

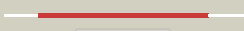


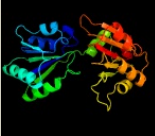


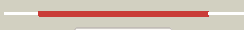















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2071c_cobM_2328230_2328985
Date	Mon Aug 5 13:25:18 BST 2019
Unique Job ID	4e59b82e2d102744

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1pjtB_	 Alignment		100.0	28	PDB header: transferase/oxidoreductase/lyase Chain: B: PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatase for3 siroheme synthesis
2	c1cbfA_	 Alignment		100.0	40	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
3	d1cbfa_	 Alignment		100.0	40	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
4	d1s4da_	 Alignment		100.0	29	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
5	c2yboA_	 Alignment		100.0	30	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
6	c3ndcB_	 Alignment		100.0	55	PDB header: transferase Chain: B: PDB Molecule: precorrin-4 c(11)-methyltransferase; PDBTitle: crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
7	c4e16A_	 Alignment		100.0	36	PDB header: transferase Chain: A: PDB Molecule: precorrin-4 c(11)-methyltransferase; PDBTitle: precorrin-4 c(11)-methyltransferase from clostridium difficile
8	d1pjqa2	 Alignment		100.0	28	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
9	c3kwpA_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: predicted methyltransferase; PDBTitle: crystal structure of putative methyltransferase from lactobacillus2 brevis
10	d1ve2a1	 Alignment		100.0	30	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
11	d1va0a1	 Alignment		100.0	28	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase

12	c5hw4C_	Alignment		100.0	16	PDB header: transferase Chain: C: PDB Molecule: ribosomal rna small subunit methyltransferase i; PDBTitle: crystal structure of escherichia coli 16s rrna methyltransferase rsmi2 in complex with adomet
13	c2zvba_	Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: precorrin-3 c17-methyltransferase; PDBTitle: crystal structure of tt0207 from thermus thermophilus hb8
14	d2deka1	Alignment		100.0	20	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
15	d1vhva_	Alignment		100.0	15	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
16	d1wdea_	Alignment		100.0	18	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
17	c3nutC_	Alignment		100.0	24	PDB header: transferase Chain: C: PDB Molecule: precorrin-3 methylase; PDBTitle: crystal structure of the methyltransferase cobj
18	d1wyza1	Alignment		100.0	10	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
19	c3i4tA_	Alignment		100.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: diphthine synthase; PDBTitle: crystal structure of putative diphthine synthase from entamoeba2 histolytica
20	c2e0kA_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: precorrin-2 c20-methyltransferase; PDBTitle: crystal structure of cbil, a methyltransferase involved in anaerobic2 vitamin b12 biosynthesis
21	c2qbuA_	Alignment	not modelled	100.0	27	PDB header: transferase Chain: A: PDB Molecule: precorrin-2 methyltransferase; PDBTitle: crystal structure of methanothermobacter thermautotrophicus cbil
22	c2nnpA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: putative cobalamin synthesis related protein; PDBTitle: crystal structure of putative cobalamin synthesis related protein2 (cobf) from corynebacterium diphtheriae
23	c5n0sA_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: A: PDB Molecule: peptide n-methyltransferase; PDBTitle: crystal structure of opha-deltac6 mutant y98a in complex with sam
24	c3nd1B_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: B: PDB Molecule: precorrin-6a synthase/cobf protein; PDBTitle: crystal structure of precorrin-6a synthase from rhodobacter capsulatus
25	c2bb3B_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: cobalamin biosynthesis precorrin-6y methylase (cbie); PDBTitle: crystal structure of cobalamin biosynthesis precorrin-6y methylase2 (cbie) from archaeoglobus fulgidus
26	d2bb3a1	Alignment	not modelled	100.0	18	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
27	c3hh1D_	Alignment	not modelled	99.9	21	PDB header: transferase Chain: D: PDB Molecule: tetrapyrrole methylase family protein; PDBTitle: the structure of a tetrapyrrole methylase family protein domain from2 chlorobium tepidum t1s
28	c3fq6A_	Alignment	not modelled	99.5	19	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi

29	d2o8ra3	Alignment	not modelled	88.4	14	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
30	c2o8rA	Alignment	not modelled	82.6	14	PDB header: transferase Chain: A: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of polyphosphate kinase from porphyromonas2 gingivalis
31	c5v1tA	Alignment	not modelled	74.6	18	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis suib bound to precursor2 peptide suia
32	d2p1ra1	Alignment	not modelled	68.4	13	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
33	c5th5C	Alignment	not modelled	67.5	24	PDB header: lyase Chain: C: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from bacillus subtilis with 6-carboxypterin-2 5'-deoxyadenosyl ester bound
34	c6efnA	Alignment	not modelled	64.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: sporulation killing factor maturation protein skfb; PDBTitle: structure of a ripp maturase, skfb
35	d1j5pa4	Alignment	not modelled	64.1	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
36	c5er0D	Alignment	not modelled	63.1	19	PDB header: oxidoreductase Chain: D: PDB Molecule: nadh oxidase; PDBTitle: water-forming nadh oxidase from lactobacillus brevis (lbnx)
37	c4njka	Alignment	not modelled	59.7	19	PDB header: lyase Chain: A: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from burkholderia multivorans in complex2 with adomet, 7-carboxy-7-deazaguanine, and mg2+
38	d1p3y1	Alignment	not modelled	59.2	9	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
39	d7reqa2	Alignment	not modelled	58.8	10	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
40	c3mcuF	Alignment	not modelled	58.7	19	PDB header: oxidoreductase Chain: F: PDB Molecule: dipicolinate synthase, b chain; PDBTitle: crystal structure of the dipicolinate synthase chain b from bacillus2 cereus. northeast structural genomics consortium target bcr215.
41	c5tueB	Alignment	not modelled	58.2	19	PDB header: oxidoreductase Chain: B: PDB Molecule: tetracycline destructase tet(50); PDBTitle: crystal structure of tetracycline destructase tet(50)
42	c3bioB	Alignment	not modelled	58.0	11	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
43	c2dc1A	Alignment	not modelled	57.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
44	d2jgra1	Alignment	not modelled	56.6	13	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
45	c3lqkA	Alignment	not modelled	55.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit b; PDBTitle: crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
46	c2cduB	Alignment	not modelled	54.1	21	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh oxidase; PDBTitle: the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
47	c3ic5A	Alignment	not modelled	52.7	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
48	c1xdoB	Alignment	not modelled	52.5	14	PDB header: transferase Chain: B: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of escherichia coli polyphosphate kinase
49	c5dboA	Alignment	not modelled	51.4	15	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of the tetrameric eif2b-beta2-delta2 complex from c.2 thermophilum
50	c6p2iA	Alignment	not modelled	51.3	7	PDB header: oxidoreductase, biosynthetic protein Chain: A: PDB Molecule: glycerate dehydrogenase; PDBTitle: acyclic imino acid reductase (bsp5) in complex with nadph and d-arg
51	c4bucA	Alignment	not modelled	51.1	17	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanine--d-glutamate ligase; PDBTitle: crystal structure of murd ligase from thermotoga maritima in apo form
52	c6cluC	Alignment	not modelled	51.0	15	PDB header: antimicrobial protein Chain: C: PDB Molecule: dihydropteroate synthase; PDBTitle: staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
53	c3oc4A	Alignment	not modelled	50.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, pyridine nucleotide-disulfide family; PDBTitle: crystal structure of a pyridine nucleotide-disulfide family2 oxidoreductase from the enterococcus faecalis v583

54	dlyxya1	Alignment	not modelled	49.2	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
55	c3wb9A	Alignment	not modelled	48.5	8	PDB header: oxidoreductase Chain: A; PDB Molecule: diaminopimelate dehydrogenase; PDBTitle: crystal structures of meso-diaminopimelate dehydrogenase from <i>Symbiobacterium thermophilum</i>
56	c6a4tB	Alignment	not modelled	48.3	13	PDB header: hydrolase Chain: B; PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from <i>Deinococcus radiodurans</i> r1
57	c1nhqA	Alignment	not modelled	47.8	19	PDB header: oxidoreductase (h2o2(a)) Chain: A; PDB Molecule: nadh peroxidase; PDBTitle: crystallographic analyses of nadh peroxidase cys42ala and cys42ser2 mutants: active site structure, mechanistic implications, and an unusual environment of arg303
58	c5tchG	Alignment	not modelled	46.9	21	PDB header: lyase Chain: G; PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from <i>M. tuberculosis</i> -2 ligand-free form, trpa-g66v mutant
59	d1lssa	Alignment	not modelled	42.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
60	d2jfga2	Alignment	not modelled	42.7	27	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
61	c2a5hC	Alignment	not modelled	40.6	25	PDB header: isomerase Chain: C; PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from <i>Clostridium subterminale</i> sb4, with Michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
62	d1xdpa3	Alignment	not modelled	40.3	16	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
63	c2z2vA	Alignment	not modelled	40.2	15	PDB header: oxidoreductase Chain: A; PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from <i>Hyperthermophilic archaeon Pyrococcus horikoshii</i>
64	c4txkA	Alignment	not modelled	40.0	23	PDB header: oxidoreductase Chain: A; PDB Molecule: protein-methionine sulfoxide oxidase mical1; PDBTitle: construct of mical-1 containing the monooxygenase and calponin2 homology domains
65	c2ppvA	Alignment	not modelled	39.4	6	PDB header: transferase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein belonging to the upf0052 (se_0549) from <i>Staphylococcus epidermidis</i> ATCC 12228 at 2.00 Å resolution
66	c5jg7A	Alignment	not modelled	38.5	20	PDB header: metal transport Chain: A; PDB Molecule: fur regulated salmonella iron transporter; PDBTitle: crystal structure of putative periplasmic binding protein from <i>Salmonella typhimurium</i> lt2
67	c4u0pB	Alignment	not modelled	38.5	12	PDB header: transferase Chain: B; PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
68	c2yx0A	Alignment	not modelled	35.8	19	PDB header: metal binding protein Chain: A; PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
69	c3kpgA	Alignment	not modelled	35.8	26	PDB header: oxidoreductase Chain: A; PDB Molecule: sulfide-quinone reductase, putative; PDBTitle: crystal structure of sulfide:quinone oxidoreductase from <i>Acidithiobacillus ferrooxidans</i> in complex with decylubiquinone
70	c1u1iC	Alignment	not modelled	35.7	32	PDB header: isomerase Chain: C; PDB Molecule: myo-inositol-1-phosphate synthase; PDBTitle: myo-inositol phosphate synthase mips from <i>A. fulgidus</i>
71	c6c8vA	Alignment	not modelled	35.6	16	PDB header: oxidoreductase Chain: A; PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from <i>Methylobacterium extorquens</i>
72	c3lk7A	Alignment	not modelled	35.2	15	PDB header: ligase Chain: A; PDB Molecule: udp-n-acetylmuramoylalanine--d-glutamate ligase; PDBTitle: the crystal structure of udp-n-acetylmuramoylalanine-d-glutamate2 (murD) ligase from <i>Streptococcus agalactiae</i> to 1.5 Å
73	d1u1ia1	Alignment	not modelled	34.9	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
74	c1j5pA	Alignment	not modelled	34.8	15	PDB header: oxidoreductase Chain: A; PDB Molecule: aspartate dehydrogenase; PDBTitle: crystal structure of aspartate dehydrogenase (tm1643) from <i>Thermotoga2 maritima</i> at 1.9 Å resolution
75	c5b04G	Alignment	not modelled	34.5	17	PDB header: translation Chain: G; PDB Molecule: probable translation initiation factor eif-2b subunit PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from <i>Schizosaccharomyces pombe</i>
76	d2jfga1	Alignment	not modelled	33.3	21	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
77	d2q4qa1	Alignment	not modelled	33.2	11	Fold: MTH938-like Superfamily: MTH938-like Family: MTH938-like
78	c2z2uA	Alignment	not modelled	33.1	27	PDB header: metal binding protein Chain: A; PDB Molecule: upf0026 protein mj0257;

						PDBTitle: crystal structure of archaeal tyw1
79	d1umdb2	Alignment	not modelled	32.7	20	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
80	c3kd9B	Alignment	not modelled	32.6	24	PDB header: oxidoreductase Chain: B: PDB Molecule: coenzyme a disulfide reductase; PDBTitle: crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii
81	d2ffea1	Alignment	not modelled	32.3	14	Fold: CofD-like Superfamily: CofD-like Family: CofD-like
82	d2ozlb2	Alignment	not modelled	31.7	17	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
83	c5j7xA	Alignment	not modelled	31.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylaniline monooxygenase, putative; PDBTitle: baeyer-villiger monooxygenase bvmoaf1838 from aspergillus flavus
84	d1k0ia1	Alignment	not modelled	31.6	26	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
85	d1f0ka	Alignment	not modelled	30.8	12	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Peptidoglycan biosynthesis glycosyltransferase MurG
86	c6b4cH	Alignment	not modelled	30.4	20	PDB header: antiviral protein Chain: H: PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens
87	c2bcpA	Alignment	not modelled	30.3	9	PDB header: oxidoreductase Chain: A: PDB Molecule: nahd oxidase; PDBTitle: structural analysis of streptococcus pyogenes nahd oxidase: c44s nox2 with azide
88	d1iuKa	Alignment	not modelled	29.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
89	d2voua1	Alignment	not modelled	28.9	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
90	c5z2fA	Alignment	not modelled	28.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: nadph/pda bound dihydrodipicolinate reductase from paenisporosarcina2 sp. tg-14
91	c2bryA	Alignment	not modelled	28.7	27	PDB header: transport Chain: A: PDB Molecule: nedd9 interacting protein with calponin homology PDBTitle: crystal structure of the native monooxygenase domain of2 mical at 1.45 a resolution
92	c3rhtB	Alignment	not modelled	27.4	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: (gatase1)-like protein; PDBTitle: crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
93	c1gqqA	Alignment	not modelled	27.1	11	PDB header: cell wall biosynthesis Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: murc - crystal structure of the apo-enzyme from haemophilus influenzae
94	c4s1vD	Alignment	not modelled	26.9	11	PDB header: oxidoreductase Chain: D: PDB Molecule: d-3-phosphoglycerate dehydrogenase-related protein; PDBTitle: crystal structure of phosphoglycerate oxidoreductase from vibrio2 cholerae o395
95	c3uclA	Alignment	not modelled	26.4	23	PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexanone monooxygenase; PDBTitle: cyclohexanone-bound crystal structure of cyclohexanone monooxygenase2 in the rotated conformation
96	c3cgbB	Alignment	not modelled	26.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridine nucleotide-disulfide oxidoreductase, class i; PDBTitle: pyridine nucleotide complexes with bacillus anthracis coenzyme a-2 disulfide reductase: a structural analysis of dual nad(p)h3 specificity
97	c5b3uB	Alignment	not modelled	26.0	15	PDB header: transferase Chain: B: PDB Molecule: biliverdin reductase; PDBTitle: crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803
98	c3zidB	Alignment	not modelled	25.9	11	PDB header: gtp-binding protein Chain: B: PDB Molecule: tubulin/ftsZ, gtpase; PDBTitle: cetZ from methanoseta thermophila strain dsm 6194
99	c6bz5B	Alignment	not modelled	25.8	12	PDB header: oxidoreductase Chain: B: PDB Molecule: salicylate hydroxylase; PDBTitle: structure and mechanism of salicylate hydroxylase from pseudomonas2 putida g7
100	c2gr2A	Alignment	not modelled	25.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase, bpha4 (oxidized form)
101	c5do7B	Alignment	not modelled	25.4	17	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 8; PDBTitle: crystal structure of the human sterol transporter abcg5/abcg8
102	c2p0yA	Alignment	not modelled	25.3	0	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein lp_0780; PDBTitle: crystal structure of q88yi3_lacpl from lactobacillus plantarum.2 northeast structural genomics consortium target lpr6
103	d2naca2	Alignment	not modelled	25.0	9	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like

						Family: Formate/glycerate dehydrogenases, substrate-binding domain
104	c5b04B_	Alignment	not modelled	24.9	18	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
105	c4zeoH_	Alignment	not modelled	24.1	15	PDB header: translation Chain: H: PDB Molecule: translation initiation factor eif-2b-like protein; PDBTitle: crystal structure of eif2b delta from chaetomium thermophilum
106	c1vqwB_	Alignment	not modelled	23.9	37	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein with similarity to flavin-containing PDBTitle: crystal structure of a protein with similarity to flavin-2 containing monooxygenases and to mammalian dimethylalanine3 monooxygenases
107	c3h8lA_	Alignment	not modelled	23.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh oxidase; PDBTitle: the first x-ray structure of a sulfide:quinone2 oxidoreductase: insights into sulfide oxidation mechanism
108	c2bonB_	Alignment	not modelled	23.4	14	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
109	c1ir6A_	Alignment	not modelled	23.0	22	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease recj; PDBTitle: crystal structure of exonuclease recj bound to manganese
110	d1ir6a_	Alignment	not modelled	23.0	22	Fold: DHH phosphoesterases Superfamily: DHH phosphoesterases Family: Exonuclease RecJ
111	d1w85b2	Alignment	not modelled	22.5	26	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
112	c4gmfD_	Alignment	not modelled	22.4	15	PDB header: oxidoreductase Chain: D: PDB Molecule: yersiniabactin biosynthetic protein ybtu; PDBTitle: apo structure of a thiazolanyl imine reductase from yersinia2 enterocolitica (irp3)
113	d2bona1	Alignment	not modelled	22.3	14	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
114	d1gpua3	Alignment	not modelled	22.1	23	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Transketolase C-terminal domain-like
115	d2gv8a1	Alignment	not modelled	22.0	33	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
116	d1ydwa1	Alignment	not modelled	21.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
117	d1a9xa4	Alignment	not modelled	21.8	19	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
118	c3ezyB_	Alignment	not modelled	21.5	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of probable dehydrogenase tm_0414 from thermotoga2 maritima
119	c5jciA_	Alignment	not modelled	21.2	9	PDB header: hydrolase Chain: A: PDB Molecule: os09g0567300 protein; PDBTitle: structure and catalytic mechanism of monodehydroascorbate reductase,2 mdhar, from oryza sativa l. japonica
120	c2axqA_	Alignment	not modelled	21.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae