Phyre2

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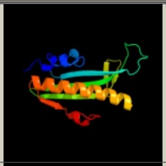
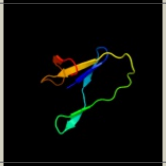
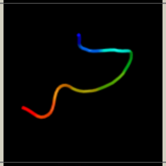
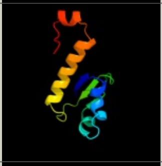
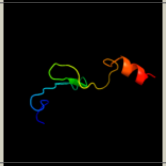
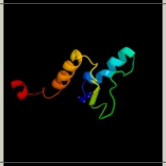
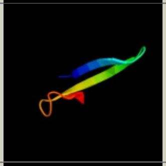
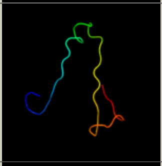
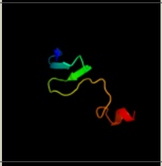
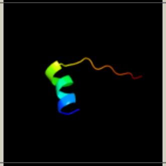
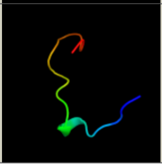
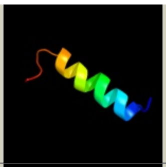
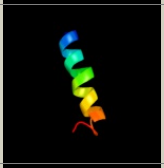
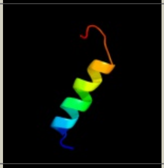
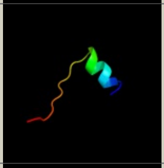
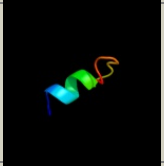
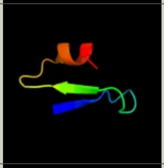
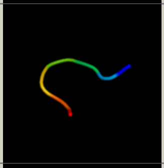
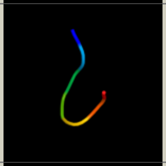
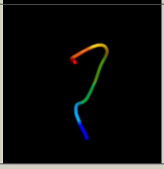
Description	P24251
Date	Thu Jan 5 11:41:37 GMT 2012
Unique Job ID	b7a85e0f3efeed58

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rpjA_	Alignment		100.0	48	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**curlin genes transcriptional regulator; **PDBTitle:** structure of a curlin genes transcriptional regulator protein from2 proteus mirabilis hi4320.
2	d2bhua1	Alignment		67.4	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
3	c2b9bA_	Alignment		62.2	44	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**fusion glycoprotein f0; **PDBTitle:** structure of the parainfluenza virus 5 f protein in its metastable,2 pre-fusion conformation
4	d2a1va1	Alignment		49.9	18	**Fold:**Secretion chaperone-like **Superfamily:**YjbR-like **Family:**YjbR-like
5	d3duea1	Alignment		45.9	23	**Fold:**BLIP-like **Superfamily:**BT0923-like **Family:**BT0923-like
6	d2fkia1	Alignment		32.8	22	**Fold:**Secretion chaperone-like **Superfamily:**YjbR-like **Family:**YjbR-like
7	c3nrlB_	Alignment		22.2	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rumgna_01417; **PDBTitle:** crystal structure of protein rumgna_01417 from ruminococcus gnavus,2 northeast structural genomics consortium target ugr76
8	d1axib1	Alignment		18.0	28	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
9	d3elga1	Alignment		17.7	15	**Fold:**BLIP-like **Superfamily:**BT0923-like **Family:**BT0923-like
10	c1agqB_	Alignment		16.4	31	**PDB header:**growth factor **Chain:** B: **PDB Molecule:**glial cell-derived neurotrophic factor; **PDBTitle:** glial cell-derived neurotrophic factor from rat
11	d1b63a1	Alignment		16.0	21	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain

12	d2p02a2	Alignment		15.1	35	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
13	d1mxaa2	Alignment		14.3	30	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
14	d1qm4a2	Alignment		13.0	30	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
15	c2gyrB_	Alignment		11.9	13	**PDB header:**hormone/growth factor **Chain:** B: **PDB Molecule:**neurotrophic factor artemin, isoform 3; **PDBTitle:** crystal structure of human artemin
16	d1zyma1	Alignment		10.4	19	**Fold:**SAM domain-like **Superfamily:**Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain **Family:**Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain
17	c2w82C_	Alignment		9.7	28	**PDB header:**replication inhibitor **Chain:** C: **PDB Molecule:**orf18; **PDBTitle:** the structure of arda
18	c1lu0A_	Alignment		9.6	86	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**trypsin inhibitor i; **PDBTitle:** atomic resolution structure of squash trypsin inhibitor: unexpected2 metal coordination
19	d1lu0a_	Alignment		9.6	86	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant inhibitors of proteinases and amylases **Family:**Plant inhibitors of proteinases and amylases
20	c3ctiA_	Alignment		9.6	86	**PDB header:**proteinase inhibitor (trypsin) **Chain:** A: **PDB Molecule:**trypsin inhibitor; **PDBTitle:** relaxation matrix refinement of the solution structure of2 squash trypsin inhibitor
21	c2ctiA_	Alignment	not modelled	9.6	86	**PDB header:**proteinase inhibitor (trypsin) **Chain:** A: **PDB Molecule:**trypsin inhibitor; **PDBTitle:** determination of the complete three-dimensional structure2 of the trypsin inhibitor from squash seeds in aqueous3 solution by nuclear magnetic resonance and a combination4 of distance geometry and dynamical simulated annealing
22	c1ppel_	Alignment	not modelled	9.6	86	**PDB header:**hydrolase(serine proteinase) **Chain:** I: **PDB Molecule:**trypsin inhibitor cmti-i; **PDBTitle:** the refined 2.0 angstroms x-ray crystal structure of the2 complex formed between bovine beta-trypsin and cmti-i, a3 trypsin inhibitor from squash seeds (cucurbita maxima):4 topological similarity of the squash seed inhibitors with5 the carboxypeptidase a inhibitor from potatoes
23	c1ctiA_	Alignment	not modelled	9.6	86	**PDB header:**proteinase inhibitor (trypsin) **Chain:** A: **PDB Molecule:**trypsin inhibitor; **PDBTitle:** determination of the complete three-dimensional structure2 of the trypsin inhibitor from squash seeds in aqueous3 solution by nuclear magnetic resonance and a combination4 of distance geometry and dynamical simulated annealing
24	c2stal_	Alignment	not modelled	9.6	86	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** I: **PDB Molecule:**protein (trypsin inhibitor); **PDBTitle:** anionic salmon trypsin in complex with squash seed2 inhibitor (cucurbita maxima trypsin inhibitor i)
25	d2id1a1	Alignment	not modelled	9.5	25	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
26	c1lu0B_	Alignment	not modelled	9.5	86	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**trypsin inhibitor i; **PDBTitle:** atomic resolution structure of squash trypsin inhibitor: unexpected2 metal coordination
						PDB header:hydrolase inhibitor

27	c2v1vA_	Alignment	not modelled	9.5	86	**Chain:** A: **PDB Molecule:**trypsin inhibitor 1; **PDBTitle:** 3d structure of the m8l mutant of squash trypsin inhibitor2 cmti-i
28	c2a7oA_	Alignment	not modelled	9.2	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**huntingtin interacting protein b; **PDBTitle:** solution structure of the hset2/hypb sri domain
29	d2c4ba2	Alignment	not modelled	9.2	86	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant inhibitors of proteinases and amylases **Family:**Plant inhibitors of proteinases and amylases
30	c2vpzG_	Alignment	not modelled	9.2	50	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**hypothetical membrane spanning protein; **PDBTitle:** polysulfide reductase native structure
31	d1h9ii_	Alignment	not modelled	9.1	60	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant inhibitors of proteinases and amylases **Family:**Plant inhibitors of proteinases and amylases
32	d1h9hi_	Alignment	not modelled	8.8	86	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant inhibitors of proteinases and amylases **Family:**Plant inhibitors of proteinases and amylases
33	c1mcvI_	Alignment	not modelled	8.8	86	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**hei-toe i; **PDBTitle:** crystal structure analysis of a hybrid squash inhibitor in2 complex with porcine pancreatic elastase
34	d1mcvi_	Alignment	not modelled	8.8	86	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant inhibitors of proteinases and amylases **Family:**Plant inhibitors of proteinases and amylases
35	c2it7A_	Alignment	not modelled	8.7	86	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**trypsin inhibitor 2; **PDBTitle:** solution structure of the squash trypsin inhibitor eeti-ii
36	d2it7a1	Alignment	not modelled	8.7	86	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant inhibitors of proteinases and amylases **Family:**Plant inhibitors of proteinases and amylases
37	c2letA_	Alignment	not modelled	8.5	86	**PDB header:**proteinase inhibitor(trypsin) **Chain:** A: **PDB Molecule:**trypsin inhibitor ii; **PDBTitle:** an 1h nmr determination of the three dimensional structures2 of mirror image forms of a leu-5 variant of the trypsin3 inhibitor ecballium elaterium (eeti-ii)
38	d1rpya_	Alignment	not modelled	8.1	19	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
39	c3m07A_	Alignment	not modelled	8.0	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative alpha amylase; **PDBTitle:** 1.4 angstrom resolution crystal structure of putative alpha2 amylase from salmonella typhimurium.
40	c3fg7A_	Alignment	not modelled	7.6	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**villin-1; **PDBTitle:** the crystal structure of villin domain 6
41	d1xa6a2	Alignment	not modelled	7.6	18	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
42	d2evra2	Alignment	not modelled	7.3	26	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
43	c1ik9C_	Alignment	not modelled	7.3	38	**PDB header:**gene regulation/ligase **Chain:** C: **PDB Molecule:**dna ligase iv; **PDBTitle:** crystal structure of a xrcc4-dna ligase iv complex
44	d2o62a1	Alignment	not modelled	7.2	23	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**All1756-like
45	d2i1sa1	Alignment	not modelled	6.9	27	**Fold:**MM3350-like **Superfamily:**MM3350-like **Family:**MM3350-like
46	d1exbe_	Alignment	not modelled	6.6	21	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
47	d2btci_	Alignment	not modelled	6.5	71	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant inhibitors of proteinases and amylases **Family:**Plant inhibitors of proteinases and amylases
48	c2btcI_	Alignment	not modelled	6.5	71	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** I: **PDB Molecule:**protein (trypsin inhibitor); **PDBTitle:** bovine trypsin in complex with squash seed inhibitor2 (cucurbita pepo trypsin inhibitor ii)
49	c2stbI_	Alignment	not modelled	6.5	71	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** I: **PDB Molecule:**protein (trypsin inhibitor); **PDBTitle:** anionic salmon trypsin in complex with squash seed2 inhibitor (cucurbita pepo trypsin inhibitor ii)
50	c3h9xB_	Alignment	not modelled	6.3	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein pspto_3016; **PDBTitle:** crystal structure of the pspto_3016 protein from2 pseudomonas syringae, northeast structural genomics3 consortium target psr293
51	c2ysxA_	Alignment	not modelled	6.2	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signaling inositol polyphosphate phosphatase **PDBTitle:** solution structure of the human ship sh2 domain
52	c2yh5A_	Alignment	not modelled	6.1	12	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**dapx protein; **PDBTitle:** structure of the c-terminal domain of bamc
53	c2xznZ_	Alignment	not modelled	6.1	11	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**rps21e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2

						subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
54	d1t6aa_	Alignment	not modelled	6.0	12	**Fold:**TBP-like **Superfamily:**Rbstp2229 protein **Family:**Rbstp2229 protein
55	d2eyva1	Alignment	not modelled	6.0	19	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
56	d1eysl_	Alignment	not modelled	5.9	67	**Fold:**Bacterial photosystem II reaction centre, L and M subunits **Superfamily:**Bacterial photosystem II reaction centre, L and M subunits **Family:**Bacterial photosystem II reaction centre, L and M subunits
57	c2kkuA_	Alignment	not modelled	5.8	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein af2351 from archaeoglobus2 fulgidus. northeast structural genomics consortium target3 att9/ontario center for structural proteomics target af2351
58	d2bcqa3	Alignment	not modelled	5.5	25	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
59	c2nvgA_	Alignment	not modelled	5.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit; **PDBTitle:** soluble domain of rieske iron sulfur protein.
60	c2qv5A_	Alignment	not modelled	5.5	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
61	c3rv2B_	Alignment	not modelled	5.4	43	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosylmethionine synthase; **PDBTitle:** crystal structure of s-adenosylmethionine synthetase from2 mycobacterium marinum