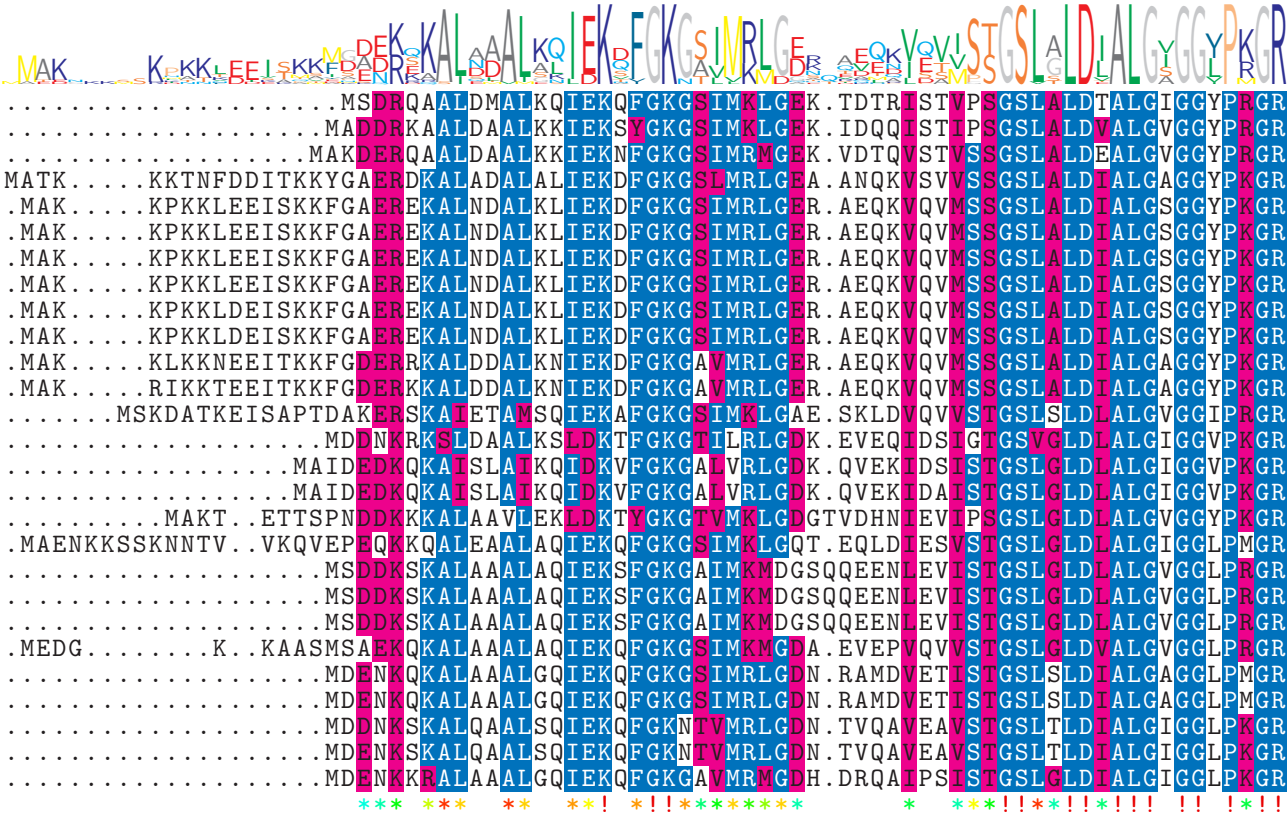


logo

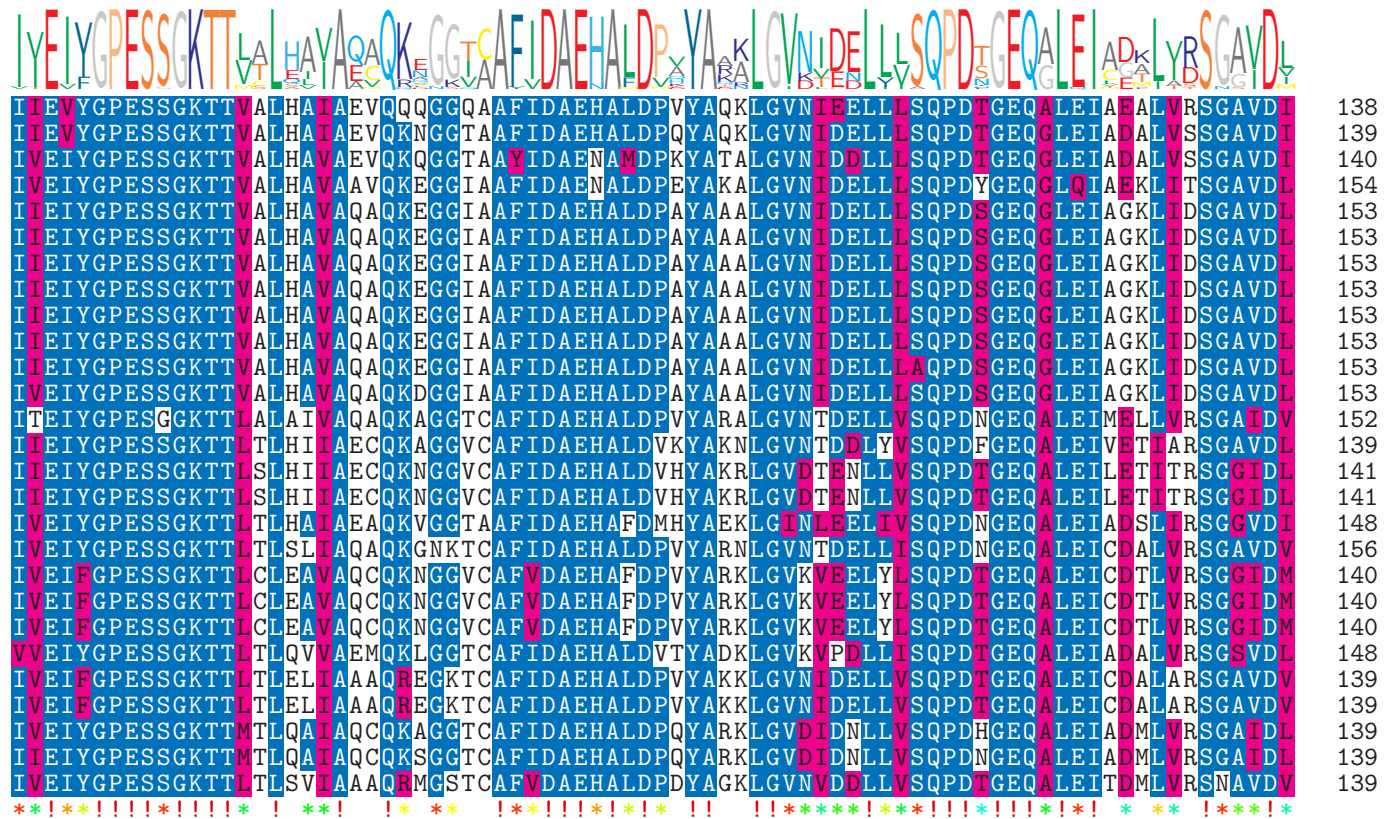
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NTDB id 194 SPR RS08825 WP 001085462.1
NTDB id 159 SP RS09750 WP 001085462.1
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NTDB id 408 SMU RS09530 WP 002262392.1
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NTDB id 1334 RAOC RS04870 WP 004918236.1
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consensus



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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

Sequence	Score
DEERLGGGRENAAKQFLKENKDTIMLTIQEQIREHYGLDNNGVVQQQAEEETQEEL.....EFEE.....	348
EDRIGGGRENAAKIYMANHPPEMAEVSALVRAAYGIGEEVAPPEDEKG.QEEL.....PLVEE.....	349
SERIGGGRENAAKNYLADHEDVEDEVRLKVRRAAYGISDVPEEDLPTTE.DEQI.....NILPDDSTEE..	355
DEKIGGGAEKAKKNYLKEHQDVFEIDHKKVRAAHGLDDSEVAETEEETTASKTAKAKKKEEKAVETEEIELELED....	387
DEKIGGGSSENAAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGSSENAAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
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GEKIGGGSSENAAKFLADNPFIIDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
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DKKLGGRRENAAKALLKEDKALADEITLKIKESIGSNEEI.....MPLPDE..PLEEM.....E.....	347
DKKLGGRRENAAKALLKEDKALADEITLKIKESIGSNEEI.....MPLPDE..PLEEM.....E.....	347
DTKLGGGRDITVKELIKDNPELAEELEAKIREKLQAK.....	343
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GAKIGGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGTQDET DGER.....PEE.....	348
GAKIGGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGTQDET DGER.....PEE.....	348
GERIGGGRDNCREFLNAR EIAENKVR EHLGVTPMG.....AVTLA.EEEVE.....	352
GDKIGGGKANACKYLKENPEIAKTLDDKKLREMLLNPNEM.....QLIAETSSAADDV.....EFGAVPEEF....	354
GDKIGGGKANACKYLKENPEIAKTLDDKKLREMLLNPNEM.....QLIAETSSAADDV.....EFGAVPEEF....	354
GNKIGGGKNNVIRYLEENPQISTEIEIAVIREQLLTKASD.....QTAA.HDETEEEP.....DLL..ES.....	349
GNKIGGGKNNVIRYFEENNQIAEIEIERNIREQLLTTGTN.....GAVQ..I.EDEEEP.....DLL..LES.....	349
GSKIGGGKANAAKYLEENPEIQQEIRAKLLVTSAN.....TKATPVAEDLADA.....DI.....	347

logo

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consensus			

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