Phyre2

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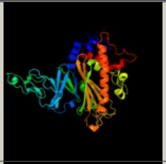
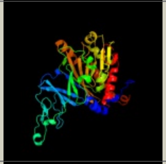
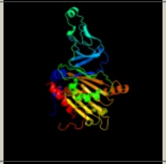
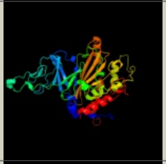
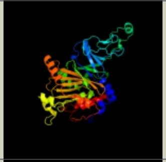
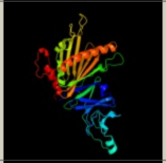
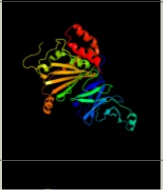
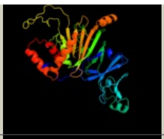
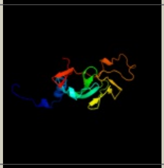
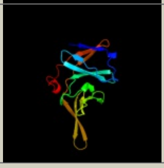
Description	P0ABR7
Date	Thu Jan 5 11:16:09 GMT 2012
Unique Job ID	def27a0b7e02e877

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3n0qA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative aromatic-ring hydroxylating dioxygenase; **PDBTitle:** crystal structure of a putative aromatic-ring hydroxylating2 dioxygenase (tm1040_3219) from silicibacter sp. tm1040 at 1.80 a3 resolution
2	c1uljA_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**biphenyl dioxygenase large subunit; **PDBTitle:** biphenyl dioxygenase (bpha1a2) in complex with the substrate
3	c2b1xE_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**naphthalene dioxygenase large subunit; **PDBTitle:** crystal structure of naphthalene 1,2-dioxygenase from rhodococcus sp.
4	c1wqlA_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-sulfur protein large subunit of cumene dioxygenase; **PDBTitle:** cumene dioxygenase (cuma1a2) from pseudomonas fluorescens ip01
5	c2hmnA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**naphthalene 1,2-dioxygenase alpha subunit; **PDBTitle:** crystal structure of the naphthalene 1,2-dioxygenase f352v2 mutant bound to anthracene.
6	c2gbxE_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**biphenyl 2,3-dioxygenase alpha subunit; **PDBTitle:** crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl
7	c3gteB_	Alignment		100.0	18	**PDB header:**electron transport, oxidoreductase **Chain:** B: **PDB Molecule:**ddmc; **PDBTitle:** crystal structure of dicamba monooxygenase with non-heme2 iron
8	c3gkqB_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**terminal oxygenase component of carbazole 1,9a- **PDBTitle:** terminal oxygenase of carbazole 1,9a-dioxygenase from2 novosphingobium sp. ka1
9	c2zylA_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**possible oxidoreductase; **PDBTitle:** crystal structure of 3-ketosteroid-9-alpha-hydroxylase2 (ksha) from m. tuberculosis
10	c2de7B_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**terminal oxygenase component of carbazole; **PDBTitle:** the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
11	c3gcfC_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**terminal oxygenase component of carbazole 1,9a- **PDBTitle:** terminal oxygenase of carbazole 1,9a-dioxygenase from2 nocardioides aromaticivorans ic177

12	c1z01D_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**2-oxo-1,2-dihydroquinoline 8-monooxygenase, **PDBTitle:** 2-oxoquinoline 8-monooxygenase component: active site2 modulation by rieske-[2fe-2s] center oxidation/reduction
13	d2b1xa1	Alignment		100.0	30	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
14	d1wqla1	Alignment		100.0	30	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
15	d1ulia1	Alignment		100.0	29	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
16	d2bmoa1	Alignment		100.0	27	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
17	d1o7na1	Alignment		100.0	28	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
18	d1z01a1	Alignment		100.0	24	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
19	d2de6a1	Alignment		100.0	28	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
20	c3d89A_	Alignment		99.9	16	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rieske domain-containing protein; **PDBTitle:** crystal structure of a soluble rieske ferredoxin from mus musculus
21	d1vm9a_	Alignment	not modelled	99.9	21	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
22	d1fqta_	Alignment	not modelled	99.9	17	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
23	d3c0da1	Alignment	not modelled	99.9	19	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
24	c2de7E_	Alignment	not modelled	99.9	23	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ferredoxin component of carbazole; **PDBTitle:** the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
25	c3dqyA_	Alignment	not modelled	99.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**toluene 1,2-dioxygenase system ferredoxin **PDBTitle:** crystal structure of toluene 2,3-dioxygenase ferredoxin
26	c3gceA_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin component of carbazole 1,9a- **PDBTitle:** ferredoxin of carbazole 1,9a-dioxygenase from nocardioides2 aromaticivorans ic177
27	d2jzaa1	Alignment	not modelled	99.8	19	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
28	c2qpzA_	Alignment	not modelled	99.8	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**naphthalene 1,2-dioxygenase system ferredoxin **PDBTitle:** naphthalene 1,2-dioxygenase rieske ferredoxin
29	d2jo6a1	Alignment	not modelled	99.8	17	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like

30	c2i7fB_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin component of dioxygenase; **PDBTitle:** sphingomonas yanoikuyae b1 ferredoxin
31	d2bmoa2	Alignment	not modelled	99.8	20	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Ring hydroxylating alpha subunit catalytic domain
32	d2b1xa2	Alignment	not modelled	99.8	16	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Ring hydroxylating alpha subunit catalytic domain
33	d1ulia2	Alignment	not modelled	99.8	12	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Ring hydroxylating alpha subunit catalytic domain
34	d1wqla2	Alignment	not modelled	99.8	17	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Ring hydroxylating alpha subunit catalytic domain
35	d1o7na2	Alignment	not modelled	99.8	21	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Ring hydroxylating alpha subunit catalytic domain
36	d1rfsa_	Alignment	not modelled	99.6	22	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
37	d1q90c_	Alignment	not modelled	99.6	20	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
38	d3cx5e1	Alignment	not modelled	99.5	18	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
39	d1g8kb_	Alignment	not modelled	99.5	28	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
40	d2e74d1	Alignment	not modelled	99.5	21	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
41	d1riea_	Alignment	not modelled	99.4	18	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
42	c2nvgA_	Alignment	not modelled	99.3	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit; **PDBTitle:** soluble domain of rieske iron sulfur protein.
43	d1nyka_	Alignment	not modelled	99.3	15	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
44	c2e76D_	Alignment	not modelled	99.2	19	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
45	d1z01a2	Alignment	not modelled	99.1	10	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Ring hydroxylating alpha subunit catalytic domain
46	c2fyuE_	Alignment	not modelled	99.1	20	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
47	c2fynO_	Alignment	not modelled	99.0	21	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
48	d2de6a2	Alignment	not modelled	98.9	15	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Ring hydroxylating alpha subunit catalytic domain
49	c1p84E_	Alignment	not modelled	98.8	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
50	d1jm1a_	Alignment	not modelled	97.9	35	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
51	d1pwka_	Alignment	not modelled	40.6	13	**Fold:**DLC **Superfamily:**DLC **Family:**DLC
52	c2c3yA_	Alignment	not modelled	25.8	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
53	c2z0rA_	Alignment	not modelled	24.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0547; **PDBTitle:** crystal structure of hypothetical protein ttha0547
54	c2ba1B_	Alignment	not modelled	23.9	13	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
55	d1w44a_	Alignment	not modelled	22.9	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
						PDB header:lyase

56	c2w3nA_	Alignment	not modelled	22.2	26	**Chain:** A: **PDB Molecule:**carbonic anhydrase 2; **PDBTitle:** structure and inhibition of the co2-sensing carbonic2 anhydrase can2 from the pathogenic fungus cryptococcus3 neoformans
57	c3kv0A_	Alignment	not modelled	22.0	40	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**het-c2; **PDBTitle:** crystal structure of het-c2: a fungal glycolipid transfer protein2 (gltp)
58	c1ddzA_	Alignment	not modelled	21.3	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1
59	d2c42a2	Alignment	not modelled	21.0	9	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**PFOR PP module
60	d1swxa_	Alignment	not modelled	20.4	60	**Fold:**Glycolipid transfer protein, GLTP **Superfamily:**Glycolipid transfer protein, GLTP **Family:**Glycolipid transfer protein, GLTP
61	c2i3fA_	Alignment	not modelled	19.6	40	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glycolipid transfer-like protein; **PDBTitle:** crystal structure of a glycolipid transfer-like protein2 from galdieria sulphuraria
62	d1cmia_	Alignment	not modelled	19.1	13	**Fold:**DLC **Superfamily:**DLC **Family:**DLC
63	c1dfcB_	Alignment	not modelled	18.5	18	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**fascin; **PDBTitle:** crystal structure of human fascin, an actin-crosslinking protein
64	d1ddza2	Alignment	not modelled	17.7	25	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
65	c3k2tA_	Alignment	not modelled	17.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2511 protein; **PDBTitle:** crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
66	d1t62a_	Alignment	not modelled	17.3	15	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical protein EF3133
67	d1ubdc1	Alignment	not modelled	17.1	67	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
68	d1igqa_	Alignment	not modelled	16.8	14	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Transcriptional repressor protein KorB
69	c3s9xA_	Alignment	not modelled	16.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**asch domain; **PDBTitle:** high resolution crystal structure of asch domain from lactobacillus2 crispatus jv v101
70	c3izbP_	Alignment	not modelled	16.6	40	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**40s ribosomal protein rps11 (s17p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
71	d1uhva1	Alignment	not modelled	16.1	18	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
72	c3iz6P_	Alignment	not modelled	16.1	40	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**40s ribosomal protein s11 (s17p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
73	c3nwiC_	Alignment	not modelled	16.0	12	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**zinc transport protein zntb; **PDBTitle:** the soluble domain structure of the zntb zn2+ efflux system
74	d1igub_	Alignment	not modelled	15.1	14	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Transcriptional repressor protein KorB
75	d1d1la_	Alignment	not modelled	14.9	29	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
76	c3lasA_	Alignment	not modelled	14.6	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution
77	c2xznQ_	Alignment	not modelled	14.5	40	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**ribosomal protein s17 containing protein; **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
78	c3ka5A_	Alignment	not modelled	14.4	14	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**ribosome-associated protein y (psrp-1); **PDBTitle:** crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
79	c3fcgB_	Alignment	not modelled	14.4	11	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**f1 capsule-anchoring protein; **PDBTitle:** crystal structure analysis of the middle domain of the2 caf1a usher
80	d4croa_	Alignment	not modelled	14.2	29	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
						Fold:lambda repressor-like DNA-binding domains

81	d3orca_	Alignment	not modelled	14.2	29	**Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
82	d1nfga1	Alignment	not modelled	14.1	22	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase)
83	c2yrtA_	Alignment	not modelled	14.1	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**chord containing protein-1; **PDBTitle:** solution structure of the chord domain of human chord-2 containing protein 1
84	c2kppA_	Alignment	not modelled	13.6	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0431 protein; **PDBTitle:** solution nmr structure of lin0431 protein from listeria innocua.2 northeast structural genomics consortium target lkr112
85	c2jv2A_	Alignment	not modelled	13.6	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1500; **PDBTitle:** solution structure of the n-terminal domain of ph1500
86	c2pijB_	Alignment	not modelled	13.4	29	**PDB header:**transcription **Chain:** B: **PDB Molecule:**prophage pfl 6 cro; **PDBTitle:** structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
87	c3ozbF_	Alignment	not modelled	13.3	19	**PDB header:**transferase **Chain:** F: **PDB Molecule:**methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
88	d1ddza1	Alignment	not modelled	13.0	21	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
89	d1wida_	Alignment	not modelled	12.7	21	**Fold:**DNA-binding pseudobarrel domain **Superfamily:**DNA-binding pseudobarrel domain **Family:**B3 DNA binding domain
90	d1ugpa_	Alignment	not modelled	12.6	10	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
91	c1ylkA_	Alignment	not modelled	12.5	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv1284/mt1322; **PDBTitle:** crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate
92	c2a8cE_	Alignment	not modelled	12.1	36	**PDB header:**lyase **Chain:** E: **PDB Molecule:**carbonic anhydrase 2; **PDBTitle:** haemophilus influenzae beta-carbonic anhydrase
93	d1v29a_	Alignment	not modelled	12.0	14	**Fold:**Nitrile hydratase alpha chain **Superfamily:**Nitrile hydratase alpha chain **Family:**Nitrile hydratase alpha chain
94	d3e2ba1	Alignment	not modelled	11.8	11	**Fold:**DLC **Superfamily:**DLC **Family:**DLC
95	d1ei5a2	Alignment	not modelled	11.6	15	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
96	d1en2a2	Alignment	not modelled	11.2	19	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant lectins/antimicrobial peptides **Family:**Hevein-like agglutinin (lectin) domain
97	c2fhdA_	Alignment	not modelled	11.2	5	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair protein rhp9/crb2; **PDBTitle:** crystal structure of crb2 tandem tudor domains
98	d1do5a_	Alignment	not modelled	11.1	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Cu,Zn superoxide dismutase-like **Family:**Cu,Zn superoxide dismutase-like
99	d1ehda2	Alignment	not modelled	10.7	19	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant lectins/antimicrobial peptides **Family:**Hevein-like agglutinin (lectin) domain