SCOPe

Lineage for d1t1ga_ (1t1g A:)

1. Root: SCOPe 2.06
2. Class c: Alpha and beta proteins (a/b) [51349] (148 folds)
3. Fold c.41: Subtilisin-like [52742] (1 superfamily)
   3 layers: a/b/a, parallel beta-sheet of 7 strands, order 2314567; left-handed crossover connection between strands 2 & 3
4. Superfamily c.41.1: Subtilisin-like [52743] (3 families) $\mathcal{S}$
5. Family c.41.1.2: Serine-carboxyl proteinase, SCP [52764] (2 protein domains)
   elaborated with additional structures
6. Protein Serine-carboxyl proteinase, SCP [52765] (3 species)
7. Species Bacillus novosp. MN-32, kumamolisin [TaxId:198803] [75226] (7 PDB entries)
   Uniprot Q8RR56 ! Uniprot Q8RR56
8. Domain d1t1ga_: 1t1g A: [106246]
   complexed with ca, so4; mutant
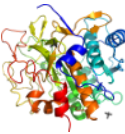
Details for d1t1ga_

PDB Entry: 1t1g (more details), 1.18 Å

PDB Description: High Resolution Crystal Structure of Mutant E23A of Kumamolisin, a sedolisin type proteinase (previously called Kumamolysin or KSCP)
PDB Compounds: (A:) kumamolisin

SCOPe Domain Sequences for d1t1ga_:

Sequence; same for both **SEQRES** and **ATOM** records: (download)

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>d1t1ga_ c.41.1.2 (A:) Serine-carboxyl proteinase, SCP {Bacillus novosp. MN-32, kumamolisin [TaxId: 198803]}
aaptaytpldvaqayqfpegldgqgqciaiialgggydetslaqyfaslgvsapqvvsvs
vdgatnqptgdpngpdgeveldievagalapgakiavyfapntdagflnaittavhdpth
kpsivsiswggpedswapasiaamnrafldaaalgvtvlaaagdsgstdgeqdglyhvdf
paaspyvlacggtrlvasagrieretvwndgpdggstgggvsrifplpswqeranvppsa
npgagsgrgvpdvagnadpatgyevvidgettviggtsavaplfaalvarinqklgkpvg
ylnptlyqlppevfhditegnndianrariyqagpgwdpctglgspigirllqallp
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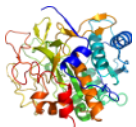
SCOPe Domain Coordinates for d1t1ga_:

Click to download the PDB-style file with coordinates for d1t1ga_.
   (The format of our PDB-style files is described here.)

Timeline for d1t1ga_:

- d1t1ga_ first appeared in SCOP 1.69
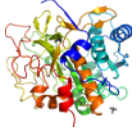- d1t1ga_ appears in SCOPe 2.05

Thumbnails for d1t1ga_:

d1t1ga_
(click for larger image)
View in 3D

d1t1ga_ in context of chain
View in 3D

SCOPe