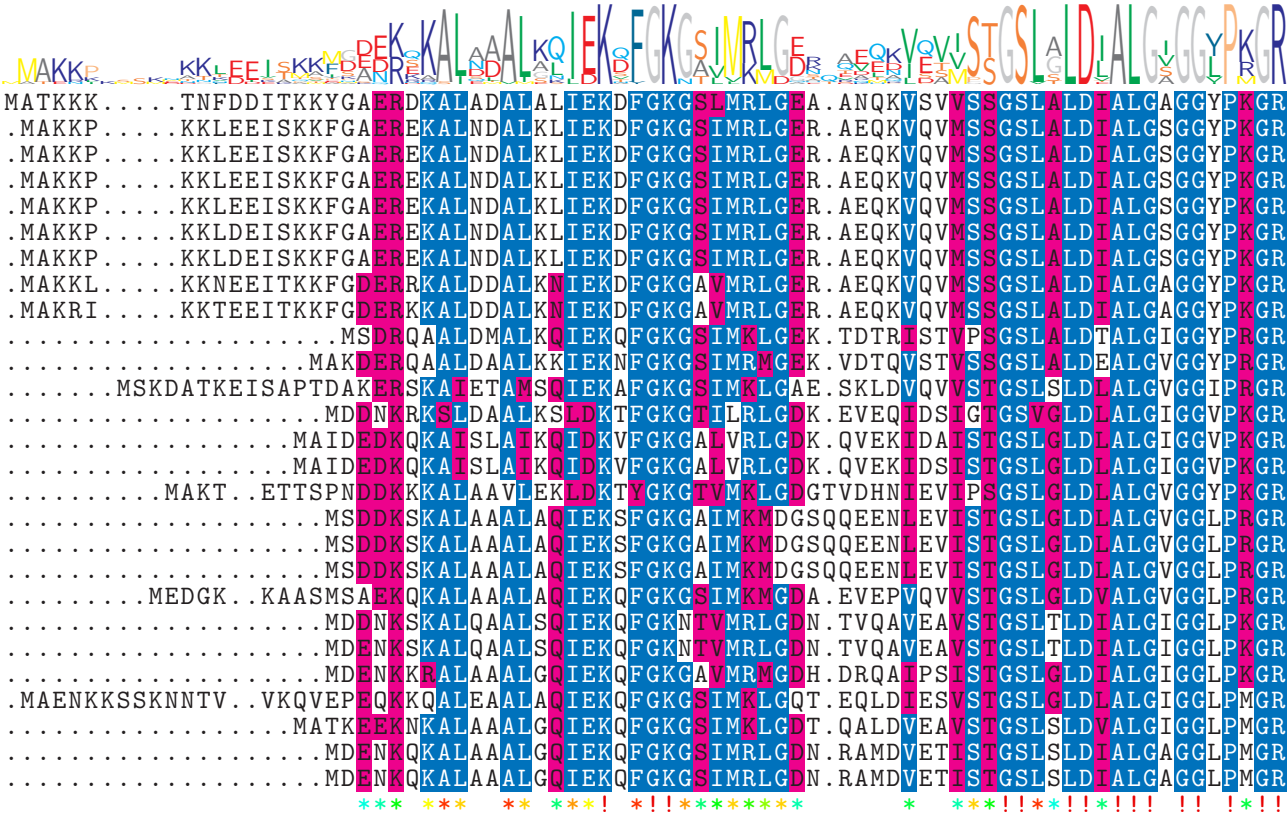


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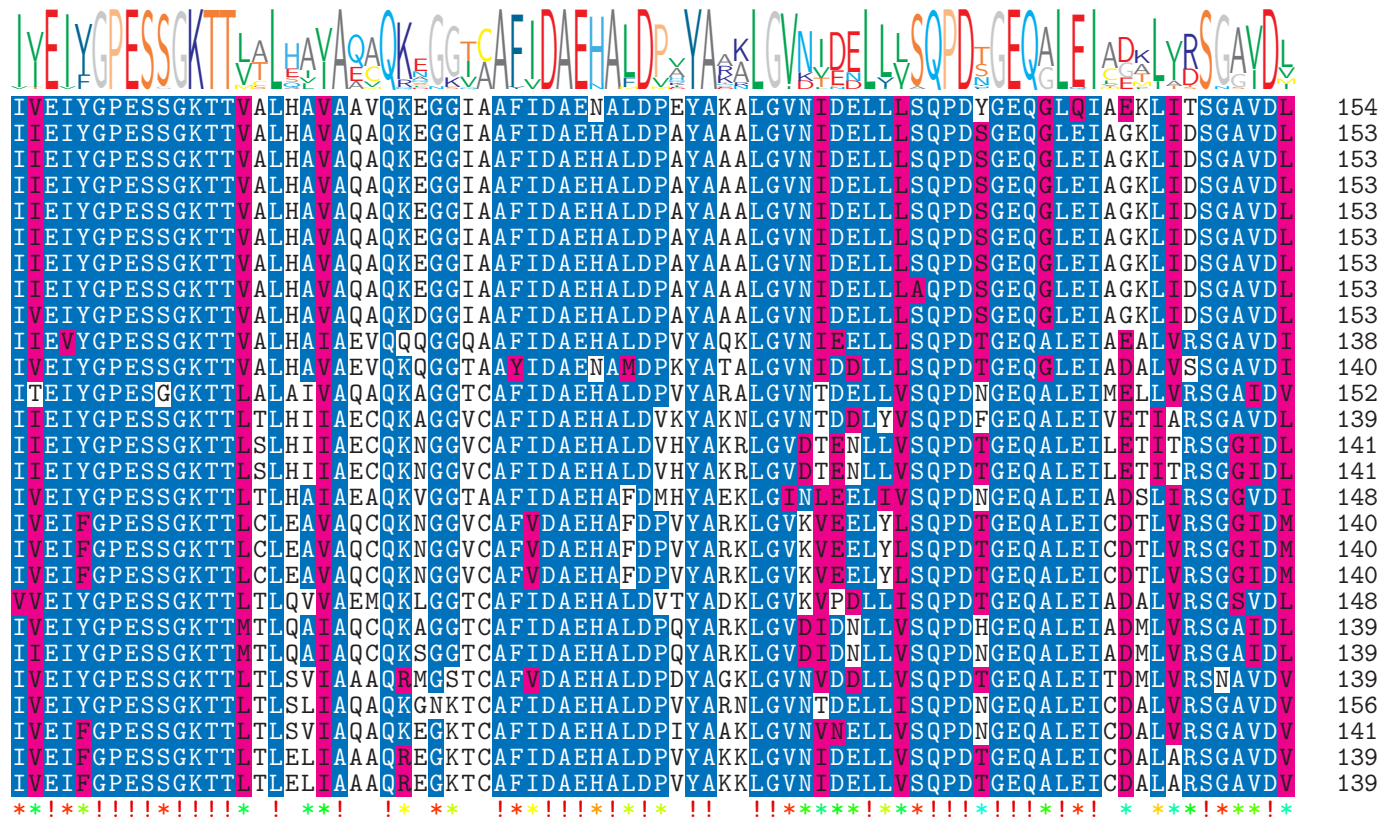


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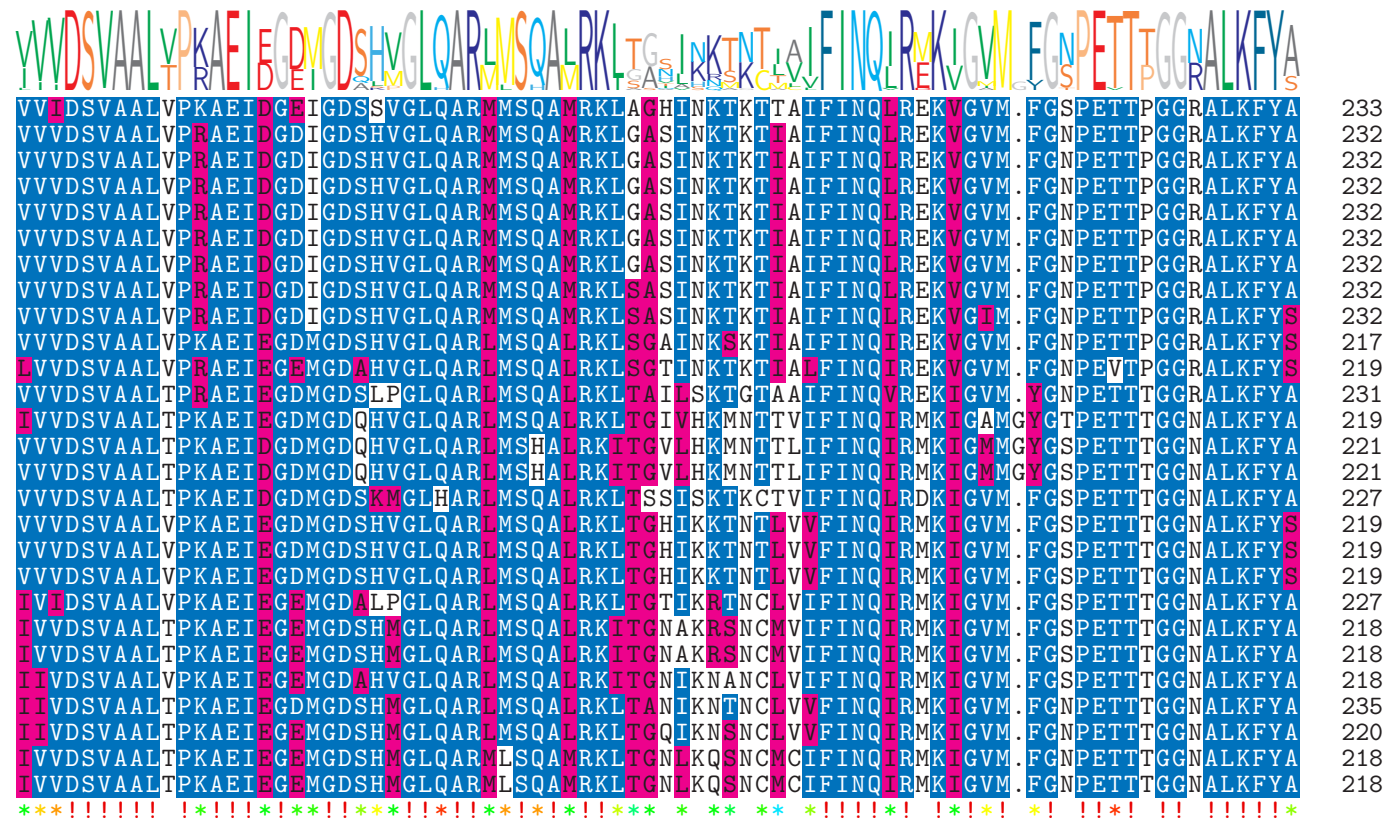
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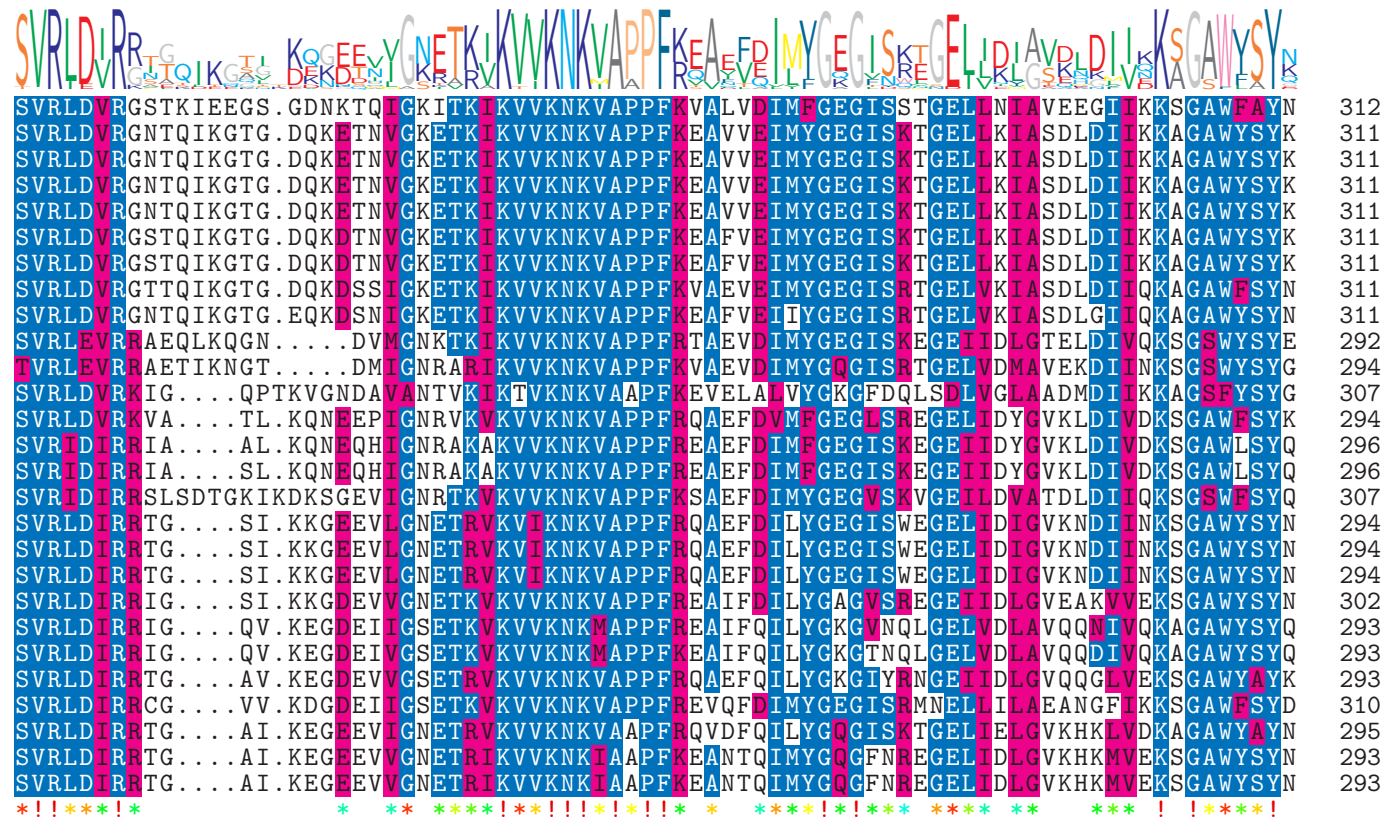
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Sequence	Score
DEKIGGGA ¹ E ² KA ³ KN ⁴ YL ⁵ KE ⁶ HQ ⁷ DV ⁸ FD ⁹ EID ¹⁰ HK ¹¹ VRAA ¹² HG ¹³ LDDSEVAETEEETTAS ¹⁴ KT ¹⁵ KAKAKKEEK ¹⁶ AVETEEIELE ¹⁷ D.....	387
DEKIGGGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SK ¹² FG ¹³ LIDGEEVSEQD ¹⁴ TENKKDE...PKKEEA...VNEEVPLDLGDELEIE	385
DEKIGGGS 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 TENKKDE...PKKEEA...VNEEVPLDLGDELEIE	385
DEKIGGGS 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 TENKKDE...PKKEEA...VNEEVPLDLGDELEIE	385
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DEKIGGGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ HQ ¹⁰ VR ¹¹ VQ ¹² FG ¹³ LIDGEEIAE...SKKDE...AAQVDS...VNEEVTLDLGDLEIE	381
GEKIGGGS ¹ EN ² AK ³ RYLA ⁴ DHP ⁵ QL ⁶ FD ⁷ EID ⁸ DR ⁹ KV ¹⁰ RV ¹¹ KF ¹² GLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGGGS ¹ EN ² AK ³ KFLA ⁴ DN ⁵ PE ⁶ IF ⁷ DD ⁸ ID ⁹ HK ¹⁰ VR ¹¹ VQ ¹² YGLIEEDNTEEKQSSKEK.....ETDEK...ADKNLVLELDDTIELE	382
EE ¹ RL ² GQGR ³ EN ⁴ AK ⁵ QFL ⁶ KN ⁷ KDIM ⁸ LM ⁹ IQEQ ¹⁰ IREHY ¹¹ GLD ¹² NNGVVQQQAETQEEL ¹³ .EFE.E.....	348
SERIGGGR ¹ EN ² AK ³ NYLA ⁴ DH ⁵ ED ⁶ VE ⁷ VL ⁸ KV ⁹ RAAY ¹⁰ GISDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGGG ¹ KE ² KTI ³ AY ⁴ IA ⁵ ER ⁶ PE ⁷ ME ⁸ QIE ⁹ DR ¹⁰ VM ¹¹ AA ¹² IRAGNAGEAPALAPAPAAPEAA.EA.....	363
DKKL ¹ GQGR ² EN ³ SKA ⁴ FL ⁵ KN ⁶ PEIA ⁷ DE ⁸ IT ⁹ KA ¹⁰ IQNSM ¹¹ G ¹² IEGMI.....SGSEDDGEE.....	343
DKKL ¹ GQGR ² EN ³ AK ⁴ ALL ⁵ KED ⁶ KALADE ⁷ IT ⁸ LK ⁹ IKESIG ¹⁰ SNEEI....MPLPDEPLEEME.....	347
DKKL ¹ GQGR ² EN ³ AK ⁴ ALL ⁵ KED ⁶ KALADE ⁷ IT ⁸ LK ⁹ IKESIG ¹⁰ SNEEI....MPLPDEPLEEME.....	347
DTKL ¹ GQGRD ² TV ³ KEL ⁴ IK ⁵ DN ⁶ PE ⁷ LAE ⁸ ELE ⁹ AK ¹⁰ IREKLQAK.....	343
GAKIGGG ¹ KDN ² VR ³ VWL ⁴ KN ⁵ PEIS ⁶ DE ⁷ IDA ⁸ KI ⁹ RALN ¹⁰ GVEMHI....TEGTQDET ¹¹ DGE.....RPEE.....	348
GAKIGGG ¹ KDN ² VR ³ VWL ⁴ KN ⁵ PEIS ⁶ DE ⁷ IDA ⁸ KI ⁹ RALN ¹⁰ GVEMHI....TEGTQDET ¹¹ DGE.....RPEE.....	348
GAKIGGG ¹ KDN ² VR ³ VWL ⁴ KN ⁵ PEIS ⁶ DE ⁷ IDA ⁸ KI ⁹ RALN ¹⁰ GVEMHI....TEGTQDET ¹¹ DGE.....RPEE.....	348
GER ¹ IGQGRD ² NC ³ REFL ⁴ RENA ⁵ ELARE ⁶ IE ⁷ NKV ⁸ REHL ⁹ GVTPMG....AVTLAAEEVEED.....	352
GNKIGGG ¹ KNN ² VIR ³ YLEEN ⁴ PQ ⁵ ISTE ⁶ IE ⁷ AV ⁸ IREQLLT ⁹ KASD....QTAAHDET ¹⁰ .EEEPDL....LES.....	349
GNKIGGG ¹ KNN ² VIR ³ YFEE ⁴ NNQIA ⁵ EE ⁶ IE ⁷ ARN ⁸ IREQLLT ⁹ TGNT....GAVQI ¹⁰ .ED ¹¹ .EEEPDL....LLES.....	349
GSKIGGG ¹ KANA ² AA ³ KYLEEN ⁴ PEIG ⁵ QIE ⁶ IE ⁷ QQ ⁸ IRAKLL ⁹ VTAN....TKATPVAEDLADADI.....	347
GTKIGGG ¹ KNN ² AVK ³ WL ⁴ KN ⁵ PEIA ⁶ DK ⁷ LQE ⁸ IRNTL ⁹ ASNPNS....VLKATASDSNDES ¹⁰ VDV...EEFSEEL.....	372
GEKIGGG ¹ KANAM ² KW ³ LEEH ⁴ PEE ⁵ ALALE ⁶ TK ⁷ LRNELLAN ⁸ PEK....VLAADIAEKN ⁹ .ESST...GLEADY.....	354
GDKIGGG ¹ KANACK ² YL ³ KN ⁴ PEIA ⁵ TA ⁶ KT ⁷ LD ⁸ KKL ⁹ REMLLN ¹⁰ PNEM....QLIAETSSAADDVEF...GAVPEEF.....	354
GD ¹ KIGGG ² KANACK ³ YL ⁴ KN ⁵ PEIA ⁶ TA ⁷ KT ⁸ LD ⁹ KKL ¹⁰ REMLLN ¹¹ PNEM....QLIAETSSAADDVEF...GAVPEEF.....	354

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consensus			

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