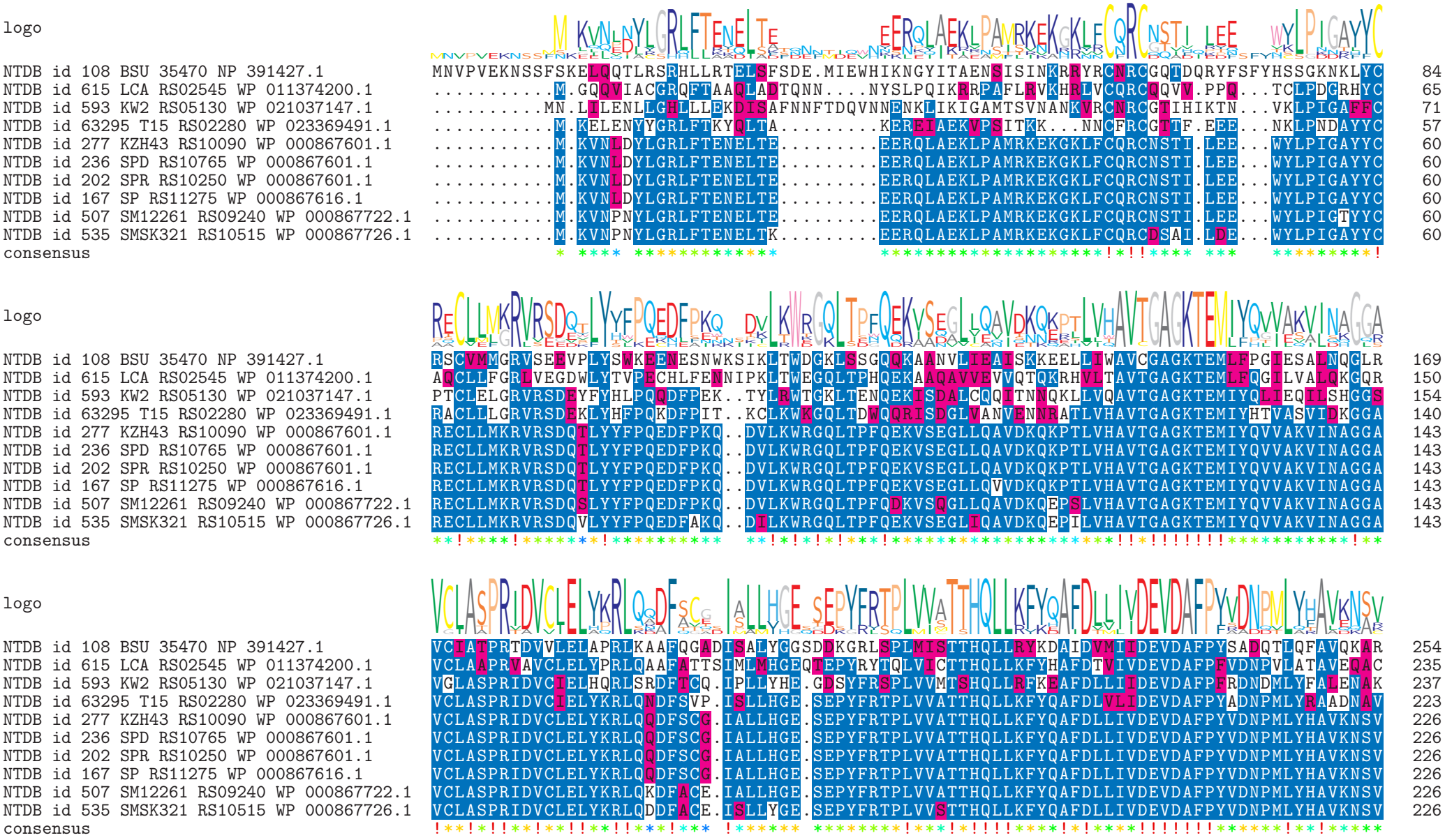
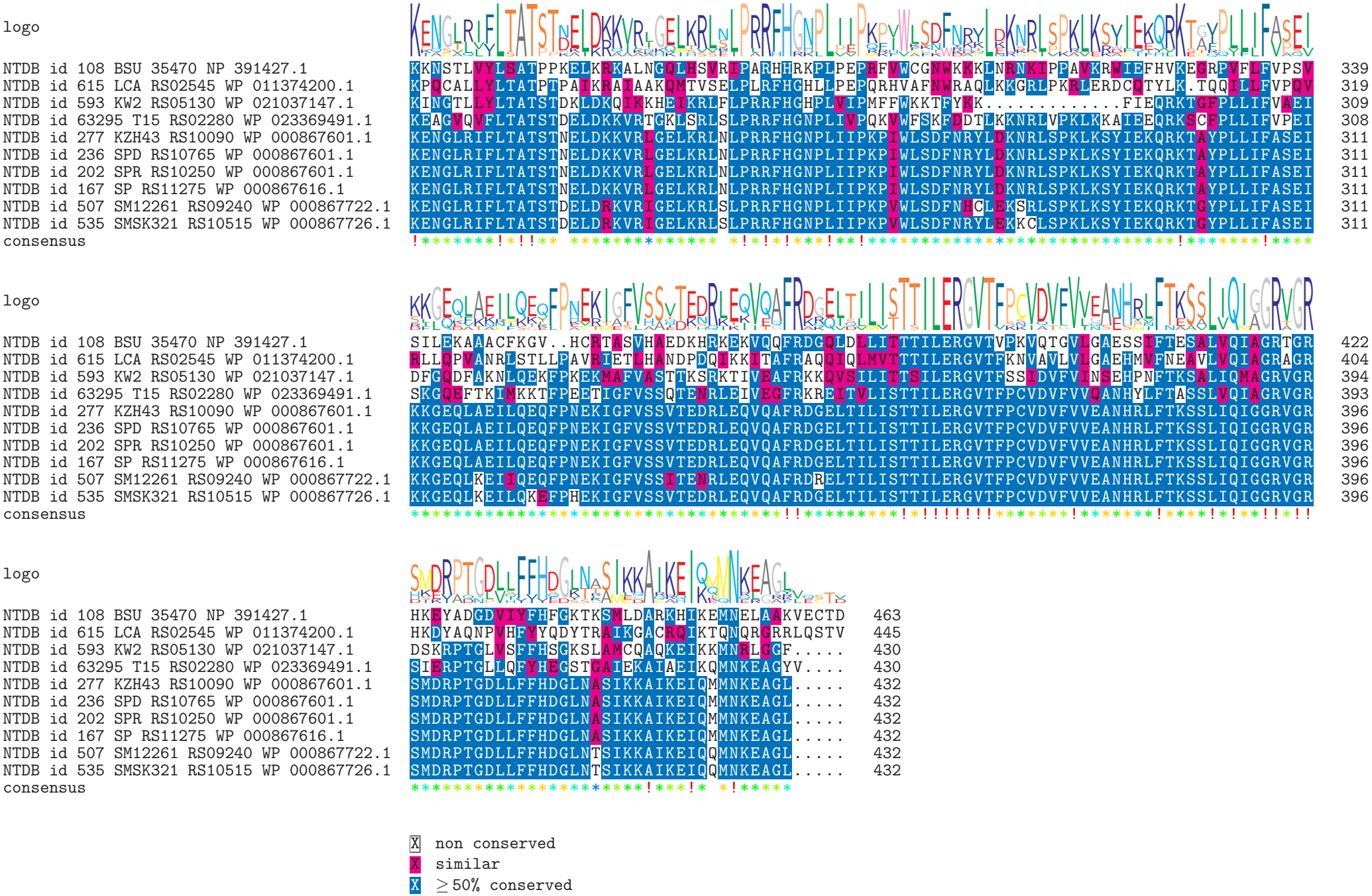

logo
NTDB id 108 BSU 35470 NP 391427.1 MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDE.MIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHSSGKNKLYC 84
NTDB id 615 LCA RS02545 WP 011374200.1 ..........M.GQQVIACGRQFTAAQLADTQNN....NYSLPQIKRRPAFLRVKHRLVCQRCQQVV.PPQ...TCLPDGRHYC 65
NTDB id 593 KW2 RS05130 WP 021037147.1 ..........MN.LILENLLGHLLLEKDISAFNNFTDQVNNENKLIKIGAMTSVNANKVRCNRCGTIHIKTN...VKLPIGAFFC 71
NTDB id 63295 T15 RS02280 WP 023369491.1 ..........M.KELENYYGRLFTKYQLTA.........KEREIAEKVPSITKK...NNCFRCGTTF.EEE...NKLPNDAYYC 57
NTDB id 277 KZH43 RS10090 WP 000867601.1 ..........M.KVNLDYLGRLFTENELTE.........EERQLAEKLPAMRKEKGKLFCQRCNSTI.LEE...WYLPIGAYYC 60
NTDB id 236 SPD RS10765 WP 000867601.1 ..........M.KVNLDYLGRLFTENELTE.........EERQLAEKLPAMRKEKGKLFCQRCNSTI.LEE...WYLPIGAYYC 60
NTDB id 202 SPR RS10250 WP 000867601.1 ..........M.KVNLDYLGRLFTENELTE.........EERQLAEKLPAMRKEKGKLFCQRCNSTI.LEE...WYLPIGAYYC 60
NTDB id 167 SP RS11275 WP 000867616.1 ..........M.KVNLDYLGRLFTENELTE.........EERQLAEKLPAMRKEKGKLFCQRCNSTI.LEE...WYLPIGAYYC 60
NTDB id 507 SM12261 RS09240 WP 000867722.1 ..........M.KVNPNYLGRLFTENELTE.........EERQLAEKLPAMRKEKGKLFCQRCNSTI.LEE...WYLPICTYYC 60
NTDB id 535 SMSK321 RS10515 WP 000867726.1 ..........M.KVNPNYLGRLFTENELTK.........EERQLAEKLPAMRKEKGKLFCQRCDSAI.LDE...WYLPIGAYYC 60
consensus
logo
NTDB id 108 BSU 35470 NP 391427.1 RSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFPGIESALNQGLR 169
NTDB id 615 LCA RS02545 WP 011374200.1 AQCLLFGRLVEGDWLYTVPECHLFENNIPKLTWEGQLTPHQEKAAQAVVEVVQTQKRHVLTAVTGAGKTEMLFQGILVALQKGQR 150
NTDB id 593 KW2 RS05130 WP 021037147.1 PTCLELGRVRSDEYFYHLPQQDFPEK..TYLRWTGKLTENQEKISDALCQQITNNQKLLVQAVTGAGKTEMIYQLIEQILSHGGS 154
NTDB id 63295 T15 RS02280 WP 023369491.1 RACLLLGRVRSDEKLYHFPQKDFPIT..KCLKWKGQLTDWQQRISDGLVANVENNRATLVHAVTGAGKTEMIYHTVASVIDKGGA 140
NTDB id 277 KZH43 RS10090 WP 000867601.1 RECLLMKRVRSDQTLYYFPQEDFPKQ..DVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMIYQVVAKVINAGGA 143
NTDB id 236 SPD RS10765 WP 000867601.1 RECLLMKRVRSDQTLYYFPQEDFPKQ..DVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMIYQVVAKVINAGGA 143
NTDB id 202 SPR RS10250 WP 000867601.1 RECLLMKRVRSDQTLYYFPQEDFPKQ..DVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMIYQVVAKVINAGGA 143
NTDB id 167 SP RS11275 WP 000867616.1 RECLLMKRVRSDQTLYYFPQEDFPKQ..DVLKWRGQLTPFQEKVSEGLLQVVDKQKPTLVHAVTGAGKTEMIYQVVAKVINAGGA 143
NTDB id 507 SM12261 RS09240 WP 000867722.1 RECLLMKRVRSDQSLYYFPQEDFPKQ..DVLKWRGQLTPFQDKVSQGLLQAVDKQEPSLVHAVTGAGKTEMIYQVVAKVINAGGA 143
NTDB id 535 SMSK321 RS10515 WP 000867726.1 RECLLMKRVRSDQVLYYFPQEDFAKQ..DILKWRGQLTPFQEKVSEGLIQAVDKQEPILVHAVTGAGKTEMIYQVVAKVINAGGA 143
consensus
logo
NTDB id 108 BSU 35470 NP 391427.1 VCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAFPYSADQTLQFAVQKAR 254
NTDB id 615 LCA RS02545 WP 011374200.1 VCLAAPRVAVCLELYPRLQAAFATTSIMLMHGEQTEPYRYTQLVICTTHQLLKFYHAFDTVIVDEVDAFPFVDNPVLATAVEQAC 235
NTDB id 593 KW2 RS05130 WP 021037147.1 VGLASPRIDVCIELHQRLSRDFTCQ.IPLLYHE.GDSYFRSPLVVMTSHQLLRFKEAFDLLIIDEVDAFPFRDNDMLYFALENAK 237
NTDB id 63295 T15 RS02280 WP 023369491.1 VCLASPRIDVCIELYKRLQNDFSVP.ISLLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLVLIDEVDAFPYADNPMLYRAADNAV 223
NTDB id 277 KZH43 RS10090 WP 000867601.1 VCLASPRIDVCLELYKRLQQDFSCG.IALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNSV 226
NTDB id 236 SPD RS10765 WP 000867601.1 VCLASPRIDVCLELYKRLQQDFSCG.IALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNSV 226
NTDB id 202 SPR RS10250 WP 000867601.1 VCLASPRIDVCLELYKRLQQDFSCG.IALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNSV 226
NTDB id 167 SP RS11275 WP 000867616.1 VCLASPRIDVCLELYKRLQQDFSCG.IALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNSV 226
NTDB id 507 SM12261 RS09240 WP 000867722.1 VCLASPRIDVCLELYKRLQKDFACE.IALLHGE.SEPYFRTPLVVATTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNSV 226
NTDB id 535 SMSK321 RS10515 WP 000867726.1 VCLASPRIDVCLELYKRLQDDFACE.ISLLYGE.SEPYFRTPLVVSTTHQLLKFYQAFDLLIVDEVDAFPYVDNPMLYHAVKNSV 226
consensus


logo
NTDB id 108 BSU 35470 NP 391427.1 KKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAVKRWIEFHVKEGRPVFLFVPSV 339
NTDB id 615 LCA RS02545 WP 011374200.1 KPQCALLYLTATPTPAIKRATAAKQMTVSELPLRFHGHLLPEPQRHVAFNWRAQLKKGRLPKRLERDCQTYLK.TQQILLFVPQV 319
NTDB id 593 KW2 RS05130 WP 021037147.1 KINGTLLYLTATSTDKLDKQIKKHEIKRLFLPRRFHGHPLVIPMFFWKKTFYKK.............FIEQRKTGFPLLIFVAEI 309
NTDB id 63295 T15 RS02280 WP 023369491.1 KEAGVQVFLTATSTDELDKKVRTGKLSRLSLPRRFHGNPLIVPQKVWFSKFDDTLKKNRLVPKLKKAIEEQRKSCFPLLIFVPEI 308
NTDB id 277 KZH43 RS10090 WP 000867601.1 KENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLKSYIEKQRKTAYPLLIFASEI 311
NTDB id 236 SPD RS10765 WP 000867601.1 KENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLKSYIEKQRKTAYPLLIFASEI 311
NTDB id 202 SPR RS10250 WP 000867601.1 KENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLKSYIEKQRKTAYPLLIFASEI 311
NTDB id 167 SP RS11275 WP 000867616.1 KENGLRIFLTATSTNELDKKVRLGELKRLNLPRRFHGNPLIIPKPIWLSDFNRYLDKNRLSPKLKSYIEKQRKTAYPLLIFASEI 311
NTDB id 507 SM12261 RS09240 WP 000867722.1 KENGLRIFLTATSTDELDRKVRIGELKRLSLPRRFHGNPLIIPKPVWLSDFNHCLEKSRLSPKLKSYIEKQRKTGYPLLIFASEI 311
NTDB id 535 SMSK321 RS10515 WP 000867726.1 KENGLRIFLTATSTDELDRKVRIGELKRLSLPRRFHGNPLIIPKPVWLSDFNRYLEKKCLSPKLKSYIEKQRKTGYPLLIFASEI 311
consensus
logo
NTDB id 108 BSU 35470 NP 391427.1 SILEKAAACFKGV..HCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQTGVLGAESSIFTESALVQIAGRTGR 422
NTDB id 615 LCA RS02545 WP 011374200.1 RLLQPVANRLSTLLPAVRIETLHANDPDQIKKITAFRAQQIQLMVTTTILERGVTFKNVAVLVLGAEHMVFNEAVLVQIAGRAGR 404
NTDB id 593 KW2 RS05130 WP 021037147.1 DFGQDFAKNLQEKFPKEKMAFVASTTKSRKTIVEAFRKKQVSILITTSILERGVTFSSIDVFVINSEHPNFTKSALIQMAGRVGR 394
NTDB id 63295 T15 RS02280 WP 023369491.1 SKGQEFTKIMKKTFPEETIGFVSSQTENRLEIVEGFRKREITVLISTTILERGVTFPCVDVFVVQANHYLFTASSLVQIAGRVGR 393
NTDB id 277 KZH43 RS10090 WP 000867601.1 KKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVGR 396
NTDB id 236 SPD RS10765 WP 000867601.1 KKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVGR 396
NTDB id 202 SPR RS10250 WP 000867601.1 KKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVGR 396
NTDB id 167 SP RS11275 WP 000867616.1 KKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVGR 396
NTDB id 507 SM12261 RS09240 WP 000867722.1 KKGEQLKEIIQEQFPNEKIGFVSSITENRLEQVQAFRDRELTILISTTILERGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVGR 396
NTDB id 535 SMSK321 RS10515 WP 000867726.1 KKGEQLKEILQKEFPHEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFPCVDVFVVEANHRLFTKSSLIQIGGRVGR 396
consensus
logo
NTDB id 108 BSU 35470 NP 391427.1 HKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD 463
NTDB id 615 LCA RS02545 WP 011374200.1 HKDYAQNPVHFYYQDYTRAIKGACRQIKTQNQRGRRLQSTV 445
NTDB id 593 KW2 RS05130 WP 021037147.1 DSKRPTGLVSFFHSGKSLAMCQAQKEIKKMNRLGGF..... 430
NTDB id 63295 T15 RS02280 WP 023369491.1 SIERPTGLLQFYHEGSTGAIEKAIAEIKQMNKEAGYV..... 430
NTDB id 277 KZH43 RS10090 WP 000867601.1 SMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL..... 432
NTDB id 236 SPD RS10765 WP 000867601.1 SMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL..... 432
NTDB id 202 SPR RS10250 WP 000867601.1 SMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL..... 432
NTDB id 167 SP RS11275 WP 000867616.1 SMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL..... 432
NTDB id 507 SM12261 RS09240 WP 000867722.1 SMDRPTGDLLFFHDGLNTSIKKAIKEIQQMNKEAGL..... 432
NTDB id 535 SMSK321 RS10515 WP 000867726.1 SMDRPTGDLLFFHDGLNTSIKKAIKEIQQMNKEAGL..... 432
consensus
X non conserved
X similar
X ≥ 50% conserved