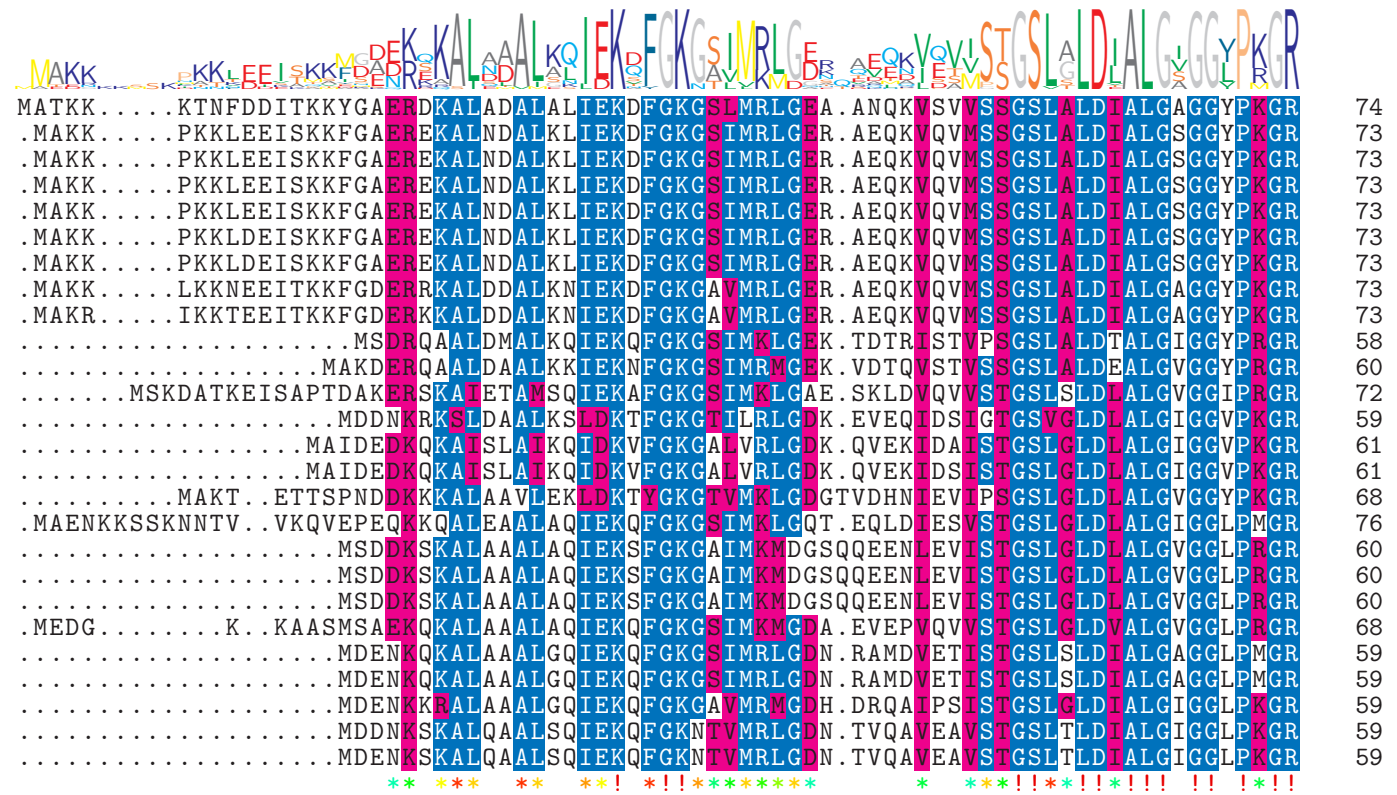


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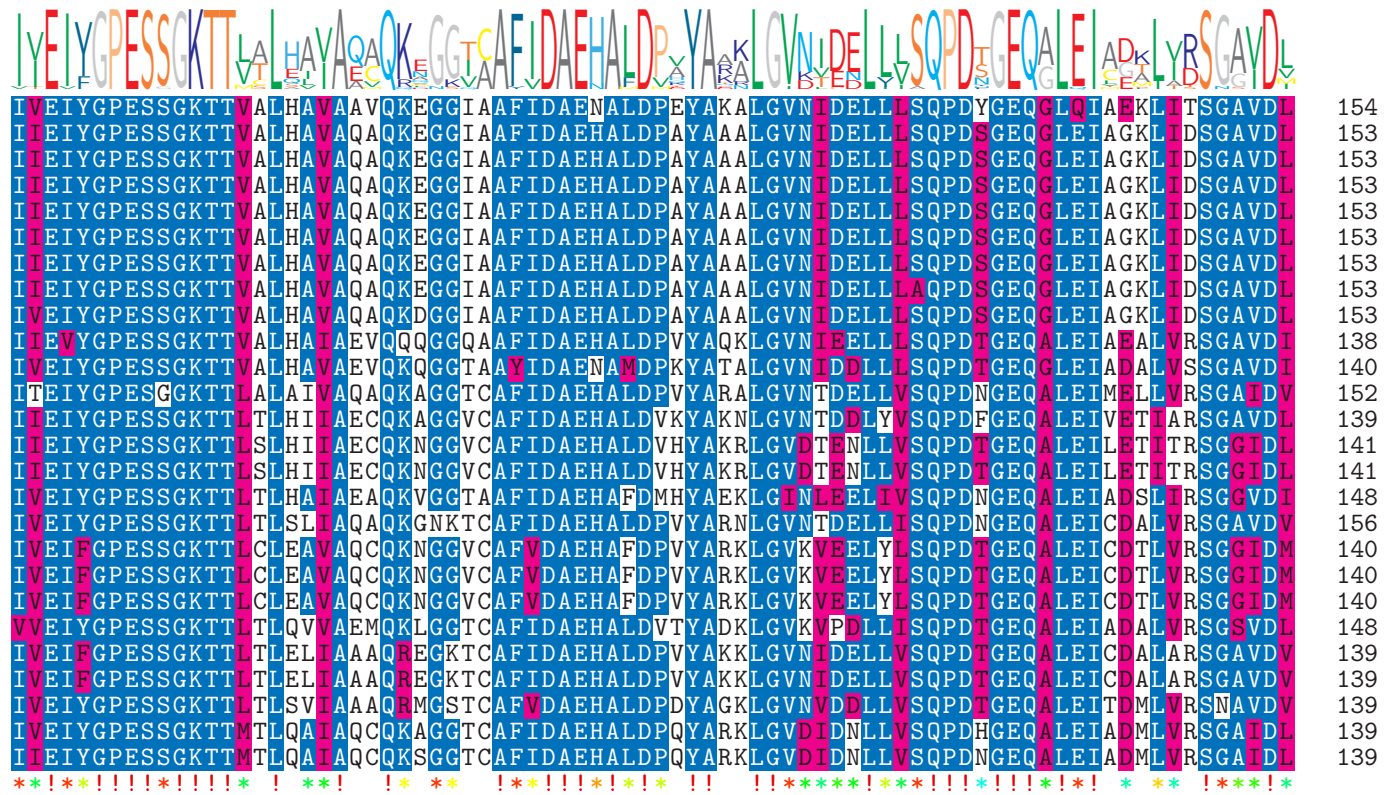
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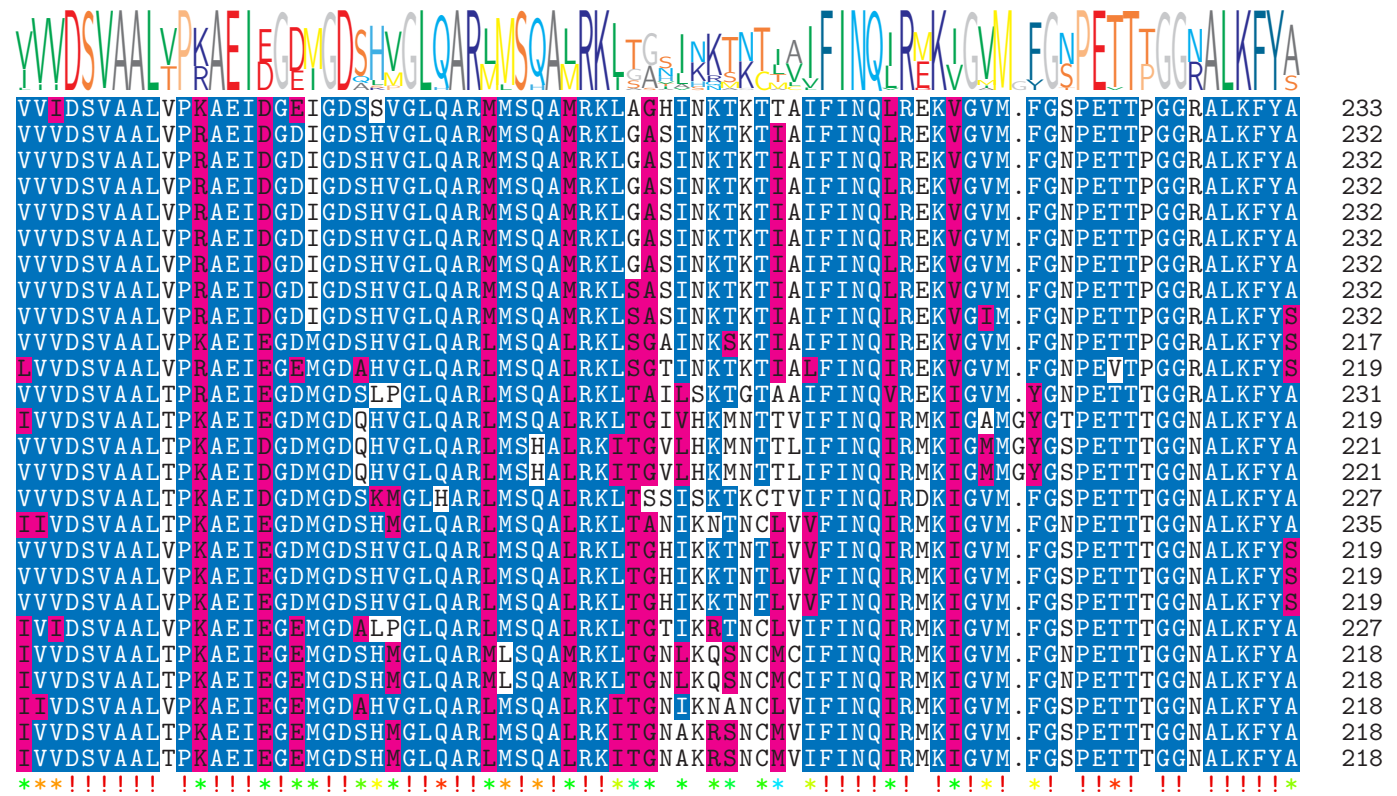
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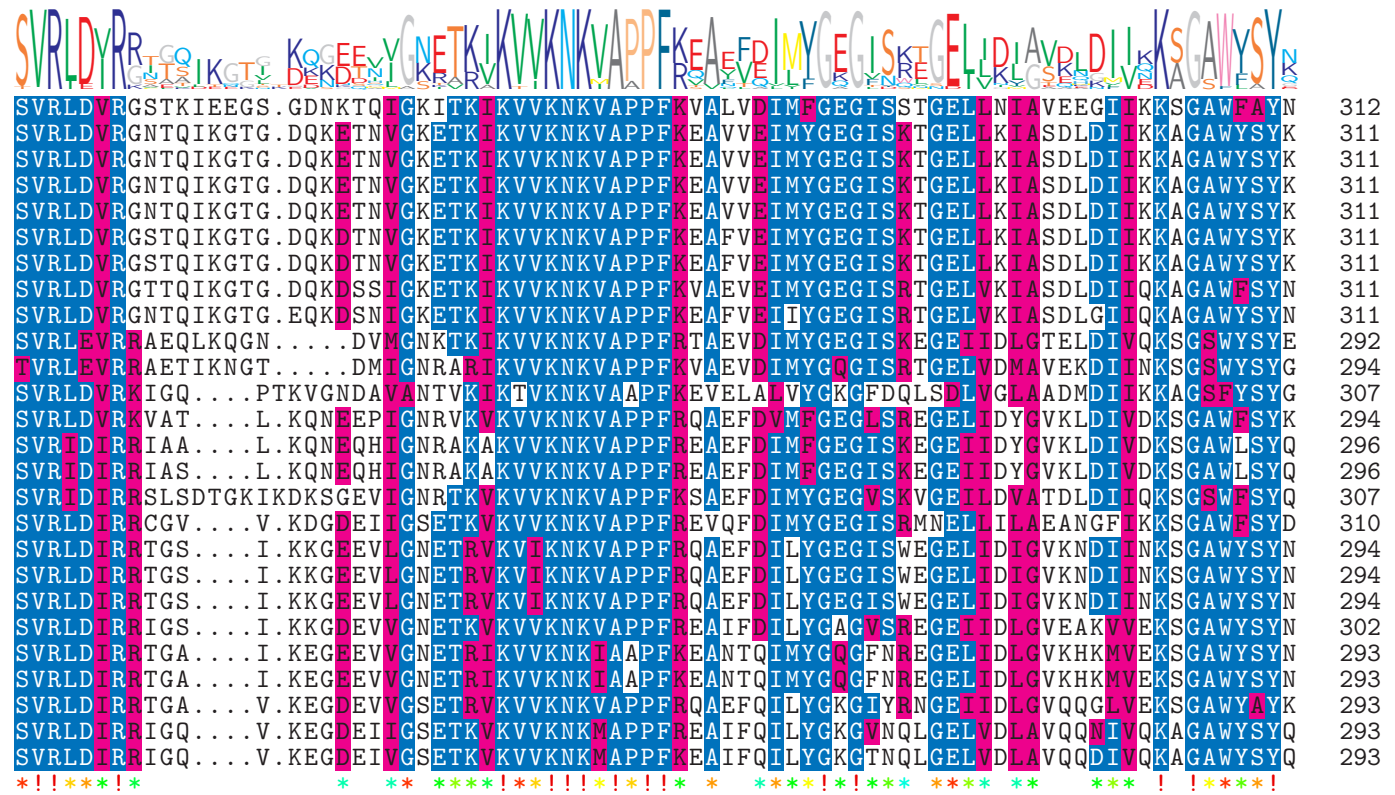
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Sequence	Score
DEKIGQGA ¹ E ² KA ³ KN ⁴ YL ⁵ KE ⁶ HQ ⁷ DV ⁸ F ⁹ DE ¹⁰ ID ¹¹ HK ¹² V ¹³ RA ¹⁴ AH ¹⁵ GI ¹⁶ LDDSEVAETEETTASKTKAKAKKEEKAVETEEIELELED....	387
DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EIF ⁷ DE ⁸ ID ⁹ DK ¹⁰ QV ¹¹ RS ¹² KF ¹³ GLIDGEEVSEQD ¹⁴ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EIF ⁷ DE ⁸ ID ⁹ DK ¹⁰ QV ¹¹ RS ¹² KF ¹³ GLIDGEEVSEQD ¹⁴ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EIF ⁷ DE ⁸ ID ⁹ DK ¹⁰ QV ¹¹ RS ¹² KF ¹³ GLIDGEEVSEQD ¹⁴ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
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GEKIGQGS ¹ EN ² AK ³ RYL ⁴ AD ⁵ HP ⁶ QL ⁷ FDE ⁸ ID ⁹ DK ¹⁰ V ¹¹ RV ¹² KF ¹³ GLIDEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGS ¹ EN ² AK ³ KFL ⁴ AD ⁵ NPE ⁶ IF ⁷ DD ⁸ ID ⁹ HK ¹⁰ V ¹¹ RV ¹² QY ¹³ CLIEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EER ¹ L ² GG ³ GR ⁴ EN ⁵ AK ⁶ FL ⁷ KEN ⁸ KD ⁹ IM ¹⁰ LI ¹¹ QE ¹² IRE ¹³ HY ¹⁴ CLDNNGVVQQQAETQEEL.EFE.E.....	348
SER ¹ IG ² QGR ³ EN ⁴ AK ⁵ NYL ⁶ AD ⁷ HED ⁸ VE ⁹ DEV ¹⁰ LR ¹¹ KV ¹² RA ¹³ AY ¹⁴ GISDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DER ¹ IG ² QGE ³ KTI ⁴ AI ⁵ Y ⁶ AER ⁷ PE ⁸ ME ⁹ QE ¹⁰ IR ¹¹ DRV ¹² MA ¹³ AIR ¹⁴ AG ¹⁵ NAGE ¹⁶ AP ¹⁷ AL ¹⁸ AP ¹⁹ AP ²⁰ AA ²¹ PE ²² AAE.....A.....	363
DKKL ¹ GG ² GR ³ EN ⁴ SK ⁵ AFL ⁶ KEN ⁷ PE ⁸ IA ⁹ DE ¹⁰ IT ¹¹ KAI ¹² QNSM ¹³ CTEGMI....SGSEDDE..GE..E.....	343
DKKL ¹ GG ² GR ³ EN ⁴ AK ⁵ ALL ⁶ KED ⁷ KAL ⁸ ADE ⁹ IT ¹⁰ LK ¹¹ IK ¹² ES ¹³ GSNEEI....MPLPDEP..LE..EME.....	347
DKKL ¹ GG ² GR ³ EN ⁴ AK ⁵ ALL ⁶ KED ⁷ KAL ⁸ ADE ⁹ IT ¹⁰ LK ¹¹ IK ¹² ES ¹³ GSNEEI....MPLPDEP..LE..E.....EME.....	347
DTKL ¹ GG ² GR ³ D ⁴ TV ⁵ KE ⁶ L ⁷ IK ⁸ DN ⁹ PE ¹⁰ LA ¹¹ EEL ¹² EAK ¹³ IRE ¹⁴ KLQAK.....	343
GTKIGQGN ¹ NAV ² KWL ³ KEN ⁴ PE ⁵ IA ⁶ DK ⁷ LE ⁸ QEI ⁹ RNT ¹⁰ LA ¹¹ SNPNS.....VLKATASDSND..ESDVVEEFSEEEEL.....	372
GAKIGQGK ¹ D ² NVR ³ VWL ⁴ KEN ⁵ PE ⁶ IS ⁷ DE ⁸ IDA ⁹ KIR ¹⁰ AL ¹¹ NG ¹² VEMHI....TEGT.....Q..DET ¹³ DGER ¹⁴ PEE.....	348
GAKIGQGK ¹ D ² NVR ³ VWL ⁴ KEN ⁵ PE ⁶ IS ⁷ DE ⁸ IDA ⁹ KIR ¹⁰ AL ¹¹ NG ¹² VEMHI....TEGT.....Q..DET ¹³ DGER ¹⁴ PEE.....	348
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GE ¹ RIG ² QGR ³ DN ⁴ CRE ⁵ FL ⁶ RNA ⁷ EL ⁸ ARE ⁹ EN ¹⁰ KV ¹¹ REHL ¹² CVTPMG....AV.TLAEVEVE..D.....	352
GDKIGQGK ¹ AN ² ACK ³ YL ⁴ KEN ⁵ PE ⁶ IA ⁷ AK ⁸ TL ⁹ DK ¹⁰ KL ¹¹ REML ¹² LN ¹³ PENM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GDKIGQGK ¹ AN ² ACK ³ YL ⁴ KEN ⁵ PE ⁶ IA ⁷ AK ⁸ TL ⁹ DK ¹⁰ KL ¹¹ REML ¹² LN ¹³ PENM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GSKIGQGK ¹ ANA ² AK ³ YLE ⁴ EN ⁵ PE ⁶ IG ⁷ QEI ⁸ EQ ⁹ IR ¹⁰ AK ¹¹ LY ¹² TSAN....TKATPVAEDLA..DADI.....	347
GNKIGQGK ¹ NN ² VIR ³ YLE ⁴ EN ⁵ PE ⁶ IQ ⁷ ISTE ⁸ IE ⁹ AV ¹⁰ IRE ¹¹ QLL ¹² TKASD....QTAA.HDETEE..EPDLL..ES.....	349
GNKIGQGK ¹ NN ² VIR ³ YLE ⁴ EN ⁵ PE ⁶ IQ ⁷ ISTE ⁸ IE ⁹ AV ¹⁰ IRE ¹¹ QLL ¹² TKGTN....GAVQ.I.EDEE..EPDLL..LES.....	349

logo

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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved