Phyre^2

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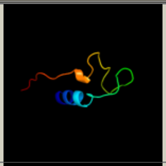
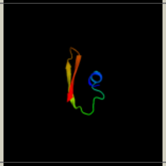
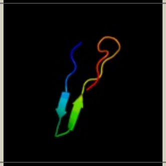
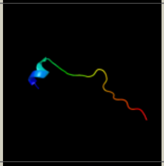
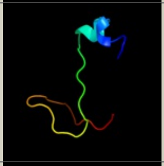
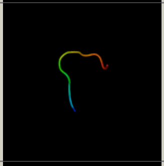
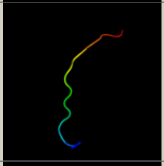
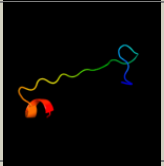
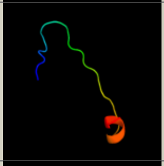
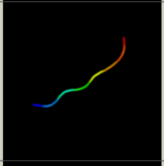
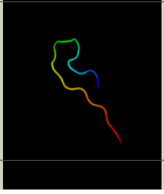
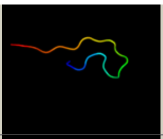
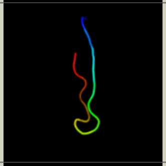
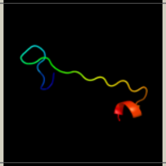
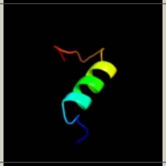
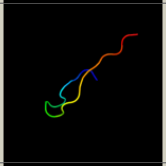
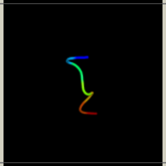
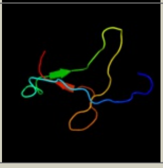
Description	Q9JMT9
Date	Thu Jan 5 12:38:15 GMT 2012
Unique Job ID	2a15cd3f9519b020

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gr0a1	Alignment		29.5	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
2	d1uwca_	Alignment		14.1	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
3	d1mkfa_	Alignment		13.5	33	**Fold:**Viral chemokine binding protein m3 **Superfamily:**Viral chemokine binding protein m3 **Family:**Viral chemokine binding protein m3
4	d1oe4a_	Alignment		12.8	29	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Single-strand selective monofunctional uracil-DNA glycosylase SMUG1
5	c3dmlA_	Alignment		11.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the periplasmic thioredoxin soxs from2 paracoccus pantotrophus (reduced form)
6	c3ofeB_	Alignment		10.0	38	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**ldlr chaperone boca; **PDBTitle:** structured domain of drosophila melanogaster boca p41 2 2 crystal form
7	d2qn6a1	Alignment		8.9	41	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
8	c2yr1B_	Alignment		8.7	35	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426
9	d1gqna_	Alignment		8.2	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
10	c2eoyA_	Alignment		7.7	63	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 557-2 589) of human zinc finger protein 473
11	d2p6ba1	Alignment		7.0	26	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase

12	c2p6bC_	Alignment		7.0	26	**PDB header:**hydrolase/hydrolase regulator **Chain:** C: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha **PDBTitle:** crystal structure of human calcineurin in complex with2 pvivit peptide
13	c2exuA_	Alignment		6.4	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation protein spt4/spt5; **PDBTitle:** crystal structure of saccharomyces cerevisiae transcription elongation2 factors spt4-spt5ngn domain
14	c3js3C_	Alignment		6.3	22	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of type i 3-dehydroquinate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
15	d1zu1a1	Alignment		6.2	23	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**HkH motif-containing C2H2 finger
16	c2jogA_	Alignment		5.6	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha **PDBTitle:** structure of the calcineurin-nfat complex
17	c2l3iA_	Alignment		5.5	71	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**aoxki4a, antimicrobial peptide in spider venom; **PDBTitle:** oxki4a, spider derived antimicrobial peptide
18	c3h7hB_	Alignment		5.3	31	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
19	c4a56A_	Alignment		5.3	56	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**pullulanase secretion protein puls; **PDBTitle:** crystal structure of the type 2 secretion system pilotin2 from klebsiella oxytoca
20	c3n2oA_	Alignment		5.2	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**biosynthetic arginine decarboxylase; **PDBTitle:** x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
21	c3utkA_	Alignment	not modelled	5.2	56	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**lipoprotein outs; **PDBTitle:** structure of the pilotin of the type ii secretion system
22	c3solA_	Alignment	not modelled	5.2	56	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**type ii secretion pathway related protein; **PDBTitle:** crystal structure of the type 2 secretion system pilotin gsps