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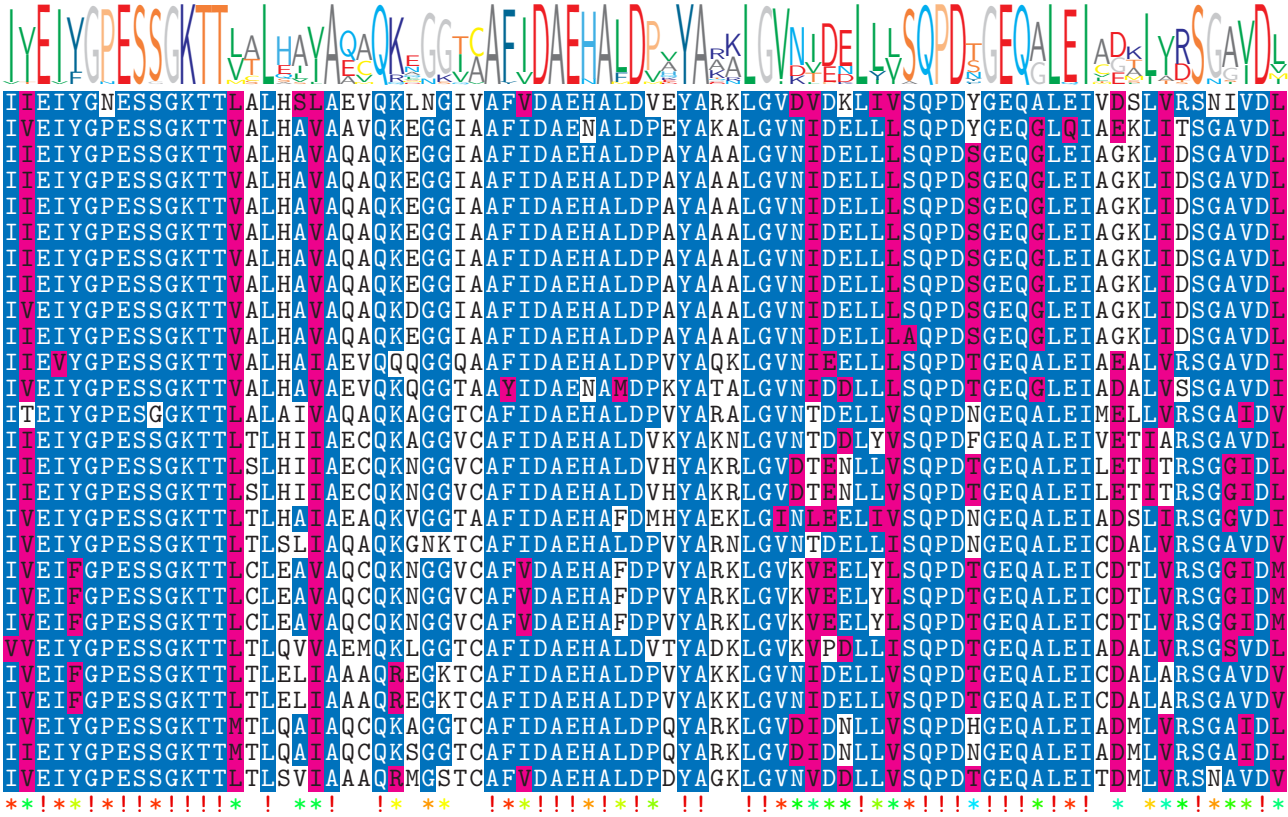
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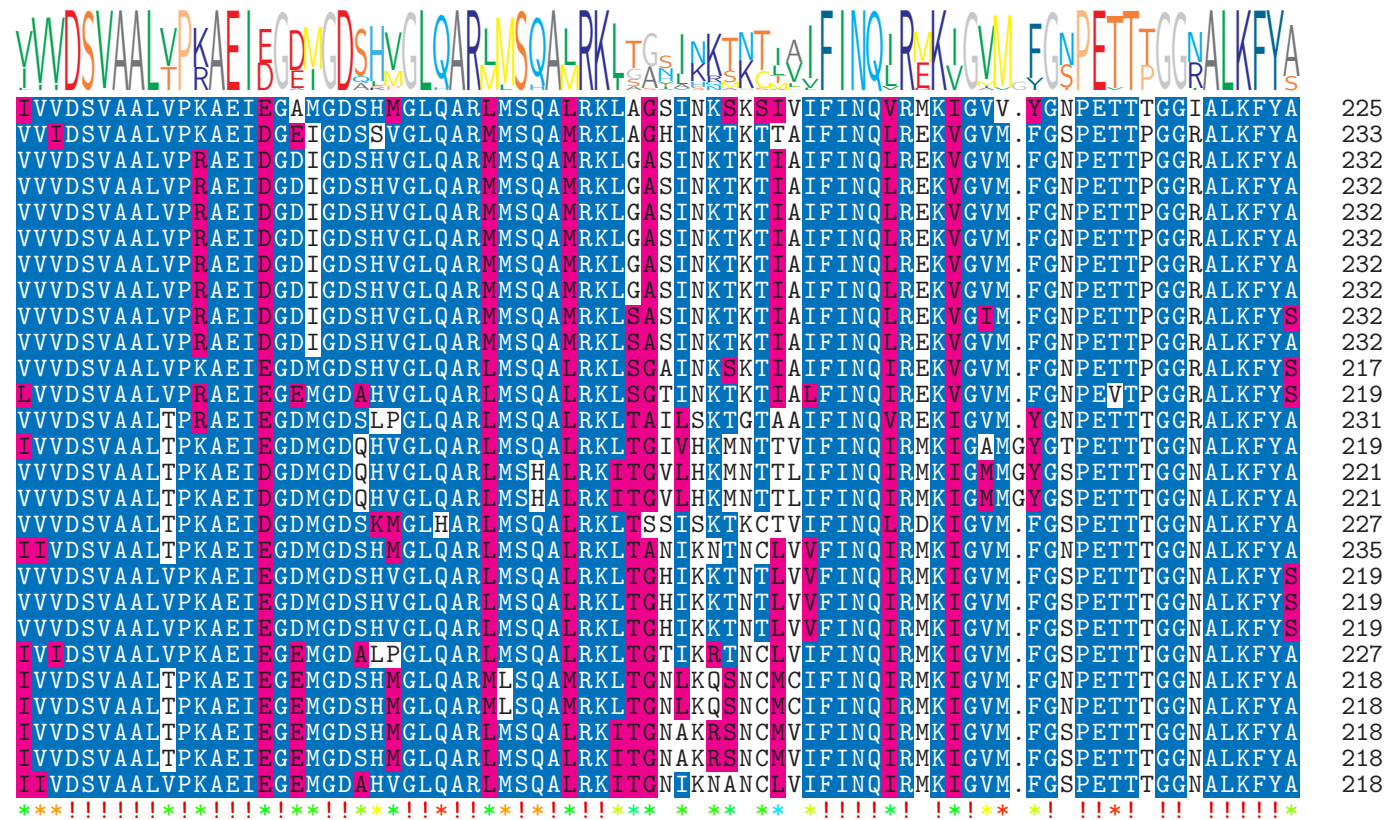


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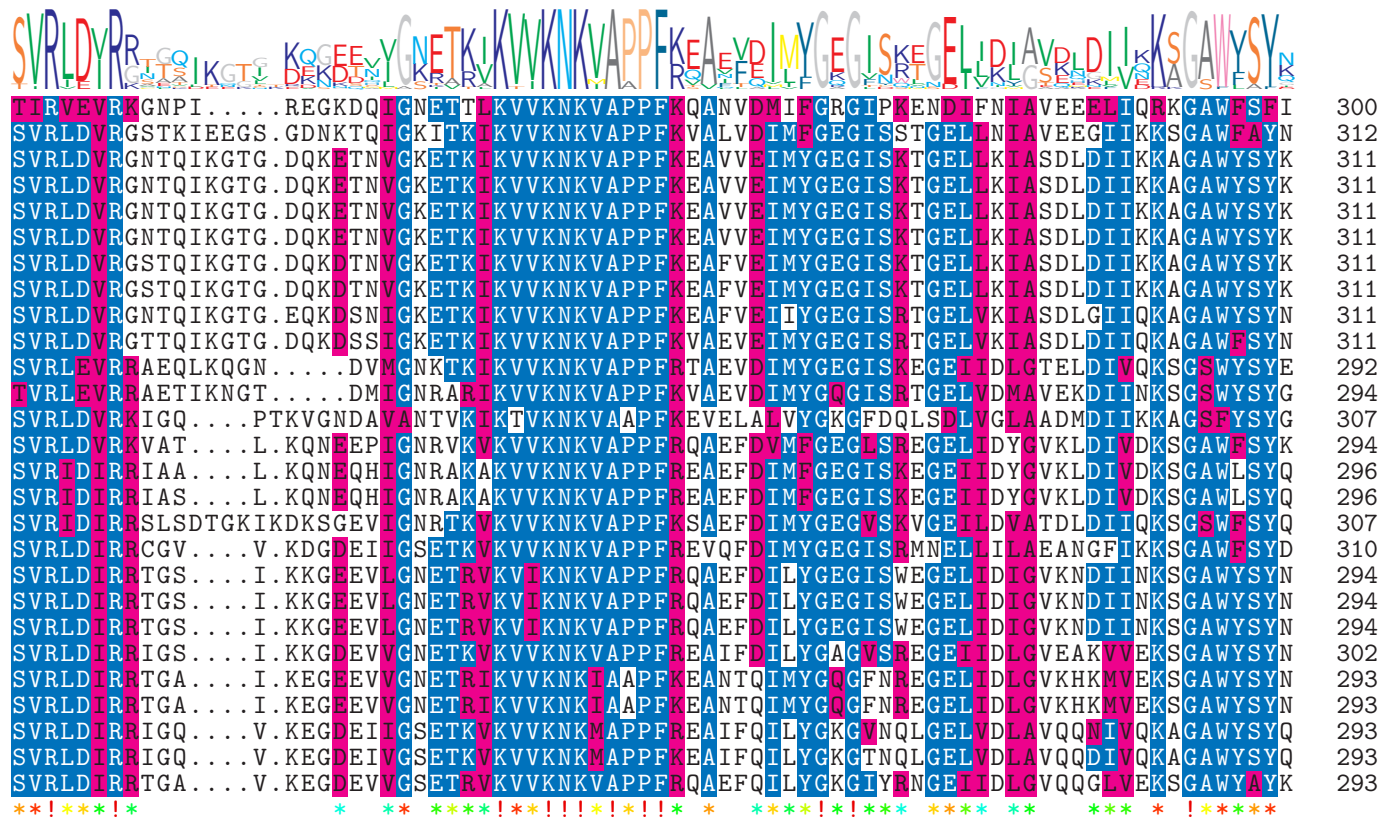
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consensus

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consensus

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Sequence	Score
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DE....KIGQGSSENAKKYLAHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGD	380
DE....KIGQGSSENAKKYLAHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGD	380
DE....KIGQGSSENAKKYLAHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGD	380
DE....KIGQGSSENAKKYLAHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGD	380
DE....KIGQGSSENAKKYLANPEIFDEIDHQVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGD	376
DE....KIGQGSSENAKKYLANPEVFAEIDHQVRVQFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGD	376
GE....KIGQGSSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDD	377
GE....KIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLDN	372
EE....RLGGGRENAKYFLKENKDIMLMIQEQIREHYGLDNGGVVQQQAETQEEL.EFE.E.....	348
SE....RIGQGRENAKNYLADHEDVEDEVLKVRAAAGISDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DE....RIGGQKEKTIAYIAERPEMEQEIRDRVMAAIRAGNAGEAPALAPAAPEAAE..A.....	363
DK....KLGGGRENASKAFLKENPEIADEITKAIQNSMGIEGMI.....SGSEDD..EGE.E.....	343
DK....KLGGGRENAKALLKEDKALADEITLKIKESIGSNEEI.....MPLPDE..PLE..EME.....	347
DK....KLGGGRENAKALLKEDKALADEITLKIKESIGSNEEI.....MPLPDE..PLE..EME.....	347
DT....KLGGGRDVTVELIKDNPELAEELEAKIREKLQAK.....	343
GT....KIGQKKNNAVKWLKENPEIADKLEQEIINTLASNPNS.....VLKATASDSND..ESDVEEFSEEEL.....	372
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GA....KIGQKKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGTQDETGE..R.....PEE.....	348
GA....KIGQKKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGTQDETGE..R.....PEE.....	348
GE....RIGGGRDNCREFLRNAAELAREIENKVRHLGVTPMG.....AVTLA.EEEVE..D.....	352
GD....KIGQKKANACKYLLKENPEIAKTLDDKKLREMLLNPNEM...QLIAETSSAAD..DVEFGAVPEEF.....	354
GD....KIGQKKANACKYLLKENPEIAKTLDDKKLREMLLNPNEM...QLIAETSSAAD..DVEFGAVPEEF.....	354
GN....KIGQKKNNVIRYLEENPQISTEIEAVIREQLLTKASD...QTAA.HDETEE..EPDLL..ES.....	349
GN....KIGQKKNNVIRYFEENNQIAEIEIENIREQLLTGTN...GAVQ.I.EDEE..EPDLL..LES.....	349
GS....KIGQKKANAAYLLENPEIIGQIEEQIRAKLLVTSAN....TKATPVAEDLA..DADI.....	347

logo

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consensus			

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