Phyre^2

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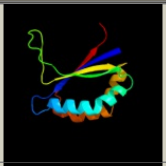
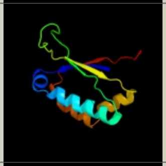
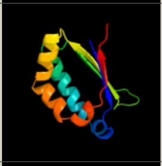
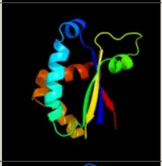
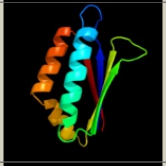
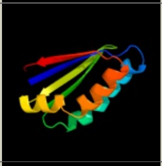
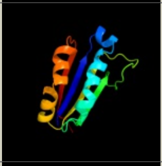
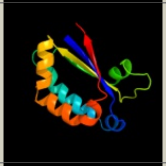
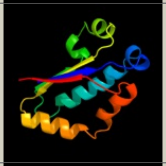
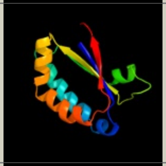
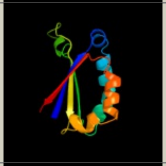
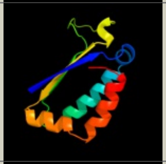
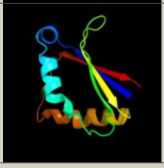
Description	P0ADU2
Date	Thu Jan 5 11:21:51 GMT 2012
Unique Job ID	03412844ec81b45e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tuva_	Alignment		100.0	100	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
2	c3mcsB_	Alignment		100.0	20	**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
3	c3f44A_	Alignment		99.9	18	**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
4	c3kkfA_	Alignment		99.9	18	**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
5	d1x7va_	Alignment		99.9	32	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
6	c3bm7A_	Alignment		99.9	21	**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
7	c3e8oB_	Alignment		99.9	21	**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
8	d2pd1a1	Alignment		99.9	21	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
9	c2bbeA_	Alignment		99.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein so0527; **PDBTitle:** crystal structure of protein so0527 from shewanella oneidensis
10	c2omoC_	Alignment		99.9	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**duf176; **PDBTitle:** putative antibiotic biosynthesis monooxygenase from nitrosomonas2 europaea
11	c2fb0A_	Alignment		99.9	22	**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

12	d2omoa1	Alignment		99.9	15	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
13	c3fgvB_	Alignment		99.9	20	**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
14	d1y0ha_	Alignment		99.9	26	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PA3566-like
15	d1q8ba_	Alignment		99.9	17	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Hypothetical protein YjcS
16	c2gffB_	Alignment		99.9	16	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**lsrg protein; **PDBTitle:** crystal structure of yersinia pestis lsrg
17	c3gz7B_	Alignment		99.9	22	**PDB header:**biosynthetic protein **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
18	d1iuja_	Alignment		99.8	18	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
19	c3kngA_	Alignment		99.8	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
20	c3hx9B_	Alignment		99.8	16	**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
21	d2zdpa1	Alignment	not modelled	99.3	15	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
22	c2rilA_	Alignment	not modelled	99.2	13	**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
23	c3fj2A_	Alignment	not modelled	98.9	13	**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
24	d1xbwa_	Alignment	not modelled	98.5	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
25	d1tz0a_	Alignment	not modelled	98.5	18	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
26	d1lq9a_	Alignment	not modelled	98.3	12	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Actinorhodin biosynthesis monooxygenase ActVa-Orf6
27	d1tr0a_	Alignment	not modelled	98.0	11	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Plant stress-induced protein
28	c3hfkB_	Alignment	not modelled	97.8	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-methylmuconolactone methylisomerase; **PDBTitle:** crystal structure of 4-methylmuconolactone methylisomerase2 (h52a) in complex with 4-methylmuconolactone

29	c3bdeA_	Alignment	not modelled	97.8	9	**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
30	c2qycA_	Alignment	not modelled	97.7	9	**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
31	c3bn7A_	Alignment	not modelled	97.7	7	**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
32	c3bguA_	Alignment	not modelled	97.3	12	**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
33	d1rjja_	Alignment	not modelled	97.3	10	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Plant stress-induced protein
34	d1q4ra_	Alignment	not modelled	97.3	9	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Plant stress-induced protein
35	c3fmbA_	Alignment	not modelled	96.9	8	**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
36	d1vqsa_	Alignment	not modelled	96.9	15	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**NIPSNAP
37	d1vqya1	Alignment	not modelled	96.9	14	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**NIPSNAP
38	c3bb5B_	Alignment	not modelled	96.6	8	**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
39	d1x8da1	Alignment	not modelled	96.3	22	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YiiL-like
40	c2qlwA_	Alignment	not modelled	94.8	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**rhau; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
41	c2qlxA_	Alignment	not modelled	94.8	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**l-rhamnose mutarotase; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
42	d2ftra1	Alignment	not modelled	93.3	15	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**EthD-like
43	d2go8a1	Alignment	not modelled	87.4	14	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**PG130-like
44	c2jdjB_	Alignment	not modelled	86.0	18	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**redy-like protein; **PDBTitle:** crystal structure of hapk from hahella chejuensis
45	d2cb2a1	Alignment	not modelled	85.2	21	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**SOR-like
46	d2ifxa1	Alignment	not modelled	67.4	12	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**MmlI-like
47	d2hiqa1	Alignment	not modelled	60.3	13	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Hypothetical protein YdhR
48	c1wd6B_	Alignment	not modelled	51.3	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydhr; **PDBTitle:** crystal structure of jw1657 from escherichia coli
49	c3bf4B_	Alignment	not modelled	45.8	12	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**ethyl tert-butyl ether degradation ethd protein; **PDBTitle:** crystal structure of an ethd-like protein (reut_b5694) from ralstonia2 eutropha jmp134 at 2.10 a resolution
50	d2cs4a1	Alignment	not modelled	43.1	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
51	c3dcaC_	Alignment	not modelled	31.2	16	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**rpa0582; **PDBTitle:** crystal structure of the rpa0582- protein of unknown2 function from rhodopseudomonas palustris- a structural3 genomics target
52	d2fiua1	Alignment	not modelled	31.1	16	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Atu0297-like
53	c2kl8A_	Alignment	not modelled	21.6	21	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**or15; **PDBTitle:** solution nmr structure of de novo designed ferredoxin-

						like2 fold protein, northeast structural genomics consortium3 target or15
54	c3bpjD_	Alignment	not modelled	13.6	8	**PDB header:**translation **Chain:** D: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit j; **PDBTitle:** crystal structure of human translation initiation factor 3, subunit 12 alpha
55	c2k9hA_	Alignment	not modelled	13.3	22	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**glycoprotein; **PDBTitle:** the hantavirus glycoprotein g1 tail contains a dual cchc-2 type classical zinc fingers
56	c3gn6B_	Alignment	not modelled	13.0	27	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ct0912, orfan protein with a ferredoxin-like domain repeat; **PDBTitle:** crystal structure of ct0912, orfan protein from chlorobium tepidum2 with a ferredoxin-like domain repeat (np_661805.1) from chlorobium3 tepidum tls at 1.80 a resolution
57	c2e1aD_	Alignment	not modelled	8.7	15	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
58	d1a8ya3	Alignment	not modelled	8.1	7	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Calsequestrin
59	d1zr9a1	Alignment	not modelled	7.9	12	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**HkH motif-containing C2H2 finger
60	c1zr9A_	Alignment	not modelled	7.9	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 593; **PDBTitle:** solution structure of a human c2h2-type zinc finger protein