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NTDB id 1056691 ACFIOF RS07780 WP 000368166.1
NTDB id 115 BSU 16940 NP 389576.2
NTDB id 1313 DR RS12030 WP 010888966.1
NTDB id 1245 Cj1673c YP 002345041.1
NTDB id 1211 C694 RS00795 WP 000963128.1
NTDB id 1214 NCTC11637 00359 SQJ03206.1
NTDB id 1334 RA0C RS04870 WP 004918236.1
NTDB id 1389 A4U84 RS07560 WP 021112712.1
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NTDB id 1124 NGFG RS03960 WP 003688695.1
NTDB id 1123 OK783 RS03845 WP 003688695.1
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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consensus

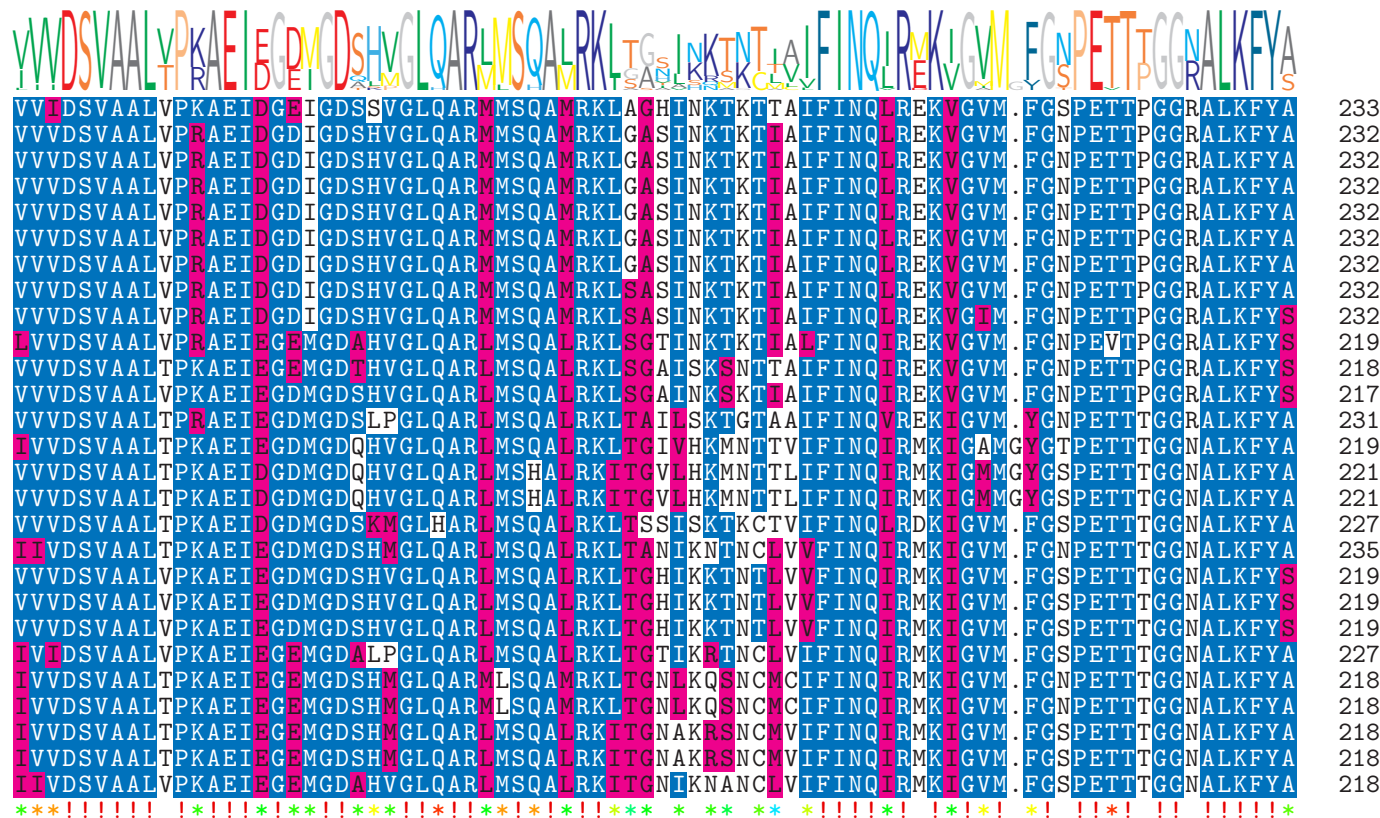
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1205 PSJ3M300 05545 AFN77183.1

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Sequence	Score
DEKIGQGA EKAKNYLKEHQDV FDEIDHKVRAAHGLDDSEVAETEEETTASKTAKAKKKEEKAVETEEIELELED	387
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDE . . . PKKEEA . VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAADNPEIFDEIDHQVRVQFLIDGEEIAES . . . KKDE . . . AAQVDS . VNEEVTLDLGDELEIE	381
DEKIGQGS ENAKKYLAADNPEVFAEIDHQVRVQFLIDGEEIAES . . . KKDE . . . VAQVDS . VNEEVTLDLGDELEIE	381
GEKIGQGS ENAKRYLADHPQLFDEIDRKVRVKFLLEESEESAMAVASE E TDDLALDLNGIEIE	377
GEKIGQGS ENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK ETDEK . ADKNLVLELDDTIELE	382
SERIGQGR ENAKNYLADHEDVEDEVRLKVRAAYGISDVPEEDLPTTEDEQINILPDDSTEE	355
GERMGQGG KENVKMYLKENPQIKEEIDRKLRKLGISDGDVEETEDA . . PKSLFDEE	347
EERLGGGR ENAKQFLKENKDIMLMIQEIQIREHYGLDNNGVVQQQAETQEELEFEE	348
DERIGQGEKKTIAIYIAERPEMEQEIRDRVMAAIRAGNAGEAPALAPAAPEAAEA	363
DKKLGGGR ENSKAFLENPEIAD EITKAIQNSMGTIEGMI SGSEDD . EGEE	343
DKKLGGGR ENAKALLKEDKALADEITLKIKESIGSNEEI MPLPDE . PLEEME	347
DKKLGGGR ENAKALLKEDKALADEITLKIKESIGSNEEI MPLPDE . PLEEME	347
DTKLGGGRD TVKELIKDNPELAEELEAKIREKLQAK	343
GKIGQGKNN AVKWLKENPEIADKLEQEI RNTLASNPNS VLKATASDSNDESD . VEEFSEEEL	372
GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI TEGTQDETGDGER PEE	348
GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI TEGTQDETGDGER PEE	348
GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI TEGTQDETGDGER PEE	348
GERIGQGRDNCREFLRENAELAREIENKVRHGLVTPMG AVTLA . EEEVE	352
GDKIGQGKANACKYLKENPEIAKTLDDKKLREMLLNPNEM QLIAETSSAADDVE . FGAVPEEF	354
GDKIGQGKANACKYLKENPEIAKTLDDKKLREMLLNPNEM QLIAETSSAADDVE . FGAVPEEF	354
GNKIGQGKNNVIRYLEENPQISTEIEAVIREQLLTKASD QTAA . HDETEEEP . LL . ES	349
GNKIGQGKNNVIRYFEENNQIAEIEIERNIREQLLTTGTN GAVQ . I . EDEEEP . LL . LES	349
GSKIGQGGKANAACKYLENPEI GQIEEQIRAKLLVTSAN TKATPVAEDLADAD . I	347

logo

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NTDB id 228 SPD RS09265 WP 001085462.1	IEE 388
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consensus	

-  non conserved
-  similar
-  ≥ 50% conserved