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NTDB id 600 KW2 RS01765 WP 011675413.1
NTDB id 269 KZH43 RS08665 WP 001085462.1
NTDB id 228 SPD RS09265 WP 001085462.1
NTDB id 194 SPR RS08825 WP 001085462.1
NTDB id 159 SP RS09750 WP 001085462.1
NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 527 SMSK321 RS11065 WP 001085454.1
NTDB id 453 Spy49 1753c ACI62003.1
NTDB id 408 SMU RS09530 WP 002262392.1
NTDB id 625 LCA RS02525 WP 011374196.1
NTDB id 142776 FCFHV36 RS06135 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 RAOC RS04870 WP 004918236.1
NTDB id 1389 A4U84 RS07560 WP 021112712.1
NTDB id 1130 NGFG RS03960 WP 003688695.1
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NTDB id 1123 OK783 RS03845 WP 003688695.1
NTDB id 1427 RS RS02760 WP 011000510.1
NTDB id 1165 A1552VC RS01565 WP 000344154.1
NTDB id 1142 GTF74 RS11550 WP 000344154.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1205 PSJM300 05545 AFN77183.1

consensus



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Sequence	Position
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VVVDSVAALVPRAEIDGDI GDSHVGLQARLMSQAMRKLGASINKTKTTAIFINQLREKVGVM.FGNPETTPGGRALKFYA	232
VVVDSVAALVPRAEIDGDI GDSHVGLQARLMSQAMRKLGASINKTKTTAIFINQLREKVGVM.FGNPETTPGGRALKFYA	232
VVVDSVAALVPRAEIDGDI GDSHVGLQARLMSQAMRKLGASINKTKTTAIFINQLREKVGVM.FGNPETTPGGRALKFYA	232
VVVDSVAALVPRAEIDGDI GDSHVGLQARLMSQAMRKLGASINKTKTTAIFINQLREKVGVM.FGNPETTPGGRALKFYA	232
VVVDSVAALVPRAEIDGDI GDSHVGLQARLMSQAMRKLGASINKTKTTAIFINQLREKVGVM.FGNPETTPGGRALKFYA	232
VVVDSVAALVPRAEIDGDI GDSHVGLQARLMSQAMRKLGASINKTKTTAIFINQLREKVGVM.FGNPETTPGGRALKFYA	232
VVVDSVAALVPRAEIDGDI GDSHVGLQARLMSQAMRKLGASINKTKTTAIFINQLREKVGVM.FGNPETTPGGRALKFYA	232
VVVDSVAALVPRAEIDGDI GDSHVGLQARLMSQAMRKLGASINKTKTTAIFINQLREKVGIM.FGNPETTPGGRALKFYS	232
LVVDSVAALVPRAEIEGEMGD AHVGLQARLMSQALRKLSGTINKTKTTIALFINQIREKVGVM.FGNPEVTPGGRALKFYS	219
VVVDSVAALTPKAEIEGEMGDTHVGLQARLMSQALRKLSGATSKSNTTAIFINQIREKVGVM.FGNPETTPGGRALKFYS	218
VVVDSVAALVPKAEIDGDMGDTHVGLQARLMSQALRKLSGAINSKTTAIFINQIREKVGVM.FGNPETTPGGRALKFYS	217
VVVDSVAALTPRAEIEGDMGDSLPLGLQARLMSQALRKLTAILSKTGTAIFINQIREKIGVM.YGNPETTPGGRALKFYA	231
IVVDSVAALTPKAEIEGDMGDQHVGVLQARLMSQALRKLTGIVHKMNTTVIFINQIRMKIGAMGYGTPETTTGGNALKFYA	219
VVVDSVAALTPKAEIDGDMGDQHVGVLQARLMSHALRKITGV LHKMNTTLIFINQIRMKIGMMGYGSPETTTGGNALKFYA	221
VVVDSVAALTPKAEIDGDMGDQHVGVLQARLMSHALRKITGV LHKMNTTLIFINQIRMKIGMMGYGSPETTTGGNALKFYA	221
VVVDSVAALTPKAEIDGDMGDKMGLHARLMSQALRKLTSSIKTKCTVIFINQLRDKIGVM.FGSPETTTGGNALKFYA	227
IIVDSVAALTPKAEIEGDMGDSSHGLQARLMSQALRKLTANIKNTNCLVIFINQIRMKIGVM.FGNPETTTGGNALKFYA	235
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IVI DSVAALVPKAEIEGEMDALPGLQARLMSQALRKLTGTIKRTNCLVIFINQIRMKIGVM.FGSPETTTGGNALKFYA	227
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IVVDSVAALTPKAEIEGEMGDSSHGLQARLMSQALRKITGNAKRSNCMVIFINQIRMKIGVM.FGSPETTTGGNALKFYA	218
IVVDSVAALVPKAEIEGEMGD AHVGLQARLMSQALRKITGNANKNANCLVIFINQIRMKIGVM.FGSPETTTGGNALKFYA	218

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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 ENAKKYLAADNPEIFDEIDHQVRVQFGLIDGEEIAES . . . KKDE . . . AAQVDS . VNEEVTLDLGDELEIE	381
DEKIGQGS ENAKKYLAADNPEVFAEIDHQVRVQFGLIDGEEIAES . . . KKDE . . . VAQVDS . VNEEVTLDLGDELEIE	381
GEKIGQGS ENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE 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
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GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI TEGTQDETGDGER PEE	348
GERIGQGRDNCREFLRENAELAREIENKVRHGLVTPMG AVTLA . EEEVE	352
GDKIGQGKANACKYLKENPEIAKTLDDKKLREMLLNPNEM QLIAETSSAADDVE . FGAVPEEF	354
GDKIGQGKANACKYLKENPEIAKTLDDKKLREMLLNPNEM QLIAETSSAADDVE . FGAVPEEF	354
GNKIGQGKNNVIRYLEENPQISTEIEAVIREQLLTKASD QTAA . HDETEEEPD . LL . ES	349
GNKIGQGKNNVIRYFEENNQIAEIEIERNIREQLLTTGTN GAVQ . I . EDEEEPD . LL . LES	349
GSKIGQGGKANAACKYLENPEIQEIEEQIRAKLLVTSAN TKATPVAEDLADAD . I	347

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

-  non conserved
-  similar
-  ≥ 50% conserved