

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus



80
80

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus



160
160

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus



235
230

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus



314
298

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus



394
378

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus



474
458

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus



554
538

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus

SYANVPLPIAGQRETRDAEGNITKYYYAVQSKIRNLFQDVSAAVADGSLTKISTSGTNLLKIPAAPPEETNPFDTVANTA
SYANVPLPIAGQRETRDAEGNITKYYYAVQSKIRNLFQDVSAAVADGSLTKISTSGTNLLKIPAAPPEETNPFDTVANTA
SYANVPLPIAGQRETRDAEGNITKYYYAVQSKIRNLFQDVSAAVADGSLTKISTSGTNLLKIPAAPPEETNPFDTVANTA
*!!

634
618

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus

SYVLGKFDPSGTGNILKAFPIISLKLKILNYLGYSTDINATTLPSLVTSEPEYLSMGGSIHSLPVQLTYNGTLDDNGNLT
SYVLGKFDPSGTGNILKAFPIISLKLKILNYLGYSTDINATTLPSLVTSEPEYLSMGGSIHSLPVQLTYNGTLDDNGNLT
SYVLGKFDPSGTGNILKAFPIISLKLKILNYLGYSTDINATTLPSLVTSEPEYLSMGGSIHSLPVQLTYNGTLDDNGNLT
!!

714
698

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus

SAREQSILYGTMEGGLHIVDASSGIEQMVFPADILNDSVASKALVVGQSDASAPAHGMDGAWVSDPAYNITTVGSGSSA
SAREQSILYGTMEGGLHIVDASSGIEQMVFPADILNDSVASKALVVGQSDASAPAHGMDGAWVSDPAYNITTVGSGSSA
SAREQSILYGTMEGGLHIVDASSGIEQMVFPADILNDSVASKALVVGQSDASAPAHGMDGAWVSDPAYNITTVGSGSSA
!!

794
778

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus

VSKVTAKQMNLYGGMRMGGSSYYGLDVLSPSTPKLLFRIGADQNDYSRMGQSWSKPVLANIRYNGSIRRVLIVGGGYDQC
VSKVTAKQMNLYGGMRMGGSSYYGLDVLSPSTPKLLFRIGADQNDYSRMGQSWSKPVLANIRYNGSIRRVLIVGGGYDQC
VSKVTAKQMNLYGGMRMGGSSYYGLDVLSPSTPKLLFRIGADQNDYSRMGQSWSKPVLANIRYNGSIRRVLIVGGGYDQC
!!

874
858

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus

YEKPNITLTDACFTNGKAKGNAVYIIDAKTGQRLWWTSDTGSNTDNANMKHSIVSRISTLDGDADGLVDHLYFGDLGGQI
YEKPNITLTDACFTNGKAKGNAVYIIDAKTGQRLWWTSDTGSNTDNANMKHSIVSRISTLDGDADGLVDHLYFGDLGGQI
YEKPNITLTDACFTNGKAKGNAVYIIDAKTGQRLWWTSDTGSNTDNANMKHSIVSRISTLDGDADGLVDHLYFGDLGGQI
!!

954
938

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus

FRVDLNNNQTKTNSTYSSFGVRVRLANLATNDSTYDGTNDYTGGNAPRFYEPPTVTIHDYGIHTFITVGIASGDRSTPL
FRVDLNNNQTKTNSTYSSFGVRVRLANLATNDSTYDGTNDYTGGNAPRFYEPPTVTIHDYGIHTFITVGIASGDRSTPL
FRVDLNNNQTKTNSTYSSFGVRVRLANLATNDSTYDGTNDYTGGNAPRFYEPPTVTIHDYGIHTFITVGIASGDRSTPL
!!

1034
1018

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus

DVYPLTGREGMTPASALSGRPVNNVYGIIDRDFVKKNLMSLTDNQLETKDITRTGLRKNPQILRTGETRVAQIFFPPTTG
DVYPLTGREGMTPASALSGRPVNNVYGIIDRDFVKKNLMSLTDNQLETKDITRTGLRKNPQILRTGETRVAQIFFPPTTG
DVYPLTGREGMTPASALSGRPVNNVYGIIDRDFVKKNLMSLTDNQLETKDITRTGLRKNPQILRTGETRVAQIFFPPTTG
!!

1114
1098

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus



1194
1178

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus



1274
1258

logo

NTDB id 110070 ACAK35 RS01860 WP 216076437.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus



1284
1268

- non conserved
- similar
- ≥ 50% conserved