```
logo
NTDB id 193655 BARD7 RS15675 WP 065982452.1  ....MSGGASEFSEVRDFFYGKHLLRSEIPFSDQCIKRFIEEKYITAEPSVIRRKNRYVCRRCGQSDQARFAVFWAPSAK   76
NTDB id 108 BSU 35470 NP 391427.1            MNVPVEKNSSFSKELQQTLRSRHLLRTELSFSDEMIEWHIKNGYITAENSISINKRRYRCNRCGQTDQRYFSFYHS..SG   78
consensus                                    *****    !   !*      *!!!!*!**!!! *!  *!   !!!!!*!*   ! !! ! !!!!*!!  !   ** **

logo

NTDB id 193655 BARD7 RS15675 WP 065982452.1  RHITYCRSCVVMGRADELTSLYSWNQVAEKSWEPIKLSWEGTLTDGQKQAADALIEAIKEKQELLVWAVCGSGKTEMLFP  156
NTDB id 108 BSU 35470 NP 391427.1            KNKLYCRSCVMMGRVSEEVPLYSWKEENESNWKSIKLTWDGKLSSGQQKAANVLIEAISKKEELLIWAVCGAGKTEMLFP  158
consensus                                    **  !!!!!!*!!!  !  *!!!!   !  ! *!!!*!*! !* !!  !!  !!!!!  ! !!!*!!!!! !!!!!!!!

logo

NTDB id 193655 BARD7 RS15675 WP 065982452.1  GIEFALNHGLRVCVATPRTDVVLELLPRLKKAFEKVEVSALYGGSEDKGSLTPLMISTTHQLMRYRDIFDVMIIDEVDAF  236
NTDB id 108 BSU 35470 NP 391427.1            GIESALNQGLRVCIATPRTDVVLELAPRLKAAFQGADISALYGGSDDKGRLSPLMISTTHQLLRYKDAIDVMIIDEVDAF  238
consensus                                    !!! !!!*!!!!!*!!!!!!!!!!! !!!! !!   **!!!!!!!*!!! !*!!!!!! !!!*!!*!  !!!!!!!!!!!

logo

NTDB id 193655 BARD7 RS15675 WP 065982452.1  PFSADETLRFAVDKARKKNSALVYVTATPSETLKKRAEASLLKSVRIPARYHRKPLPEPRFLWCGNWKKKLEKGKLPRSV  316
NTDB id 108 BSU 35470 NP 391427.1            PYSADQTLQFAVQKARKKNSTLVYLSATPPKELKRKALNGQLHSVRIPARHHRKPLPEPRFVWCGNWKKKLNRNKIPPAV  318
consensus                                    !*!!! !! !!! !!!!!!! !!!**!!!*  !!**!    !*!!!!!!!*!!!!!!!!!!*!!!!!!!!! * !*!* !

logo

NTDB id 193655 BARD7 RS15675 WP 065982452.1  TDWVRQKLQSRVPVFLFVPSVHILRKTTDYFQKLNIRAEGVHAEDTCRKDKVKRFREGRVDLLVTTTILERGVTVPKVQT  396
NTDB id 108 BSU 35470 NP 391427.1            KRWIEFHVKEGRPVFLFVPSVSILEKAAACFKGVHCRTASVHAEDKHRKEKVQQFRDGQLDLLITTTILERGVTVPKVQT  398
consensus                                      !*  **    !!!!!!!!!!*!! !   *!  ***!   !!!!!  !!*!!  !!*! *!!!*!!!!!!!!!!!!!!!!!

logo

NTDB id 193655 BARD7 RS15675 WP 065982452.1  CVLGAEAPIFTESALVQIAGRTGRHYKHFSGDVVMFHFGMTNGMKKAKKHIEYMNKLAQKNKLLD   461
NTDB id 108 BSU 35470 NP 391427.1            GVLGAESSIFTESALVQIAGRTGRHKEYADGDVIYFHFGKTKSMLDARKHIKEMNELAAKVECTD   463
consensus                                    *!!!!! *!!!!!!!!!!!!!!!!!  *  !!!* !!!! !  !  !*!!!  !! !! !  * !
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X non conserved

X similar

X ≥ 50% conserved