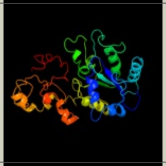
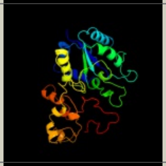
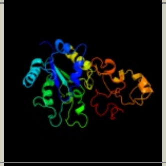
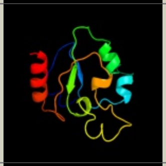
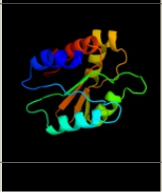
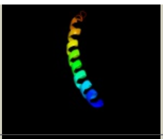
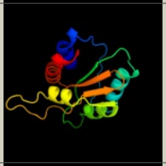
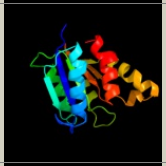
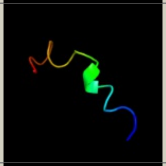
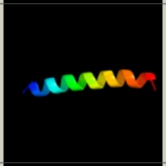
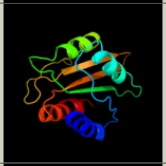
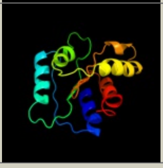
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P69741
Date	Thu Jan 5 12:11:49 GMT 2012
Unique Job ID	4e0f64c439fde4f3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rgwS_	Alignment		100.0	41	**PDB header:**oxidoreductase/oxidoreductase **Chain:** S: **PDB Molecule:**membrane-bound hydrogenase (nife) small subunit hoxk; **PDBTitle:** crystal structure at 1.5 a resolution of an h2-reduced, o2-tolerant2 hydrogenase from ralstonia eutropha unmasks a novel iron-sulfur3 cluster
2	c3myrE_	Alignment		100.0	48	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**hydrogenase (nife) small subunit hyda; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
3	d1wuis1	Alignment		100.0	45	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
4	c1h2aS_	Alignment		100.0	45	**PDB header:**oxidoreductase **Chain:** S: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
5	d1frfs_	Alignment		100.0	47	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
6	d1e3da_	Alignment		100.0	42	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
7	d1yq9a1	Alignment		100.0	45	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
8	d1cc1s_	Alignment		100.0	37	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nickel-iron hydrogenase, small subunit
9	c2wpnA_	Alignment		100.0	39	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic [nifese] hydrogenase, small subunit; **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
10	d2fug61	Alignment		99.6	22	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nq06-like
11	c2g4rB_	Alignment		90.5	15	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis mog protein; **PDBTitle:** anomalous substructure of moga

12	c2e76D_	Alignment		85.5	18	**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
13	d2nqra3	Alignment		84.5	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
14	c2is8A_	Alignment		84.2	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
15	d1y5ea1	Alignment		83.8	9	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
16	c2pq4B_	Alignment		82.8	60	**PDB header:**chaperone/oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic nitrate reductase precursor; **PDBTitle:** nmr solution structure of napd in complex with napa1-352 signal peptide
17	c2fynO_	Alignment		82.3	23	**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
18	d1xi8a3	Alignment		81.1	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
19	d2ftsa3	Alignment		80.1	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
20	c2pjkA_	Alignment		77.6	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor **PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
21	c1p84E_	Alignment	not modelled	76.7	3	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
22	d1jlja_	Alignment	not modelled	73.0	11	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
23	c2fu3A_	Alignment	not modelled	72.2	14	**PDB header:**biosynthetic protein/structural protein **Chain:** A: **PDB Molecule:**gephyrin; **PDBTitle:** crystal structure of gephyrin e-domain
24	c2nqqA_	Alignment	not modelled	71.2	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
25	d1ovma1	Alignment	not modelled	70.6	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
26	d1uuya_	Alignment	not modelled	65.5	11	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
27	d1uz5a3	Alignment	not modelled	64.2	21	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
28	c2fyuE_	Alignment	not modelled	62.4	14	**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
29	d1mkza_	Alignment	not modelled	60.1	9	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins

						Family: MogA-like
30	c3rfqC_	Alignment	not modelled	58.9	14	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
31	d2h1qa1	Alignment	not modelled	57.5	14	**Fold:**PLP-dependent transferase-like **Superfamily:**Dhaf3308-like **Family:**Dhaf3308-like
32	c2wcvI_	Alignment	not modelled	57.2	24	**PDB header:**isomerase **Chain:** I: **PDB Molecule:**l-fucose mutarotase; **PDBTitle:** crystal structure of bacterial fucu
33	d1pvda1	Alignment	not modelled	54.1	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
34	d2g2ca1	Alignment	not modelled	52.8	11	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
35	d1ik6a2	Alignment	not modelled	51.4	16	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
36	d2djia1	Alignment	not modelled	50.1	16	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
37	c3ilhA_	Alignment	not modelled	50.1	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** crystal structure of two component response regulator from cytophaga2 hutchinsonii
38	d1zpda1	Alignment	not modelled	49.5	20	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
39	d1ogda_	Alignment	not modelled	49.3	16	**Fold:**RbsD-like **Superfamily:**RbsD-like **Family:**RbsD-like
40	c3e7nB_	Alignment	not modelled	48.6	28	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**d-ribose high-affinity transport system; **PDBTitle:** crystal structure of d-ribose high-affinity transport system from2 salmonella typhimurium lt2
41	d2f7wa1	Alignment	not modelled	46.5	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
42	d1wu2a3	Alignment	not modelled	41.6	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
43	d2ob5a1	Alignment	not modelled	40.7	20	**Fold:**RbsD-like **Superfamily:**RbsD-like **Family:**RbsD-like
44	c3mvkA_	Alignment	not modelled	40.1	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein fucu; **PDBTitle:** the crystal structure of fucu from bifidobacterium longum to 1.65a
45	d1ozha1	Alignment	not modelled	36.6	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
46	c1ovmC_	Alignment	not modelled	36.4	18	**PDB header:**lyase **Chain:** C: **PDB Molecule:**indole-3-pyruvate decarboxylase; **PDBTitle:** crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
47	c2wcuB_	Alignment	not modelled	36.1	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**protein fucu homolog; **PDBTitle:** crystal structure of mammalian fucu
48	d1t9ba1	Alignment	not modelled	34.1	25	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
49	d2r25b1	Alignment	not modelled	34.0	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
50	d1qopa_	Alignment	not modelled	33.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
51	c3a52A_	Alignment	not modelled	30.9	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cold-active alkaline phosphatase; **PDBTitle:** crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
52	c1uz5A_	Alignment	not modelled	26.8	19	**PDB header:**molybdopterin biosynthesis **Chain:** A: **PDB Molecule:**402aa long hypothetical molybdopterin **PDBTitle:** the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
53	d1y6va1	Alignment	not modelled	26.6	21	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
54	d1k7ha_	Alignment	not modelled	25.3	17	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
55	c2x98A_	Alignment	not modelled	25.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
56	d1xhja_	Alignment	not modelled	24.4	19	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like

						Family: NifU C-terminal domain-like
57	c3e2dB_	Alignment	not modelled	23.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** the 1.4 a crystal structure of the large and cold-active2 vibrio sp. alkaline phosphatase
58	d2g39a1	Alignment	not modelled	23.5	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
59	c3uhjE_	Alignment	not modelled	22.2	17	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**probable glycerol dehydrogenase; **PDBTitle:** crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
60	c2jnvA_	Alignment	not modelled	21.6	24	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**nifu-like protein 1, chloroplast; **PDBTitle:** solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
61	c1ew2A_	Alignment	not modelled	19.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatase; **PDBTitle:** crystal structure of a human phosphatase
62	d1zeda1	Alignment	not modelled	19.9	21	**Fold:**Alkaline phosphatase-like **Superfamily:**Alkaline phosphatase-like **Family:**Alkaline phosphatase
63	c2iucB_	Alignment	not modelled	19.7	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** structure of alkaline phosphatase from the antarctic2 bacterium tab5
64	c2kveA_	Alignment	not modelled	19.6	56	**PDB header:**hormone **Chain:** A: **PDB Molecule:**mesencephalic astrocyte-derived neurotrophic factor; **PDBTitle:** c-terminal domain of mesencephalic astrocyte-derived neurotrophic2 factor (manf)
65	c2zwmA_	Alignment	not modelled	19.4	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein yycf; **PDBTitle:** crystal structure of yycf receiver domain from bacillus2 subtilis
66	c2oasA_	Alignment	not modelled	18.6	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coenzyme a transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coenzyme a transferase (atoa)2 in complex with coa from shewanella oneidensis, northeast structural3 genomics target sor119.
67	c3nhzA_	Alignment	not modelled	17.3	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**two component system transcriptional regulator mtra; **PDBTitle:** structure of n-terminal domain of mtra
68	d2g2xa1	Alignment	not modelled	16.9	15	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
69	c3iv7B_	Alignment	not modelled	16.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alcohol dehydrogenase iv; **PDBTitle:** crystal structure of iron-containing alcohol dehydrogenase2 (np_602249.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.07 a resolution
70	d2ez9a1	Alignment	not modelled	15.6	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
71	c2r8bA_	Alignment	not modelled	15.1	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2452; **PDBTitle:** the crystal structure of the protein atu2452 of unknown function from2 agrobacterium tumefaciens str. c58
72	d1kgsa2	Alignment	not modelled	14.5	20	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
73	d1ys7a2	Alignment	not modelled	14.4	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
74	d1xhfa1	Alignment	not modelled	14.2	21	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
75	d1ofcx1	Alignment	not modelled	14.0	31	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
76	c3fq6A_	Alignment	not modelled	12.7	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
77	c3eh7A_	Alignment	not modelled	12.4	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** the structure of a putative 4-hydroxybutyrate coa-transferase from2 porphyromonas gingivalis w83
78	c2zayA_	Alignment	not modelled	12.4	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
79	c2ju5A_	Alignment	not modelled	11.7	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin disulfide isomerase; **PDBTitle:** dsbh oxidoreductase
80	d1zh2a1	Alignment	not modelled	11.6	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
81	d1peya_	Alignment	not modelled	11.5	23	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
						PDB header:hydrolase

82	c2w0yB_	Alignment	not modelled	11.1	12	**Chain:** B: **PDB Molecule:**alkaline phosphatase; **PDBTitle:** h.salinarum alkaline phosphatase
83	c2nvvF_	Alignment	not modelled	11.0	18	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**acetyl-coa hydrolase/transferase family protein; **PDBTitle:** crystal structure of the putative acetyl-coa hydrolase/transferase2 pg1013 from porphyromonas gingivalis, northeast structural genomics3 target pgr16.
84	d1evsa_	Alignment	not modelled	10.9	33	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
85	c2qvgA_	Alignment	not modelled	10.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** the crystal structure of a two-component response regulator2 from legionella pneumophila
86	c2j48A_	Alignment	not modelled	10.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two-component sensor kinase; **PDBTitle:** nmr structure of the pseudo-receiver domain of the cika2 protein.
87	c2z1dA_	Alignment	not modelled	10.1	27	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hypd; **PDBTitle:** crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
88	d1z6na1	Alignment	not modelled	10.0	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
89	c3d3uA_	Alignment	not modelled	9.9	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase (abft-2) from2 porphyromonas gingivalis. northeast structural genomics consortium3 target pgr26
90	d1c4ea_	Alignment	not modelled	9.8	34	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Gurmarin-like **Family:**Gurmarin, a sweet taste-suppressing polypeptide
91	c3gk7A_	Alignment	not modelled	9.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum
92	d2a9pa1	Alignment	not modelled	9.7	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
93	d1uhua_	Alignment	not modelled	9.6	16	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**MMLV matrix protein-like
94	d1omba_	Alignment	not modelled	9.6	43	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
95	d2f6ma1	Alignment	not modelled	9.5	21	**Fold:**Long alpha-hairpin **Superfamily:**Endosomal sorting complex assembly domain **Family:**VPS23 C-terminal domain
96	d2ar1a1	Alignment	not modelled	9.4	12	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
97	d1xwdb1	Alignment	not modelled	9.0	25	**Fold:**Cystine-knot cytokines **Superfamily:**Cystine-knot cytokines **Family:**Gonadodropin/Follitropin
98	c2omkB_	Alignment	not modelled	9.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of the bacteroides thetaiotaomicron thiamin2 pyrophosphokinase
99	c3jteA_	Alignment	not modelled	9.0	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver domain2 protein from clostridium thermocellum