Phyre2

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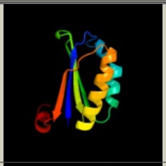
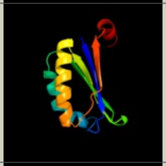
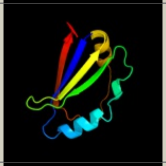
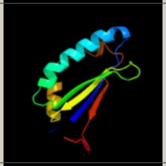
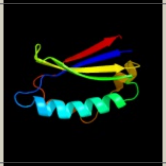
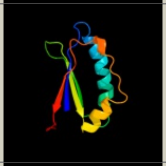
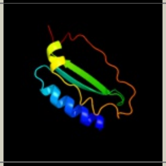
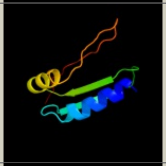
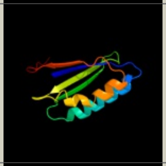
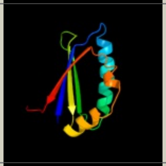
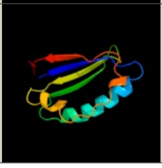
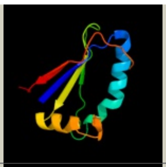
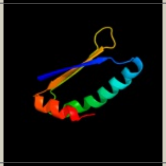
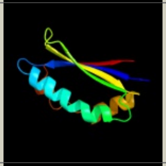
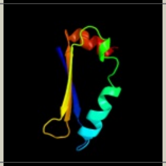
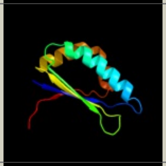
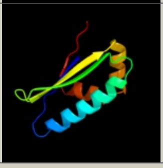
Description	P0ACX3
Date	Thu Jan 5 11:19:20 GMT 2012
Unique Job ID	d636cf9a08df520c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2hiqa1	Alignment		100.0	100	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Hypothetical protein YdhR
2	c1wd6B_	Alignment		100.0	99	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydhr; **PDBTitle:** crystal structure of jw1657 from escherichia coli
3	c3hx9B_	Alignment		97.0	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein rv3592; **PDBTitle:** structure of heme-degrader, mhud (rv3592), from2 mycobacterium tuberculosis with two hemes bound in its3 active site
4	d1y0ha_	Alignment		96.4	16	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
5	c3fgvB_	Alignment		95.1	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized protein with ferredoxin-like fold; **PDBTitle:** crystal structure of a putative antibiotic biosynthesis monooxygenase2 (spo2313) from silicibacter pomeroyi dss-3 at 1.30 a resolution
6	c2omoC_	Alignment		95.1	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**duf176; **PDBTitle:** putative antibiotic biosynthesis monooxygenase from nitrosomonas2 europaea
7	c2gffB_	Alignment		95.1	19	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**lsrg protein; **PDBTitle:** crystal structure of yersinia pestis lsrg
8	c3bm7A_	Alignment		94.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein of unknown function with ferredoxin-like fold; **PDBTitle:** crystal structure of a putative antibiotic biosynthesis monooxygenase2 (cc_2132) from caulobacter crescentus cb15 at 1.35 a resolution
9	c3e8oB_	Alignment		94.3	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized protein with erredoxin-like fold; **PDBTitle:** crystal structure of a putative antibiotic biosynthesis monooxygenase2 (dr_2100) from deinococcus radiodurans at 1.40 a resolution
10	c3kngA_	Alignment		93.7	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**snoab; **PDBTitle:** crystal structure of snoab, a cofactor-independent oxygenase2 from streptomyces nogalater, determined to 1.9 resolution
11	d2omoa1	Alignment		92.7	16	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like

12	d1iuja_	Alignment		92.5	16	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
13	c3fj2A_	Alignment		89.9	6	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**monooxygenase-like protein; **PDBTitle:** crystal structure of a monooxygenase-like protein (lin2316) from2 listeria innocua at 1.85 a resolution
14	d2pd1a1	Alignment		87.4	17	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
15	c3bn7A_	Alignment		86.3	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**ferredoxin-like protein; **PDBTitle:** crystal structure of a dimeric ferredoxin-like protein (cc_2267) from2 caulobacter crescentus cb15 at 1.64 a resolution
16	d1x7va_	Alignment		85.0	14	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
17	c2bbeA_	Alignment		84.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein so0527; **PDBTitle:** crystal structure of protein so0527 from shewanella oneidensis
18	d2zdpa1	Alignment		84.3	14	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
19	c2rilA_	Alignment		72.7	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**antibiotic biosynthesis monooxygenase; **PDBTitle:** crystal structure of a putative monooxygenase (yp_001095275.1) from2 shewanella loihica pv-4 at 1.26 a resolution
20	c2fb0A_	Alignment		71.1	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of conserved protein of unknown function from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution, possible3 oxidoreductase
21	d1xbwa_	Alignment	not modelled	69.0	15	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
22	d1lq9a_	Alignment	not modelled	68.2	17	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Actinorhodin biosynthesis monooxygenase ActVa-Orf6
23	c2qycA_	Alignment	not modelled	66.1	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**ferredoxin-like protein; **PDBTitle:** crystal structure of a dimeric ferredoxin-like protein (bb1511) from2 bordetella bronchiseptica rb50 at 1.90 a resolution
24	c3f44A_	Alignment	not modelled	63.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative monooxygenase; **PDBTitle:** crystal structure of putative monooxygenase (yp_193413.1) from2 lactobacillus acidophilus ncfm at 1.55 a resolution
25	d1xrsb2	Alignment	not modelled	63.1	27	**Fold:**Dodecin subunit-like **Superfamily:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain **Family:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
26	d1q8ba_	Alignment	not modelled	62.6	19	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Hypothetical protein YjcS
27	c3kkfA_	Alignment	not modelled	59.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative antibiotic biosynthesis monooxygenase; **PDBTitle:** crystal structure of putative antibiotic biosynthesis2 monooxygenase (np_810307.1) from bacteriodes3 thetaiotaomicron vpi-5482 at 1.30 a resolution
						PDB header:biosynthetic protein

28	c3gz7B_	Alignment	not modelled	55.5	5	**Chain:** B: **PDB Molecule:**putative antibiotic biosynthesis monooxygenase; **PDBTitle:** crystal structure of putative antibiotic biosynthesis2 monooxygenase (np_888398.1) from bordetella bronchiseptica3 at 2.15 a resolution
29	c3mcsB_	Alignment	not modelled	53.1	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative monooxygenase; **PDBTitle:** crystal structure of putative monooxygenase (fn1347) from2 fusobacterium nucleatum subsp. nucleatum atcc 25586 at 2.55 a3 resolution
30	d1tuva_	Alignment	not modelled	43.4	11	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
31	c3bdeA_	Alignment	not modelled	42.4	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**mll5499 protein; **PDBTitle:** crystal structure of a dabb family protein with a ferredoxin-like fold2 (mll5499) from mesorhizobium loti maff303099 at 1.79 a resolution
32	c2jyaA_	Alignment	not modelled	41.3	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1810; **PDBTitle:** nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
33	d1tr0a_	Alignment	not modelled	29.8	14	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Plant stress-induced protein
34	d1q4ra_	Alignment	not modelled	25.7	16	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Plant stress-induced protein
35	d1tz0a_	Alignment	not modelled	24.9	11	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
36	d1rjja_	Alignment	not modelled	21.9	17	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Plant stress-induced protein
37	c3bb5B_	Alignment	not modelled	21.9	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**stress responsive alpha-beta protein; **PDBTitle:** crystal structure of a dimeric ferredoxin-like protein of unknown2 function (jann_3925) from jannaschia sp. ccs1 at 2.30 a resolution
38	c3hfkB_	Alignment	not modelled	20.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-methylmuconolactone methylisomerase; **PDBTitle:** crystal structure of 4-methylmuconolactone methylisomerase2 (h52a) in complex with 4-methylmuconolactone
39	c1qysA_	Alignment	not modelled	19.5	12	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
40	d1tvna1	Alignment	not modelled	19.3	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
41	d2fzia1	Alignment	not modelled	18.7	14	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
42	c3bguA_	Alignment	not modelled	18.0	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**ferredoxin-like protein of unknown function; **PDBTitle:** crystal structure of a dimeric ferredoxin-like protein of unknown2 function (tfu_0763) from thermobifida fusca yx at 1.50 a resolution
43	c3a24A_	Alignment	not modelled	17.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of bt1871 retaining glycosidase
44	c2jvfA_	Alignment	not modelled	16.9	16	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
45	d2ftsa2	Alignment	not modelled	16.3	33	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
46	d1iyjb2	Alignment	not modelled	15.8	24	**Fold:**BRCA2 tower domain **Superfamily:**BRCA2 tower domain **Family:**BRCA2 tower domain
47	c3h2zA_	Alignment	not modelled	14.8	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mannitol-1-phosphate 5-dehydrogenase; **PDBTitle:** the crystal structure of mannitol-1-phosphate dehydrogenase from2 shigella flexneri
48	d1mlia_	Alignment	not modelled	11.6	11	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Muconalactone isomerase, MLI
49	c3fmbA_	Alignment	not modelled	11.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dimeric protein of unknown function and ferredoxin-like **PDBTitle:** crystal structure of dimeric protein of unknown function and2 ferredoxin-like fold (yp_212648.1) from bacteroides fragilis nctc3 9343 at 1.85 a resolution
50	c3bsuF_	Alignment	not modelled	10.2	38	**PDB header:**hydrolase/rna/dna **Chain:** F: **PDB Molecule:**ribonuclease h1; **PDBTitle:** hybrid-binding domain of human rnase h1 in complex with 12-2 mer rna/dna
51	d1tp6a_	Alignment	not modelled	10.2	25	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PA1314-like

52	d1lj8a3	Alignment	not modelled	9.8	15	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Mannitol 2-dehydrogenase
53	c2khdA_	Alignment	not modelled	8.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein vc_a0919; **PDBTitle:** solution nmr structure of vc_a0919 from vibrio cholerae.2 northeast structural genomics consortium target vcr52
54	d2nn6g2	Alignment	not modelled	8.6	20	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
55	c2hq3A_	Alignment	not modelled	8.1	13	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nosl protein; **PDBTitle:** solution nmr structure of the apo-nosl protein from2 achromobacter cycloclastes
56	c2zq0B_	Alignment	not modelled	7.9	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-glucosidase (alpha-glucosidase susb); **PDBTitle:** crystal structure of susb complexed with acarbose
57	c2wb1J_	Alignment	not modelled	7.6	14	**PDB header:**transcription **Chain:** J: **PDB Molecule:**dna-directed rna polymerase rpo13 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
58	d1mjea2	Alignment	not modelled	7.4	16	**Fold:**BRCA2 tower domain **Superfamily:**BRCA2 tower domain **Family:**BRCA2 tower domain
59	c2waqQ_	Alignment	not modelled	7.3	14	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase rpo13 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
60	c2z0rA_	Alignment	not modelled	7.0	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0547; **PDBTitle:** crystal structure of hypothetical protein ttha0547
61	c2wb1Q_	Alignment	not modelled	6.9	15	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase rpo13 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
62	d1qhka_	Alignment	not modelled	6.6	27	**Fold:**MbtH/L9 domain-like **Superfamily:**L9 N-domain-like **Family:**N-terminal domain of RNase HI
63	d1s6la2	Alignment	not modelled	6.6	27	**Fold:**NosL/MerB-like **Superfamily:**NosL/MerB-like **Family:**MerB-like
64	c3hkzY_	Alignment	not modelled	6.5	9	**PDB header:**transferase **Chain:** Y: **PDB Molecule:**dna-directed rna polymerase subunit 13; **PDBTitle:** the x-ray crystal structure of rna polymerase from archaea
65	d1mwqa_	Alignment	not modelled	6.3	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YciI-like
66	c2gjhA_	Alignment	not modelled	6.1	14	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein; **PDBTitle:** nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7)
67	d2hpua1	Alignment	not modelled	5.9	13	**Fold:**NosL/MerB-like **Superfamily:**NosL/MerB-like **Family:**NosL-like