logo
NTDB id 615 LCA RS02545 WP 011374200.1 ..................MGQQVIACGRQFTAAQLADTQNNNYSLPQIKRRPAFLRVKHRLVCQRCQQVVPPQ....TC..LPD 60
NTDB id 139048 SB48 RS13460 WP 014095892.1 ......MPSVFSEQLQRHLAGRILFEPEIPFSPELLD....QHFKQGWIRAEPAIQGEFPHCVCLRCGNRAPHLFAEFPCAHCGK 75
NTDB id 108 BSU 35470 NP 391427.1 MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIE....WHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYH..SSGK 79
consensus
logo
NTDB id 615 LCA RS02545 WP 011374200.1 GRHYCAQCLLFGRLVEGDWLYTVPE.CHLFENNIPKLTWEGQLTPHQEKAAQAVVEVVQTQKRHVLTAVTGAGKTEMLFQGILVA 144
NTDB id 139048 SB48 RS13460 WP 014095892.1 TSIYCRNCLMMGRVTACKPLITWAGPAPAFHSPRHPLHWDGTLSEGQQAASEAVKAAILQKNELLIWAVCGSGKTEIVFKGIEAA 160
NTDB id 108 BSU 35470 NP 391427.1 NKLYCRSCVMMGRVSEEVPLYSWKEENESN.WKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFPGIESA 163
consensus
logo
NTDB id 615 LCA RS02545 WP 011374200.1 LQKGQRVCLAAPRVAVCLELYPRLQAAFATTSIMLMHGEQTEPYRYTQLVICTTHQLLKFYHAFDTVIVDEVDAFPFVDNPVLAT 229
NTDB id 139048 SB48 RS13460 WP 014095892.1 LANGERVCIATPRTDVVLELAPRFRRVFPDIPIAALYGGSPDRHKWAQLVISTTHQLYRFASAFDVVIVDEVDAFPYTFDETLQC 245
NTDB id 108 BSU 35470 NP 391427.1 LNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAFPYSADQTLQF 248
consensus
logo
NTDB id 615 LCA RS02545 WP 011374200.1 AVEQACKPQCALLYLTATPTPAIKRAIAAKQMTVSELPLRFHGHLLPEPQRHVAFNWRAQLKKGRLPKRLERDCQTYLK.TQQIL 313
NTDB id 139048 SB48 RS13460 WP 014095892.1 AVQKAAKDRCARIYLTATPSETWQLECKTGKRPFVTIPARYHRKPLPVPVFKWAGNWRKKFEKGKLPVPVEAWVKKRLESGKQAL 330
NTDB id 108 BSU 35470 NP 391427.1 AVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAVKRWIEFHVKEGRPVF 333
consensus
logo
NTDB id 615 LCA RS02545 WP 011374200.1 LFVPQVRLLQPVANRLSTLLPAVRIETLHANDPDQIKKITAFRAQQIQLMVTTTILERGVTFKNVAVLVLGAEHMVFNEAVLVQI 398
NTDB id 139048 SB48 RS13460 WP 014095892.1 LFLPNIRLMKKAEPVFKQLHP..AIESVHAEDPDRKEKVERMRAGKTPLLLTTTILERGVTFPNIDVCVVGAEDAIFTEAALVQI 413
NTDB id 108 BSU 35470 NP 391427.1 LFVPSVSILEKAAACFKGVHC..RTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQTGVLGAESSIFTESALVQI 416
consensus
logo
NTDB id 615 LCA RS02545 WP 011374200.1 AGRAGRHKDYAQNPVHFYYQDYTRAIKGACRQIKTQNQRGRRLQSTV. 445
NTDB id 139048 SB48 RS13460 WP 014095892.1 AGRAGRSADFPSGDVTFFHYGKSNAMVKAQRHILSMNEEAGKRGLLDA 461
NTDB id 108 BSU 35470 NP 391427.1 AGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD. 463
consensus
X non conserved
X similar
X ≥ 50% conserved