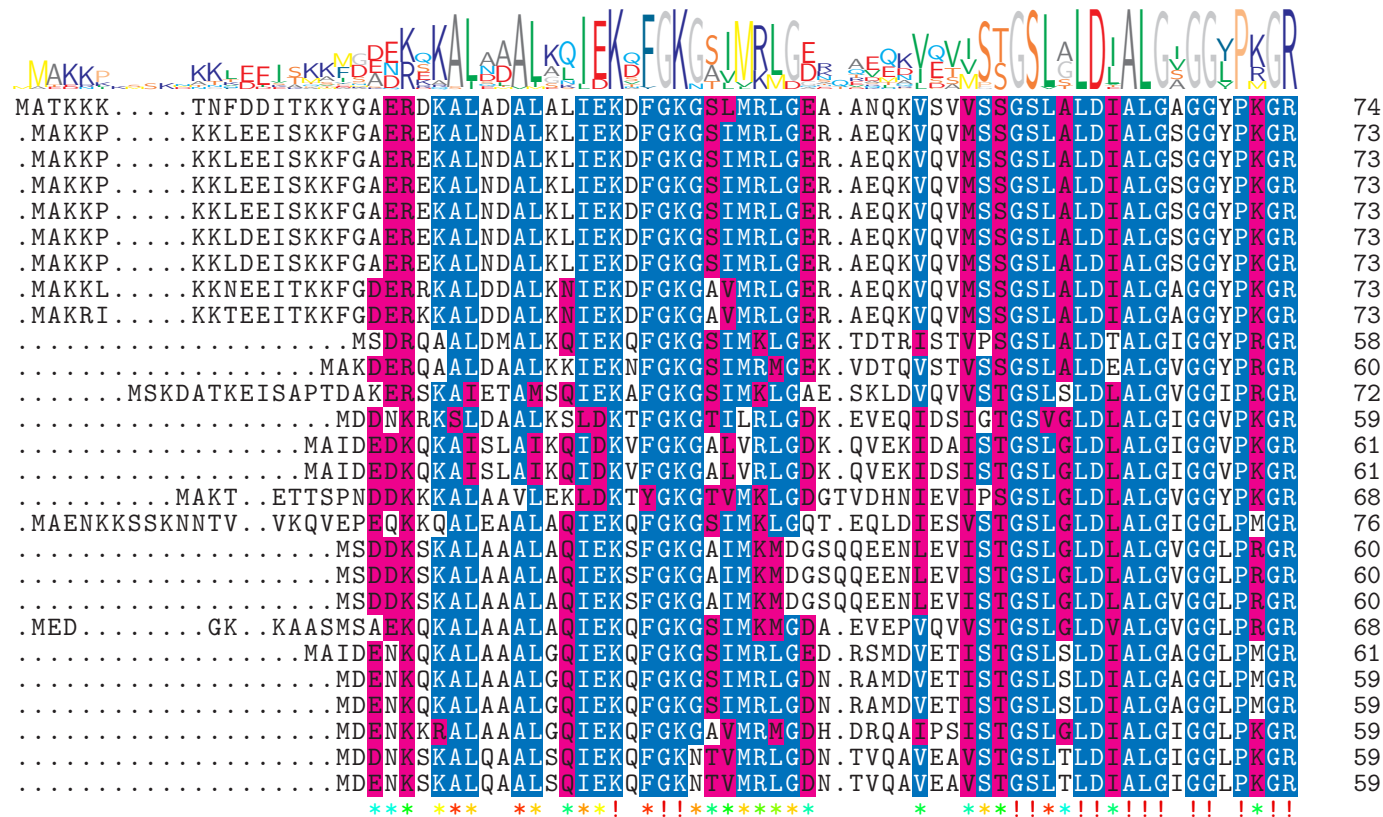


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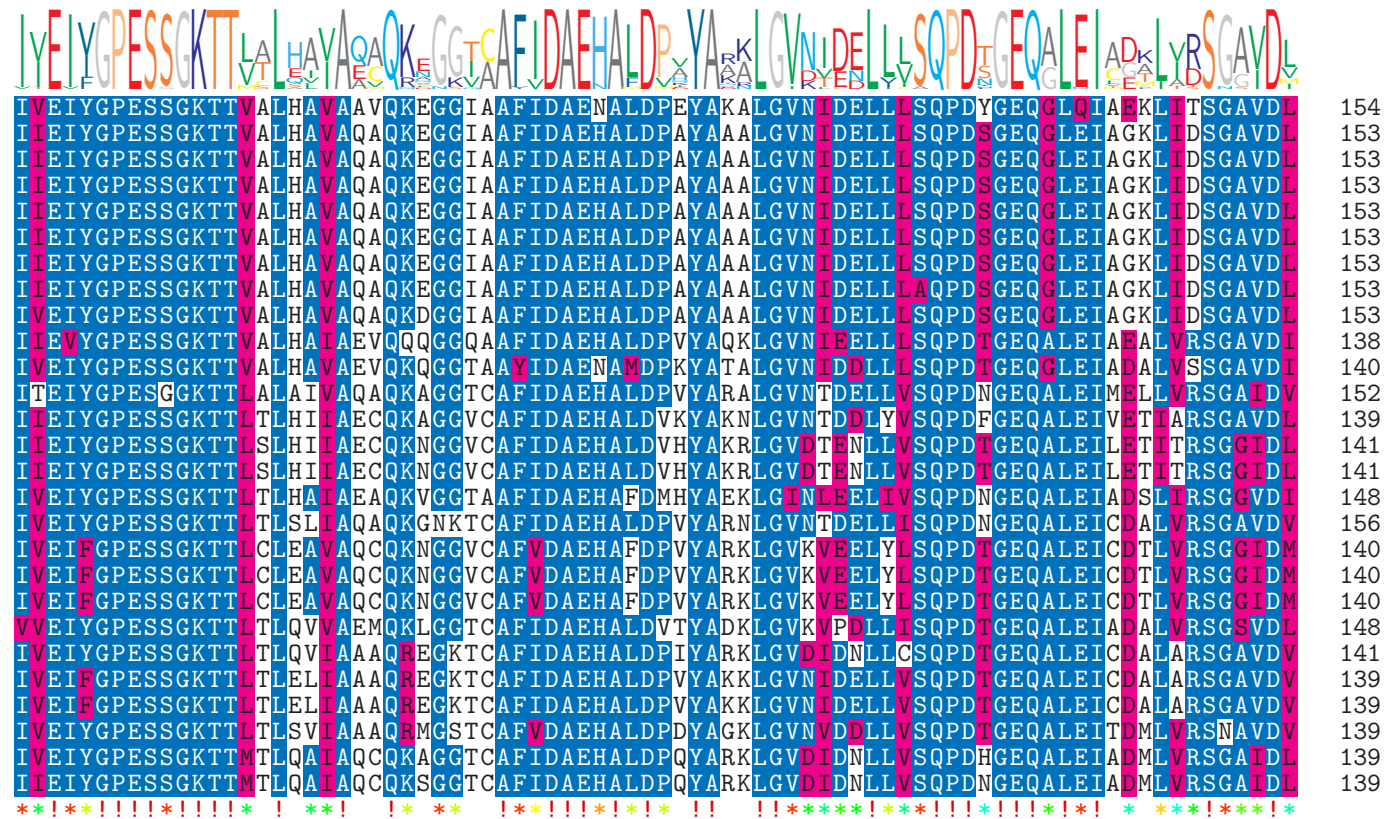
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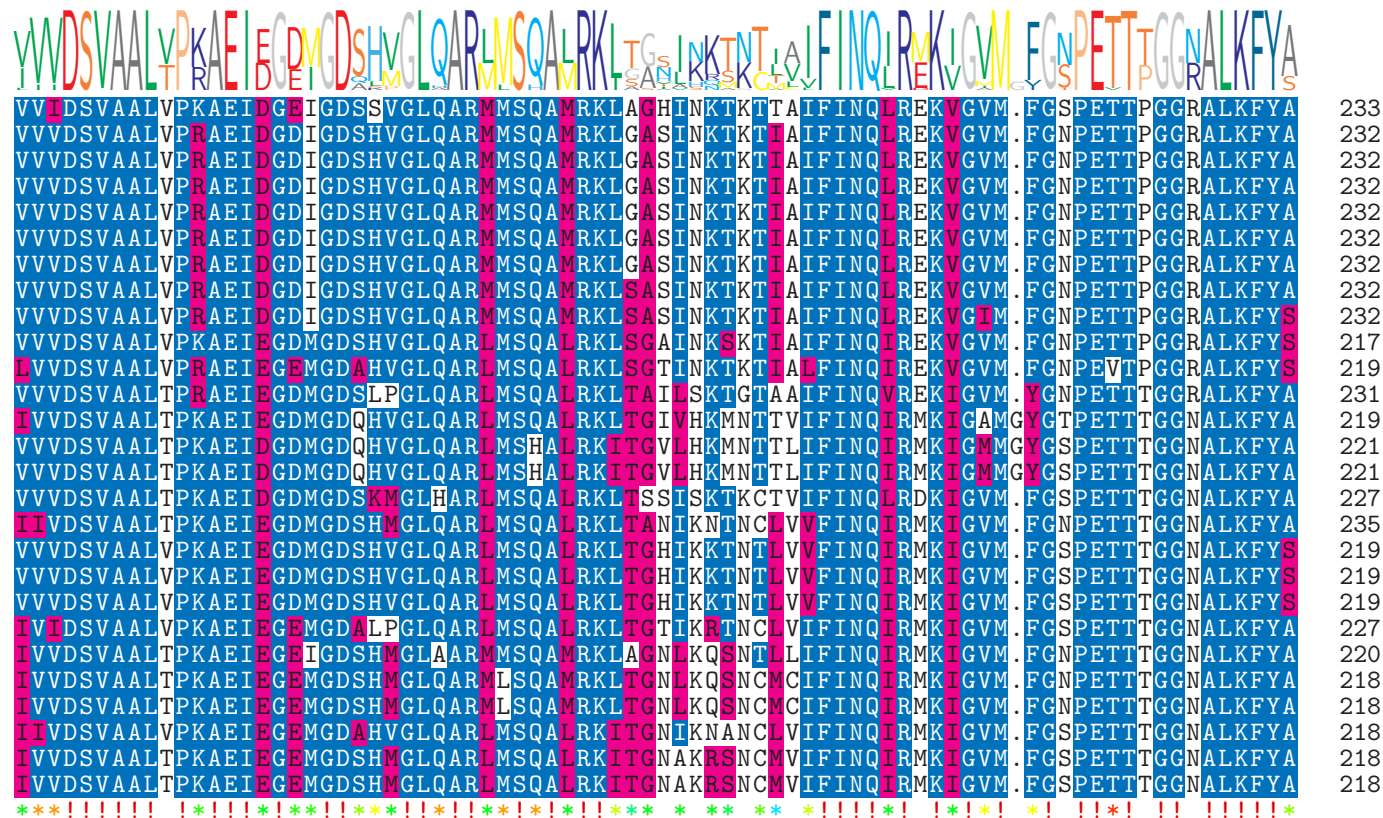
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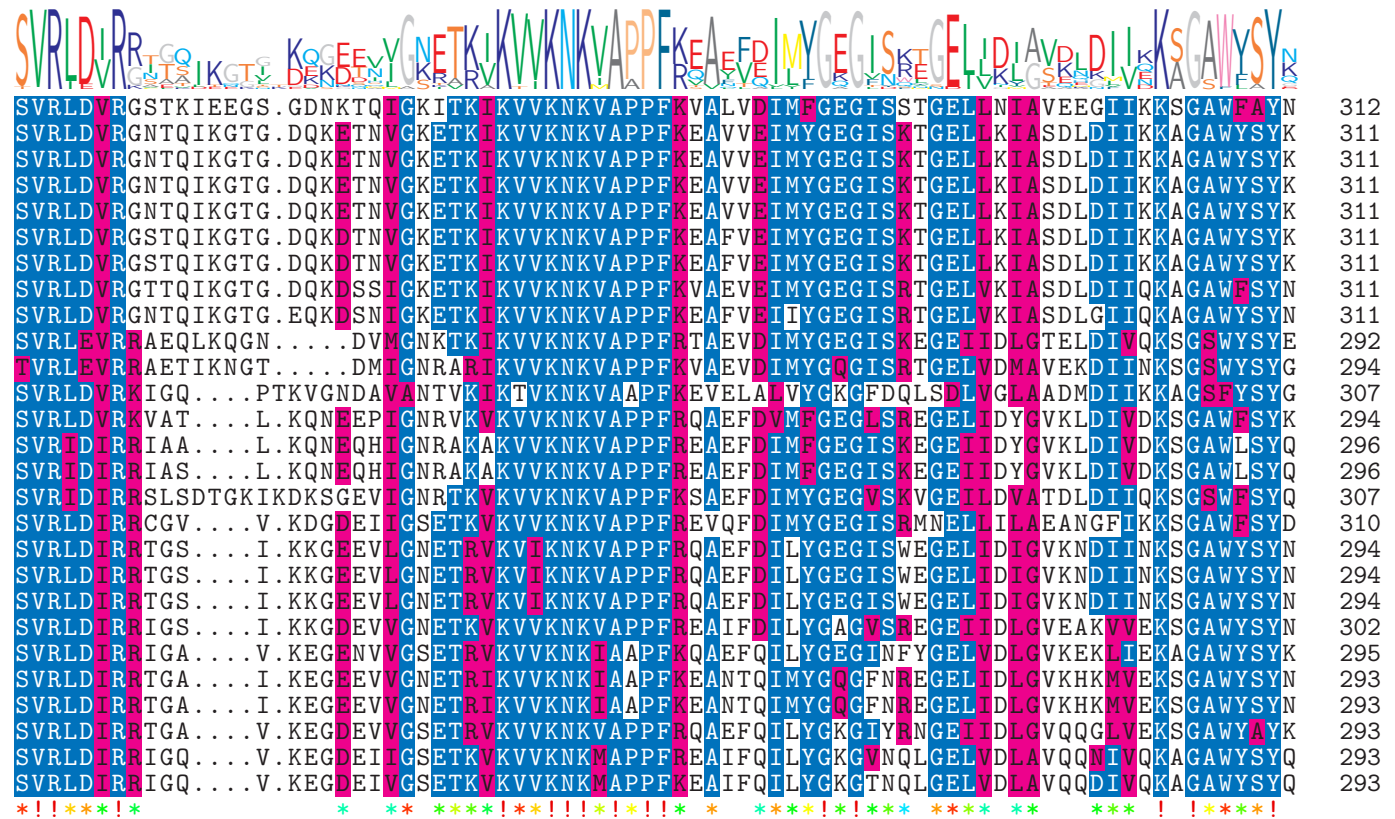
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consensus

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Sequence	Score
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DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ 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 QG ³ REN ⁴ AK ⁵ QFL ⁶ KN ⁷ KDIM ⁸ LI ⁹ QE ¹⁰ QIRE ¹¹ HY ¹² GL ¹³ DNNGVVQQAEETQEEL ¹⁴ .EFE ¹⁵ .E ¹⁶	348
SERIGQGR ¹ EN ² AK ³ NYLA ⁴ DH ⁵ ED ⁶ VE ⁷ RL ⁸ KV ⁹ RAAY ¹⁰ GIS ¹¹ SDVPEEDLPTTEDE ¹² .QI ¹³ .NILPDDST ¹⁴EE ¹⁵	355
DERIGQG ¹ KE ² KTI ³ AY ⁴ IA ⁵ ERP ⁶ EME ⁷ QE ⁸ IRDR ⁹ VMAA ¹⁰ IRAGNAGEAPALAPAPAAPEAA ¹¹ ...EA ¹²	363
DKKL ¹ GG ² RENS ³ KA ⁴ FL ⁵ IKEN ⁶ PEIA ⁷ DEIT ⁸ KA ⁹ IQNSM ¹⁰ GI ¹¹ EGM ¹²ISGSEDDEG ¹³EE ¹⁴	343
DKKL ¹ GG ² RENS ³ AK ⁴ ALL ⁵ KED ⁶ KALA ⁷ DEIT ⁸ LK ⁹ IKES ¹⁰ IG ¹¹ SNEE ¹²IMPLPDEPL ¹³EEME ¹⁴	347
DKKL ¹ GG ² RENS ³ AK ⁴ ALL ⁵ KED ⁶ KALA ⁷ DEIT ⁸ LK ⁹ IKES ¹⁰ IG ¹¹ SNEE ¹²IMPLPDEPL ¹³EEME ¹⁴	347
DTKL ¹ GG ² RD ³ TV ⁴ KEL ⁵ IK ⁶ DN ⁷ PELA ⁸ E ⁹ LE ¹⁰ AK ¹¹ IREKLQAK ¹²	343
GTKIGQG ¹ KNN ² AVK ³ WL ⁴ KEN ⁵ PEIA ⁶ DK ⁷ LE ⁸ QE ⁹ IRNTLA ¹⁰ SNPN ¹¹SVLKATASDSN ¹² ...DES ¹³ DVEEFSEEL ¹⁴	372
GAKIGGQ ¹ KDN ² VR ³ VWL ⁴ KEN ⁵ PEIS ⁶ DEID ⁷ AK ⁸ IRALNG ⁹ VMH ¹⁰ITEG ¹¹T ¹² ...QDET ¹³ DGERPEE ¹⁴	348
GAKIGGQ ¹ KDN ² VR ³ VWL ⁴ KEN ⁵ PEIS ⁶ DEID ⁷ AK ⁸ IRALNG ⁹ VMH ¹⁰ITEG ¹¹T ¹² ...QDET ¹³ DGERPEE ¹⁴	348
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GER ¹ IGQGR ² DN ³ CRE ⁴ FL ⁵ RENA ⁶ E ⁷ LARE ⁸ EIEN ⁹ KV ¹⁰ REHL ¹¹ GV ¹² TPM ¹³GAVTLAEE ¹⁴ .VE ¹⁵ ...ED ¹⁶	352
GEKIGGQ ¹ KAN ² ATA ³ WL ⁴ KN ⁵ PETAK ⁶ EIE ⁷ KKV ⁸ RELLLSNPN ⁹STPDFSV ¹⁰ ...D ¹¹ ...DSEGVAETNEDF ¹²	353
GDKIGGQ ¹ KAN ² ACKYL ³ KEN ⁴ PEIA ⁵ AKT ⁶ L ⁷ DKKL ⁸ REMLLN ⁹ PEN ¹⁰MQLIAETSSAA ¹¹ ...DDVEFGAVPEEF ¹²	354
GDKIGGQ ¹ KAN ² ACKYL ³ KEN ⁴ PEIA ⁵ AKT ⁶ L ⁷ DKKL ⁸ REMLLN ⁹ PEN ¹⁰MQLIAETSSAA ¹¹ ...DDVEFGAVPEEF ¹²	354
GSKIGGQ ¹ KANA ² AKYLE ³ EN ⁴ PEIG ⁵ QIE ⁶ EQ ⁷ IRAKLL ⁸ VTSA ⁹NTKATPVAEDL ¹⁰ ...ADADI ¹¹	347
GNKIGGQ ¹ KNN ² VIRY ³ LEEN ⁴ PQISTE ⁵ EIE ⁶ AV ⁷ IREQLLTKAS ⁸DQTA ⁹ A ¹⁰ .HDETE ¹¹ ...EED ¹² LLLES ¹³	349
GNKIGGQ ¹ KNN ² VIRY ³ FEENN ⁴ QIAE ⁵ EIE ⁶ ERN ⁷ IREQLLTGT ⁸NGAVQ ⁹ .I ¹⁰ .EDE ¹¹ ...EED ¹² LLLES ¹³	349

logo

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consensus			

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