

logo

NTDB id 328874 EHF38 RS01665 WP 128385708.1
NTDB id 1063 ABD1 RS15730 WP 000768961.1
consensus

MKLKLKNFKPNNLWYAVCSSSMIFTWMTSSVVQASDLQIYASPTAGKKTIVMMLDTSGSMTSNSYGENRLAMLKNGMNA
.....
MKLKLKNFKPNNLWYAVCSSSMIFTWMTSSVVQASDLQIYASPTAGKKTIVMMLDTSGSMTSNSYGENRLAMLKNGMNA

0
80

logo

NTDB id 328874 EHF38 RS01665 WP 128385708.1
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consensus

FLASNNPVLNDTRVGLGNFSADGDSRSGQILVAAAPLGDASTLNTMGSQRYKLKQAVASLTASGYTPSAHAYAEAAAYLM
.....
FLASNNPVLNDTRVGLGNFSADGDSRSGQILVAAAPLGDASTLNTMGSQRYKLKQAVASLTASGYTPSAHAYAEAAAYLM

0
160

logo

NTDB id 328874 EHF38 RS01665 WP 128385708.1
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consensus

GTTTLKNINLVDAPIYFSYVTYDRRGRVITNYHACTEWNTEGTICNSWDSSSLSNPPVISGLQQASCTANIGWQLLSGTC
.....
GTTTLKNINLVDAPIYFSYVTYDRRGRVITNYHACTEWNTEGTICNSWDSSSLSNPPVISGLQQASCTANIGWQLLSGTC

0
240

logo

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consensus

YKKTGLITINNLDSGFNKISGSKNTDQSQYNSPLPAVANRQSCDGQGIYFLSDGEPNKTTDTRSASIMSTALGSTFGAD
.....
YKKTGLITINNLDSGFNKISGSKNTDQSQYNSPLPAVANRQSCDGQGIYFLSDGEPNKTTDTRSASIMSTALGSTFGAD

0
320

logo

NTDB id 328874 EHF38 RS01665 WP 128385708.1
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consensus

FNCSSGLSNTTADSGWACMGFEFAKRLFDKTKNPAGVSIQTAFVGFSGDFSSLSSSDVKNAACRLSSRTQFDRGGDDL CSPN
.....
FNCSSGLSNTTADSGWACMGFEFAKRLFDKTKNPAGVSIQTAFVGFSGDFSSLSSSDVKNAACRLSSRTQFDRGGDDL CSPN

0
400

logo

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consensus

QTTNAITAPGYNGGFFSTQSAQGVTDSVIAFINNLDKVPLEPLTTGAISVPYDALNPKNLQEYGYLRAFEPNPANTYLT
.....
QTTNAITAPGYNGGFFSTQSAQGVTDSVIAFINNLDKVPLEPLTTGAISVPYDALNPKNLQEYGYLRAFEPNPANTYLT

0
480

logo

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consensus

WRGNLKKYHVLSGTNAGAFEANTGGLVYNATGAFRTGTDYWNSSSTYNDGGKVFFGGSYAKVPLPIAGQNETRDAEGNI
.....
WRGNLKKYHVLSGTNAGAFEANTGGLVYNATGAFRTGTDYWNSSSTYNDGGKVFFGGSYAKVPLPIAGQNETRDAEGNI

0
560

logo

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consensus

TKYYYAVQSKI RNLF TDVSAVAADGSLTKISTSGTNLLKIPAAPPEGTNPFDTVANTASYVLGKFDPSTGQNILKAFPIS
TKYYYAVQSKIRNLF TDVSAVAADGSLTKISTSGTNLLKIPAAPPEGTNPFDTVANTASYVLGKFDPSTGQNILKAFPIS

0
640

logo

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consensus

LKLKILNLYLGYSTDISATTL PSSLVTSNEPYLSMGGSIHSLPVQLTYNGTLD DNGNLTSAREQSILYGTMEGGLHIVDAS
LKLKILNLYLGYSTDISATTL PSSLVTSNEPYLSMGGSIHSLPVQLTYNGTLD DNGNLTSAREQSILYGTMEGGLHIVDAS

0
720

logo

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consensus

SGIEQWVFVPADILNDSVASKALVVGQSDASAPAHGMDGAWVSDPAYNITTVGSGSSAVSKVTAKQMNIYGGMRMGSSY
SGIEQWVFVPADILNDSVASKALVVGQSDASAPAHGMDGAWVSDPAYNITTVGSGSSAVSKVTAKQMNIYGGMRMGSSY

0
800

logo

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consensus

YGLDVLSP TSPKLLFRIGADQTDYSRMGQSWSKPVLANIRYNGSIRRVLI VGGGYDQCYEKPNI TLTDACFTNGKAKGNA
YGLDVLSP TSPKLLFRIGADQTDYSRMGQSWSKPVLANIRYNGSIRRVLI VGGGYDQCYEKPNI TLTDACFTNGKAKGNA

0
880

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consensus

VYIIDAKTGQRLWWTSDTGSNTDNANMKHSIVSRISTLDRDADGLVDHLYFGDLGGQIFRVDLNNNQTKTNSTYSSFVGR
VYIIDAKTGQRLWWTSDTGSNTDNANMKHSIVSRISTLDRDADGLVDHLYFGDLGGQIFRVDLNNNQTKTNSTYSSFVGR

0
960

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consensus

VR LANLATNDSTYDGTNDYTGGNAPRFYEPPTVTIHDYGIHTFITVGIASGDRSTPLDVYPLTGREGMTPTSALSGRPV
VR LANLATNDSTYDGTNDYTGGNAPRFYEPPTVTIHDYGIHTFITVGIASGDRSTPLDVYPLTGREGMTPTSALSGRPV

0
1040

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consensus

NNVYGIIDRDFVKKNLMSLTDNQLETKDITRTGLRKNPQILRTGETRVAQIFFPTTGVGKGGWYRSLSSTSDGTEKANNS
NNVYGIIDRDFVKKNLMSLTDNQLETKDITRTGLRKNPQILRTGETRVAQIFFPTTGVGKGGWYRSLSSTSDGTEKANNS

0
1120

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consensus



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