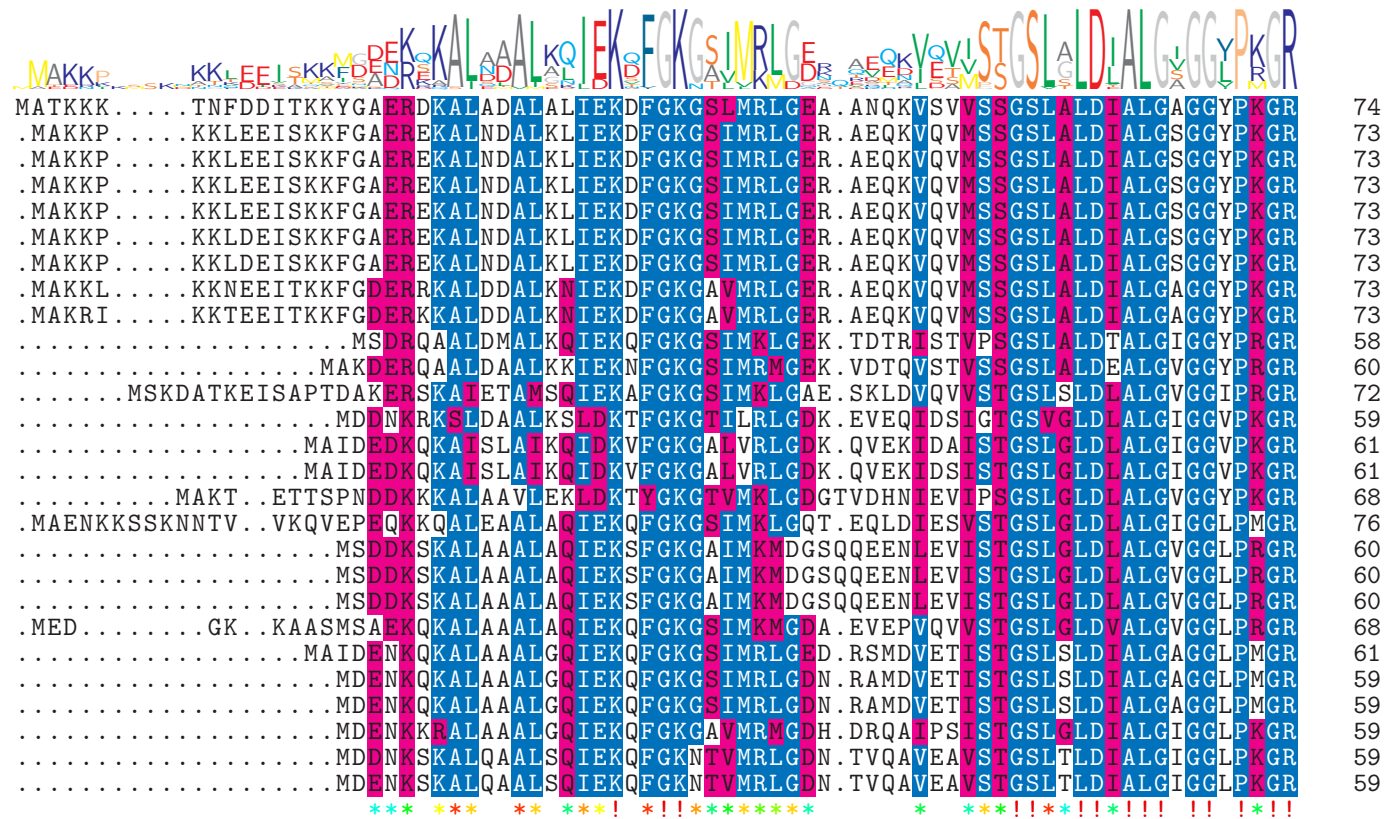


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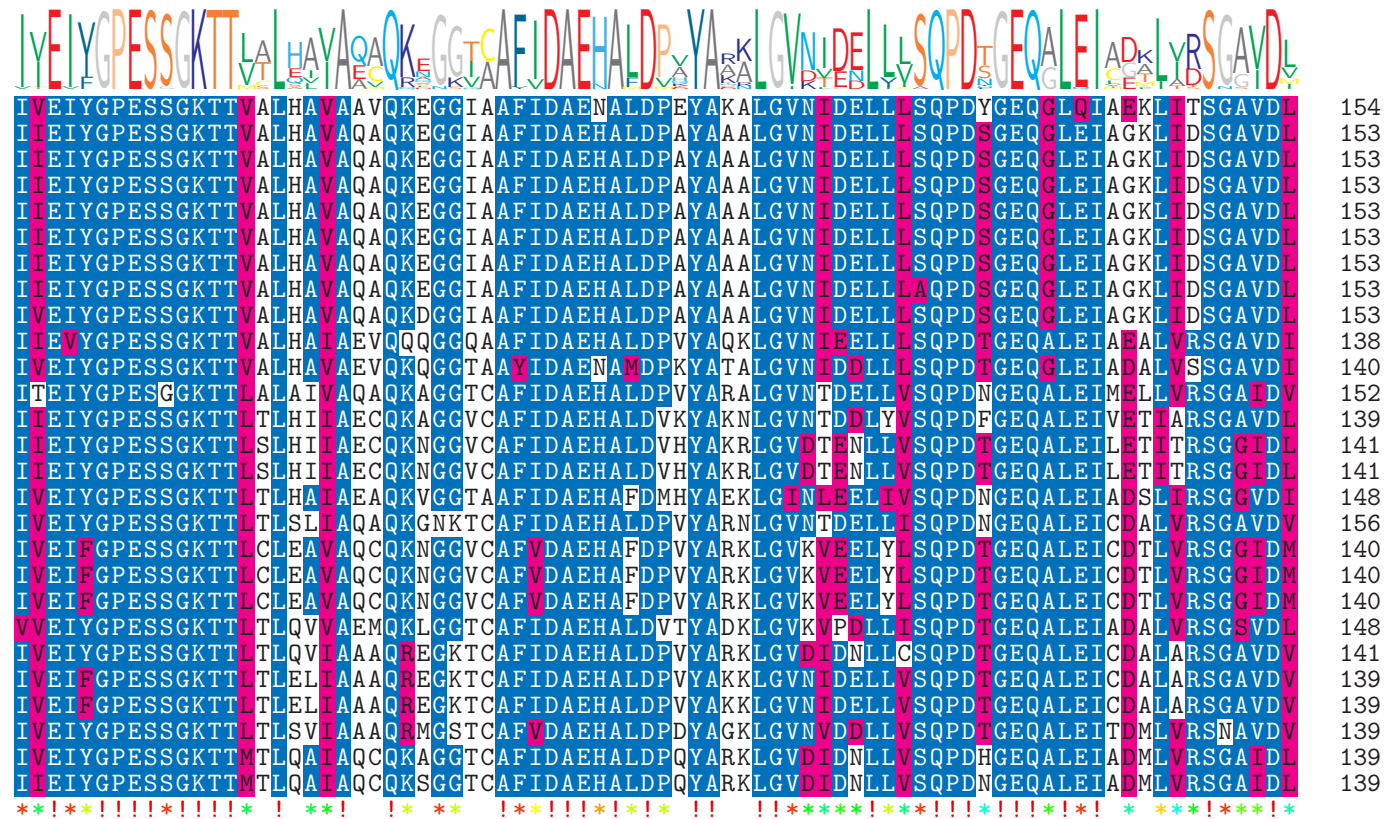
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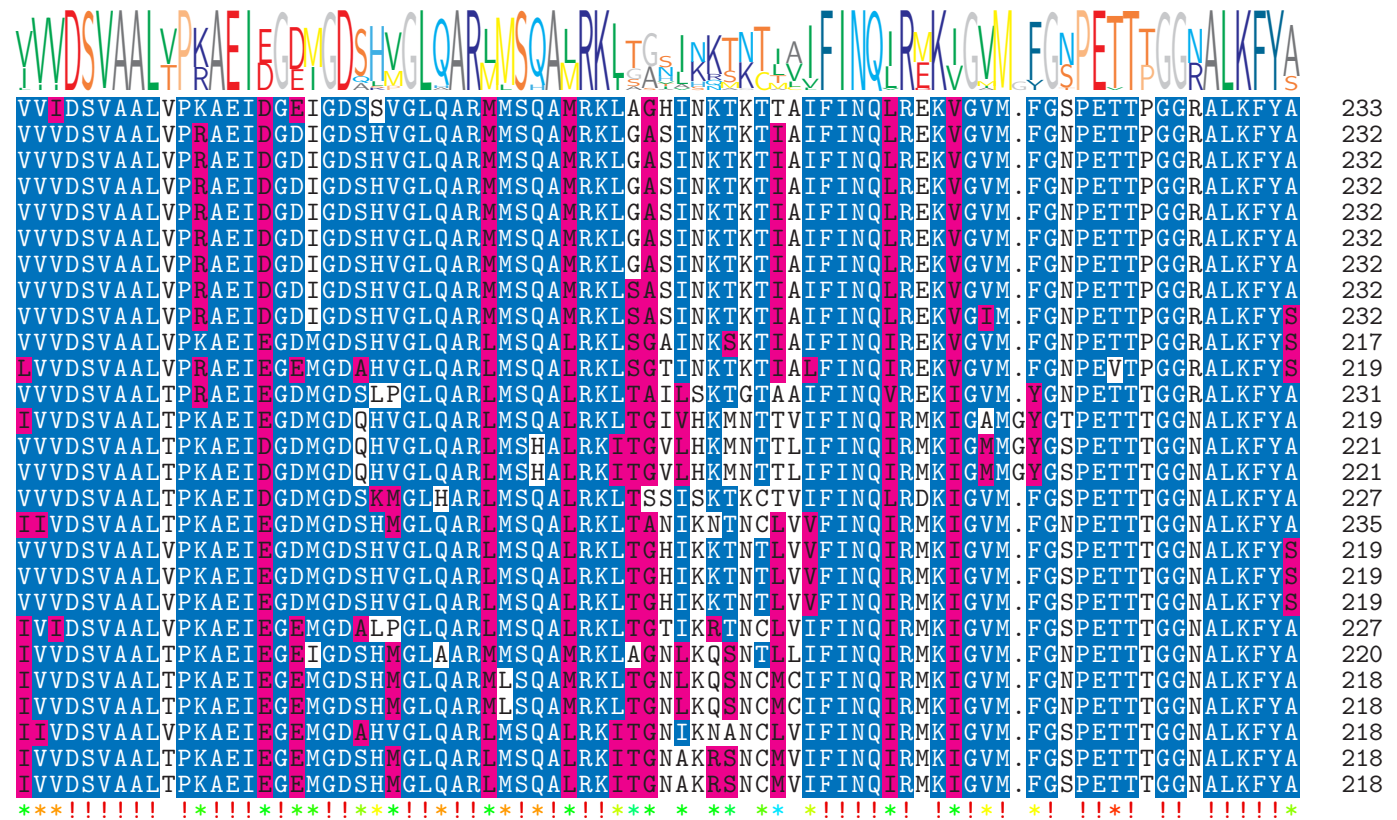
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consensus

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Sequence	Score
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DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SK ¹² FG ¹³ LIDGEEVSEQD ¹⁴ TEN ¹⁵ KK ¹⁶ DE ¹⁷ ...PK ¹⁸ KEEA ¹⁹ ..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SK ¹² FG ¹³ LIDGEEVSEQD ¹⁴ TEN ¹⁵ KK ¹⁶ DE ¹⁷ ...PK ¹⁸ KEEA ¹⁹ ..VNEEVPLDLGDELEIE	385
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GEKIGQGS ¹ EN ² AK ³ KFLA ⁴ DNP ⁵ EIF ⁶ DD ⁷ ID ⁸ HK ⁹ VR ¹⁰ VQ ¹¹ GLIEEDNTEEKQSSKEK ¹²ET ¹³ DE ¹⁴ K ¹⁵ ..ADKNLVL ¹⁶ ELDD ¹⁷ TIELE	382
EE ¹ RL ² GG ³ RENA ⁴ KQ ⁵ FL ⁶ KN ⁷ KD ⁸ IM ⁹ LI ¹⁰ QE ¹¹ QI ¹² RE ¹³ HY ¹⁴ GLD ¹⁵ NNGVV ¹⁶ QQ ¹⁷ AE ¹⁸ ET ¹⁹ QE ²⁰ EL ²¹ .EFE ²² .E ²³	348
SERIGQGS ¹ EN ² AK ³ NYLA ⁴ DH ⁵ ED ⁶ VE ⁷ DE ⁸ VR ⁹ LK ¹⁰ VRAA ¹¹ YG ¹² ISDVPEEDLPTTEDE ¹³ .QI ¹⁴ .NILPDDST ¹⁵EE ¹⁶	355
DERIGQG ¹ KE ² KTI ³ AI ⁴ YIA ⁵ ER ⁶ PE ⁷ ME ⁸ QE ⁹ IT ¹⁰ RD ¹¹ RV ¹² MA ¹³ IRAGNAGEAPALAPAPAAPEAA ¹⁴ ...EA ¹⁵	363
DKKLGGGREN ¹ SKA ² FL ³ KN ⁴ PEIA ⁵ DE ⁶ IT ⁷ KA ⁸ IQ ⁹ NSM ¹⁰ GI ¹¹ EGM ¹²ISGSEDDE ¹³GEF ¹⁴	343
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KALA ⁵ DE ⁶ IT ⁷ LK ⁸ IKES ⁹ IG ¹⁰ SNEE ¹¹IMPLPDEP ¹²LEEME ¹³	347
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KALA ⁵ DE ⁶ IT ⁷ LK ⁸ IKES ⁹ IG ¹⁰ SNEE ¹¹IMPLPDEP ¹²LEEME ¹³	347
DTKLGGGRD ¹ TV ² KEL ³ IK ⁴ DN ⁵ PELA ⁶ E ⁷ LE ⁸ AK ⁹ IREKLQAK ¹⁰	343
GTKIGQG ¹ KNN ² AVK ³ WL ⁴ KN ⁵ PEIA ⁶ DK ⁷ LE ⁸ QEI ⁹ RNTL ¹⁰ ASNP ¹¹SVLKATASDSN ¹² ...DES ¹³ DVEEFSEEL ¹⁴	372
GAKIGGQKDN ¹ VR ² VL ³ KN ⁴ PEIS ⁵ DE ⁶ IDAK ⁷ IRAL ⁸ NG ⁹ VMH ¹⁰IT ¹¹EGT ¹² ...QDET ¹³ DGERPEE ¹⁴	348
GAKIGGQKDN ¹ VR ² VL ³ KN ⁴ PEIS ⁵ DE ⁶ IDAK ⁷ IRAL ⁸ NG ⁹ VMH ¹⁰IT ¹¹EGT ¹² ...QDET ¹³ DGERPEE ¹⁴	348
GAKIGGQKDN ¹ VR ² VL ³ KN ⁴ PEIS ⁵ DE ⁶ IDAK ⁷ IRAL ⁸ NG ⁹ VMH ¹⁰IT ¹¹EGT ¹² ...QDET ¹³ DGERPEE ¹⁴	348
GERIGGGRD ¹ NC ² REFL ³ RENA ⁴ EL ⁵ ARE ⁶ EI ⁷ EN ⁸ KV ⁹ REHL ¹⁰ GV ¹¹ TPM ¹²GAVTL ¹³ .AEEVE ¹⁴ ...ED ¹⁵	352
GEKIGGQKAN ¹ ATAWL ² KN ³ PTTAK ⁴ EIEKK ⁵ VREMLLNQD ⁶DKPAFTVDD ⁷GEGVAETNEDF ⁸	353
GDKIGGQKAN ¹ ACKYL ² KN ³ PEIAKT ⁴ LDKKL ⁵ REMLLNPN ⁶MQLIAETSSAA ⁷ ..DDVEFGAVPEEF ⁸	354
GDKIGGQKAN ¹ ACKYL ² KN ³ PEIAKT ⁴ LDKKL ⁵ REMLLNPN ⁶MQLIAETSSAA ⁷ ..DDVEFGAVPEEF ⁸	354
GSKIGGQKANA ¹ AKY ² LEEN ³ PEIG ⁴ QIE ⁵ EQQ ⁶ IRAKLL ⁷ VTSA ⁸NTKATPVAEDL ⁹ ..ADADI ¹⁰	347
GNKIGGQKNN ¹ VIRY ² LEEN ³ PQISTE ⁴ EIEAV ⁵ IREQLLTKAS ⁶DQ ⁷ TAA ^{8</}	

logo

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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349

consensus

 non conserved
 similar
 ≥ 50% conserved