logo
NTDB id 1152130 MMH06 RS10380 WP 000244158.1 MVLQRNERNEINEKDTWDLSTIYPTDQAWEEALKDLTEQLETVAQYEGHLLDSADNLLEITEFSLEMERQMEKLYVYAHM 80
NTDB id 480 HSISS4 RS02090 WP 002890133.1 ...MSDNRTHLEEKYTWDLTTIFATDADWETEYESTVQDLKKASAYAGHLLDSAKNLLGATELYMSLMRRLEKIYVYASM 77
consensus

logo
NTDB id 1152130 MMH06 RS10380 WP 000244158.1 KNDQDTREAKYQEYYAKAMTLYSQLDQAFSFYDPEFMEISEKQYADFLEAQPKLQVYQHYFDKLLQGKDHVLSQREEELL 160
NTDB id 480 HSISS4 RS02090 WP 002890133.1 KNDQDTTVGLYQEYQAKASNLYSQLSEAFAYFEPEFMALDDKKLAEFKEQEPGLGLYDHYFERLLANKDHVLSQEAEELL 157
consensus

logo
NTDB id 1152130 MMH06 RS10380 WP 000244158.1 AGAGEIFGSASETFAILDNADIVFPYVLDDDGKEVQLSHGTYTRLMESKKREVRRGAYQALYATYEQFQHTYAKTLQTNV 240
NTDB id 480 HSISS4 RS02090 WP 002890133.1 AAAGDIFNGPTDTFNVLDNADILFPWVSDGQGDVVELTHGNFITLMESKDRDIRKGAYEAMYGTYEQFQHTYAQTLQGVV 237
consensus

logo
NTDB id 1152130 MMH06 RS10380 WP 000244158.1 KVQNYRAKVRNYKSARHAALAANFVPESVYDNLVAAVRKHLPLLHRYLELRSKILGISDLKMYDVYTPLSSVEYNFTYQE 320
NTDB id 480 HSISS4 RS02090 WP 002890133.1 KVHNYQAKVRHYNSARHAALAANFIPESVYDSLLESVNKHLPLLHRYLDLRKKVLGLDELKMYDVYTPLSETETALTYEE 317
consensus

logo
NTDB id 1152130 MMH06 RS10380 WP 000244158.1 ALKKAEDALAVLGEDYLSRVKRAFSERWIDVYENQGKRSGAYSGGSYDTNAFMLLNWQDNLDNLFTLVHETGHSMHSSYT 400
NTDB id 480 HSISS4 RS02090 WP 002890133.1 SLKKAEEVLAIFGEEYSKGVHAAFTERWIDVHPNKGKRSGAYSGGAYDTNAFMLLNWQDTLDNLFTLVHETGHSLHSTFT 397
consensus

logo
NTDB id 1152130 MMH06 RS10380 WP 000244158.1 RETQPYVYGDYSIFLAEIASTTNENILTEKLLEEVEDDATRFAILNNFLDGFRGTVFRQTQFAEFEHAIHQADQNGEVLT 480
NTDB id 480 HSISS4 RS02090 WP 002890133.1 RQTQPYVYGDYPIFLAEIASTTNENILTETLLKEVKDDKTRFAILNHYLDGFKGTVFRQTQFAEFEHAIHEADASGQILT 477
consensus

logo
NTDB id 1152130 MMH06 RS10380 WP 000244158.1 SDFLNKLYADLNQEYYGLSKEDNPEIQYEWARIPHFYYNYYVYQYSTGFAAASALAEKIVHGSQEDRDRYIDYLKAGKSD 560
NTDB id 480 HSISS4 RS02090 WP 002890133.1 ADFMNKLYADLNEKYYNLKAEDNYEIQFEWERIPHFYMNYYVYQYATGFAAASYLAEKIVHGTEEDKEAYLTYLKAGSSD 557
consensus

logo

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NTDB id 1152130 MMH06 RS10380 WP 000244158.1  YPLNVMRKAGVDMEKEDYLNDAFAVFERRLNEFEALVEKLGLA.  603
NTDB id 480 HSISS4 RS02090 WP 002890133.1     YPLEVIKKAGVDMTNTDYLDAAFKVFEDRLVELEALVEKGVHLS  601
consensus                                     !!! !**!!!!!!   !!!  !! !!! !! ! !!!!!!  * *
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X non conserved

X similar

X $\geq$ 50% conserved