Phyre2

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Description	P0ABY2
Date	Thu Jan 5 11:16:41 GMT 2012
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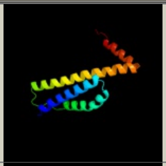
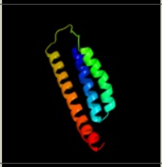
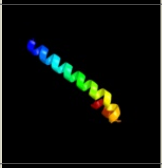
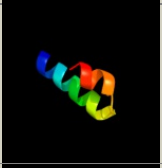
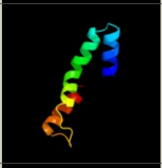
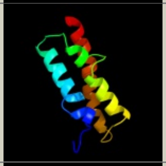
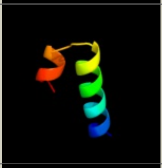
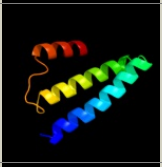
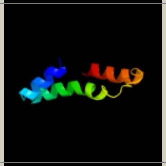
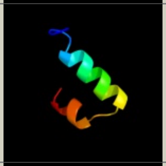
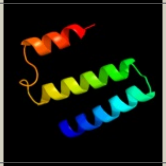
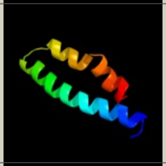
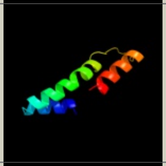
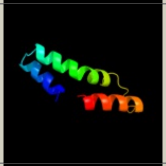
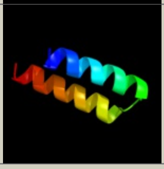
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3a7mA_	Alignment		100.0	33	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**flagellar protein flit; **PDBTitle:** structure of flit, the flagellar type iii chaperone for flid
2	c3nkzD_	Alignment		100.0	43	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**flagellar protein flit; **PDBTitle:** the crystal structure of a flagella protein from yersinia2 enterocolitica subsp. enterocolitica 8081
3	c3h3mB_	Alignment		99.9	20	**PDB header:**structural genomics **Chain:** B: **PDB Molecule:**flagellar protein flit; **PDBTitle:** crystal structure of flagellar protein flit from bordetella2 bronchiseptica
4	c3bc1F_	Alignment		40.2	13	**PDB header:**signaling protein/transport protein **Chain:** F: **PDB Molecule:**synaptotagmin-like protein 2; **PDBTitle:** crystal structure of the complex rab27a-slp2a
5	d2f86b1	Alignment		31.5	16	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
6	c3bi8A_	Alignment		28.6	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from clostridium2 botulinum
7	d1wr0a1	Alignment		27.0	18	**Fold:**Spectrin repeat-like **Superfamily:**MIT domain **Family:**MIT domain
8	d2ux0a1	Alignment		25.2	4	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
9	c3k17A_	Alignment		23.3	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lin0012 protein; **PDBTitle:** crystal structure of a lin0012 protein from listeria innocua
10	d2a1ja1	Alignment		22.3	17	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
11	c3fsdA_	Alignment		21.1	4	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ntf2-like protein of unknown function in nutrient uptake; **PDBTitle:** crystal structure of ntf2-like protein of unknown function in nutrient2 uptake (yp_427473.1) from rhodospirillum rubrum atcc 11170 at 1.70 a3 resolution

12	d1hkxa_	Alignment		20.9	4	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
13	c3fluD_	Alignment		17.5	14	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
14	c3echC_	Alignment		16.5	29	**PDB header:**transcription, transcription regulation **Chain:** C: **PDB Molecule:**25-mer fragment of protein armr; **PDBTitle:** the marr-family repressor mexr in complex with its antirepressor armr
15	d2r4ia1	Alignment		16.0	8	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**CHU142-like
16	d1k47a2	Alignment		15.1	12	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Phosphomevalonate kinase (PMK)
17	d1wuua2	Alignment		14.1	18	**Fold:**Ferredoxin-like **Superfamily:**GHMP Kinase, C-terminal domain **Family:**Galactokinase
18	c3s5oA_	Alignment		13.8	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase, mitochondrial; **PDBTitle:** crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
19	c3na8A_	Alignment		13.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
20	d1sr2a_	Alignment		12.9	8	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Sensor-like histidine kinase YojN, C-terminal domain
21	c2ehhE_	Alignment	not modelled	12.6	14	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
22	c3si9B_	Alignment	not modelled	12.1	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
23	c3lciA_	Alignment	not modelled	12.1	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
24	c2hz8A_	Alignment	not modelled	12.1	29	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo designed diiron protein; **PDBTitle:** qm/mm structure refined from nmr-structure of a single2 chain diiron protein
25	d1yqha1	Alignment	not modelled	11.6	16	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
26	d2crua1	Alignment	not modelled	11.4	18	**Fold:**RuvA C-terminal domain-like **Superfamily:**Double-stranded DNA-binding domain **Family:**Double-stranded DNA-binding domain
27	c2ka3C_	Alignment	not modelled	11.3	20	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**emilin-1; **PDBTitle:** structure of emilin-1 c1q-like domain
28	c1u7mB_	Alignment	not modelled	11.2	24	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**four-helix bundle model; **PDBTitle:** solution structure of a diiron protein model: due ferri(ii)2 turn mutant
						PDB header:isomerase

29	c1zvuA_	Alignment	not modelled	11.2	28	**Chain:** A: **PDB Molecule:**topoisomerase iv subunit a; **PDBTitle:** structure of the full-length e. coli parc subunit
30	d1wn0a1	Alignment	not modelled	10.6	11	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Phosphorelay protein-like
31	d2cpta1	Alignment	not modelled	10.6	18	**Fold:**Spectrin repeat-like **Superfamily:**MIT domain **Family:**MIT domain
32	d1e9ya2	Alignment	not modelled	10.5	11	**Fold:**Urease, gamma-subunit **Superfamily:**Urease, gamma-subunit **Family:**Urease, gamma-subunit
33	d1vk8a_	Alignment	not modelled	10.4	6	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
34	d1ug7a_	Alignment	not modelled	10.1	15	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain from hypothetical 2610208m17rik protein **Family:**Domain from hypothetical 2610208m17rik protein
35	d1lxja_	Alignment	not modelled	10.0	16	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
36	c3qgaD_	Alignment	not modelled	9.8	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**fusion of urease beta and gamma subunits; **PDBTitle:** 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae
37	c3eb2A_	Alignment	not modelled	9.3	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative dihydrodipicolinate synthetase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
38	d3en8a1	Alignment	not modelled	9.3	8	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Rpa4348-like
39	c2zetD_	Alignment	not modelled	9.1	9	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**melanophilin; **PDBTitle:** crystal structure of the small gtpase rab27b complexed with2 the slp homology domain of slac2-a/melanophilin
40	c3efgA_	Alignment	not modelled	9.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein slyx homolog; **PDBTitle:** structure of slyx protein from xanthomonas campestris pv. campestris2 str. atcc 33913
41	c1e9zA_	Alignment	not modelled	9.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**urease subunit alpha; **PDBTitle:** crystal structure of helicobacter pylori urease
42	c3gzrA_	Alignment	not modelled	9.0	4	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein with a ntf2-like fold; **PDBTitle:** crystal structure of an uncharacterized protein with a cystatin-like2 fold (cc_2572) from caulobacter vibrioides at 1.40 a resolution
43	c2epiA_	Alignment	not modelled	8.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0045 protein mj1052; **PDBTitle:** crystal structure pf hypothetical protein mj1052 from2 methanocaldococcus jannascii (form 2)
44	d1ngka_	Alignment	not modelled	8.5	8	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
45	d1ejxa_	Alignment	not modelled	8.4	11	**Fold:**Urease, gamma-subunit **Superfamily:**Urease, gamma-subunit **Family:**Urease, gamma-subunit
46	c3robC_	Alignment	not modelled	8.3	8	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved protein from planctomyces2 limnophilus dsm 3776
47	d4ubpa_	Alignment	not modelled	7.9	5	**Fold:**Urease, gamma-subunit **Superfamily:**Urease, gamma-subunit **Family:**Urease, gamma-subunit
48	c2oi2A_	Alignment	not modelled	7.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mevalonate kinase; **PDBTitle:** streptococcus pneumoniae mevalonate kinase in complex with2 diphosphomevalonate
49	c2yxgD_	Alignment	not modelled	7.5	14	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
50	d2a0ba_	Alignment	not modelled	7.0	11	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Aerobic respiration control sensor protein, ArcB
51	c2fvhB_	Alignment	not modelled	6.8	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**urease gamma subunit; **PDBTitle:** crystal structure of rv1848, a urease gamma subunit urea (urea2 amidohydrolase), from mycobacterium tuberculosis
52	d2g3ba2	Alignment	not modelled	6.7	10	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
53	c3f7sA_	Alignment	not modelled	6.6	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized ntf2-like protein; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function (pp_4556)2 from pseudomonas putida kt2440 at 2.11 a resolution
54	d1yvia1	Alignment	not modelled	6.5	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Phosphorelay protein-like

55	c2v6xA_	Alignment	not modelled	6.4	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** stractural insight into the interaction between escrt-iii2 and vps4
56	d1xsfa1	Alignment	not modelled	6.4	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**RPF-like
57	d1yzma1	Alignment	not modelled	6.2	13	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
58	c1fi4A_	Alignment	not modelled	6.2	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mevalonate 5-diphosphate decarboxylase; **PDBTitle:** the x-ray crystal structure of mevalonate 5-diphosphate decarboxylase2 at 2.3 angstrom resolution.
59	c3hx8A_	Alignment	not modelled	6.2	0	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative ketosteroid isomerase; **PDBTitle:** crystal structure of putative ketosteroid isomerase2 (np_103587.1) from mesorhizobium loti at 1.45 a resolution
60	d2iboa1	Alignment	not modelled	6.1	17	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
61	c3jw4C_	Alignment	not modelled	6.0	19	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator, marr/emrr family; **PDBTitle:** the structure of a putative marr family transcriptional regulator from2 clostridium acetobutylicum
62	d2g5ca1	Alignment	not modelled	6.0	12	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**TyrA dimerization domain-like
63	c2rfgB_	Alignment	not modelled	5.8	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
64	d3b8la1	Alignment	not modelled	5.7	7	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**BaiE/LinA-like
65	d1s5aa_	Alignment	not modelled	5.7	7	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PhzA/PhzB-like
66	c1k47F_	Alignment	not modelled	5.4	5	**PDB header:**transferase **Chain:** F: **PDB Molecule:**phosphomevalonate kinase; **PDBTitle:** crystal structure of the streptococcus pneumoniae2 phosphomevalonate kinase (pmk)
67	d1y6da_	Alignment	not modelled	5.4	13	**Fold:**Four-helical up-and-down bundle **Superfamily:**Histidine-containing phosphotransfer domain, HPT domain **Family:**Phosphorelay protein luxU
68	c2xcqA_	Alignment	not modelled	5.4	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit b, dna gyrase subunit a; **PDBTitle:** the 2.98a crystal structure of the catalytic core (b'a'2 region) of staphylococcus aureus dna gyrase
69	d1m98a1	Alignment	not modelled	5.3	18	**Fold:**Orange carotenoid protein, N-terminal domain **Superfamily:**Orange carotenoid protein, N-terminal domain **Family:**Orange carotenoid protein, N-terminal domain
70	c1m98A_	Alignment	not modelled	5.3	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**orange carotenoid protein; **PDBTitle:** crystal structure of orange carotenoid protein
71	d1z05a2	Alignment	not modelled	5.2	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
72	d1o5ka_	Alignment	not modelled	5.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
73	c2rrlA_	Alignment	not modelled	5.2	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar hook-length control protein; **PDBTitle:** solution structure of the c-terminal domain of the flik
74	d1zbdb_	Alignment	not modelled	5.1	13	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
75	d1q3ma_	Alignment	not modelled	5.1	39	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
76	c1u6tA_	Alignment	not modelled	5.1	5	**PDB header:**protein binding, signaling protein **Chain:** A: **PDB Molecule:**sh3 domain-binding glutamic acid-rich-like **PDBTitle:** crystal structure of the human sh3 binding glutamic-rich2 protein like
77	c3q4iA_	Alignment	not modelled	5.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase (mutt/nudix family protein); **PDBTitle:** crystal structure of cdp-chase in complex with gd3+
78	d2cqea1	Alignment	not modelled	5.0	25	**Fold:**CCCH zinc finger **Superfamily:**CCCH zinc finger **Family:**CCCH zinc finger
79	c3g0eA_	Alignment	not modelled	5.0	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mast/stem cell growth factor receptor; **PDBTitle:** kit kinase domain in complex with sunitinib
80	d1q8ha_	Alignment	not modelled	5.0	38	**Fold:**GLA-domain **Superfamily:**GLA-domain

Family:GLA-domain