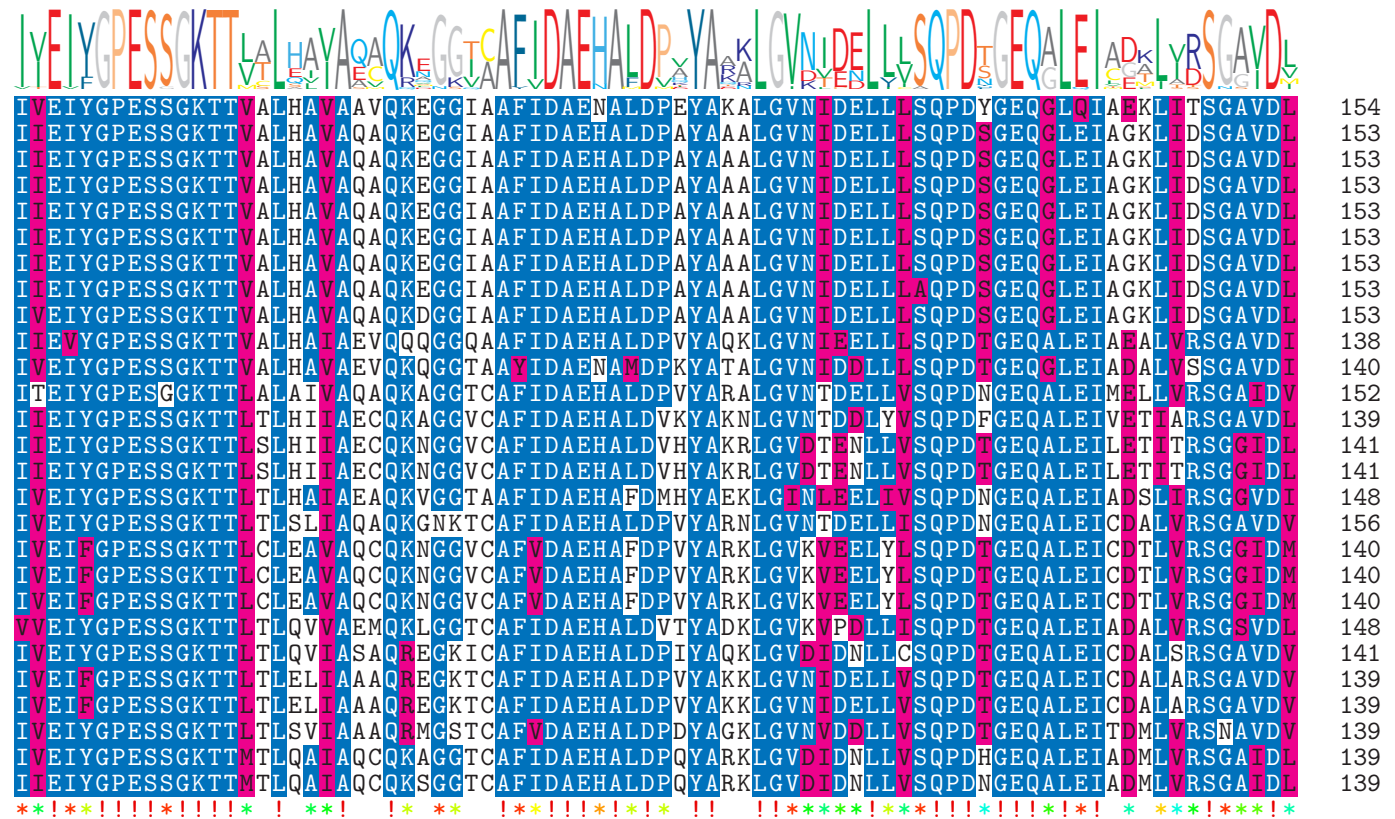


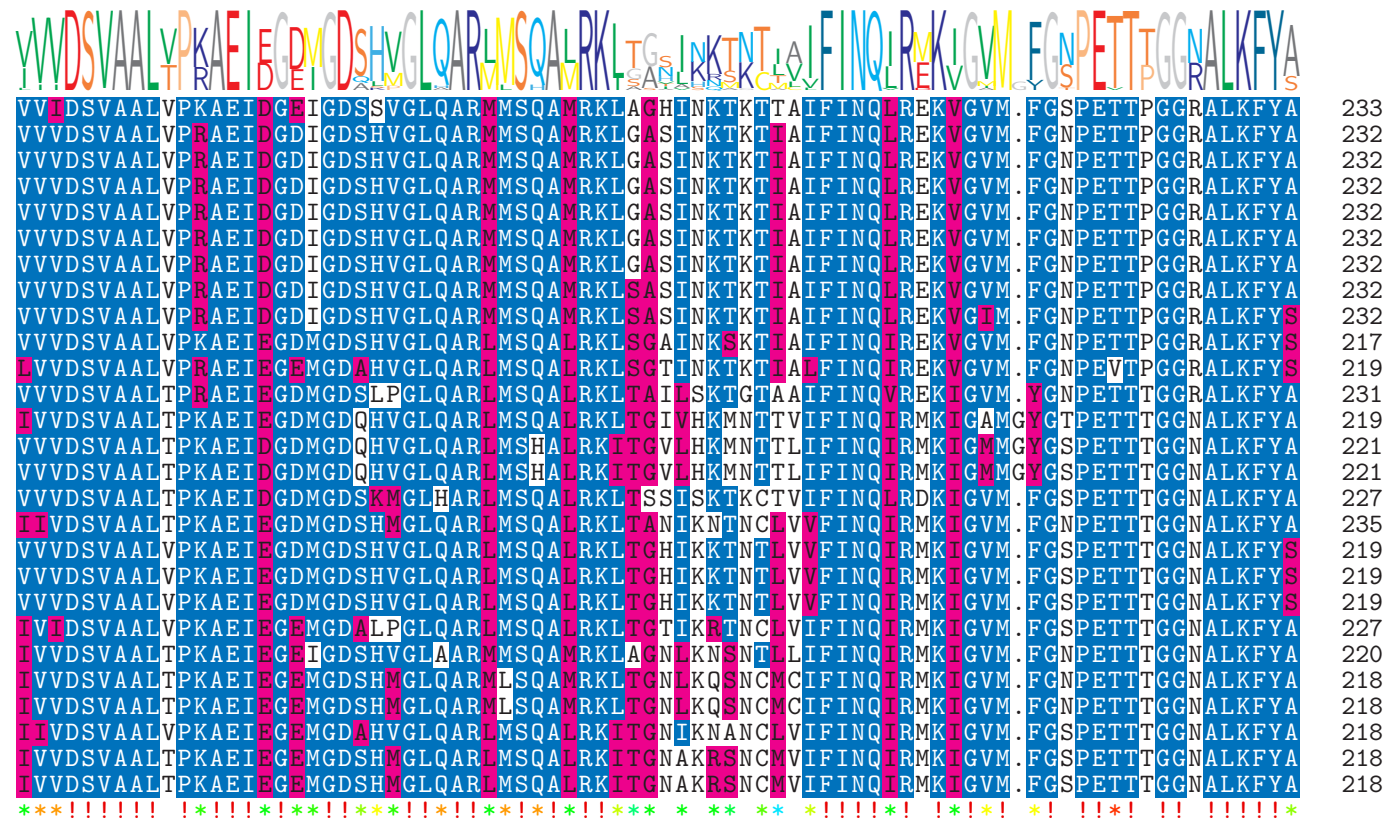
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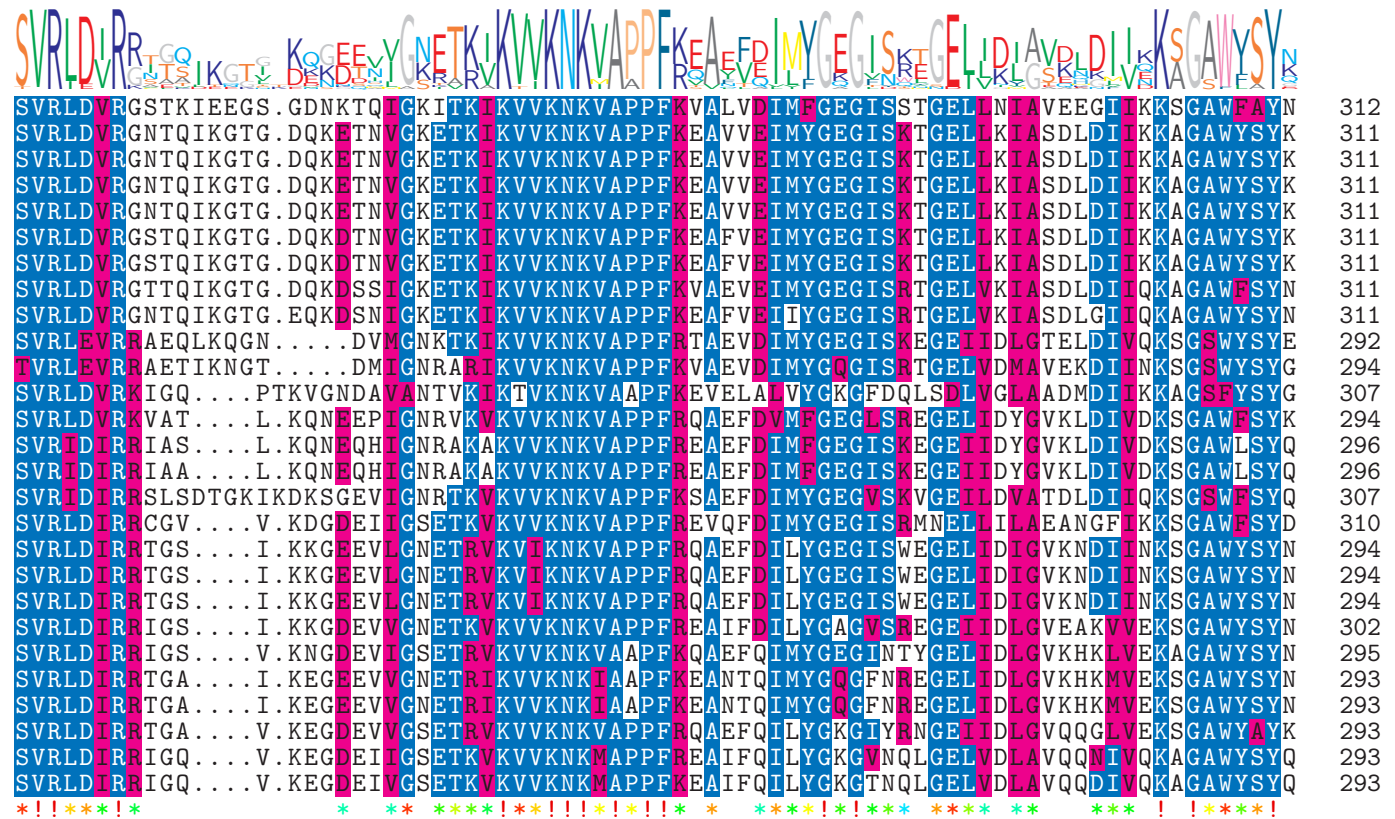
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGGGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EIF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SK ¹² FLIDGEEVSEQD ¹³ TENKKDE...PKKEEA...VNEEVPLDLGDELEIE	385
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GEKIGGGS ¹ EN ² AK ³ KFL ⁴ AD ⁵ NPEIF ⁶ DD ⁷ ID ⁸ HK ⁹ VR ¹⁰ VQ ¹¹ GLIEEDNTEEKQSSKEK.....ETDEK...ADKNLVLELDDTIELE	382
EE ¹ RL ² GQGR ³ EN ⁴ AK ⁵ QFL ⁶ KN ⁷ KDIM ⁸ LI ⁹ QE ¹⁰ Q ¹¹ IRE ¹² HY ¹³ GLD ¹⁴ NNGVVQQQAETQEEL.EFE.E.....	348
SERIGGGR ¹ EN ² AK ³ NY ⁴ LAD ⁵ HD ⁶ VE ⁷ DE ⁸ VR ⁹ LK ¹⁰ V ¹¹ RA ¹² AY ¹³ GISDVPPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGGG ¹ KE ² KTI ³ AY ⁴ IA ⁵ ER ⁶ PE ⁷ ME ⁸ QE ⁹ IR ¹⁰ DR ¹¹ VMAA ¹² IRAGNAGEAPALAPA.....PAAPEAAEA.....	363
DKKLGGGR ¹ EN ² SK ³ AF ⁴ LKEN ⁵ PEI ⁶ AD ⁷ EIT ⁸ KA ⁹ IQ ¹⁰ SM ¹¹ GIEGMISGSEDDEGEE.....	343
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GTKIGGQK ¹ NN ² AV ³ KL ⁴ KEN ⁵ PEI ⁶ AD ⁷ KL ⁸ QE ⁹ IR ¹⁰ N ¹¹ TL ¹² ASN ¹³ PNSVLKATASDSNDES.D...VEEFSE...EEL.....	372
GAKIGGQK ¹ DN ² VR ³ VWL ⁴ KEN ⁵ PEI ⁶ SD ⁷ EID ⁸ AK ⁹ IRAL ¹⁰ NG ¹¹ VEMHIT ¹² EGTQDE.....TDGERPEE.....	348
GAKIGGQK ¹ DN ² VR ³ VWL ⁴ KEN ⁵ PEI ⁶ SD ⁷ EID ⁸ AK ⁹ IRAL ¹⁰ NG ¹¹ VEMHIT ¹² EGTQDE.....TDGERPEE.....	348
GAKIGGQK ¹ DN ² VR ³ VWL ⁴ KEN ⁵ PEI ⁶ SD ⁷ EID ⁸ AK ⁹ IRAL ¹⁰ NG ¹¹ VEMHIT ¹² EGTQDE.....TDGERPEE.....	348
GERIGGGR ¹ DN ² CR ³ REFL ⁴ RENA ⁵ EL ⁶ AREI ⁷ EN ⁸ KV ⁹ REHL ¹⁰ GVTPMGAVTLAAEEVEED.....	352
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GDKIGGQK ¹ AN ² ACK ³ YL ⁴ KEN ⁵ PEI ⁶ AK ⁷ LD ⁸ KKL ⁹ REMLLN ¹⁰ PNEMQLI.AET.....SSAADDVEFGAVPEEF.....	354
GDKIGGQK ¹ AN ² ACK ³ YL ⁴ KEN ⁵ PEI ⁶ AK ⁷ LD ⁸ KKL ⁹ REMLLN ¹⁰ PNEMQLI.AET.....SSAADDVEFGAVPEEF.....	354
GSKIGGQK ¹ ANA ² AK ³ YLEEN ⁴ PEI ⁵ GQ ⁶ EIE ⁷ QQ ⁸ IRAK ⁹ LL ¹⁰ V ¹¹ TSANTKA.TPVAEDLA...DADI.....	347
GNKIGGQK ¹ NN ² VIR ³ YLEEN ⁴ PEI ⁵ QISTE ⁶ IEAV ⁷ IREQLLTKASDQTA.A.HDETEE...EPDLLS.....	349
GNKIGGQK ¹ NN ² VIR ³ YFEENN ⁴ QIA ⁵ EIE ⁶ ERN ⁷ IREQLLTGTNGAV.Q.I.EDEE...EPDLLLES.....	349

logo

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 non conserved
 similar
 ≥ 50% conserved