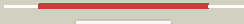



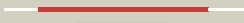



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3054c_(-)_3415432_3415986
Date	Thu Aug 8 16:20:23 BST 2019
Unique Job ID	790afa8d637e8427

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3svlB_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: protein yief; PDBTitle: structural basis of the improvement of chrr - a multi-purpose enzyme
2	c3s2yB_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: B: PDB Molecule: chromate reductase; PDBTitle: crystal structure of a chromate/uranium reductase from2 gluconacetobacter hansenii
3	c3u7rB_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent fmn reductase; PDBTitle: ferb - flavoenzyme nad(p)h:(acceptor) oxidoreductase (ferb) from2 paracoccus denitrificans
4	c2q62A_	 Alignment		100.0	22	PDB header: flavoprotein Chain: A: PDB Molecule: arsh; PDBTitle: crystal structure of arsh from sinorhizobium meliloti
5	c4c76A_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn reductase (nadph); PDBTitle: crystal structure of the fmn-reductase msue from pseudomonas putida2 kt2440.
6	c2fzvC_	 Alignment		100.0	23	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: putative arsenical resistance protein; PDBTitle: crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
7	d1rtta_	 Alignment		100.0	31	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
8	c4ptzC_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: C: PDB Molecule: fmn reductase ssue; PDBTitle: crystal structure of the escherichia coli alkanesulfonate fmn2 reductase ssue in fmn-bound form
9	d2fzva1	 Alignment		100.0	24	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
10	d1nni1_	 Alignment		100.0	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
11	d1t0ia_	 Alignment		100.0	21	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase

12	c3fvwA_	Alignment		100.0	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative nad(p)h-dependent fmn reductase; PDBTitle: crystal structure of the q8dwd8_strmu protein from streptococcus2 mutans. northeast structural genomics consortium target smr99.
13	d1sqsa_	Alignment		100.0	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein SP1951
14	c3k1yE_	Alignment		100.0	19	PDB header: oxidoreductase Chain: E: PDB Molecule: oxidoreductase; PDBTitle: x-ray structure of oxidoreductase from corynebacterium diphtheriae.2 orthorombic crystal form, northeast structural genomics consortium3 target cdr100d
15	c3lcmB_	Alignment		100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of smu.1420 from streptococcus mutans ua159
16	c5mjiA_	Alignment		100.0	17	PDB header: flavoprotein Chain: A: PDB Molecule: bramp domain protein; PDBTitle: crystal structure of rosb with bound intermediate ohc-rp (8-demethyl-2-8-formylriboflavin-5'-phosphate)
17	c2vzha_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-dependent fmn reductase; PDBTitle: structures of nadh:fmn oxidoreductase (emob)-fmn complex
18	c4r81C_	Alignment		100.0	16	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh dehydrogenase; PDBTitle: nad(p)h:quinone oxidoreductase from methanothermobacter marburgensis
19	c4c0xA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn-dependent nadh-azoreductase 1; PDBTitle: the crystal structure of ppazor in complex with anthraquinone-2-2 sulfonate
20	c2hpaA_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn-dependent nadh-azoreductase; PDBTitle: crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
21	c3w7aD_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: D: PDB Molecule: fmn-dependent nadh-azoreductase; PDBTitle: crystal structure of azoreductase azrc fin complex with sulfone-2 modified azo dye acid red 88
22	d2qwa1	Alignment	not modelled	100.0	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
23	c6dxdD_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: fmn-dependent nadh-azoreductase; PDBTitle: the crystal structure of an fmn-dependent nadh-azoreductase from2 klebsiella pneumoniae
24	c3p0rA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: azoreductase; PDBTitle: crystal structure of azoreductase from bacillus anthracis str. Sterne
25	d1t5ba_	Alignment	not modelled	100.0	21	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
26	d2z98a1	Alignment	not modelled	100.0	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
27	c3u7iB_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: fmn-dependent nadh-azoreductase 1; PDBTitle: the crystal structure of fmn-dependent nadh-azoreductase 1 (gbaa0966)2 from bacillus anthracis str. ames ancestor
28	d1dxqa_	Alignment	not modelled	100.0	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase

29	c4gi5B_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: quinone reductase; PDBTitle: crystal structure of a putative quinone reductase from klebsiella2 pneumoniae (target psi-013613)
30	d1qrda_	Alignment	not modelled	100.0	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
31	d1d4aa_	Alignment	not modelled	100.0	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
32	d1ydga_	Alignment	not modelled	100.0	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
33	c2v9cA_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn-dependent nadh-azoreductase 1; PDBTitle: x-ray crystallographic structure of a pseudomonas2 aeruginosa azoreductase in complex with methyl red.
34	c5lvaA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nad(p)h-fmn oxidoreductase; PDBTitle: crystal structure of thermophilic tryptophan halogenase (th-hal)2 enzyme from streptomycin violaceusniger.
35	d1rlia_	Alignment	not modelled	100.0	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein YwqN
36	c2zkiH_	Alignment	not modelled	99.9	16	PDB header: transcription Chain: H: PDB Molecule: 199aa long hypothetical trp repressor binding PDBTitle: crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
37	c5mp4C_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: C: PDB Molecule: protoplast secreted protein 2; PDBTitle: the structure of pst2p from saccharomyces cerevisiae
38	c3b6iB_	Alignment	not modelled	99.9	16	PDB header: flavoprotein Chain: B: PDB Molecule: flavoprotein wrba; PDBTitle: wrba from escherichia coli, native structure
39	c3f2vA_	Alignment	not modelled	99.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: general stress protein 14; PDBTitle: crystal structure of the general stress protein 14 (tde0354) in2 complex with fmn from treponema denticola, northeast structural3 genomics consortium target tdr58.
40	c4lafB_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p)h dehydrogenase (quinone); PDBTitle: crystal structure of pnpb complex with fmn
41	c3rpeA_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: modulator of drug activity b; PDBTitle: 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92.
42	c3eywA_	Alignment	not modelled	99.9	24	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
43	c3ha2B_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-quinone reductase; PDBTitle: crystal structure of protein (nadph-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a
44	c2amjD_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: D: PDB Molecule: modulator of drug activity b; PDBTitle: crystal structure of modulator of drug activity b from escherichia2 coli o157:h7
45	d2a5la1	Alignment	not modelled	99.9	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
46	c5f4bB_	Alignment	not modelled	99.9	22	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p)h dehydrogenase (quinone); PDBTitle: structure of b. abortus wrba-related protein a (wrpa)
47	c3d7nA_	Alignment	not modelled	99.9	18	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin, wrba-like protein; PDBTitle: the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens
48	d2arka1	Alignment	not modelled	99.8	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
49	d1e5da1	Alignment	not modelled	99.8	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
50	d1ycga1	Alignment	not modelled	99.8	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
51	c1ychD_	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: D: PDB Molecule: nitric oxide reductase; PDBTitle: x-ray crystal structures of moorella thermoacetica fpra. novel diiron2 site structure and mechanistic insights into a scavenging nitric3 oxide reductase
52	c6h0cA_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: flv1 flavodiiron core from synechocystis sp. pcc6803
53	c2ohiB_	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: type a flavoprotein fpra; PDBTitle: crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
						PDB header: electron transport Chain: A: PDB Molecule: anaerobic nitric oxide reductase

54	c4d02A_	Alignment	not modelled	99.7	16	flavorubredoxin; PDBTitle: the crystallographic structure of flavorubredoxin from escherichia2 coli
55	d1vmea1	Alignment	not modelled	99.7	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
56	c5widB_	Alignment	not modelled	99.7	13	PDB header: flavoprotein Chain: B: PDB Molecule: flavodoxin; PDBTitle: structure of a flavodoxin from the domain archaea
57	c2q9uB_	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
58	c1e5dA_	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin\oxygen oxidoreductase; PDBTitle: rubredoxin oxygen:oxidoreductase (roo) from anaerobe desulfovibrio2 gigas
59	c4iciA_	Alignment	not modelled	99.6	17	PDB header: flavoprotein Chain: A: PDB Molecule: putative flavoprotein; PDBTitle: crystal structure of a putative flavoprotein (bacegg_01620) from2 bacteroides eggerthii dsm 20697 at 1.40 a resolution
60	c4j8pA_	Alignment	not modelled	99.6	17	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin; PDBTitle: crystal structure of a putative flavoprotein (bacuni_04544) from2 bacteroides uniformis atcc 8492 at 1.50 a resolution
61	c3edoA_	Alignment	not modelled	99.5	14	PDB header: flavoprotein Chain: A: PDB Molecule: putative trp repressor binding protein; PDBTitle: crystal structure of flavoprotein in complex with fmn (yp_193882.1)2 from lactobacillus acidophilus ncfm at 1.20 a resolution
62	c3fniA_	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
63	c3k1bA_	Alignment	not modelled	99.5	17	PDB header: flavoprotein Chain: A: PDB Molecule: putative flavoprotein; PDBTitle: crystal structure of putative flavoprotein in complex with fmn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
64	c3hlyA_	Alignment	not modelled	99.4	14	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from synechococcus sp2 q5mzp6_synp6 protein. northeast structural genomics consortium target3 snr135d.
65	c1vmeB_	Alignment	not modelled	99.4	14	PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
66	c6gaqB_	Alignment	not modelled	99.4	18	PDB header: electron transport Chain: B: PDB Molecule: flavodoxin; PDBTitle: crystal structure of oxidised flavodoxin 2 from bacillus cereus
67	c6fsiA_	Alignment	not modelled	99.3	15	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: crystal structure of semiquinone flavodoxin 1 from bacillus cereus2 (1.32 a resolution)
68	c5vegC_	Alignment	not modelled	99.3	16	PDB header: electron transport Chain: C: PDB Molecule: flavodoxin; PDBTitle: structure of a short-chain flavodoxin associated with a non-canonical2 pdu bacterial microcompartment
69	d2fz5a1	Alignment	not modelled	99.2	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
70	c5ljiA_	Alignment	not modelled	99.2	21	PDB header: oxidoreductase Chain: A: PDB Molecule: flavodoxin; PDBTitle: streptococcus pneumonia tigr4 flavodoxin: structural and biophysical2 characterization of a novel drug target
71	d5nula_	Alignment	not modelled	99.1	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
72	c2mtbA_	Alignment	not modelled	99.1	17	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin-2; PDBTitle: solution structure of apo_fldb
73	d1czna_	Alignment	not modelled	99.1	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
74	c3f6sl_	Alignment	not modelled	99.0	13	PDB header: electron transport Chain: I: PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin alternate2 conformers
75	d1oboa_	Alignment	not modelled	99.0	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
76	c4oxxA_	Alignment	not modelled	99.0	18	PDB header: electron transport Chain: A: PDB Molecule: cindoxin; PDBTitle: crystal structure of cindoxin, surface entropy reduction mutant
77	c4heqB_	Alignment	not modelled	98.9	18	PDB header: electron transport Chain: B: PDB Molecule: flavodoxin; PDBTitle: the crystal structure of flavodoxin from desulfovibrio gigas
78	d1ag9a_	Alignment	not modelled	98.9	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
						Fold: Flavodoxin-like

79	d2fcra_	Alignment	not modelled	98.9	22	Superfamily: Flavoproteins Family: Flavodoxin-related
80	c5b3kA_	Alignment	not modelled	98.8	22	PDB header: electron transport Chain: A: PDB Molecule: uncharacterized protein pa3435; PDBTitle: c101a mutant of flavodoxin from pseudomonas aeruginosa
81	c6ohkA_	Alignment	not modelled	98.8	14	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: crystal structure of fusobacterium nucleatum flavodoxin mutant k13g2 bound to flavin mononucleotide
82	c2wc1A_	Alignment	not modelled	98.8	21	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
83	d1yoba1	Alignment	not modelled	98.8	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
84	d1f4pa_	Alignment	not modelled	98.7	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
85	d1tla2	Alignment	not modelled	98.6	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
86	d1fuea_	Alignment	not modelled	98.6	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
87	d1bvyf_	Alignment	not modelled	98.5	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
88	c1bvyF_	Alignment	not modelled	98.5	20	PDB header: oxidoreductase Chain: F: PDB Molecule: protein (cytochrome p450 bm-3); PDBTitle: complex of the heme and fnn-binding domains of the2 cytochrome p450(bm-3)
89	c2hnbA_	Alignment	not modelled	98.4	17	PDB header: electron transport Chain: A: PDB Molecule: protein mioc; PDBTitle: solution structure of a bacterial holo-flavodoxin
90	d1b1ca_	Alignment	not modelled	98.4	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
91	d1ykqa1	Alignment	not modelled	98.4	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
92	c4h2dB_	Alignment	not modelled	98.3	20	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent diflavin oxidoreductase 1; PDBTitle: crystal structure of ndor1
93	c3hr4C_	Alignment	not modelled	98.2	12	PDB header: oxidoreductase/metal binding protein Chain: C: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: human inos reductase and calmodulin complex
94	c2m6rA_	Alignment	not modelled	98.2	14	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: apo_yqca
95	d1ja1a2	Alignment	not modelled	98.0	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
96	c4n82B_	Alignment	not modelled	97.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: ribonucleotide reductase; PDBTitle: x-ray crystal structure of streptococcus sanguinis nrdox
97	c5gxuA_	Alignment	not modelled	97.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh--cytochrome p450 reductase 2; PDBTitle: cystal structure of arabidopsis atr2
98	c6efvA_	Alignment	not modelled	96.8	17	PDB header: flavoprotein Chain: A: PDB Molecule: sulfite reductase [nadh] flavoprotein alpha-component; PDBTitle: the nadph-dependent sulfite reductase flavoprotein adopts an extended2 conformation that is unique to this diflavin reductase
99	c1tla_	Alignment	not modelled	96.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide synthase, brain; PDBTitle: crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
100	c6j7aB_	Alignment	not modelled	95.2	14	PDB header: oxidoreductase Chain: B: PDB Molecule: heme oxygenase 1,nadh--cytochrome p450 reductase; PDBTitle: fusion protein of heme oxygenase-1 and nadph cytochrome p450 reductase2 (17aa)
101	c1j9zB_	Alignment	not modelled	95.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-cytochrome p450 reductase; PDBTitle: cypor-w677g
102	c5lq5F_	Alignment	not modelled	94.9	16	PDB header: isomerase Chain: F: PDB Molecule: allantoin racemase; PDBTitle: crystal structure of allantoin racemase from pseudomonas fluorescens2 allr
103	c3qvjB_	Alignment	not modelled	94.9	11	PDB header: isomerase Chain: B: PDB Molecule: putative hydantoin racemase; PDBTitle: allantoin racemase from klebsiella pneumoniae
104	c2x2oA_	Alignment	not modelled	94.6	15	PDB header: flavoprotein Chain: A: PDB Molecule: nrdi protein; PDBTitle: the flavoprotein nrdi from bacillus cereus with the initially oxidized2 fnn cofactor in an intermediate radiation reduced state
105	c6ehaB	Alignment	not modelled	94.5	11	PDB header: flavoprotein Chain: B: PDB Molecule: protein nrdi;

105	c6e0qb_	Alignment	not modelled	94.3	11	PDBTitle: crystal structure of the flavoprotein nrld from aerococcus urinae in2 oxidized form
106	d2a9va1	Alignment	not modelled	91.4	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
107	d1u7za_	Alignment	not modelled	91.2	15	Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
108	c4qjib_	Alignment	not modelled	89.9	19	PDB header: ligase Chain: B: PDB Molecule: phosphopantothenate--cysteine ligase; PDBTitle: crystal structure of the c-terminal ctp-binding domain of a2 phosphopantothenoylcysteine decarboxylase/phosphopantothenate-3 cysteine ligase with bound ctp from mycobacterium smegmatis
109	c2bpoA_	Alignment	not modelled	89.8	18	PDB header: reductase Chain: A: PDB Molecule: nadph-cytochrom p450 reductase; PDBTitle: crystal structure of the yeast cpr triple mutant: d74g, y75f, k78a.
110	d1r1ja_	Alignment	not modelled	88.7	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavoprotein NrdI
111	c5l3za_	Alignment	not modelled	88.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide ketoreductase simc7; PDBTitle: polyketide ketoreductase simc7 - binary complex with nadp+
112	c3lp6D_	Alignment	not modelled	88.6	13	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
113	c3oy2A_	Alignment	not modelled	86.0	11	PDB header: viral protein,transferase Chain: A: PDB Molecule: glycosyltransferase b736l; PDBTitle: crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
114	d2d1pa1	Alignment	not modelled	84.6	14	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
115	c4grdA_	Alignment	not modelled	84.1	14	PDB header: lyase,isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
116	c3c4vB_	Alignment	not modelled	84.1	19	PDB header: transferase Chain: B: PDB Molecule: predicted glycosyltransferases; PDBTitle: structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
117	d2hy5a1	Alignment	not modelled	83.9	13	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
118	c3ic5A_	Alignment	not modelled	82.3	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
119	d1txga2	Alignment	not modelled	82.2	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
120	c5intB_	Alignment	not modelled	81.9	13	PDB header: ligase Chain: B: PDB Molecule: phosphopantothenate--cysteine ligase; PDBTitle: crystal structure of the c-terminal domain of coenzyme a biosynthesis2 bifunctional protein coabc