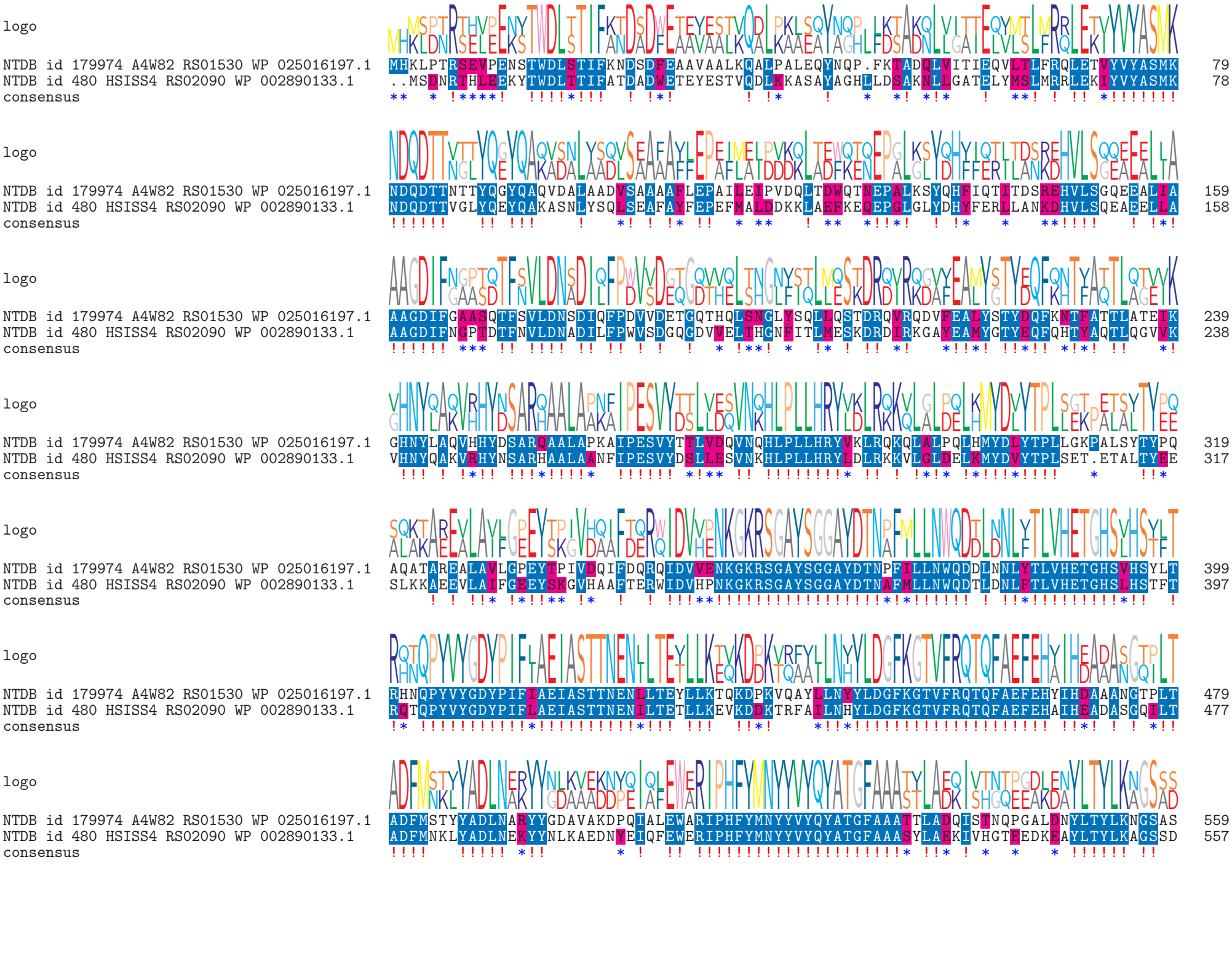
logo
NTDB id 179974 A4W82 RS01530 WP 025016197.1 MHKLPTRSEVPENSTWDLSTIFKNDSDFEAAVAALKQALPALEQYNQP.FKTADQLVITIEQVLTLFRQLETVYVYASMK 79
NTDB id 480 HSISS4 RS02090 WP 002890133.1 ..MSDNRTHLEEKYTWDLTTIFATDADWETEYESTVQDLKKASAYAGHLLDSAKNLLGATELYMSLMRRLEKIYVYASMK 78
consensus
logo
NTDB id 179974 A4W82 RS01530 WP 025016197.1 NDQDTTNTTYQGYQAQVDALAADVSAAAARLEPAILEIPVDQLTDWQTNEPALKSYQHFIQTITDSREHVLSGQEEALIA 159
NTDB id 480 HSISS4 RS02090 WP 002890133.1 NDQDTTVGLYQEYQAKASNLYSQLSEAFAYFEPEFMALDDKKLAEFKEQEPGLGLYDHYFERLLANKDHVLSQEAEELLA 158
consensus
logo
NTDB id 179974 A4W82 RS01530 WP 025016197.1 AAGDIFGAASQTFSVLDNSDIQFPDVVDETGQTHQLSNGLYSQLLQSTDRQVRQDVFEALYSTYDQFKNTFATTLATEIK 239
NTDB id 480 HSISS4 RS02090 WP 002890133.1 AAGDIFNGPTDTFNVLDNADILFPWVSDGQGDVVELTHGNFITLMESKDRDIRKGAYEAMYGTYEQFQHTYAQTLQGVVK 238
consensus
logo
NTDB id 179974 A4W82 RS01530 WP 025016197.1 GHNYLAQVHHYDSARQAALAPKAIPESVYTTLVDQVNQHLPLLHRYVKLRQKQLALPQLHMYDLYTPLLGKPALSYTYPQ 319
NTDB id 480 HSISS4 RS02090 WP 002890133.1 VHNYQAKVRHYNSARHAALAANFIPESVYDSLLESVNKHLPLLHRYLDLRKKVLGLDELKMYDVYTPLSET.ETALTYEE 317
consensus
logo
NTDB id 179974 A4W82 RS01530 WP 025016197.1 AQATAREALAVLGPEYTPIVDQIFDQRQIDVVENKGKRSGAYSGGAYDTNPFILLNWQDDLNNLYTLVHETGHSVHSYLT 399
NTDB id 480 HSISS4 RS02090 WP 002890133.1 SLKKAEEVLAIFGEEYSKGVHAAFTERWIDVHPNKGKRSGAYSGGAYDTNAFMLLNWQDTLDNLFTLVHETGHSLHSTFT 397
consensus
logo
NTDB id 179974 A4W82 RS01530 WP 025016197.1 RHNQPYVYGDYPIFIAEIASTTNENLLTEYLLKTQKDPKVQAYLLNYYLDGFKGTVFRQTQFAEFEHYIHDAAANGTPLT 479
NTDB id 480 HSISS4 RS02090 WP 002890133.1 RQTQPYVYGDYPIFLAEIASTTNENILTETLLKEVKDDKTRFAILLNHYLDGFKGTVFRQTQFAEFEHAIHEADASGQILT 477
consensus
logo
NTDB id 179974 A4W82 RS01530 WP 025016197.1 ADFMSTYYADLNARYYGDAVAKDPQIALEWARIPHFYMNYYVYQYATGFAAATTLADQISTNQPGALDNYLTYLKNGSAS 559
NTDB id 480 HSISS4 RS02090 WP 002890133.1 ADFMNKLYADLNEKYYNLKAEDNYEIQFEWERIPHFYMNYYVYQYATGFAAASYLAEKIVHGTEEDKEAYLTYLKAGSSD 557
consensus

```
logo
```

```
NTDB id 179974 A4W82 RS01530 WP 025016197.1   YPIETMQKAGVDMTNADYLERAFDVFEQRLDQLEALLADM....   599
NTDB id 480 HSISS4 RS02090 WP 002890133.1     YPLEVIKKAGVDMTNTDYLDAAFKVFEDRLVELEALVEKGVHLS   601
consensus                                     !!*! * !!!!!!!!! !!!* !! !!! !!  !!!!*    ****
```

X non conserved
X similar
X ≥ 50% conserved