







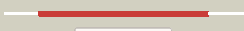










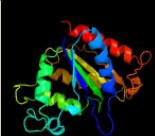

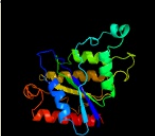


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0925c_(-)_1031900_1032637
Date	Fri Jul 26 01:50:52 BST 2019
Unique Job ID	cb9b2cf199627fac

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5mjiA_	 Alignment		100.0	38	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)
2	d1sqsa_	 Alignment		100.0	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein SP1951
3	d1ydg_	 Alignment		100.0	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
4	c3s2yB_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: chromate reductase; PDBTitle: crystal structure of a chromate/uranium reductase from2 gluconacetobacter hansenii
5	c2zkiH_	 Alignment		100.0	13	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)
6	d1t0ia_	 Alignment		100.0	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
7	c3lcmB_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of smu.1420 from streptococcus mutans ua159
8	c2q62A_	 Alignment		100.0	12	PDB header: flavoprotein Chain: A: PDB Molecule: arsh; PDBTitle: crystal structure of arsh from sinorhizobium meliloti
9	c4r81C_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh dehydrogenase; PDBTitle: nad(p)h:quinone oxidoreductase from methanothermobacter marburgensis
10	c4ptzC_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: C: PDB Molecule: fmn reductase issue; PDBTitle: crystal structure of the escherichia coli alkanesulfonate fmn2 reductase issue in fmn-bound form
11	c3svlB_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: proteinye if; PDBTitle: structural basis of the improvement of chrr - a multi-purpose enzyme

12	c3u7rB_	Alignment		100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent fmn reductase; PDBTitle: ferb - flavoenzyme nad(p)h:(acceptor) oxidoreductase (ferb) from2 paracoccus denitrificans
13	d2qwxal	Alignment		100.0	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
14	c3w7aD_	Alignment		100.0	13	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
15	d1rtta_	Alignment		100.0	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
16	d1nni1_	Alignment		100.0	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
17	c2fzvC_	Alignment		100.0	14	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
18	c4c76A_	Alignment		100.0	10	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn reductase (nadph); PDBTitle: crystal structure of the fmn-reductase msue from pseudomonas putida2 kt2440.
19	c4lafB_	Alignment		99.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p)h dehydrogenase (quinone); PDBTitle: crystal structure of pnpb complex with fmn
20	c6dxdD_	Alignment		99.9	13	PDB header: oxidoreductase Chain: D: PDB Molecule: fmn-dependent nadh-azoreductase; PDBTitle: the crystal structure of an fmn-dependent nadh-azoreductase from2 klebsiella pneumoniae
21	d1t5ba_	Alignment	not modelled	99.9	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
22	d2fzva1	Alignment	not modelled	99.9	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
23	c3u7iB_	Alignment	not modelled	99.9	15	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
24	c3b6iB_	Alignment	not modelled	99.9	13	PDB header: flavoprotein Chain: B: PDB Molecule: flavoprotein wrba; PDBTitle: wrba from escherichia coli, native structure
25	c2hpaA_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn-dependent nadh-azoreductase; PDBTitle: crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
26	c4c0xA_	Alignment	not modelled	99.9	14	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
27	c3fvwA_	Alignment	not modelled	99.9	13	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.
28	c2v9cA_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn-dependent nadh-azoreductase 1;

28	c2v9aA	Alignment	not modelled	99.9	15	PDBTitle: x-ray crystallographic structure of a pseudomonas2 aeruginosa azoreductase in complex with methyl red. PDB header: oxidoreductase
29	c2vzhA	Alignment	not modelled	99.9	17	Chain: A; PDB Molecule: nadh-dependent fmn reductase; PDBTitle: structures of nadh:fmn oxidoreductase (emob)-fmn complex
30	c5mp4C	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: C; PDB Molecule: protoplast secreted protein 2; PDBTitle: the structure of pst2p from saccharomyces cerevisiae
31	c4gi5B	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: B; PDB Molecule: quinone reductase; PDBTitle: crystal structure of a putative quinone reductase from klebsiella2 pneumoniae (target psi-013613)
32	d1d4aa	Alignment	not modelled	99.9	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
33	d2z98a1	Alignment	not modelled	99.9	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
34	d1dxqa	Alignment	not modelled	99.9	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
35	d2a5la1	Alignment	not modelled	99.9	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
36	c3k1yE	Alignment	not modelled	99.9	18	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
37	d1qrda	Alignment	not modelled	99.9	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
38	c3p0rA	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A; PDB Molecule: azoreductase; PDBTitle: crystal structure of azoreductase from bacillus anthracis str. sterne
39	c5f4bB	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B; PDB Molecule: nad(p)h dehydrogenase (quinone); PDBTitle: structure of b. abortus wrba-related protein a (wrpa)
40	d1rlia	Alignment	not modelled	99.9	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein YwqN
41	c5lvaA	Alignment	not modelled	99.9	9	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.
42	c3d7nA	Alignment	not modelled	99.9	9	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
43	c3rpeA	Alignment	not modelled	99.8	23	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.
44	c3f2vA	Alignment	not modelled	99.8	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.
45	d2arka1	Alignment	not modelled	99.8	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
46	d1e5da1	Alignment	not modelled	99.7	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
47	d1ycga1	Alignment	not modelled	99.7	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
48	c6h0cA	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A; PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: flv1 flavodiiron core from synechocystis sp. pcc6803
49	c2amjD	Alignment	not modelled	99.7	26	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
50	c1ychD	Alignment	not modelled	99.7	12	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
51	c2ohiB	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: B; PDB Molecule: type a flavoprotein fpra; PDBTitle: crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
52	c2q9uB	Alignment	not modelled	99.6	9	PDB header: oxidoreductase Chain: B; PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
53	c3ha2B	Alignment	not modelled	99.6	16	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

54	c5widB_	Alignment	not modelled	99.6	13	PDB header: flavoprotein Chain: B: PDB Molecule: flavodoxin; PDBTitle: structure of a flavodoxin from the domain archaea
55	c4d02A_	Alignment	not modelled	99.6	15	PDB header: electron transport Chain: A: PDB Molecule: anaerobic nitric oxide reductase flavorubredoxin; PDBTitle: the crystallographic structure of flavorubredoxin from escherichia2 coli
56	d1vmea1	Alignment	not modelled	99.5	9	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
57	c1e5dA_	Alignment	not modelled	99.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin\oxygen oxidoreductase; PDBTitle: rubredoxin oxygen:oxidoreductase (roo) from anaerobe desulfovibrio2 gigas
58	c4iciA_	Alignment	not modelled	99.5	9	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
59	c4j8pA_	Alignment	not modelled	99.5	8	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
60	c3edoA_	Alignment	not modelled	99.4	10	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
61	c3klbA_	Alignment	not modelled	99.4	13	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
62	c3fniA_	Alignment	not modelled	99.4	17	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	c3hlyA_	Alignment	not modelled	99.3	20	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.
64	c3eywA_	Alignment	not modelled	99.3	15	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
65	c1vmeB_	Alignment	not modelled	99.3	9	PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
66	c6gagB_	Alignment	not modelled	99.0	17	PDB header: electron transport Chain: B: PDB Molecule: flavodoxin; PDBTitle: crystal structure of oxidised flavodoxin 2 from bacillus cereus
67	d2fz5a1	Alignment	not modelled	98.9	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
68	c5vegC_	Alignment	not modelled	98.9	18	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	c6fsiA_	Alignment	not modelled	98.9	18	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: crystal structure of semiquinone flavodoxin 1 from bacillus cereus2 (1.32 a resolution)
70	d5nula_	Alignment	not modelled	98.8	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
71	c5ljiA_	Alignment	not modelled	98.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: flavodoxin; PDBTitle: streptococcus pneumonia tigr4 flavodoxin: structural and biophysical2 characterization of a novel drug target
72	c3f6sl_	Alignment	not modelled	98.6	15	PDB header: electron transport Chain: I: PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin alternate2 conformers
73	c4heqB_	Alignment	not modelled	98.5	15	PDB header: electron transport Chain: B: PDB Molecule: flavodoxin; PDBTitle: the crystal structure of flavodoxin from desulfovibrio gigas
74	c5b3kA_	Alignment	not modelled	98.4	13	PDB header: electron transport Chain: A: PDB Molecule: uncharacterized protein pa3435; PDBTitle: c101a mutant of flavodoxin from pseudomonas aeruginosa
75	d1czna_	Alignment	not modelled	98.3	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
76	d1oboa_	Alignment	not modelled	98.3	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
77	c2mtbA_	Alignment	not modelled	98.2	17	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin-2; PDBTitle: solution structure of apo_fldb
78	d1ag9a_	Alignment	not modelled	98.2	14	Fold: Flavodoxin-like Superfamily: Flavoproteins

						Family: Flavodoxin-related
79	c4oxxA	Alignment	not modelled	98.2	18	PDB header: electron transport Chain: A: PDB Molecule: cinodoxin; PDBTitle: crystal structure of cinodoxin, surface entropy reduction mutant
80	d1tla2	Alignment	not modelled	98.2	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
81	d1yoba1	Alignment	not modelled	98.1	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
82	d2fcra	Alignment	not modelled	98.0	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
83	d1f4pa	Alignment	not modelled	98.0	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
84	c6ohkA	Alignment	not modelled	97.9	16	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: crystal structure of fusobacterium nucleatum flavodoxin mutant k13g2 bound to flavin mononucleotide
85	c2hnbA	Alignment	not modelled	97.9	19	PDB header: electron transport Chain: A: PDB Molecule: protein mioc; PDBTitle: solution structure of a bacterial holo-flavodoxin
86	c4h2dB	Alignment	not modelled	97.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-dependent diflavin oxidoreductase 1; PDBTitle: crystal structure of ndor1
87	d1ykga1	Alignment	not modelled	97.9	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
88	c1bvvyF	Alignment	not modelled	97.9	15	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	d1bvvyf	Alignment	not modelled	97.9	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
90	c2wc1A	Alignment	not modelled	97.8	11	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
91	c2m6rA	Alignment	not modelled	97.8	12	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: apo_yqca
92	d1b1ca	Alignment	not modelled	97.8	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
93	d1ja1a2	Alignment	not modelled	97.7	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
94	c3hr4C	Alignment	not modelled	97.5	15	PDB header: oxidoreductase/metal binding protein Chain: C: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: human inos reductase and calmodulin complex
95	d1fuea	Alignment	not modelled	97.4	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
96	c4n82B	Alignment	not modelled	97.2	14	PDB header: oxidoreductase Chain: B: PDB Molecule: ribonucleotide reductase; PDBTitle: x-ray crystal structure of streptococcus sanguinis nrdox
97	c6efvA	Alignment	not modelled	96.1	15	PDB header: flavoprotein Chain: A: PDB Molecule: sulfite reductase [nadph] flavoprotein alpha-component; PDBTitle: the nadph-dependent sulfite reductase flavoprotein adopts an extended2 conformation that is unique to this diflavin reductase
98	c5gxuA	Alignment	not modelled	94.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph--cytochrome p450 reductase 2; PDBTitle: cystal structure of arabidopsis atr2
99	c1tla	Alignment	not modelled	94.0	15	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	d1n57a	Alignment	not modelled	93.5	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
101	c2x6rA	Alignment	not modelled	92.8	11	PDB header: isomerase Chain: A: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret from p.2 horikoshi produced by soaking in trehalose
102	c3c4vB	Alignment	not modelled	92.0	17	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.
103	c1j9zB	Alignment	not modelled	91.4	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-cytochrome p450 reductase; PDBTitle: cypor-w677g
104	c2xmpB	Alignment	not modelled	90.7	11	PDB header: sugar binding protein Chain: B: PDB Molecule: trehalose-synthase tret; PDBTitle: crystal structure of trehalose synthase tret mutant

					e326a2 from p.horishiki in complex with udp
105	d1u7za_	Alignment	not modelled	89.1	15 Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
106	c4qjB_	Alignment	not modelled	88.6	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
107	c2ofpB_	Alignment	not modelled	87.9	8 PDB header: oxidoreductase Chain: B: PDB Molecule: ketopantoate reductase; PDBTitle: crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
108	d2bisa1	Alignment	not modelled	87.2	11 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
109	c2bpoA_	Alignment	not modelled	86.9	13 PDB header: reductase Chain: A: PDB Molecule: nadh-cytochrom p450 reductase; PDBTitle: crystal structure of the yeast cpr triple mutant: d74g, y75f, k78a.
110	d1ks9a2	Alignment	not modelled	86.5	8 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
111	c5n80A_	Alignment	not modelled	86.2	7 PDB header: transferase Chain: A: PDB Molecule: lipopolysaccharide 1,6-galactosyltransferase; PDBTitle: glycosyltransferase lps biosynthesis in complex with udp
112	c3vpbC_	Alignment	not modelled	85.9	11 PDB header: ligase Chain: C: PDB Molecule: putative acetylornithine deacetylase; PDBTitle: argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
113	c3d8tB_	Alignment	not modelled	84.7	12 PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: thermus thermophilus uroporphyrinogen iii synthase
114	c3c7cB_	Alignment	not modelled	84.2	11 PDB header: oxidoreductase Chain: B: PDB Molecule: octopine dehydrogenase; PDBTitle: a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
115	c6d9tA_	Alignment	not modelled	84.1	8 PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase; PDBTitle: bsha from staphylococcus aureus complexed with udp
116	c3ic5A_	Alignment	not modelled	84.0	8 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
117	c2x2oA_	Alignment	not modelled	83.8	20 PDB header: flavoprotein Chain: A: PDB Molecule: nrndi protein; PDBTitle: the flavoprotein nrndi from bacillus cereus with the initially oxidized2 fmn cofactor in an intermediate radiation reduced state
118	d1mkza_	Alignment	not modelled	83.4	22 Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
119	c3vuFA_	Alignment	not modelled	83.1	10 PDB header: transferase Chain: A: PDB Molecule: granule-bound starch synthase 1, PDBTitle: crystal structure of rice granule bound starch synthase i catalytic2 domain in complex with adp
120	c3lwzC_	Alignment	not modelled	82.9	17 PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: 1.65 angstrom resolution crystal structure of type ii 3-dehydroquinate2 dehydratase (aroq) from yersinia pestis