



























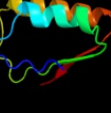




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1th8b_</a>	 Alignment		99.7	23	<b>Fold:</b> Spollaa-like <b>Superfamily:</b> Spollaa-like <b>Family:</b> Anti-sigma factor antagonist Spollaa
2	<a href="#">c3t6oA_</a>	 Alignment		99.7	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate transporter/antisigma-factor antagonist stas; <b>PDBTitle:</b> the structure of an anti-sigma-factor antagonist (stas) domain protein2 from planctomyces limnophilus.
3	<a href="#">d1vc1a_</a>	 Alignment		99.7	22	<b>Fold:</b> Spollaa-like <b>Superfamily:</b> Spollaa-like <b>Family:</b> Anti-sigma factor antagonist Spollaa
4	<a href="#">c3f43A_</a>	 Alignment		99.7	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative anti-sigma factor antagonist tm1081; <b>PDBTitle:</b> crystal structure of a putative anti-sigma factor antagonist (tm1081)2 from thermotoga maritima at 1.59 a resolution
5	<a href="#">d1auza_</a>	 Alignment		99.7	19	<b>Fold:</b> Spollaa-like <b>Superfamily:</b> Spollaa-like <b>Family:</b> Anti-sigma factor antagonist Spollaa
6	<a href="#">d1h4xa_</a>	 Alignment		99.6	16	<b>Fold:</b> Spollaa-like <b>Superfamily:</b> Spollaa-like <b>Family:</b> Anti-sigma factor antagonist Spollaa
7	<a href="#">c3mg1A_</a>	 Alignment		99.6	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate permease family protein; <b>PDBTitle:</b> crystal structure of permease family protein from vibrio2 cholerae
8	<a href="#">c3oirA_</a>	 Alignment		99.5	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate transporter sulfate transporter family protein; <b>PDBTitle:</b> crystal structure of sulfate transporter family protein from wolinetella2 succinogenes
9	<a href="#">c2vy9A_</a>	 Alignment		99.5	18	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> anti-sigma-factor antagonist; <b>PDBTitle:</b> molecular architecture of the stressosome, a signal2 integration and transduction hub
10	<a href="#">c2klnA_</a>	 Alignment		99.5	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable sulphate-transport transmembrane protein, cog0659; <b>PDBTitle:</b> solution structure of stas domain of rv1739c from m. tuberculosis
11	<a href="#">c3klkB_</a>	 Alignment		99.4	19	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> antisigma-factor antagonist stas; <b>PDBTitle:</b> crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides

12	<a href="#">c3ny7A_</a>	Alignment		99.3	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate transporter; <b>PDBTitle:</b> stas domain of ychm bound to acp
13	<a href="#">c3lloA_</a>	Alignment		99.2	14	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> prestin; <b>PDBTitle:</b> crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5)
14	<a href="#">c3ih9A_</a>	Alignment		95.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> salt-tolerant glutaminase; <b>PDBTitle:</b> crystal structure analysis of mglu in its tris form
15	<a href="#">d3c9ua2</a>	Alignment		25.7	17	<b>Fold:</b> PurM C-terminal domain-like <b>Superfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
16	<a href="#">d2q3la1</a>	Alignment		18.5	18	<b>Fold:</b> Spollaa-like <b>Superfamily:</b> Spollaa-like <b>Family:</b> Sfri0576-like
17	<a href="#">c3ghfA_</a>	Alignment		14.0	12	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> septum site-determining protein minc; <b>PDBTitle:</b> crystal structure of the septum site-determining protein2 minc from salmonella typhi murium
18	<a href="#">c3bezC_</a>	Alignment		12.1	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protease 4; <b>PDBTitle:</b> crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
19	<a href="#">d2fug61</a>	Alignment		10.3	14	<b>Fold:</b> HydA/Nqo6-like <b>Superfamily:</b> HydA/Nqo6-like <b>Family:</b> Nqo6-like
20	<a href="#">c2pr7A_</a>	Alignment		8.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase/epoxide hydrolase family; <b>PDBTitle:</b> crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
21	<a href="#">c2k42A_</a>	Alignment	not modelled	5.2	5	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> wiskott-aldrich syndrome protein; <b>PDBTitle:</b> solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehcc effector
22	<a href="#">d1xbta1</a>	Alignment	not modelled	5.1	10	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Type II thymidine kinase