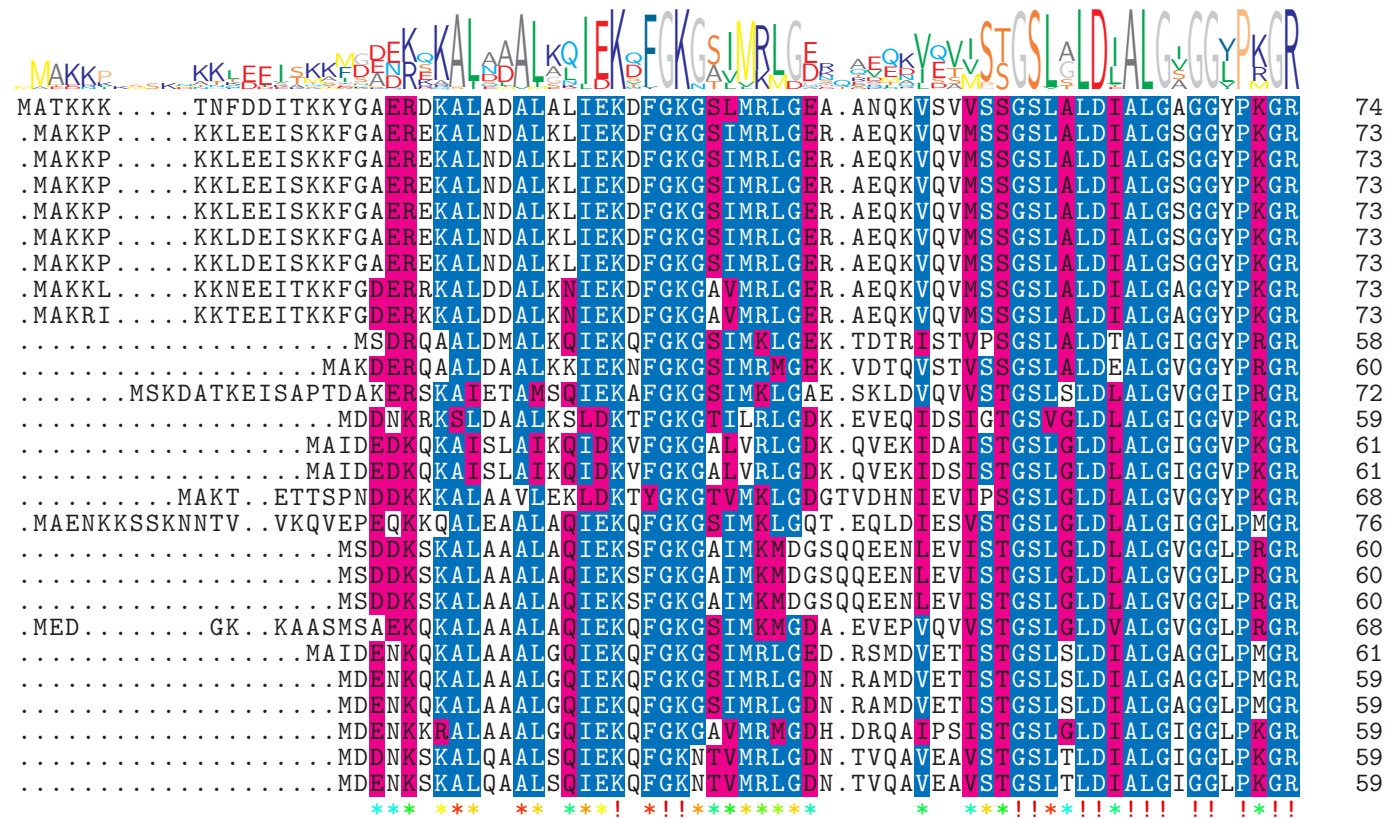


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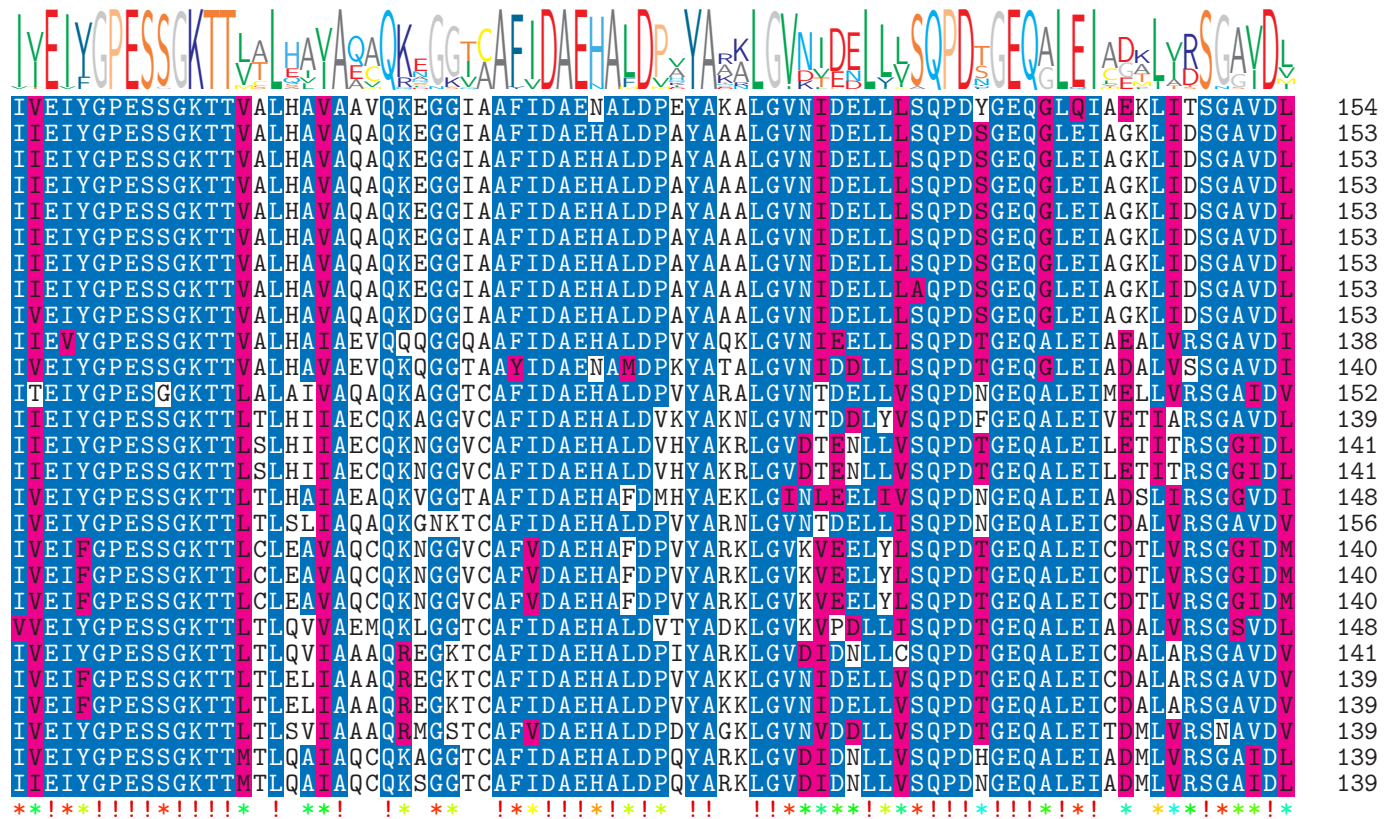
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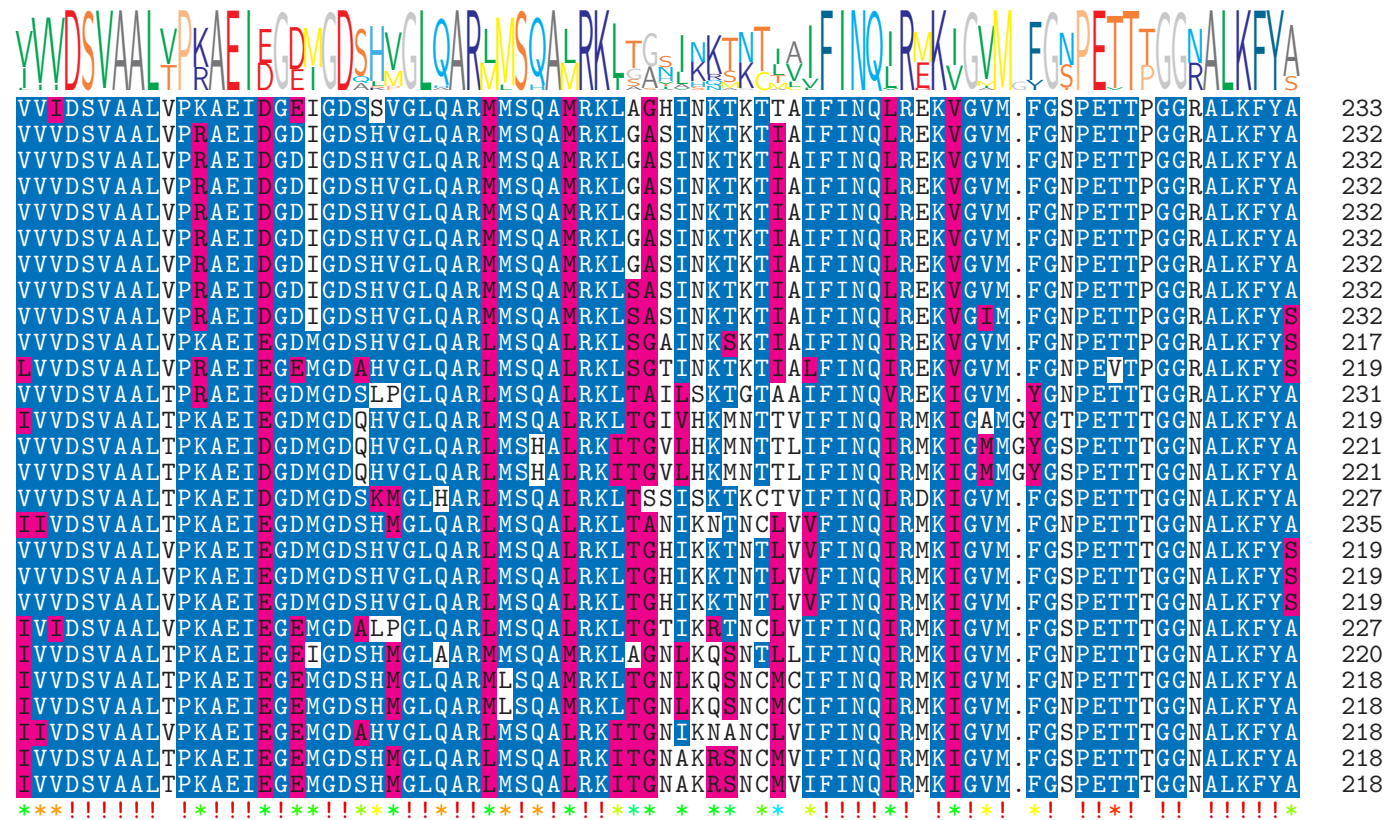
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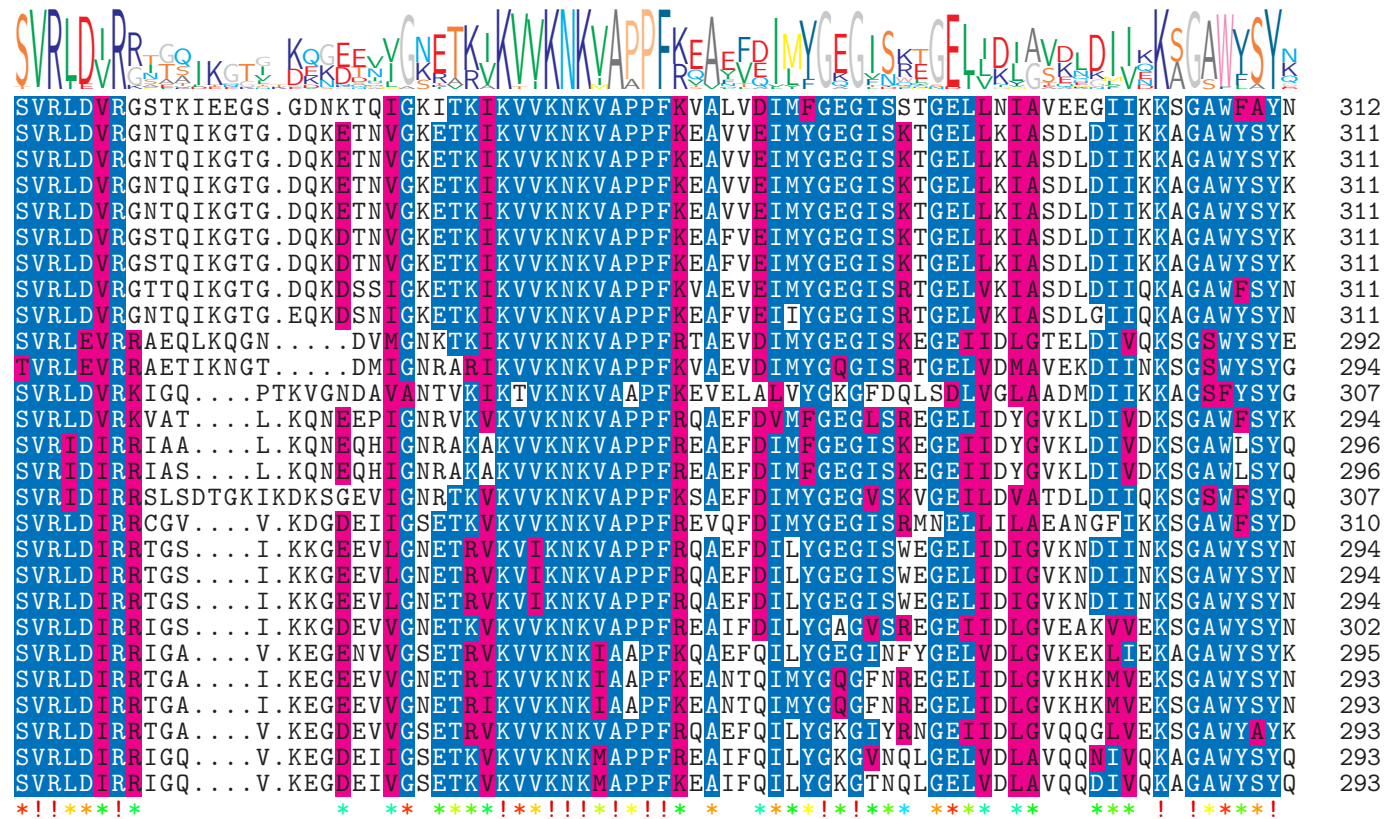
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consensus

Sequence	Score
DEKIGQGA ¹ E ² KA ³ KN ⁴ YL ⁵ KE ⁶ HQ ⁷ DV ⁸ FD ⁹ EID ¹⁰ HK ¹¹ VRAAH ¹² GL ¹³ LD ¹⁴ DDSEVAETEEETTAS ¹⁵ KTKAKAKKE ¹⁶ E ¹⁷ KAVETEEIELE ¹⁸ ED ¹⁹	387
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PEIF ⁶ DEID ⁷ KQ ⁸ VR ⁹ SKF ¹⁰ GL ¹¹ IDGEEVSEQDTENKKDE ¹² ...PKKEEA ¹³ ..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PEIF ⁶ DEID ⁷ KQ ⁸ VR ⁹ SKF ¹⁰ GL ¹¹ IDGEEVSEQDTENKKDE ¹² ...PKKEEA ¹³ ..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PEIF ⁶ DEID ⁷ KQ ⁸ VR ⁹ SKF ¹⁰ GL ¹¹ IDGEEVSEQDTENKKDE ¹² ...PKKEEA ¹³ ..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PEIF ⁶ DEID ⁷ HQ ⁸ VR ⁹ VQF ¹⁰ GL ¹¹ IDGEEIAES ¹² ...KKDE ¹³ ...AAQV ¹⁴ DS ¹⁵ ..VNEEVTLDLGDLEIE	381
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PEVFA ⁶ EID ⁷ HQ ⁸ VR ⁹ VQF ¹⁰ GL ¹¹ IDGEEAAES ¹² ...KKDE ¹³ ...VAQV ¹⁴ DS ¹⁵ ..VNEEVTLDLGDLEIE	381
GEKIGQGS ¹ EN ² AK ³ RYLA ⁴ DHPQLF ⁵ DEID ⁶ RK ⁷ VR ⁸ VKF ⁹ GL ¹⁰ LEEESEESAMAVASE ¹¹E ¹²TDDLALDLNGIEIE	377
GEKIGQGS ¹ EN ² AK ³ KFLA ⁴ DN ⁵ PEIF ⁶ DD ⁷ ID ⁸ HK ⁹ VR ¹⁰ VQY ¹¹ GL ¹² IEEDNTEEKQSSKEK ¹³ETDE ¹⁴ K ¹⁵ ..ADKNLVLELDDTIELE	382
EE ¹ RL ² GG ³ RENA ⁴ KQFL ⁵ KN ⁶ KDIMLMIQE ⁷ QIREHY ⁸ GL ⁹ DNNGVVQQAEETQEEL ¹⁰ .EFE ¹¹ .E ¹²	348
SERIGGG ¹ RENA ² KNYLA ³ DH ⁴ ED ⁵ VE ⁶ DE ⁷ VR ⁸ LK ⁹ VRAAY ¹⁰ GIS ¹¹ SDVPEEDLPTTEDE ¹² .QI ¹³ .NILPDDST ¹⁴EE ¹⁵	355
DERIGGG ¹ KE ² KTIAY ³ IA ⁴ ERP ⁵ MEQE ⁶ FEIRDRVMAAIRAGNAGEAPALAPAPAAPEAA ⁷ ...EA ⁸	363
DKKLGGG ¹ RENSKA ² FL ³ IKEN ⁴ PEIA ⁵ DEITKA ⁶ IQNSM ⁷ GI ⁸ EGM ⁹ISGSEDDEG ¹⁰EE ¹¹	343
DKKLGGG ¹ RENA ² KALL ³ KEDKALA ⁴ DEITLK ⁵ IKESIG ⁶ SNEE ⁷IMPLPDEPL ⁸EEME ⁹	347
DKKLGGG ¹ RENA ² KALL ³ KEDKALA ⁴ DEITLK ⁵ IKESIG ⁶ SNEE ⁷IMPLPDEPL ⁸EEME ⁹	347
DTKLGGGRD ¹ TV ² KEL ³ IKDN ⁴ PELA ⁵ E ⁶ LEAK ⁷ IREKLQAK ⁸	343
GTKIGQG ¹ KNN ² AVK ³ WL ⁴ KEN ⁵ PEIA ⁶ DKLE ⁷ QEIRNTLAS ⁸ NP ⁹ N.....SVLKATASDSN ¹⁰ ...DES ¹¹ DVEEFSEEL ¹²	372
GAKIGGQ ¹ KDN ² VR ³ VL ⁴ KEN ⁵ PEIS ⁶ DEIDAK ⁷ IRALNG ⁸ VMH ⁹ITEG ¹⁰T ¹¹ ...QDET ¹² DGERPEE ¹³	348
GAKIGGQ ¹ KDN ² VR ³ VL ⁴ KEN ⁵ PEIS ⁶ DEIDAK ⁷ IRALNG ⁸ VMH ⁹ITEG ¹⁰T ¹¹ ...QDET ¹² DGERPEE ¹³	348
GAKIGGQ ¹ KDN ² VR ³ VL ⁴ KEN ⁵ PEIS ⁶ DEIDAK ⁷ IRALNG ⁸ VMH ⁹ITEG ¹⁰T ¹¹ ...QDET ¹² DGERPEE ¹³	348
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GEKIGGQ ¹ KANATA ² WL ³ KN ⁴ PETAK ⁵ EIEKK ⁶ VRELLSNPN ⁷STPDFSV ⁸ ...D ⁹ ...DSEGVAETNEDF ¹⁰	353
GDKIGGQ ¹ KANACKYL ² KEN ³ PEIAKT ⁴ LD ⁵ KKLREMLLNPN ⁶MQLIAETSSAA ⁷ ...DDVEFGAVPEEF ⁸	354
GDKIGGQ ¹ KANACKYL ² KEN ³ PEIAKT ⁴ LD ⁵ KKLREMLLNPN ⁶MQLIAETSSAA ⁷ ...DDVEFGAVPEEF ⁸	354
GSKIGGQ ¹ KANA ² AKYLEN ³ PEIG ⁴ QIE ⁵ EQQIRAKLL ⁶ VTSA ⁷NTKATPVAEDL ⁸ ...ADADI ⁹	347
GNKIGGQ ¹ KNN ² VIRY ³ LEEN ⁴ PQISTE ⁵ IE ⁶ EAVIREQLLTKAS ⁷DQTA ⁸ A.HDETE ⁹ ...EED ¹⁰ LLLES ¹¹	349
GNKIGGQ ¹ KNN ² VIRY ³ FEENN ⁴ QIAE ⁵ IE ⁶ ERNIREQLLTGT ⁷NGAVQ ⁸ .I.EDE ⁹ ...EED ¹⁰ LLLES ¹¹	349

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved