logo
NTDB id 355994 E5Z46 RS07770 WP 042379620.1 MTVEEKKAKKSLPLRSEIPVEETWRLEDIFPTDDAWEEEFKQVKAMIPKLGEYKGRLGESPEVLYEALQYQDEVSMRLGK 80
NTDB id 480 HSISS4 RS02090 WP 002890133.1 .....MSDNRTHLEEKYTWDLTTIFATDADWETEYESTVQDLKKASAYAGHLLDSAKNLLGATELYMSLMRRLEK 70
consensus

logo
NTDB id 355994 E5Z46 RS07770 WP 042379620.1 LYTYAHMRYDQDTTNSFYQGLDARAKSLYSEASSAMAFIVPEILAINEAVLRSFLEQYEPLRLYAHALDEITRQRPHVLS 160
NTDB id 480 HSISS4 RS02090 WP 002890133.1 IYVYASMKNDQDTTVGLYQEYQAKASNLYSQLSEAFAYFEPEFMALDDKKLAEFKEQEPGLGLYDHYFERLLANKDHVLS 150
consensus

logo
NTDB id 355994 E5Z46 RS07770 WP 042379620.1 AEEEAILAQAAEVMQATSDTFSALNNADLTFPTIIDENGEEVEVTHGRFIRFLESTDRRVRRDAFYAVYHTYEKFQNTFA 240
NTDB id 480 HSISS4 RS02090 WP 002890133.1 QEAEELLAAAGDIFNGPTDTFNVLDNADILFPWVSDGQGDVVELTHGNFITLMESKDRDIRKGAYEAMYGTYEQFQHTYA 230
consensus

logo
NTDB id 355994 E5Z46 RS07770 WP 042379620.1 NTLAGTVKKDNFFARIRRYSSAREAALDANNIPESVYDNLIATIHEHLPLLHRYVRLRKRVLGLDELHMYDLYTPLVQDV 320
NTDB id 480 HSISS4 RS02090 WP 002890133.1 QTLQGVVKVHNYQAKVRHYNSARHAALAANFIPESVYDSLLESVNKHLPLLHRYLDLRKKVLGLDELKMYDVYTPLSET. 309
consensus

logo
NTDB id 355994 E5Z46 RS07770 WP 042379620.1 KMEVTYDEAKQYMLEGLAPLGEEYVAIVKEGLDNRWVDVRENKGKRSGAYSSGAYGTHPYILLNWQDNVNNLFTLVHEFG 400
NTDB id 480 HSISS4 RS02090 WP 002890133.1 ETALTYEESLKKAEEVLAIFGEEYSKGVHAAFTERWIDVHPNKGKRSGAYSGGAYDTNAFMLLNWQDTLDNLFTLVHETG 389
consensus

logo
NTDB id 355994 E5Z46 RS07770 WP 042379620.1 HSVHSYYTRKTQPYPYAHYSIFVAEVASTCNEALLNDYLLKTIDDEKKRLYLLNHYLEGFRGTVFRQTMFAEFEHLIHLK 480
NTDB id 480 HSISS4 RS02090 WP 002890133.1 HSLHSTFTRQTQPYVYGDYPIFLAEIASTTNENILTETLLKEVKDDKTRFAILNHYLDGFKGTVFRQTQFAEFEHAIHEA 469
consensus

logo
NTDB id 355994 E5Z46 RS07770 WP 042379620.1 AQQGEALTAEMLTALYYDLNKTYFGDDIVVDKEIGLEWARIPHFYYNYYVYQYATGFSAAIALSKQILEEGEPAVTRYID 560
NTDB id 480 HSISS4 RS02090 WP 002890133.1 DASGQILTADFMNKLYADLNEKYYNLKAEDNYEIQFEWERIPHFYMNYYVYQYATGFAAASYLAEKIVHGTEEDKEAYLT 549
consensus

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NTDB id 355994 E5Z46 RS07770 WP 042379620.1   FLKAGSSDYPIEVLKKAGVDMTSAEPIRQACQVFAEKLDEMERLLEK.....   607
NTDB id 480 HSISS4 RS02090 WP 002890133.1     YLKAGSSDYPLEVIKKAGVDMTNTDYLDAAFKVFEDRLVELEALVEKGVHLS   601
consensus                                     *!!!!!!!!!*!!*!!!!!!!!   ***  !* !! **! !*! !*!!*****
```

X non conserved
X similar
X ≥ 50% conserved