Phyre2

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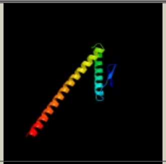
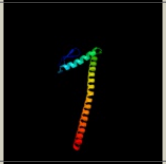
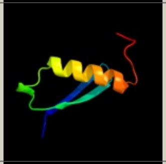
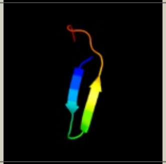
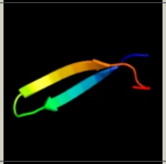
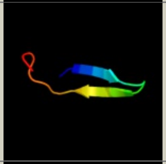
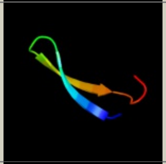
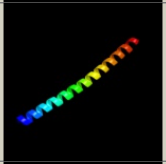
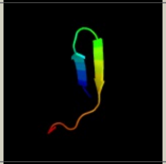
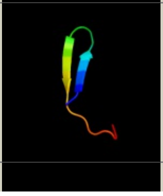
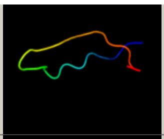
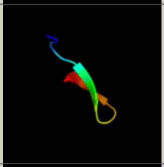
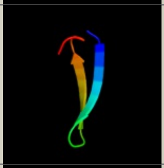
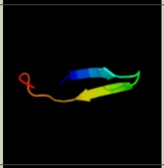
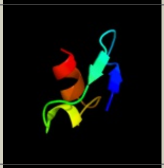
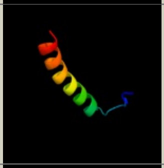
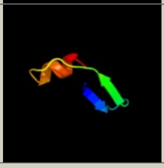
Description	P0ADS2
Date	Thu Jan 5 11:21:42 GMT 2012
Unique Job ID	a8846f0c1762e5f8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1t3ua_	Alignment		99.9	27	**Fold:**Cell division protein ZapA-like **Superfamily:**Cell division protein ZapA-like **Family:**Cell division protein ZapA-like
2	c3hnwB_	Alignment		99.8	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
3	c2ns5A_	Alignment		64.8	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**partitioning-defective 3 homolog; **PDBTitle:** the conserved n-terminal domain of par-3 adopts a novel pb1-2 like structure required for par-3 oligomerization and3 apical membrane localization
4	c3hrdH_	Alignment		64.2	13	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
5	d1t3qa2	Alignment		52.3	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
6	d1rm6c2	Alignment		50.0	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
7	d1vlba2	Alignment		45.8	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
8	d1ffva2	Alignment		44.1	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
9	c2x7aB_	Alignment		42.3	21	**PDB header:**immune system **Chain:** B: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** structural basis of hiv-1 tethering to membranes by the2 bst2-tetherin ectodomain
10	d1n62a2	Alignment		40.6	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
11	c1t3qD_	Alignment		38.8	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86

12	c1rm6F_	Alignment		37.4	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
13	d1dgja2	Alignment		37.4	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
14	c1x4rA_	Alignment		33.5	19	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**parp14 protein; **PDBTitle:** solution structure of wwe domain in parp14 protein
15	c1ffuA_	Alignment		32.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cuts, iron-sulfur protein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
16	d3c8ya2	Alignment		28.0	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
17	c1n60D_	Alignment		27.3	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**carbon monoxide dehydrogenase small chain; **PDBTitle:** crystal structure of the cu,mo-co dehydrogenase (codh); cyanide-2 inactivated form
18	d2fug33	Alignment		22.5	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
19	d1hyea2	Alignment		22.0	13	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
20	d1iuea_	Alignment		21.4	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
21	c3htkA_	Alignment	not modelled	20.2	22	**PDB header:**recombination/replication/ligase **Chain:** A: **PDB Molecule:**structural maintenance of chromosomes protein 5; **PDBTitle:** crystal structure of mms21 and smc5 complex
22	d2oq0a1	Alignment	not modelled	19.9	16	**Fold:**OB-fold **Superfamily:**HIN-2000 domain-like **Family:**HIN-200/IF120x domain
23	c2fugC_	Alignment	not modelled	17.4	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
24	d1exbe_	Alignment	not modelled	16.7	29	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
25	c3dryA_	Alignment	not modelled	16.4	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**btb/poz domain-containing protein kctd5; **PDBTitle:** x-ray crystal structure of human kctd5 protein crystallized in low-2 salt buffer
26	d1qdva_	Alignment	not modelled	16.3	29	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
27	d1t1da_	Alignment	not modelled	16.0	21	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
28	d1t95a2	Alignment	not modelled	15.8	18	**Fold:**FYSH domain **Superfamily:**FYSH domain **Family:**Hypothetical protein AF0491, N-terminal domain
29	d2pw9a1	Alignment	not modelled	15.8	17	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**FdhD/NarQ

30	c2oq0D_	Alignment	not modelled	15.7	16	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**gamma-interferon-inducible protein ifi-16; **PDBTitle:** crystal structure of the first hin-200 domain of interferon-inducible2 protein 16
31	d1dsxa_	Alignment	not modelled	15.6	33	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
32	c2kanA_	Alignment	not modelled	15.3	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ar3433a; **PDBTitle:** solution nmr structure of ubiquitin-like domain of2 arabidopsis thaliana protein at2g32350. northeast3 structural genomics consortium target ar3433a
33	c2it3B_	Alignment	not modelled	14.7	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0130 protein ph1069; **PDBTitle:** structure of ph1069 protein from pyrococcus horikoshii
34	c3b6yB_	Alignment	not modelled	14.0	21	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**gamma-interferon-inducible protein ifi-16; **PDBTitle:** crystal structure of the second hin-200 domain of interferon-inducible2 protein 16
35	c1c4cA_	Alignment	not modelled	13.8	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (fe-only hydrogenase); **PDBTitle:** binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
36	c2kd0A_	Alignment	not modelled	13.7	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**lrr repeats and ubiquitin-like domain-containing **PDBTitle:** nmr solution structure of o64736 protein from arabidopsis2 thaliana. northeast structural genomics consortium mega3 target ar3445a
37	c2x48B_	Alignment	not modelled	12.9	22	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
38	c3cwiA_	Alignment	not modelled	12.6	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this; **PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
39	c2dvkA_	Alignment	not modelled	12.2	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0130 protein ape0816; **PDBTitle:** crystal structure of hypothetical protein from aeropyrum pernix
40	d1a68a_	Alignment	not modelled	11.9	21	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
41	d1wria_	Alignment	not modelled	11.3	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
42	d1s1ga_	Alignment	not modelled	11.0	13	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
43	d1st6a4	Alignment	not modelled	10.9	24	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin
44	c3drzE_	Alignment	not modelled	10.9	13	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**btb/poz domain-containing protein kctd5; **PDBTitle:** x-ray crystal structure of the n-terminal btb domain of human kctd52 protein
45	d1frra_	Alignment	not modelled	10.7	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
46	c2yy0D_	Alignment	not modelled	10.2	12	**PDB header:**transcription **Chain:** D: **PDB Molecule:**c-myc-binding protein; **PDBTitle:** crystal structure of ms0802, c-myc-1 binding protein domain2 from homo sapiens
47	d3kvta_	Alignment	not modelled	10.0	20	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
48	c2wukD_	Alignment	not modelled	9.7	15	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**septum site-determining protein diviva; **PDBTitle:** diviva n-terminal domain, f17a mutant
49	d1i5pa1	Alignment	not modelled	9.6	31	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**delta-Endotoxin, C-terminal domain
50	d1y6ja2	Alignment	not modelled	9.2	26	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
51	d1v86a_	Alignment	not modelled	9.1	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
52	c2l5gB_	Alignment	not modelled	9.1	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative uncharacterized protein ncor2; **PDBTitle:** co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
53	c1aq5C_	Alignment	not modelled	9.0	13	**PDB header:**coiled-coil **Chain:** C: **PDB Molecule:**cartilage matrix protein; **PDBTitle:** high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
54	c1kd8E_	Alignment	not modelled	8.9	10	**PDB header:**de novo protein **Chain:** E: **PDB Molecule:**gcn4 acid base heterodimer base-d12la16l;

						PDBTitle: x-ray structure of the coiled coil gcn4 acid base2 heterodimer acid-d12ia16v base-d12la16l
55	c3ghgK_	Alignment	not modelled	8.8	10	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
56	d1ujra_	Alignment	not modelled	8.8	13	**Fold:**WWE domain **Superfamily:**WWE domain **Family:**WWE domain
57	c2gzdC_	Alignment	not modelled	8.3	16	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**rab11 family-interacting protein 2; **PDBTitle:** crystal structure of rab11 in complex with rab11-fip2
58	d1lvfa_	Alignment	not modelled	8.2	16	**Fold:**STAT-like **Superfamily:**t-snare proteins **Family:**t-snare proteins
59	c3iz5J_	Alignment	not modelled	7.9	19	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l12 (l11p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
60	c2k4mA_	Alignment	not modelled	7.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0146 protein mth_1000; **PDBTitle:** solution nmr structure of m. thermoautotrophicum protein2 mth_1000, northeast structural genomics consortium target3 tr8
61	d1hyha2	Alignment	not modelled	7.7	19	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
62	d1wqga1	Alignment	not modelled	7.4	14	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
63	c2xzrA_	Alignment	not modelled	7.3	10	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**immunoglobulin-binding protein eibd; **PDBTitle:** escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
64	d2j0111	Alignment	not modelled	7.3	10	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L28
65	d1an2a_	Alignment	not modelled	7.2	15	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
66	c3p8cF_	Alignment	not modelled	7.1	18	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**abl interactor 2; **PDBTitle:** structure and control of the actin regulatory wave complex
67	d1a70a_	Alignment	not modelled	7.1	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
68	d1gaqb_	Alignment	not modelled	7.1	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
69	d1m94a_	Alignment	not modelled	7.0	31	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
70	c1m94A_	Alignment	not modelled	7.0	31	**PDB header:**structural genomics, signaling protein **Chain:** A: **PDB Molecule:**protein ynr032c-a; **PDBTitle:** solution structure of the yeast ubiquitin-like modifier2 protein hub1
71	d1p0ra_	Alignment	not modelled	6.7	38	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
72	d1qu6a2	Alignment	not modelled	6.7	8	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
73	d1jq4a_	Alignment	not modelled	6.7	31	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
74	d1dd5a_	Alignment	not modelled	6.6	11	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
75	d1i0za2	Alignment	not modelled	6.6	26	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
76	d1oqya4	Alignment	not modelled	6.5	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
77	c2i2rK_	Alignment	not modelled	6.4	13	**PDB header:**transport protein **Chain:** K: **PDB Molecule:**potassium voltage-gated channel subfamily d member 3; **PDBTitle:** crystal structure of the kchip1/kv4.3 t1 complex
78	d1t3ta3	Alignment	not modelled	6.4	19	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**FGAM synthase PurL, PurS-like domain
79	c2odkD_	Alignment	not modelled	6.3	25	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative prevent-host-death protein from nitrosomonas europaea
80	d1nkpa_	Alignment	not modelled	6.0	15	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
81	c3fp9E	Alignment	not modelled	5.9	39	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**proteasome-associated atpase;

81	c3fp9L_	Alignment	not modelled	5.9	39	**PDBTitle:** crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis
82	d1uxja2	Alignment	not modelled	5.9	23	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
83	d1awda_	Alignment	not modelled	5.8	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
84	d1v97a2	Alignment	not modelled	5.8	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
85	d2cqla1	Alignment	not modelled	5.8	35	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
86	d1whna_	Alignment	not modelled	5.8	7	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
87	c2k1iA_	Alignment	not modelled	5.7	29	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**mucosal alpha-defensin; **PDBTitle:** synthesis, structure and activities of an oral mucosal2 alpha-defensin from rhesus macaque
88	d1gv0a2	Alignment	not modelled	5.7	14	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
89	d1nkpb_	Alignment	not modelled	5.6	10	**Fold:**HLH-like **Superfamily:**HLH, helix-loop-helix DNA-binding domain **Family:**HLH, helix-loop-helix DNA-binding domain
90	c1zmpD_	Alignment	not modelled	5.5	42	**PDB header:**antimicrobial protein **Chain:** D: **PDB Molecule:**defensin 5; **PDBTitle:** crystal structure of human defensin-5
91	d1p9qc2	Alignment	not modelled	5.5	17	**Fold:**FYSH domain **Superfamily:**FYSH domain **Family:**Hypothetical protein AF0491, N-terminal domain
92	c3m63B_	Alignment	not modelled	5.4	19	**PDB header:**ligase/protein binding **Chain:** B: **PDB Molecule:**ubiquitin domain-containing protein dsk2; **PDBTitle:** crystal structure of ufd2 in complex with the ubiquitin-like (ubl)2 domain of dsk2
93	c3mkxC_	Alignment	not modelled	5.4	19	**PDB header:**antiviral protein **Chain:** C: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** crystal structure of bst2/tetherin
94	d1krha3	Alignment	not modelled	5.3	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
95	d2b7ta1	Alignment	not modelled	5.3	14	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)