

logo

NTDB id 197365 PSA83 RS09895 WP 003163304.1
NTDB id 1196 PAKAF RS09365 WP 016253171.1
consensus

MVRLRTLVRATAAASVLTSGMAHGLGLGEITLKSALNQLDAEIELLEVRDLGSGEVIIPSLASPEEFSKAGVDRLYYLTD
MVRLRTLVRATAAASVLTSGMAHGLGLGEITLKSALNQLDAEIELLEVRDLGSGEVIIPSLASPEEFSKAGVDRLYYLTD
!!

80
80

logo

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consensus

LKFTPWKPNGKSVIRVTSSKPVQEPYLNFLVQVLPNGRLLREYTVLLDPPLYSPQAAAAPQAPVSAPRATGAPRAPQ
LKFTPVVKPNGKSVIRVTSSKPVQEPYLNFLVQVLPNGRLLREYTVLLDPPLYSPQAAAAPQAPVSAPRATGAPRAPQ
LKFTPVVKPNGKSVIRVTSSKPVQEPYLNFLVQVLPNGRLLREYTVLLDPPLYSPQAAAAPQAPVSAPRATGAPRAPQ
!!

160
160

logo

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consensus

APAPVRTTAPAGSDTYRTVSNDTLWEIAQRNRTDRVSVQAMLAHQELNPGAFVDGNINRLKSGQVLRIPTEQQMLERSP
APAPVRTTAPAGSDTYRTVSNDTLWEIAQRNRTDRVSVQAMLAHQELNPGAFVDGNINRLKSGQVLRIPTEQQMLERSP
APAPVRTTAPAGSDTYRTVSNDTLWEIAQRNRTDRVSVQAMLAHQELNPGAFVDGNINRLKSGQVLRIPTEQQMLERSP
!!

240
240

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consensus

REALSQVQAQNSWRGSRNPAAGSAGARQLDATQRNAAGSAPSKVDATDNLRLVSGEGKASKGADKGGKGDASKAIADTLA
REALSQVQAQNSWRGSRNPAAGSAGARQLDATQRNAAGSAPSKVDATDNLRLVSGEGKASKGADKGGKGDASKAIADTLA
REALSQVQAQNSWRGSRNPAAGSAGARQLDATQRNAAGSAPSKVDATDNLRLVSGEGKASKGADKGGKGDASKAIADTLA
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320
320

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consensus

VTKESLDSTRRENEELQSRMQDLQSQDKLQKLIQLKDAQLAKLQGGQGAEGQGAQPNAALPDASQPNAAAQAPAPQGT
VTKESLDSTRRENEELQSRMQDLQSQDKLQKLIQLKDAQLAKLQGGQGAEGQGAQPNAALPDASQPNAAAQAPAPQGT
VTKESLDSTRRENEELQSRMQDLQSQDKLQKLIQLKDAQLAKLQGGQGAEGQGAQPNAALPDASQPNAAAQAPAPQGT
!!

400
400

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consensus

PAAAPTAPAGEAQAAPQPPVAPPAPAAERPPAPAVPAPAPVQAAEQPAPSFDELLEANPLWLAVIGGSALLALLVL
PAAAPTAPAGEAQAAPQPPVAPPAPAAERPPAPAVPAPAPVQAAEQPAPSFDELLEANPLWLAVIGGSALLALLVL
PAAAPTAPAGEAQAAPQPPVAPPAPAAERPPAPAVPAPAPVQAAEQPAPSFDELLEANPLWLAVIGGSALLALLVL
!!

480
480

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consensus

LMILSRRNAQKEKEEAQFAADTGEQEDALDLGKDGFDLTLDEPEPQVAAPVQVEKTTAQTSDALGEADIYIAYGRF
LMILSRRNAQKEKEEAQFAADTGEQEDALDLGKDGFDLTLDEPEPQVAAPVQVEKTTAQTSDALGEADIYIAYGRF
LMILSRRNAQKEKEEAQFAADTGEQEDALDLGKDGFDLTLDEPEPQVAAPVQVEKTTAQTSDALGEADIYIAYGRF
!!

560
560

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consensus

NQAAELLQNAIYDEPQRTDLRLKLMEVYAEMGDREGFARQENELREI GGAQPQVEQLKSRYPAMVAVAAVAGLAGAKLAQ
NQAAELLQNAIYDEPQRTDLRLKLMEVYAEMGDREGFARQENELREI GGAQPQVEQLKSRYPAMVAVAAVAGLAGAKLAQ
!!

640
640

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consensus

DELDSFSLDDL SLDDSGHAAKPD AAGQDLDDAFDLSLDDLGGDDVQADLKSDSGALDDLTLDSDLDLAASTPADKPVDDL
DELDSFSLDDL SLDDSGHAAKPD AAGQDLDDAFDLSLDDLGGDDVQADLKSDSGALDDLTLDSDLDLAASTPADKPVDDL
DELDSFSLDDL SLDDSGHAAKPD AAGQDLDDAFDLSLDDLGGDDVQADLKSDSGALDDLTLDSDLDLAAST*ADKPVDDL
!!

720
720

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consensus

DFGLDFAEL AETPSQPKHDDL GDFSLDL DAPEDKLSDDDFLLSLNDEVPA AAPADNEFTLDTEAAE EPALS LPDDFDLSL
DFGLDFAEL AETPSQPKHDDL GDFSLDL DAPEDKLSDDDFLLSLNDEVPA AAPADNEFTLDTEAAE EPALS LPDDFDLSL
DFGLDFAEL AETPSQPKHDDL GDFSLDL DAPEDKLSDDDFLLSLNDEVPA AAPADNEFTLDTEAAE EPALS LPDDFDLSL
!!

800
800

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ADEPTEPAAPEKGEDSFAAQLDEVSAQLDELASNLDEPKSATPSFSAEDA AVASALDGDADDDFDL SGADEAATKLDLA
ADEPTEPAAPEKGEDSFAAQLDEVSAQLDELASNLDEPKSATPSFSAEDA AVASALDGDADDDFDL SGADEAATKLDLA
ADEPTEPAAPEKGEDSFAAQLDEVSAQLDELASNLDEPKSATPSFSAEDA AVASALDGDADDDFDL SGADEAATKLDLA
!!

880
880

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consensus

RAYIDMGDSEGARDILDEVLAEGNDSQQA EARELLERLA
RAYIDMGDSEGARDILDEVLAEGNDSQQA EARELLERLA
RAYIDMGDSEGARDILDEVLAEGNDSQQA EARELLERLA
!!

919
919

⊠ non conserved
⊠ similar
⊠ ≥ 50% conserved