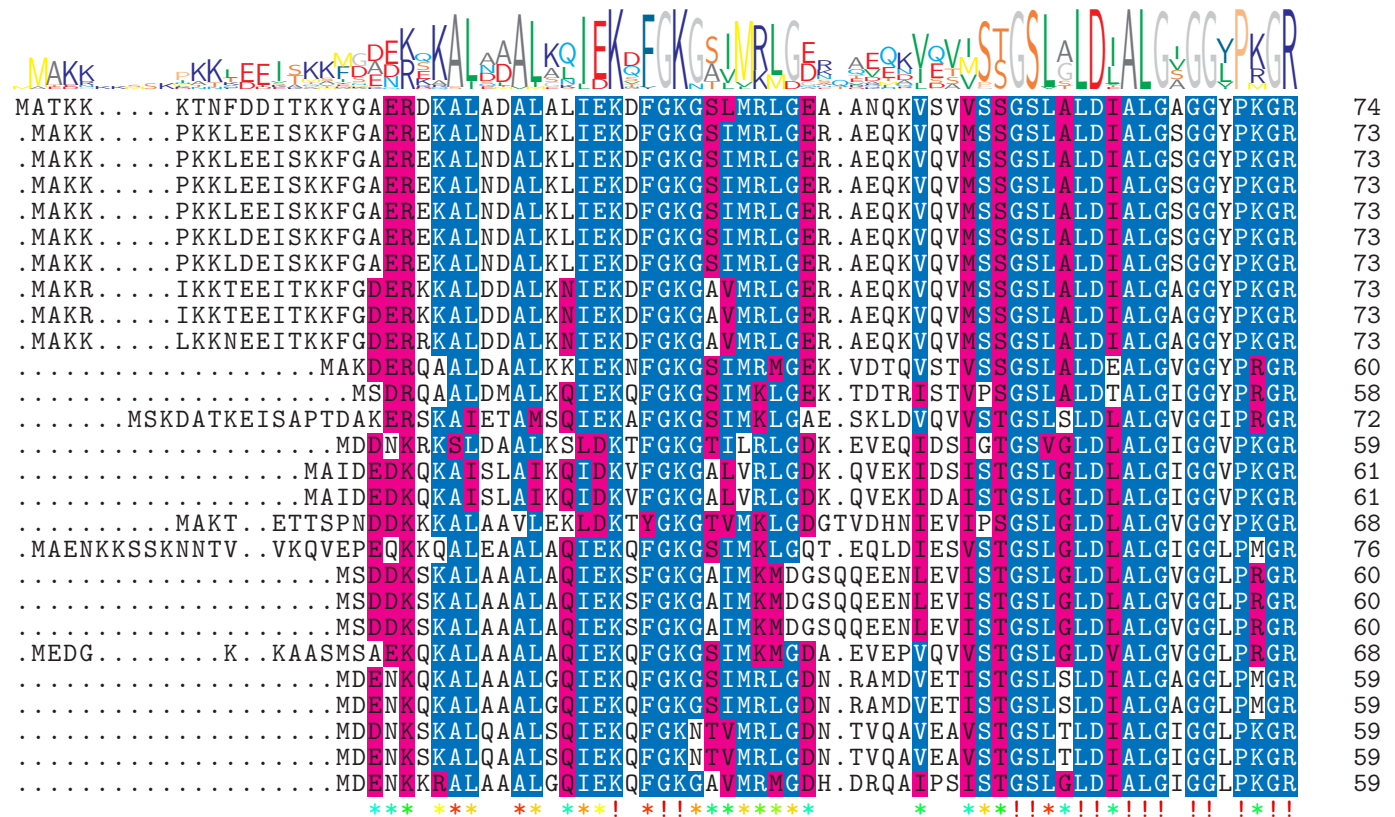


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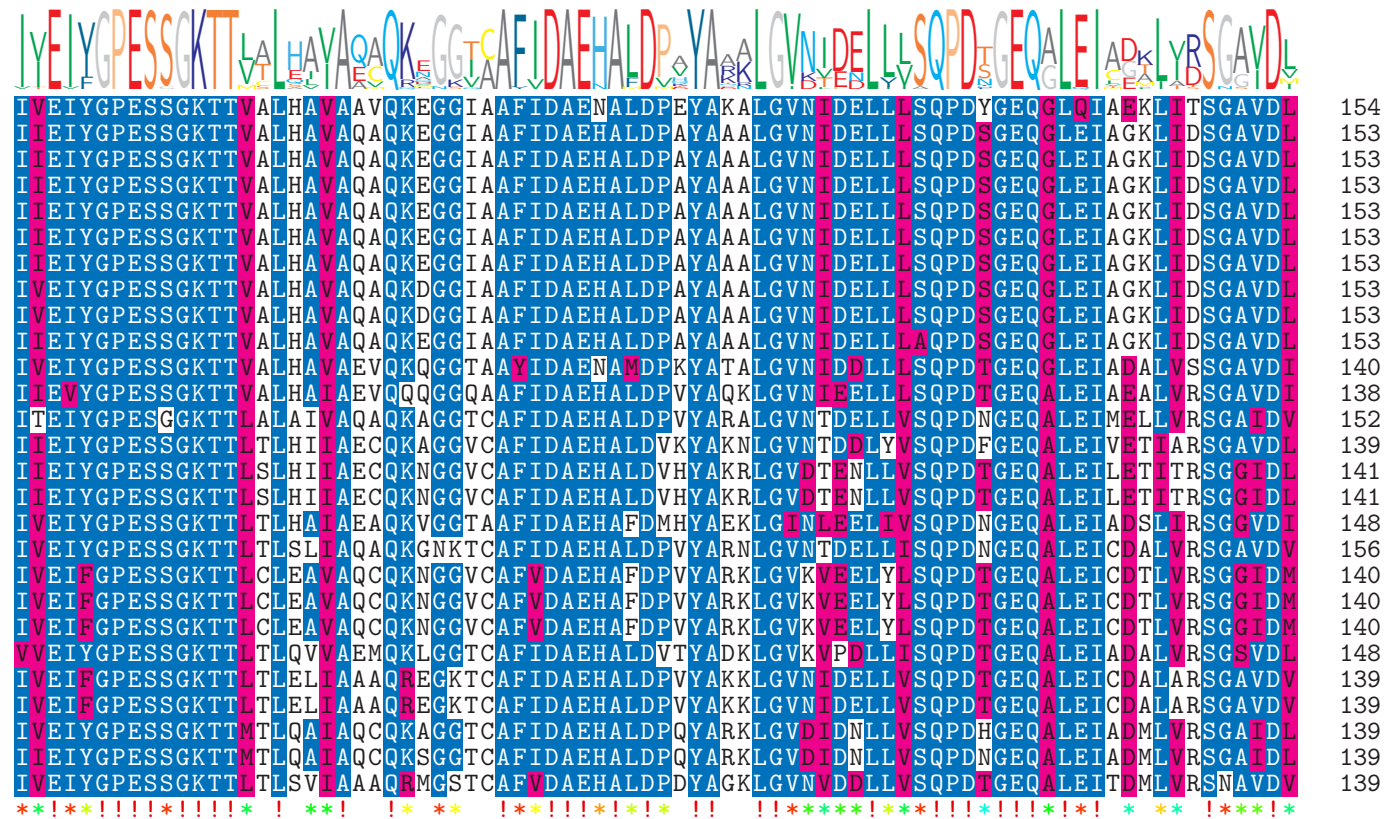
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consensus

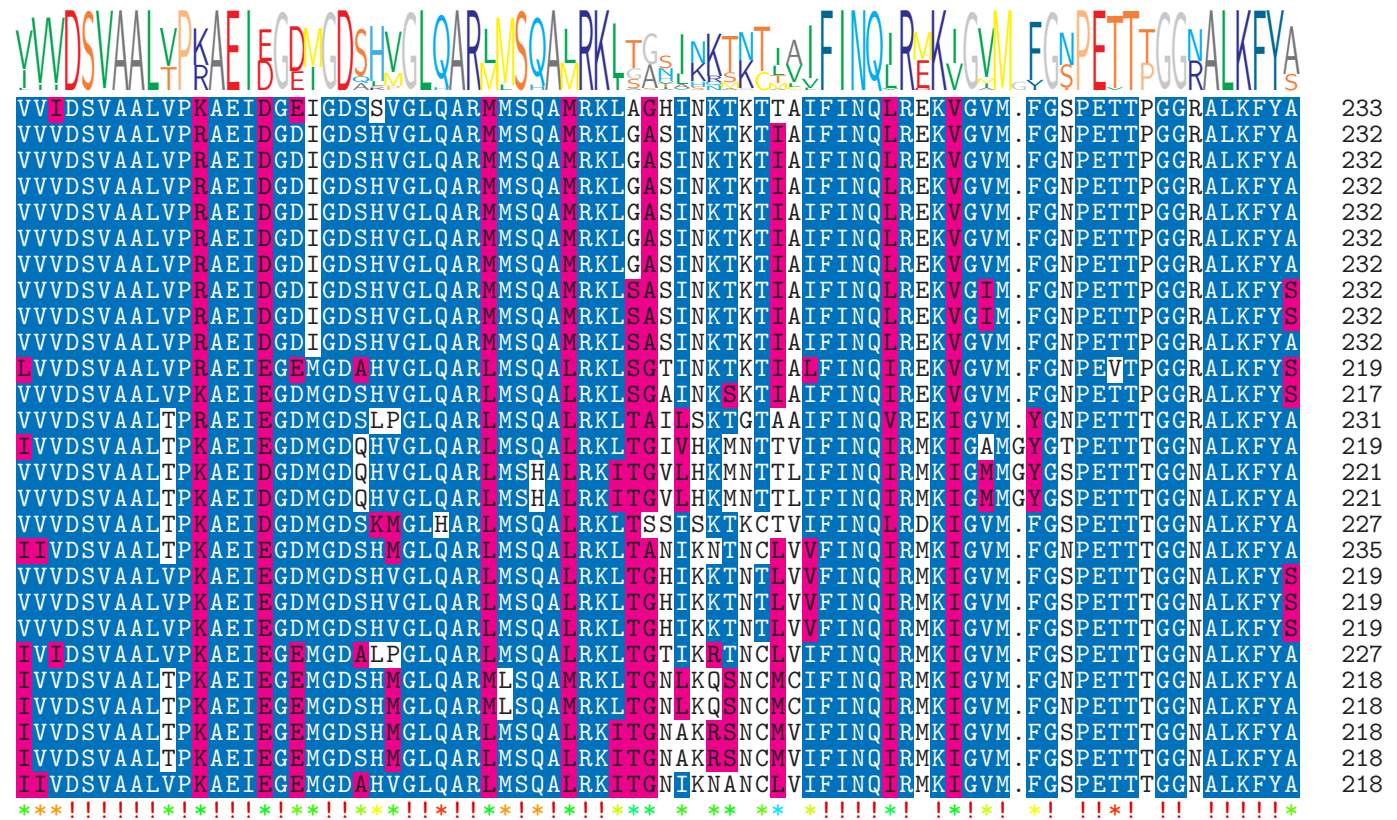
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consensus

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NTDB id 408 SMU RS09530 WP 002262392.1	SVRLDVRGNTQIKGTG.EQKDSN	IGKETKIKVVKNKVAPPFKAEFVEIITYGEGISRTGELVKIASDLGIIQKAGAWYSYN	311
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consensus

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Sequence	Score
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DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DEID ⁺ DK ⁺ QV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DEID ⁺ DK ⁺ QV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AE ⁺ HP ⁺ EIF ⁺ DEID ⁺ DK ⁺ QV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AD ⁺ NPE ⁺ IF ⁺ DEID ⁺ HQ ⁺ VR ⁺ VQF ⁺ GL ⁺ IDGEEIAES....KKDE....AAQVDS..VNEEVPLDLGDELEIE	381
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYL ⁺ AD ⁺ NPE ⁺ IF ⁺ FAE ⁺ ID ⁺ HQ ⁺ VR ⁺ VQF ⁺ GL ⁺ IDGEEAAES....KKDE....VAQVDS..VNEEVPLDLGDELEIE	381
GEKIGQGS ⁺ EN ⁺ AK ⁺ KFL ⁺ AD ⁺ NPE ⁺ IF ⁺ DD ⁺ ID ⁺ HK ⁺ VR ⁺ VQY ⁺ GL ⁺ IEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
GEKIGQGS ⁺ EN ⁺ AK ⁺ KFL ⁺ AD ⁺ NPE ⁺ IF ⁺ DD ⁺ ID ⁺ HK ⁺ VR ⁺ VQY ⁺ GL ⁺ IEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
GEKIGQGS ⁺ EN ⁺ AK ⁺ RYL ⁺ AD ⁺ HP ⁺ QL ⁺ FDEID ⁺ RK ⁺ VR ⁺ VKF ⁺ GL ⁺ LEESEEEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
SERIGQG ⁺ REN ⁺ AK ⁺ NYL ⁺ AD ⁺ HED ⁺ VE ⁺ DV ⁺ RL ⁺ KV ⁺ RAAY ⁺ GIS ⁺ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
EERLGG ⁺ REN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IRE ⁺ HY ⁺ GL ⁺ DNNGVVQQQAEEETQEEL.EFE.E.....	348
DERIGQG ⁺ EK ⁺ TIAY ⁺ IA ⁺ ER ⁺ PEME ⁺ QEIR ⁺ DRV ⁺ MAAIRAGNAGEAPALAPAPAAPEAAE..A.....	363
DKKLGG ⁺ REN ⁺ SKA ⁺ FL ⁺ KEN ⁺ PEI ⁺ ADEIT ⁺ KA ⁺ IQNSM ⁺ CT ⁺ EGMI....SGSEDD..EGE..E.....	343
DKKLGG ⁺ REN ⁺ AKA ⁺ L ⁺ LKED ⁺ KALADEIT ⁺ TLK ⁺ IKESIGSNEEI....MPLPDE..PLE..EME.....	347
DKKLGG ⁺ REN ⁺ AKA ⁺ L ⁺ LKED ⁺ KALADEIT ⁺ TLK ⁺ IKESIGSNEEI....MPLPDE..PLE..EME.....	347
DTKLGG ⁺ RD ⁺ TV ⁺ KE ⁺ L ⁺ IKDN ⁺ PEL ⁺ AE ⁺ LE ⁺ AK ⁺ IREKLQAK.....	343
GTKIGGK ⁺ NNAV ⁺ KL ⁺ KEN ⁺ PEI ⁺ ADK ⁺ L ⁺ QEIR ⁺ NTLA ⁺ SNPNS....VLKATASDSND..ESDVVEEFSEEEEL.....	372
GAKIGGK ⁺ KDN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SDEID ⁺ AK ⁺ IRALNG ⁺ VEMHI....TEGTQDET ⁺ DGE..R.....PEE.....	348
GAKIGGK ⁺ KDN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SDEID ⁺ AK ⁺ IRALNG ⁺ VEMHI....TEGTQDET ⁺ DGE..R.....PEE.....	348
GAKIGGK ⁺ KDN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SDEID ⁺ AK ⁺ IRALNG ⁺ VEMHI....TEGTQDET ⁺ DGE..R.....PEE.....	348
GERIGG ⁺ RD ⁺ NC ⁺ REFL ⁺ REN ⁺ AE ⁺ LARE ⁺ IKN ⁺ VR ⁺ EHL ⁺ CVTPMG....AVTLA.EEEVEE..D.....	352
GDKIGGK ⁺ KAN ⁺ ACKYL ⁺ KEN ⁺ PEI ⁺ AKT ⁺ LD ⁺ KKL ⁺ REMLLN ⁺ PNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GDKIGGK ⁺ KAN ⁺ ACKYL ⁺ KEN ⁺ PEI ⁺ AKT ⁺ LD ⁺ KKL ⁺ REMLLN ⁺ PNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GNKIGGK ⁺ KNNVIR ⁺ YLE ⁺ ENP ⁺ QIST ⁺ EIE ⁺ AVI ⁺ REQLLTKASD....QTAA.HDETEE..EPDLL..ES.....	349
GNKIGGK ⁺ KNNVIR ⁺ FEEN ⁺ NQIA ⁺ EIE ⁺ ERN ⁺ IREQLLTGTN....GAVQ.I.EDEE..EPDLL..LES.....	349
GSKIGGK ⁺ KANA ⁺ AKYL ⁺ LEN ⁺ PEI ⁺ GQIE ⁺ EQQIR ⁺ AKLLV ⁺ TSAN....TKATPVAEDLA..DADI.....	347

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NTDB id 194 SPR RS08825 WP 001085462.1	IEE	388	
NTDB id 159 SP RS09750 WP 001085462.1	IEE	388	
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NTDB id 527 SMSK321 RS11065 WP 001085454.1	IEE	384	
NTDB id 52070 SMUGS5 RS09450 WP 002262392.1	D..	383	
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NTDB id 1205 PSJM300 05545 AFN77183.1	...	347	
consensus			

-  non conserved
-  similar
-  ≥ 50% conserved