```
NTDB id 1103 NMB RS07590 WP 002212976.1       ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL     76
NTDB id 1131 NGFG RS05740 WP 003695064.1      ...MSLNKVILIGRLGRDPEVRYMPNGEAVCNFSVATSETWNDR.NGQRVERTEWHNITMYRKLAEIAGQYLKKGGLVYL     76
NTDB id 1390 A4U84 RS00055 WP 021115958.1     ..MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYV     78
NTDB id 355224 ArsFIN RS17630 WP 026822913.1  MASRGVNKVILIGNLGQDPEIRYMPNGGAVANLTLATSESWRDKQSGEMREKTEWHRVVIFGKLAEVAGEYLRKGSQVYI     80
NTDB id 1166 A1552VC RS00795 WP 000168289.1   MASRGVNKVILIGNLGQDPEVRYMPSGGAVANITIATSETWRDKATGEQKEKTEWHRVTLYGKLAEVAGEYLRKGSQVYI     80
consensus                                         **!!!!**!*!!*!!**!*!!*!*!!*****!!!!*!*!* *!***!*!!!!*********!!*!!*!!*!!* !!*
```

```
NTDB id 1103 NMB RS07590 WP 002212976.1       EGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAPYEE.........GYGQSQEAYQ.......RPAQQS     136
NTDB id 1131 NGFG RS05740 WP 003695064.1      EGRIQSRKYQGKDGIERTAYDIV....ANEMKMLGGRNENSGGAPYDE.........GYGQSQEAYQ.......RPAQQS     136
NTDB id 1390 A4U84 RS00055 WP 021115958.1     EGKLKTRKWQDQNGQDRYTTEIQ....GDVLQMLDSRSSGG.DFGG.......NQGSGWNQAPAQTNYNQGGYSDNYAQN     146
NTDB id 355224 ArsFIN RS17630 WP 026822913.1  EGSLQTRKWQDQSGQDRYSTEVVVN.IGGTMQMLGARGGS......QEGMPQNNPASGWGQPQQPQQ............T     141
NTDB id 1166 A1552VC RS00795 WP 000168289.1   EGQLQTRKWQDQSGQDRYSTEVVVQGYNGIMQMLGGRAQQG.GMPAQGGMNVPAQQGSWGQPQQPAK............Q     147
consensus                                     !!*****!!*!*!** !**!******    *   **!!**!  *  * *  *         ***! *   *          **
```

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NTDB id 1103 NMB RS07590 WP 002212976.1       RQPAS.DAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF     174
NTDB id 1131 NGFG RS05740 WP 003695064.1      RQPAP.DAPSHPQEAPAAPRRQPVPAAAPVEDIDDDIPF     174
NTDB id 1390 A4U84 RS00055 WP 021115958.1     NNFNGGNATRPQ.....PAQKPAAQAEPPMDNFDDDIPF     180
NTDB id 355224 ArsFIN RS17630 WP 026822913.1  QQFSG.NAPASAPAAHSGKTAPATPAEPPM.DFDDDIPF     178
NTDB id 1166 A1552VC RS00795 WP 000168289.1   HQPMQ.Q...SAP....QQYSQPQYNEPPM.DFDDDIPF     177
consensus                                      **   ***     *   *  *** ****!*****!!!!!!
```

X non conserved
X similar
X ≥ 50% conserved