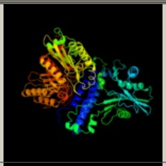
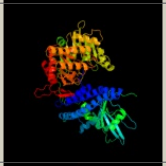
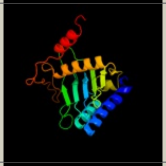
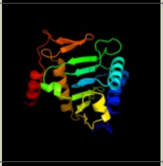
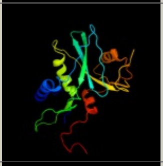
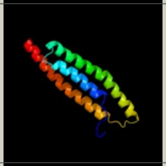
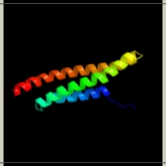
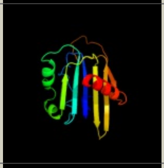
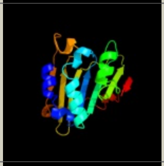
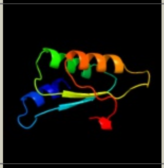
Phyre²

Email	l.a.kelley@imperial.ac.uk
Description	P0A7B1
Date	Thu Jan 5 11:05:15 GMT 2012
Unique Job ID	98789f2b846547f3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1xdoB_	Alignment		100.0	100	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of escherichia coli polyphosphate kinase
2	c2o8rA_	Alignment		100.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis
3	d1xdpa4	Alignment		100.0	100	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
4	d2o8ra4	Alignment		100.0	43	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
5	d2o8ra3	Alignment		100.0	39	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
6	d1xdpa2	Alignment		100.0	100	**Fold:**PHP14-like **Superfamily:**PHP14-like **Family:**PPK middle domain-like
7	d1xdpa3	Alignment		100.0	100	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
8	d2o8ra2	Alignment		100.0	30	**Fold:**PHP14-like **Superfamily:**PHP14-like **Family:**PPK middle domain-like
9	d1xdpa1	Alignment		100.0	100	**Fold:**Spectrin repeat-like **Superfamily:**PPK N-terminal domain-like **Family:**PPK N-terminal domain-like
10	d2o8ra1	Alignment		100.0	38	**Fold:**Spectrin repeat-like **Superfamily:**PPK N-terminal domain-like **Family:**PPK N-terminal domain-like
11	c3hsiC_	Alignment		99.9	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphatidylserine synthase; **PDBTitle:** crystal structure of phosphatidylserine synthase haemophilus2 influenzae rd kw20

12	c1v0sA_	Alignment		99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phospholipase d; **PDBTitle:** uninhibited form of phospholipase d from streptomyces sp.2 strain pmf
13	d1byra_	Alignment		99.4	15	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Nuclease
14	d1v0wa2	Alignment		99.1	17	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Phospholipase D
15	d1v0wa1	Alignment		99.0	14	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Phospholipase D
16	c2c1lA_	Alignment		92.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**restriction endonuclease; **PDBTitle:** structure of the bfii restriction endonuclease
17	c2yv2A_	Alignment		91.5	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa synthetase alpha chain; **PDBTitle:** crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1
18	d1vb5a_	Alignment		91.0	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
19	c3ecsD_	Alignment		89.5	25	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha
20	d2csua2	Alignment		87.9	15	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
21	d1eucb1	Alignment	not modelled	87.7	29	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
22	c2fpgA_	Alignment	not modelled	86.9	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa ligase [gdp-forming] alpha-chain, **PDBTitle:** crystal structure of pig gtp-specific succinyl-coa2 synthetase in complex with gdp
23	c3a11D_	Alignment	not modelled	86.2	28	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b, delta **PDBTitle:** crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
24	d1oi7a2	Alignment	not modelled	85.9	16	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
25	d1t9ka_	Alignment	not modelled	85.7	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
26	c3r2jC_	Alignment	not modelled	84.8	27	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha/beta-hydrolase-like protein; **PDBTitle:** crystal structure of pnc1 from l. infantum in complex with nicotinate
27	d2nu7a2	Alignment	not modelled	84.7	18	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
28	c2yboA_	Alignment	not modelled	84.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** the x-ray structure of the sam-dependent uroporphyrinogen2 iii methyltransferase nire from pseudomonas aeruginosa in3 complex with sah

29	d1zj8a2	Alignment	not modelled	84.6	20	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
30	d1t5oa_	Alignment	not modelled	84.5	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
31	d2a0ua1	Alignment	not modelled	82.9	8	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
32	c2nu8D_	Alignment	not modelled	82.8	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**succinyl-coa ligase [adp-forming] subunit alpha; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase
33	c3mwdB_	Alignment	not modelled	81.4	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp-citrate synthase; **PDBTitle:** truncated human atp-citrate lyase with citrate bound
34	c2yvkA_	Alignment	not modelled	81.3	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
35	c2csuB_	Alignment	not modelled	80.8	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**457aa long hypothetical protein; **PDBTitle:** crystal structure of ph0766 from pyrococcus horikoshii ot3
36	c1yd6A_	Alignment	not modelled	80.3	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uvrc; **PDBTitle:** crystal structure of the giy-yig n-terminal endonuclease2 domain of uvrc from bacillus caldotenax
37	c3gbcA_	Alignment	not modelled	78.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrazinamidase/nicotinamidas pnca; **PDBTitle:** determination of the crystal structure of the pyrazinamidase from2 m.tuberculosis : a structure-function analysis for prediction3 resistance to pyrazinamide
38	c1oi7A_	Alignment	not modelled	78.8	16	**PDB header:**synthetase **Chain:** A: **PDB Molecule:**succinyl-coa synthetase alpha chain; **PDBTitle:** the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
39	d1s4da_	Alignment	not modelled	78.8	17	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
40	c1yd2A_	Alignment	not modelled	77.8	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of the giy-yig n-terminal endonuclease domain of2 uvrc from thermotoga maritima: point mutant y19f bound to the3 catalytic divalent cation
41	d2nu7b1	Alignment	not modelled	75.6	30	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
42	c2b34C_	Alignment	not modelled	75.5	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mar1 ribonuclease; **PDBTitle:** structure of mar1 ribonuclease from caenorhabditis elegans
43	c3ndcB_	Alignment	not modelled	73.4	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**precorrin-4 c(11)-methyltransferase; **PDBTitle:** crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
44	c1nvmG_	Alignment	not modelled	73.3	9	**PDB header:**lyase/oxidoreductase **Chain:** G: **PDB Molecule:**4-hydroxy-2-oxovalerate aldolase; **PDBTitle:** crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
45	c1zj8B_	Alignment	not modelled	68.7	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable ferredoxin-dependent nitrite reductase nira; **PDBTitle:** structure of mycobacterium tuberculosis nira protein
46	c1eucB_	Alignment	not modelled	68.5	28	**PDB header:**ligase **Chain:** B: **PDB Molecule:**succinyl-coa synthetase, beta chain; **PDBTitle:** crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
47	d1jy1a1	Alignment	not modelled	67.4	13	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
48	d1qzqa1	Alignment	not modelled	67.1	13	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Tyrosyl-DNA phosphodiesterase TDP1
49	d1euca2	Alignment	not modelled	65.1	20	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
50	d2akja2	Alignment	not modelled	63.1	17	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
51	c1yzvA_	Alignment	not modelled	63.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** hypothetical protein from trypanosoma cruzi
52	d1vhna_	Alignment	not modelled	62.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
53	d1jpma1	Alignment	not modelled	60.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
54	d1nvma2	Alignment	not modelled	56.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**HMGL-like
						Fold:NAD(P)-binding Rossmann-fold domains

55	d2nu7a1	Alignment	not modelled	56.3	24	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
56	c2h0rD_	Alignment	not modelled	55.9	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nicotinamidase; **PDBTitle:** structure of the yeast nicotinamidase pnc1p
57	c2rqmA_	Alignment	not modelled	54.7	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**mesoderm development candidate 2; **PDBTitle:** nmr solution structure of mesoderm development (mesd) - open2 conformation
58	d1x9ga_	Alignment	not modelled	53.7	9	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
59	d1yaca_	Alignment	not modelled	52.2	13	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
60	c3d3kD_	Alignment	not modelled	51.1	12	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
61	d1ebda2	Alignment	not modelled	50.7	30	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
62	c3kwpA_	Alignment	not modelled	50.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**predicted methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase from lactobacillus2 brevis
63	d1im5a_	Alignment	not modelled	50.1	17	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
64	d1ve2a1	Alignment	not modelled	48.8	15	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
65	c2hxtA_	Alignment	not modelled	47.7	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**l-fuconate dehydratase; **PDBTitle:** crystal structure of l-fuconate dehydratase from xanthomonas2 campestris liganded with mg++ and d-erythronohydroxamate
66	c2pjuD_	Alignment	not modelled	47.5	19	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
67	c1rr2A_	Alignment	not modelled	46.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarboxylase 5s subunit; **PDBTitle:** propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
68	c2nu9E_	Alignment	not modelled	46.2	34	**PDB header:**ligase **Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
69	d1va0a1	Alignment	not modelled	45.8	17	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
70	c2q5cA_	Alignment	not modelled	45.7	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
71	d1dxla2	Alignment	not modelled	45.1	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
72	d1aoga2	Alignment	not modelled	44.4	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
73	c2wtaA_	Alignment	not modelled	44.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nicotinamidase; **PDBTitle:** acinetobacter baumanii nicotinamidase pyrazinamidease
74	d1lvla2	Alignment	not modelled	43.5	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
75	d1mk0a_	Alignment	not modelled	41.4	32	**Fold:**GIY-YIG endonuclease **Superfamily:**GIY-YIG endonuclease **Family:**GIY-YIG endonuclease
76	c3dmyA_	Alignment	not modelled	41.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein fdra; **PDBTitle:** crystal structure of a predicated acyl-coa synthetase from e.coli
77	d1v59a2	Alignment	not modelled	41.1	25	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
78	c1cbfA_	Alignment	not modelled	40.8	17	**PDB header:**methyltransferase **Chain:** A: **PDB Molecule:**cobalt-precorrin-4 transmethylase; **PDBTitle:** the x-ray structure of a cobalamin biosynthetic enzyme, cobalt2 precorrin-4 methyltransferase, cbif
79	d1cbfa_	Alignment	not modelled	40.8	17	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
80	c1nopB_	Alignment	not modelled	39.2	13	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**tyrosyl-dna phosphodiesterase 1; **PDBTitle:** crystal structure of human tyrosyl-dna phosphodiesterase2 (tdp1) in complex with vanadate, dna and a human3 topoisomerase i-derived peptide

81	c3eegB_	Alignment	not modelled	38.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
82	c2jlaD_	Alignment	not modelled	37.8	57	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene **PDBTitle:** crystal structure of e.coli mend, 2-succinyl-5-enolpyruvyl-2 6-hydroxy-3-cyclohexadiene-1-carboxylate synthase -semet3 protein
83	c1nu5A_	Alignment	not modelled	37.7	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**chloromuconate cycloisomerase; **PDBTitle:** crystal structure of pseudomonas sp. p51 chloromuconate lactonizing2 enzyme
84	d2pjua1	Alignment	not modelled	36.9	19	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
85	d1oi7a1	Alignment	not modelled	36.8	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
86	d1djqa2	Alignment	not modelled	35.7	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
87	c2v4jA_	Alignment	not modelled	35.5	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit **PDBTitle:** the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
88	c2akjA_	Alignment	not modelled	35.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nitrite reductase, chloroplast; **PDBTitle:** structure of spinach nitrite reductase
89	d1oy0a_	Alignment	not modelled	35.2	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
90	d3lada2	Alignment	not modelled	33.4	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
91	d2d59a1	Alignment	not modelled	31.7	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
92	d1ojta2	Alignment	not modelled	31.2	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
93	c2qvhB_	Alignment	not modelled	30.6	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**o-succinylbenzoate-coa synthase; **PDBTitle:** crystal structure of o-succinylbenzoate synthase complexed with o-2 succinyl benzoate (osb)
94	d1j2ra_	Alignment	not modelled	30.4	9	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
95	c3msyC_	Alignment	not modelled	30.3	11	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme2 from a marine actinobacterium
96	c3ivuB_	Alignment	not modelled	30.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
97	c2kglA_	Alignment	not modelled	29.9	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**mesoderm development candidate 2; **PDBTitle:** nmr solution structure of mesd
98	c3ot4F_	Alignment	not modelled	28.7	9	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative isochorismatase; **PDBTitle:** structure and catalytic mechanism of bordetella bronchiseptica nicf
99	d1pjqa2	Alignment	not modelled	28.5	16	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
100	c2i9sA_	Alignment	not modelled	27.5	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**mesoderm development candidate 2; **PDBTitle:** the solution structure of the core of mesoderm development2 (mesd).
101	c1sy7B_	Alignment	not modelled	27.1	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase 1; **PDBTitle:** crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
102	c2dc1A_	Alignment	not modelled	27.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-aspartate dehydrogenase; **PDBTitle:** crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
103	d1lpfa2	Alignment	not modelled	26.2	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
104	d1d7ya2	Alignment	not modelled	25.8	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
105	c1vixA_	Alignment	not modelled	25.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** crystal structure of a putative peptidase t
						Fold:FAD/NAD(P)-binding domain

106	d3grsa2	Alignment	not modelled	25.2	17	**Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
107	d1r6wa1	Alignment	not modelled	25.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
108	c2yv1A_	Alignment	not modelled	25.1	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa ligase [adp-forming] subunit alpha; **PDBTitle:** crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661
109	d1zpda2	Alignment	not modelled	24.6	35	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
110	d1t9ba2	Alignment	not modelled	24.4	24	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
111	c3bezC_	Alignment	not modelled	24.4	27	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease 4; **PDBTitle:** crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
112	c1pjtB_	Alignment	not modelled	23.9	16	**PDB header:**transferase/oxidoreductase/lyase **Chain:** B: **PDB Molecule:**siroheme synthase; **PDBTitle:** the structure of the ser128ala point-mutant variant of cysg,2 the multifunctional3 methyltransferase/dehydrogenase/ferrochelatase for4 siroheme synthesis
113	c2frxD_	Alignment	not modelled	23.8	5	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein yebu; **PDBTitle:** crystal structure of yebu, a m5c rna methyltransferase from e.coli
114	c3ewbX_	Alignment	not modelled	23.3	23	**PDB header:**transferase **Chain:** X: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
115	d1onfa2	Alignment	not modelled	23.2	9	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
116	d1xhca2	Alignment	not modelled	22.6	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
117	d1tuea_	Alignment	not modelled	22.5	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
118	d1tzza1	Alignment	not modelled	22.5	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
119	d2ax3a2	Alignment	not modelled	22.5	21	**Fold:**YjeF N-terminal domain-like **Superfamily:**YjeF N-terminal domain-like **Family:**YjeF N-terminal domain-like
120	d3c7bb2	Alignment	not modelled	22.3	24	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like