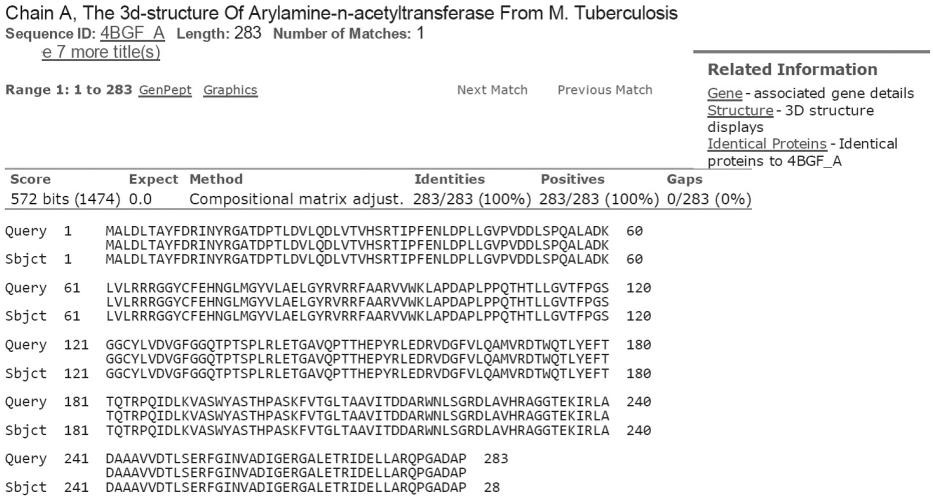

Chain A, The 3d-structure Of Arylamine-n-acetyltransferase From M. Tuberculosis
Sequence ID: 4BGF_A Length: 283 Number of Matches: 1
e 7 more title(s)

Range 1: 1 to 283 GenPept Graphics Next Match Previous Match

Related Information
Gene - associated gene details
Structure - 3D structure displays
Identical Proteins - Identical proteins to 4BGF_A

Score	Expect	Method	Identities	Positives	Gaps
572 bits (1474)	0.0	Compositional matrix adjust.	283/283 (100%)	283/283 (100%)	0/283 (0%)

```
Query  1    MALDLTAYFDRINYRGATDPTLDVLQDLVTVHSRTIPFENLDPLLGVPVDDLSPQALADK  60
            MALDLTAYFDRINYRGATDPTLDVLQDLVTVHSRTIPFENLDPLLGVPVDDLSPQALADK
Sbjct  1    MALDLTAYFDRINYRGATDPTLDVLQDLVTVHSRTIPFENLDPLLGVPVDDLSPQALADK  60

Query  61   LVLRRRGGYCFEHNGLMGYVLAELGYRVRRFAARVVWKLAPDAPLPPQTHTLLGVTFPGS  120
            LVLRRRGGYCFEHNGLMGYVLAELGYRVRRFAARVVWKLAPDAPLPPQTHTLLGVTFPGS
Sbjct  61   LVLRRRGGYCFEHNGLMGYVLAELGYRVRRFAARVVWKLAPDAPLPPQTHTLLGVTFPGS  120

Query  121  GGCYLVDVGFGGQTPTSPLRLETGAVQPTTHEPYRLEDRVDGFVLQAMVRDTWQTLYEFT  180
            GGCYLVDVGFGGQTPTSPLRLETGAVQPTTHEPYRLEDRVDGFVLQAMVRDTWQTLYEFT
Sbjct  121  GGCYLVDVGFGGQTPTSPLRLETGAVQPTTHEPYRLEDRVDGFVLQAMVRDTWQTLYEFT  180

Query  181  TQTRPQIDLKVASWYASTHPASKFVTGLTAAVITDDARWNLSGRDLAVHRAGGTEKIRLA  240
            TQTRPQIDLKVASWYASTHPASKFVTGLTAAVITDDARWNLSGRDLAVHRAGGTEKIRLA
Sbjct  181  TQTRPQIDLKVASWYASTHPASKFVTGLTAAVITDDARWNLSGRDLAVHRAGGTEKIRLA  240

Query  241  DAAAVVDTLSERFGINVADIGERGALETRIDELLARQPGADAP  283
            DAAAVVDTLSERFGINVADIGERGALETRIDELLARQPGADAP
Sbjct  241  DAAAVVDTLSERFGINVADIGERGALETRIDELLARQPGADAP  28
```

Supplementary Figure S1. pBLAST results showing maximum identity between template 4BGF and the target WT-MTB-NAT sequence Rv3566c. WT: wild type; MTB: *Mycobacterium tuberculosis*; NAT: *N*-acetyl transferase.