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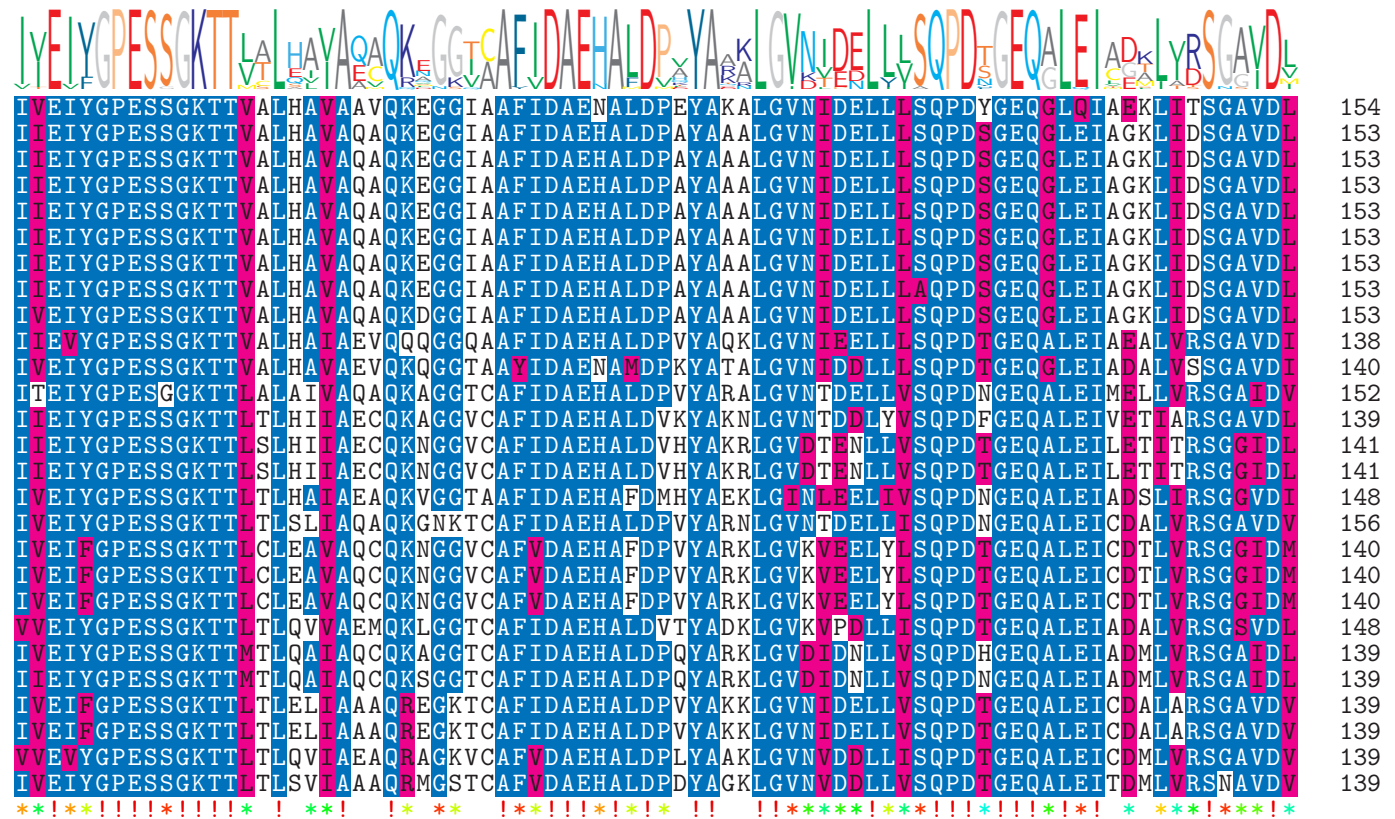
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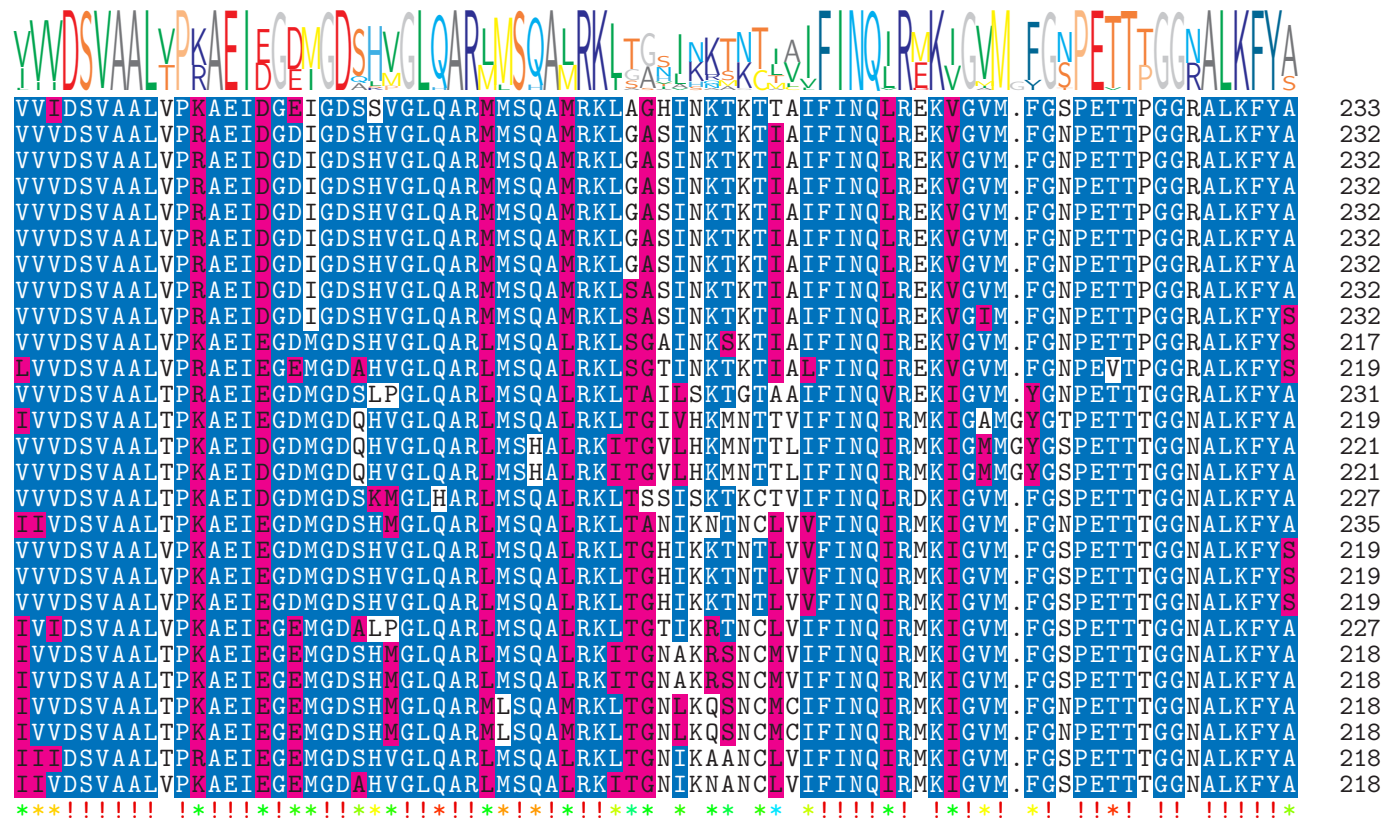
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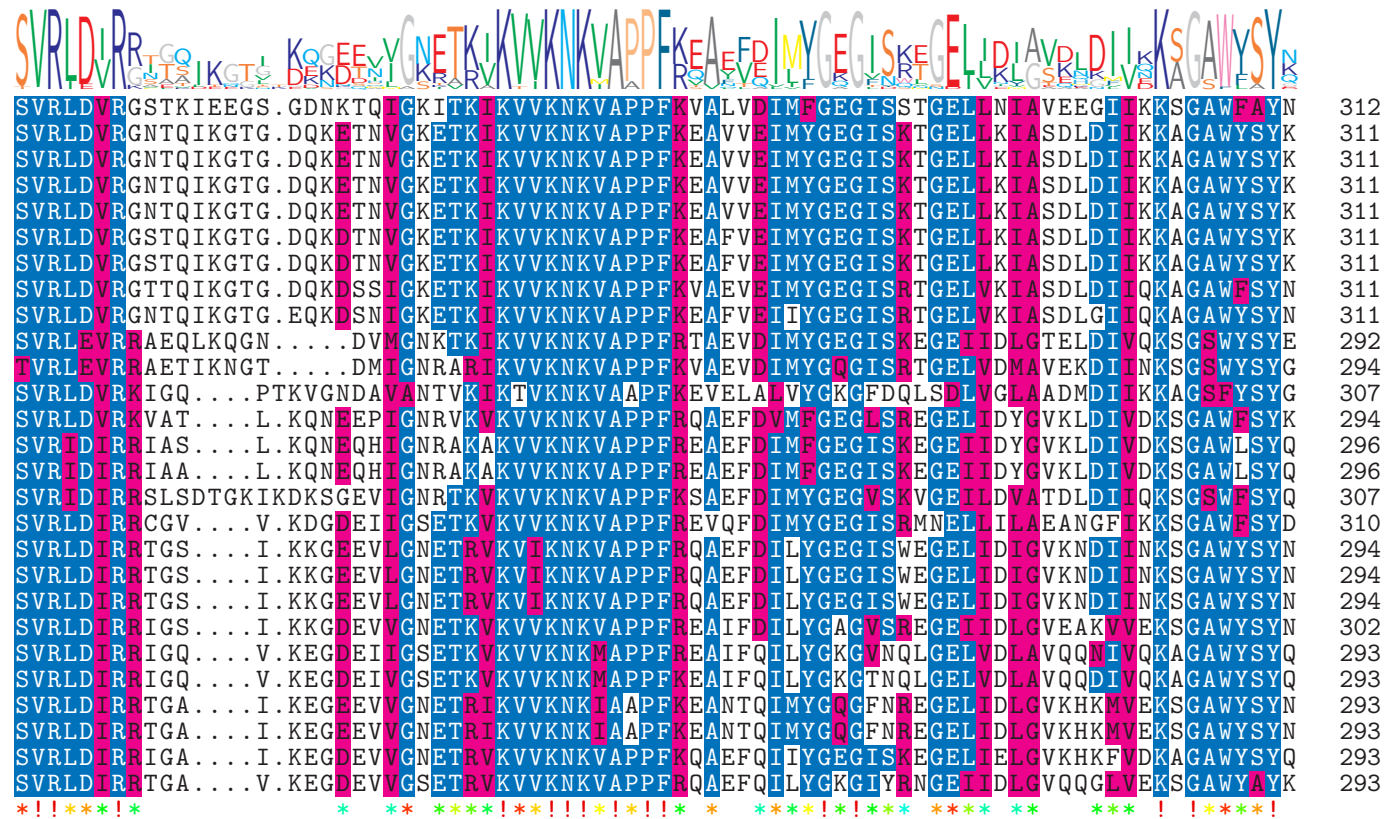
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consensus

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Sequence	Score
DEKIGGGA ¹ E ² KA ³ KN ⁴ YL ⁵ KE ⁶ HQ ⁷ DV ⁸ FDEID ⁹ HK ¹⁰ VRAAH ¹¹ GL ¹² LD ¹³ DDSEVAETEEETTAS ¹⁴ KT ¹⁵ KAKAKKEEK ¹⁶ AVET ¹⁷ EE ¹⁸ IEIELED.....	387
DEKIGGGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EIF ⁷ DEID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ GL ¹² IDGEEVSEQDTENKKDE...PKKEEA...VN ¹⁷ EE ¹⁸ VPLDLGDELEIE	385
DEKIGGGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EIF ⁷ DEID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ GL ¹² IDGEEVSEQDTENKKDE...PKKEEA...VN ¹⁷ EE ¹⁸ VPLDLGDELEIE	385
DEKIGGGS ¹ EN ² AK ³ KYL ⁴ AE ⁵ HP ⁶ EIF ⁷ DEID ⁸ KQ ⁹ VR ¹⁰ SKF ¹¹ GL ¹² IDGEEVSEQDTENKKDE...PKKEEA...VN ¹⁷ EE ¹⁸ VPLDLGDELEIE	385
DEKIGGGS ¹ EN ² AK ³ KYL ⁴ AD ⁵ NP ⁶ EIF ⁷ DEID ⁸ HQ ⁹ VR ¹⁰ VQF ¹¹ GL ¹² IDGEEIAES...KKDE...AAQVDS...VN ¹⁷ EE ¹⁸ VTLDLGDLEIE	381
DEKIGGGS ¹ EN ² AK ³ KYL ⁴ AD ⁵ NP ⁶ FA ⁷ IED ⁸ HQ ⁹ VR ¹⁰ VQF ¹¹ GL ¹² IDGEEAAES...KKDE...VAQVDS...VN ¹⁷ EE ¹⁸ VTLDLGDLEIE	381
GEKIGGGS ¹ EN ² AK ³ RYL ⁴ AD ⁵ HP ⁶ QL ⁷ F ⁸ DEID ⁹ DR ¹⁰ KV ¹¹ RK ¹² FL ¹³ LEES ¹⁴ EEESAMAVASE.....E.....TDD ¹⁸ LALDLNGIEIE	377
GEKIGGGS ¹ EN ² AK ³ KFL ⁴ AD ⁵ NP ⁶ IF ⁷ DD ⁸ ID ⁹ HK ¹⁰ VR ¹¹ VQY ¹² GL ¹³ IEED ¹⁴ NTEEKQSSKEK.....ETDEK...ADKNLVLELDDTIELE	382
EE ¹ RL ² GGGREN ³ AK ⁴ QFL ⁵ KEN ⁶ KDIM ⁷ LI ⁸ QEQ ⁹ IREHY ¹⁰ GL ¹¹ DNNGVVQQAEETQEEL ¹² .EFE.E.....EE	348
SERIGGGREN ¹ AK ² NYL ³ AD ⁴ HE ⁵ DVE ⁶ DEV ⁷ RL ⁸ KV ⁹ RAAY ¹⁰ GIS ¹¹ SDVPEEDLPTTEDE.QI.NILPDDST.....EE	355
DERIGGGKEK ¹ TI ² AY ³ IA ⁴ ERP ⁵ EME ⁶ QEIR ⁷ DRV ⁸ MAA ⁹ IRAGNAGEAPALAPAPAAP.....E.....AAEA	363
DKKLGGGREN ¹ SKA ² FL ³ KEN ⁴ PEI ⁵ ADEIT ⁶ KAI ⁷ QNSM ⁸ GI ⁹ EGMISGSEDDEGEE.....	343
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KAL ⁵ ADEIT ⁶ LK ⁷ IKES ⁸ IGS ⁹ NEEIMPLPDEPLEEME.....	347
DKKLGGGREN ¹ AK ² ALL ³ KED ⁴ KAL ⁵ ADEIT ⁶ LK ⁷ IKES ⁸ IGS ⁹ NEEIMPLPDEPLEEME.....	347
DTKLGGGRD ¹ TV ² KEL ³ IK ⁴ DN ⁵ PEL ⁶ AEE ⁷ LEAK ⁸ IREKLQAK.....	343
GTKIGGGK ¹ NN ² AV ³ KL ⁴ EN ⁵ PEI ⁶ AD ⁷ KL ⁸ QEIR ⁹ NTL ¹⁰ ASN ¹¹ PNSVLKATASDSNDES.DV...EE...FSEEL	372
GAKIGGGK ¹ DN ² VR ³ VWL ⁴ KEN ⁵ PEI ⁶ SD ⁷ IDA ⁸ KI ⁹ RAL ¹⁰ NG ¹¹ VMHIT ¹² EGTQDET ¹³ DGER...P...EE	348
GAKIGGGK ¹ DN ² VR ³ VWL ⁴ KEN ⁵ PEI ⁶ SD ⁷ IDA ⁸ KI ⁹ RAL ¹⁰ NG ¹¹ VMHIT ¹² EGTQDET ¹³ DGER...P...EE	348
GAKIGGGK ¹ DN ² VR ³ VWL ⁴ KEN ⁵ PEI ⁶ SD ⁷ IDA ⁸ KI ⁹ RAL ¹⁰ NG ¹¹ VMHIT ¹² EGTQDET ¹³ DGER...P...EE	348
GERIGGGRD ¹ NC ² REF ³ LRN ⁴ AE ⁵ LAREI ⁶ ENK ⁷ VREHL ⁸ GV ⁹ TPMGAVTLAAEEVEED.....	352
GNKIGGGK ¹ NN ² VIRY ³ LEEN ⁴ QI ⁵ STEI ⁶ EAV ⁷ IREQLLTKASDQTAAHDETEEP.....D...LLES	349
GNKIGGGK ¹ NN ² VIRY ³ FEENN ⁴ QIAE ⁵ IEI ⁶ ERN ⁷ IREQLLTGTNGAVQI.EDEEEP.....D...LLLES	349
GDKIGGGKAN ¹ ACK ² YL ³ LKEN ⁴ PEI ⁵ AKT ⁶ LD ⁷ KKL ⁸ REMLLN ⁹ PNEM.QLIAETSSAA...DDVEFG...AVPEEF	354
GDKIGGGKAN ¹ ACK ² YL ³ LKEN ⁴ PEI ⁵ AKT ⁶ LD ⁷ KKL ⁸ REMLLN ⁹ PNEM.QLIAETSSAA...DDVEFG...AVPEEF	354
GEKIGGGKAN ¹ SI ² KYL ³ LEH ⁴ KHIS ⁵ DETE ⁶ EAK ⁷ LREQLL ⁸ LP ⁹ GEEK ¹⁰ VKVDEAPGALG.NPLPKD...DTEEDF	357
GSKIGGGKAN ¹ AA ² KYL ³ LEEN ⁴ PEI ⁵ QIEI ⁶ EQ ⁷ IRAKLL ⁸ VTSANTKAT.....PVAED...LADADI	347

logo

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NTDB id 1205 PSJM300 05545 AFN77183.1	...		347
consensus			

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