Phyre2

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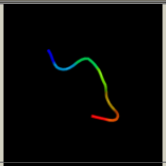
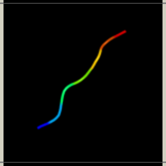
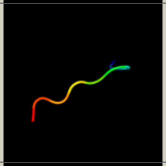
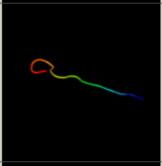
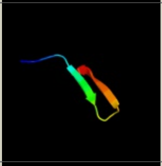
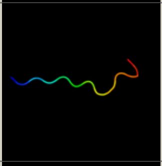
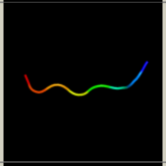
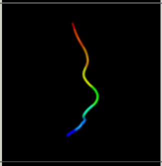
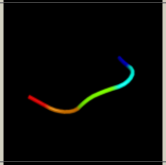
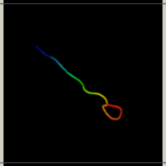
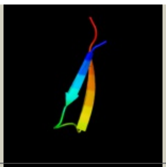
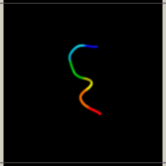
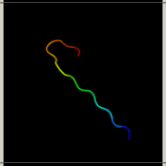
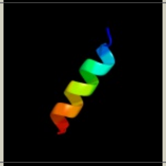
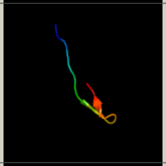
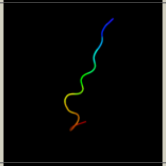
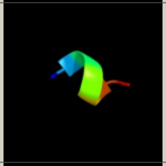
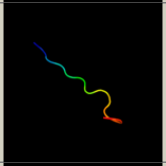
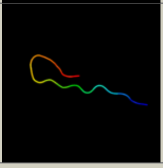
Description	P32051
Date	Wed Jan 25 15:20:49 GMT 2012
Unique Job ID	0527998f3d42f5f7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dcea2	Alignment		21.0	57	**Fold:**C2 domain-like **Superfamily:**Rab geranylgeranyltransferase alpha-subunit, insert domain **Family:**Rab geranylgeranyltransferase alpha-subunit, insert domain
2	c2vxaL_	Alignment		16.4	14	**PDB header:**flavoprotein **Chain:** L: **PDB Molecule:**dodecin; **PDBTitle:** h.halophila dodecin in complex with riboflavin
3	c2pe4A_	Alignment		15.8	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase-1; **PDBTitle:** structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis
4	d1b26a2	Alignment		11.9	31	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
5	d1u46a_	Alignment		11.6	12	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Protein kinases, catalytic subunit
6	d1euza2	Alignment		10.9	23	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
7	c2atmA_	Alignment		10.8	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** crystal structure of the recombinant allergen ves v 2
8	c3oqtP_	Alignment		10.6	63	**PDB header:**flavoprotein **Chain:** P: **PDB Molecule:**rv1498a protein; **PDBTitle:** crystal structure of rv1498a protein from mycobacterium tuberculosis
9	c2hw2A_	Alignment		10.6	80	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rifampin adp-ribosyl transferase; **PDBTitle:** crystal structure of rifampin adp-ribosyl transferase in2 complex with rifampin
10	d1bvua2	Alignment		10.5	23	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
11	c2vagA_	Alignment		10.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dual specificity protein kinase clk1; **PDBTitle:** crystal structure of di-phosphorylated human clk1 in2 complex with a novel substituted indole inhibitor

12	d1wv8a1	Alignment		10.1	24	**Fold:**TTHA1013/TTHA0281-like **Superfamily:**TTHA1013/TTHA0281-like **Family:**TTHA1013-like
13	c3s2xB_	Alignment		9.9	50	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa synthase subunit alpha; **PDBTitle:** structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
14	d1hwxa2	Alignment		9.7	13	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
15	d1gxya_	Alignment		9.4	25	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**Ecto-ART
16	d1iq9a_	Alignment		9.3	13	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
17	d1gtma2	Alignment		9.2	23	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
18	d2hlya1	Alignment		8.9	86	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Atu2299-like
19	d1bgva2	Alignment		8.8	38	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
20	d1ntxa_	Alignment		8.6	19	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
21	c3igmA_	Alignment	not modelled	8.5	33	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**pf14_0633 protein; **PDBTitle:** a 2.2a crystal structure of the ap2 domain of pf14_0633 from p.2 falciparum, bound as a domain-swapped dimer to its cognate dna
22	d1v9la2	Alignment	not modelled	8.3	31	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
23	d1qu3a1	Alignment	not modelled	8.2	44	**Fold:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Superfamily:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases **Family:**Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
24	c3fgrB_	Alignment	not modelled	8.1	43	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phospholipase b-like 2 40 kda form; **PDBTitle:** two chain form of the 66.3 kda protein at 1.8 angstroem
25	d1jq4a_	Alignment	not modelled	8.0	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
26	d1jgka_	Alignment	not modelled	7.8	6	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
27	d2byca1	Alignment	not modelled	7.7	11	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**BLUF domain
28	d2cqha1	Alignment	not modelled	7.5	60	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD

						Family: Canonical RBD
29	d1cm7a_	Alignment	not modelled	7.5	25	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
30	d1uvqb2	Alignment	not modelled	7.3	22	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
31	c4a1dH_	Alignment	not modelled	7.3	23	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**rpl35a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
32	c3izcj_	Alignment	not modelled	7.2	30	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein rpl12 (l11p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
33	c2zxeB_	Alignment	not modelled	6.9	60	**PDB header:**hydrolase/transport protein **Chain:** B: **PDB Molecule:**na+,k+-atpase beta subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
34	d1drsa_	Alignment	not modelled	6.9	50	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Dendroaspin
35	c1p0lA_	Alignment	not modelled	6.8	33	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**19-mer peptide from 50s ribosomal protein l1; **PDBTitle:** hp (2-20) substitution gln to trp modification in sds-d252 micelles
36	d1l1fa2	Alignment	not modelled	6.8	13	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
37	c3kdpD_	Alignment	not modelled	6.7	40	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**sodium/potassium-transporting atpase subunit beta-1; **PDBTitle:** crystal structure of the sodium-potassium pump
38	c1hrdA_	Alignment	not modelled	6.6	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** glutamate dehydrogenase
39	c1v9lA_	Alignment	not modelled	6.6	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
40	d1j0ga_	Alignment	not modelled	6.5	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**BM-002-like
41	c2jp2A_	Alignment	not modelled	6.4	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sprouty-related, evh1 domain-containing protein **PDBTitle:** solution structure and resonance assignment of the n-2 terminal evh1 domain from the human spred2 protein3 (sprouty-related protein with evh1 domain isoform 2)
42	c1bvuF_	Alignment	not modelled	6.4	21	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (glutamate dehydrogenase); **PDBTitle:** glutamate dehydrogenase from thermococcus litoralis
43	c3g2bA_	Alignment	not modelled	6.4	5	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
44	c2kt9A_	Alignment	not modelled	6.3	38	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**probable 30s ribosomal protein psrp-3; **PDBTitle:** solution nmr structure of probable 30s ribosomal protein2 psrp-3 (ycf65-like protein) from synechocystis sp. (strain3 pcc 6803), northeast structural genomics consortium target4 target sgr46
45	c1nr1A_	Alignment	not modelled	6.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase 1; **PDBTitle:** crystal structure of the r463a mutant of human glutamate2 dehydrogenase
46	d1ajka_	Alignment	not modelled	6.3	13	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Glycosyl hydrolases family 16
47	d2r99a1	Alignment	not modelled	6.2	23	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**Cyclophilin (peptidylprolyl isomerase)
48	d1wxsa1	Alignment	not modelled	6.2	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**BM-002-like
49	d1vb0a_	Alignment	not modelled	6.1	12	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
50	d1evha_	Alignment	not modelled	6.0	27	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Enabled/VASP homology 1 domain (EVH1 domain)
51	d2ux9a1	Alignment	not modelled	6.0	17	**Fold:**Dodecin subunit-like **Superfamily:**Dodecin-like **Family:**Dodecin-like
52	d2nnab2	Alignment	not modelled	6.0	24	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
53	d2gc9a1	Alignment	not modelled	5.9	25	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Phenolic acid decarboxylase (PAD)

54	c2zhzC_	Alignment	not modelled	5.9	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**atp:cob(i)alamin adenosyltransferase, putative; **PDBTitle:** crystal structure of a pduo-type atp:cobalamin adenosyltransferase2 from burkholderia thailandensis
55	d1fcqa_	Alignment	not modelled	5.7	50	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Bee venom hyaluronidase
56	d2rmca_	Alignment	not modelled	5.7	29	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**Cyclophilin (peptidylprolyl isomerase)
57	c3alzB_	Alignment	not modelled	5.7	50	**PDB header:**viral protein/membrane protein **Chain:** B: **PDB Molecule:**cdw150; **PDBTitle:** crystal structure of the measles virus hemagglutinin bound to its2 cellular receptor slam (form i)
58	c3aogA_	Alignment	not modelled	5.6	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
59	d1w8ma_	Alignment	not modelled	5.6	23	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**Cyclophilin (peptidylprolyl isomerase)
60	d3ebxa_	Alignment	not modelled	5.5	13	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
61	c2qyzA_	Alignment	not modelled	5.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the uncharacterized protein ctc02137 from2 clostridium tetani e88
62	c3gitA_	Alignment	not modelled	5.5	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase/acetyl-coa synthase subunit **PDBTitle:** crystal structure of a truncated acetyl-coa synthase
63	d2pxyd2	Alignment	not modelled	5.4	24	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
64	c2yfqA_	Alignment	not modelled	5.4	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of glutamate dehydrogenase from2 peptoniphilus asaccharolyticus
65	c3izbD_	Alignment	not modelled	5.4	16	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein rps4 (s4e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
66	d1ktdb2	Alignment	not modelled	5.4	26	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
67	d2hrva_	Alignment	not modelled	5.4	19	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
68	c3aoeC_	Alignment	not modelled	5.3	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glutamate dehydrogenase; **PDBTitle:** crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
69	d2i1sa1	Alignment	not modelled	5.3	14	**Fold:**MM3350-like **Superfamily:**MM3350-like **Family:**MM3350-like
70	d1c8za_	Alignment	not modelled	5.2	30	**Fold:**Tubby C-terminal domain-like **Superfamily:**Tubby C-terminal domain-like **Family:**Transcriptional factor tubby, C-terminal domain
71	d1lmia_	Alignment	not modelled	5.2	44	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Antigen MPT63/MPB63 (immunoprotective extracellular protein) **Family:**Antigen MPT63/MPB63 (immunoprotective extracellular protein)
72	d1cnza_	Alignment	not modelled	5.2	25	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
73	d1mujb2	Alignment	not modelled	5.2	29	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
74	c3dy0B_	Alignment	not modelled	5.2	23	**PDB header:**blood clotting, hydrolase inhibitor **Chain:** B: **PDB Molecule:**c-terminus plasma serine protease inhibitor; **PDBTitle:** crystal structure of cleaved pci bound to heparin
75	d1mvka_	Alignment	not modelled	5.2	50	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains
76	c3fbxA_	Alignment	not modelled	5.1	43	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phospholipase b-like 2; **PDBTitle:** crystal structure of the lysosomal 66.3 kda protein from mouse solved2 by s-sad
77	d1i3rb2	Alignment	not modelled	5.1	26	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
78	d2esla1	Alignment	not modelled	5.1	31	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**Cyclophilin (peptidylprolyl isomerase)
79	c1lq8H_	Alignment	not modelled	5.1	23	**PDB header:**blood clotting **Chain:** H: **PDB Molecule:**plasma serine protease inhibitor; **PDBTitle:** crystal structure of cleaved protein c inhibitor