logo
NTDB id 155598 AMD33 RS01300 WP 014727354.1 MSDNRCHLEEKYTWDLTTIFATDADWETEYESIVQDLKKASSFAGHLLDSAKNLLEATELYMSLMRRLEKIYVYASMKND 80
NTDB id 480 HSISS4 RS02090 WP 002890133.1 MSDNRTHLEEKYTWDLTTIFATDADWETEYESTVQDLKKASAYAGHLLDSAKNLLGATELYMSLMRRLEKIYVYASMKND 80
consensus
logo
NTDB id 155598 AMD33 RS01300 WP 014727354.1 QDTTVGLYQEYNAKASNLYSQLSEAFAYFEPEFMALEAEKLVSFKEQEPDLGLYDHYFERLLANKDHVLSQEAEELLAAA 160
NTDB id 480 HSISS4 RS02090 WP 002890133.1 QDTTVGLYQEYQAKASNLYSQLSEAFAYFEPEFMALDDKKLAEFKEQEPGLGLYDHYFERLLANKDHVLSQEAEELLAAA 160
consensus
logo
NTDB id 155598 AMD33 RS01300 WP 014727354.1 GDIFNGPTDTFNVLDNADILFPWVSDGQGDVIELTHGNFITLMESKNREVRKGAYEAMYRTYEQFQHTYAQTLQGVVKVH 240
NTDB id 480 HSISS4 RS02090 WP 002890133.1 GDIFNGPTDTFNVLDNADILFPWVSDGQGDVVELTHGNFITLMESKDRDIRKGAYEAMYGTYEQFQHTYAQTLQGVVKVH 240
consensus
logo
NTDB id 155598 AMD33 RS01300 WP 014727354.1 NYMAKVRHYNSARHAALAANFIPESVYDSLLESVNKHLPLLHRYLDLRKKVLELDKLKMYDVYAPLSETETALTYEEALK 320
NTDB id 480 HSISS4 RS02090 WP 002890133.1 NYQAKVRHYNSARHAALAANFIPESVYDSLLESVNKHLPLLHRYLDLRKKVLGLDELKMYDVYTPLSETETALTYEESLK 320
consensus
logo
NTDB id 155598 AMD33 RS01300 WP 014727354.1 KAEEVLAIFGEEYSKEVHAAFTERWIDVHPNKGKRSGAYSGGAYDTNAFMLLNWQDTLDNLFTLVHETGHSLHSTFTRQT 400
NTDB id 480 HSISS4 RS02090 WP 002890133.1 KAEEVLAIFGEEYSKGVHAAFTERWIDVHPNKGKRSGAYSGGAYDTNAFMLLNWQDTLDNLFTLVHETGHSLHSTFTRQT 400
consensus
logo
NTDB id 155598 AMD33 RS01300 WP 014727354.1 QPYVYGDYPIFLAEIASTTNENILTETLLKEVNDDKTRFAILNHYLDGFKGTVFRQTQFAEFEHAIHEADASGQILTADF 480
NTDB id 480 HSISS4 RS02090 WP 002890133.1 QPYVYGDYPIFLAEIASTTNENILTETLLKEVKDDKTRFAILNHYLDGFKGTVFRQTQFAEFEHAIHEADASGQILTADF 480
consensus
logo
NTDB id 155598 AMD33 RS01300 WP 014727354.1 MNKLYADLNEKYYNLKAEDNYEIQFEWERIPHFYMNYYVYQYATGFAAASYLAEKIVHGNEEDKEAYLTYLKAGSSDYPL 560
NTDB id 480 HSISS4 RS02090 WP 002890133.1 MNKLYADLNEKYYNLKAEDNYEIQFEWERIPHFYMNYYVYQYATGFAAASYLAEKIVHGTEEDKEAYLTYLKAGSSDYPL 560
consensus

logo

```
NTDB id 155598 AMD33 RS01300 WP 014727354.1   EVIKKAGVDMTNTDYLDAAFKVFEDRLVELEALVEKGVHLS   601
NTDB id 480 HSISS4 RS02090 WP 002890133.1     EVIKKAGVDMTNTDYLDAAFKVFEDRLVELEALVEKGVHLS   601
consensus                                     !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
```

X non conserved

X similar

X ≥ 50% conserved