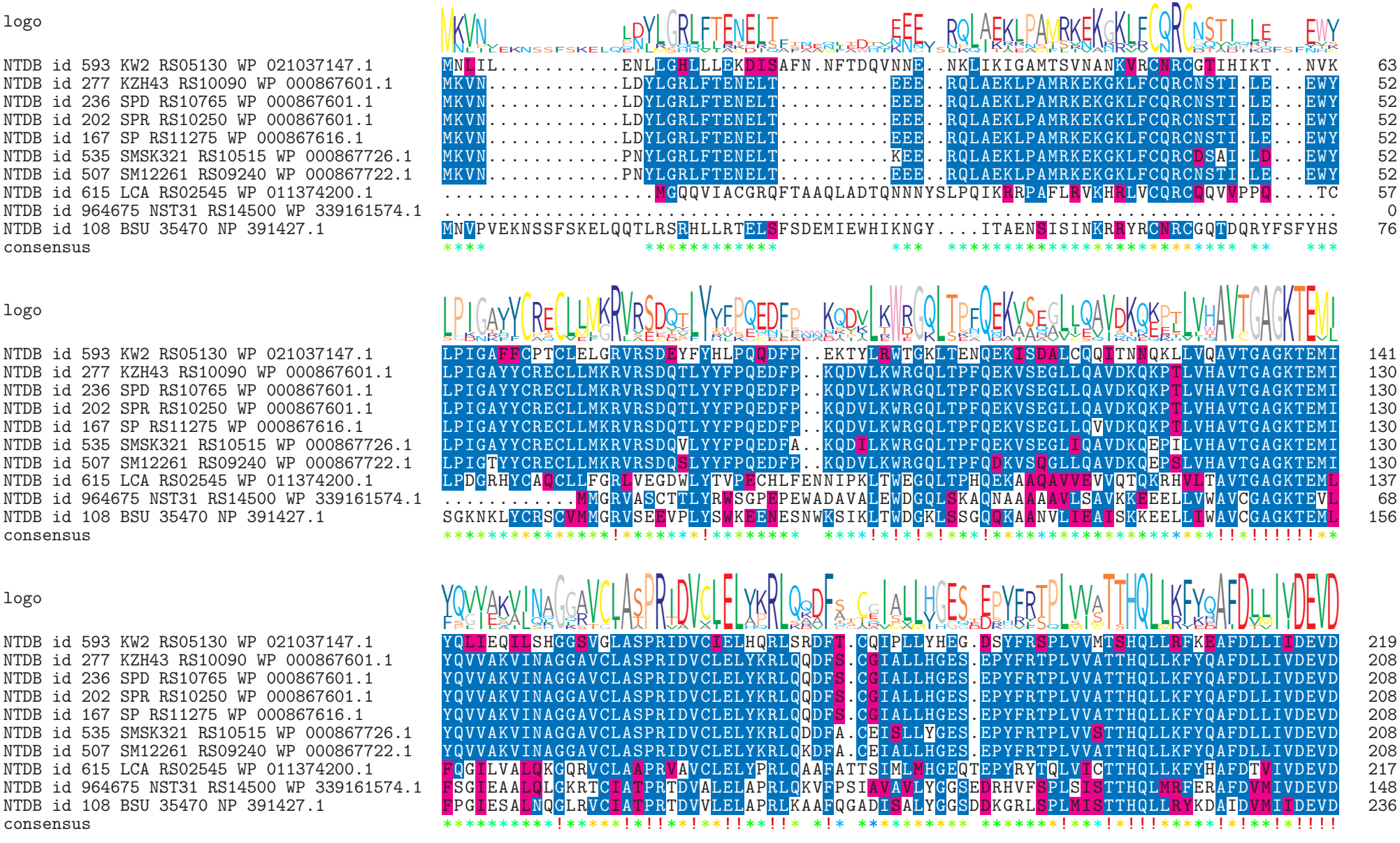
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NTDB id 277 KZH43 RS10090 WP 000867601.1 MKVN.....LDYLGRLFTENELT.....EEE..RQLAEKLPAMRKEKGKLFCQRCNSTI.LE...EWY 52
NTDB id 236 SPD RS10765 WP 000867601.1 MKVN.....LDYLGRLFTENELT.....EEE..RQLAEKLPAMRKEKGKLFCQRCNSTI.LE...EWY 52
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NTDB id 167 SP RS11275 WP 000867616.1 MKVN.....LDYLGRLFTENELT.....EEE..RQLAEKLPAMRKEKGKLFCQRCNSTI.LE...EWY 52
NTDB id 535 SMSK321 RS10515 WP 000867726.1 MKVN.....PNYLGRLFTENELT.....KEE..RQLAEKLPAMRKEKGKLFCQRCDSAI.LD...EWY 52
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NTDB id 964675 NST31 RS14500 WP 339161574.1 0
NTDB id 108 BSU 35470 NP 391427.1 MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGY....ITAENSISINKRRYRCNRCGQTDQRYFSFYHS 76
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NTDB id 236 SPD RS10765 WP 000867601.1 LPIGAYYCRECLLMKRVRSDQTLYYFPQEDFP..KQDVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMI 130
NTDB id 202 SPR RS10250 WP 000867601.1 LPIGAYYCRECLLMKRVRSDQTLYYFPQEDFP..KQDVLKWRGQLTPFQEKVSEGLLQAVDKQKPTLVHAVTGAGKTEMI 130
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NTDB id 615 LCA RS02545 WP 011374200.1 LPDGRHYCAQCLLFGRLVEGDWLYTVPECHLFENNIPKLTWEGQLTPHQEKAAQAVVEVVQTQKRHVLTAVTGAGKTEML 137
NTDB id 964675 NST31 RS14500 WP 339161574.1 .....MMGRVASCTTLYRWSGPEPEWADAVALEWDGQLSKAQNAAAAAVLSAVKKEEELLVWAVCGAGKTEVL 68
NTDB id 108 BSU 35470 NP 391427.1 SGKNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEML 156
consensus
logo
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NTDB id 167 SP RS11275 WP 000867616.1 YQVVAKVINAGGAVCLASPRIDVCLELYKRLQQDFS.CGIALLHGES.EPYFRTPLVVATTHQLLKFYQAFDLLIVDEVD 208
NTDB id 535 SMSK321 RS10515 WP 000867726.1 YQVVAKVINAGGAVCLASPRIDVCLELYKRLQDDFA.CEISLLYGES.EPYFRTPLVVSTTHQLLKFYQAFDLLIVDEVD 208
NTDB id 507 SM12261 RS09240 WP 000867722.1 YQVVAKVINAGGAVCLASPRIDVCLELYKRLQKDFA.CEIALLHGES.EPYFRTPLVVATTHQLLKFYQAFDLLIVDEVD 208
NTDB id 615 LCA RS02545 WP 011374200.1 FQGILVALQKGQRVCLAAPRVAVCLELYPRLQAAFATTSIMLMHGEQTEPYRYTQLVICTTHQLLKFYHAFDTVIVDEVD 217
NTDB id 964675 NST31 RS14500 WP 339161574.1 FSGIEAALQLGKRTCIATPRTDVALELAPRLQKVFPSIAVAVLYGGSEDRHVFSPLSLSTTHQLMRFERAFDVMIVDEVD 148
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consensus

logo

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NTDB id 535 SMSK321 RS10515 WP 000867726.1  AFPYVDNPMLYHAVKNSVKENGLRIFLTATSTDELDRKVRIGELKRLSLPRRFHGNPLIIPKPVWLSDFNRYLEKKCLSP  288
NTDB id 507 SM12261 RS09240 WP 000867722.1  AFPYVDNPMLYHAVKNSVKENGLRIFLTATSTDELDRKVRIGELKRLSLPRRFHGNPLIIPKPVWLSDFNHCLEKSRLSP  288
NTDB id 615 LCA RS02545 WP 011374200.1     AFPFVDNPVLATAVEQACKPQCALLYLTATPTPAIKRAIAAKQMTVSELPLRFHGHLLPEPQRHVAFNWRAQLKKGRLPK  297
NTDB id 964675 NST31 RS14500 WP 339161574.1 AFPYSFDQSLQWAVEKAAKKNAARIYLTATPSKRWQEECRYGKRNFIKIPARYHRKPLPAPVFVWCGNWRKSFEKSKLPR  228
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consensus                                   !!!******!**!*****!*******!*!!** ************** *!*!*!***!**!********************
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logo

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NTDB id 236 SPD RS10765 WP 000867601.1      KLKSYIEKQRKTAYPLLIFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFP  368
NTDB id 202 SPR RS10250 WP 000867601.1      KLKSYIEKQRKTAYPLLIFASEIKKGEQLAEILQEQFPNEKIGFVSSVTEDRLEQVQAFRDGELTILISTTILERGVTFP  368
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NTDB id 507 SM12261 RS09240 WP 000867722.1  KLKSYIEKQRKTGYPLLIFASEIKKGEQLKEIIQEQFPNEKIGFVSSITENRLEQVQAFRDRELTILISTTILERGVTFP  368
NTDB id 615 LCA RS02545 WP 011374200.1     RLERDCQTYL.KTQQILLFVPQVRLLQPVANRLSTLLPAVRIETLHANDPDQIKKITAFRAQQIQLMVTTTILERGVTFK  376
NTDB id 964675 NST31 RS14500 WP 339161574.1 VVLKWVRERLQAGKQALIFLPHIQLMENSLPLFKQL..HSSIQAVHAEDPLREEKVNAMRREKIPILLTTTILERGVTFS  306
NTDB id 108 BSU 35470 NP 391427.1           AVKRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGV..HCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVP  394
consensus                                   ******************!**************************************!*********!*!!!!!!!**
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logo

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NTDB id 593 KW2 RS05130 WP 021037147.1      SIDVFVINSEHPNFTKSALIQMAGRVGRDSKRPTGLVSFFHSGKSLAMCQAQKEIKKMNRLGGF......   430
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NTDB id 236 SPD RS10765 WP 000867601.1      CVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL......   432
NTDB id 202 SPR RS10250 WP 000867601.1      CVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL......   432
NTDB id 167 SP RS11275 WP 000867616.1       CVDVFVVEANHRLFTKSSLIQIGGRVGRSMDRPTGDLLFFHDGLNASIKKAIKEIQMMNKEAGL......   432
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NTDB id 964675 NST31 RS14500 WP 339161574.1 NLDVAVIGAEDPIFTEAALVQIAGRVGRSADFPGGNVTFFHHGKTKAMIQALVHINHMNKAARKAGLIDE   376
NTDB id 108 BSU 35470 NP 391427.1           KVQTGVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD.   463
consensus                                   *****!********!****!*!**!!*!!*******************  ****!***!* *!*****
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X non conserved
X similar
X ≥ 50% conserved