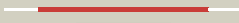


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ag9a_	 Alignment		99.9	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
2	d2arka1	 Alignment		99.9	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
3	d1yoba1	 Alignment		99.9	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
4	d1lobo_	 Alignment		99.9	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
5	c2wc1A_	 Alignment		99.9	18	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
6	d1czna_	 Alignment		99.8	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
7	d2fcra_	 Alignment		99.8	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
8	d2a5la1	 Alignment		99.8	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
9	d1e5da1	 Alignment		99.8	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
10	d1fuea_	 Alignment		99.8	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
11	d1ycga1	 Alignment		99.8	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related

12	dlvmeal	Alignment		99.8	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
13	d1tlla2	Alignment		99.8	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
14	d1ydga	Alignment		99.8	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
15	d1ykga1	Alignment		99.8	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
16	c3b6iB	Alignment		99.8	18	PDB header: flavoprotein Chain: B: PDB Molecule: flavoprotein wrba; PDBTitle: wrba from escherichia coli, native structure
17	c3f6sl	Alignment		99.8	20	PDB header: electron transport Chain: I: PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
18	c3d7nA	Alignment		99.8	15	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
19	d2fz5a1	Alignment		99.8	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
20	c3klbA	Alignment		99.8	15	PDB header: flavoprotein Chain: A: PDB Molecule: putative flavoprotein; PDBTitle: crystal structure of putative flavoprotein in complex with fnm2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
21	c1ychD	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: D: PDB Molecule: nitric oxide reductase; PDBTitle: x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
22	c2zkiH	Alignment	not modelled	99.8	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)
23	c2ohiB	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: B: PDB Molecule: type a flavoprotein fpra; PDBTitle: crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
24	c3hlyA	Alignment	not modelled	99.8	9	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
25	c1ymeB	Alignment	not modelled	99.7	17	PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
26	c2q9uB	Alignment	not modelled	99.7	10	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
27	d5nula	Alignment	not modelled	99.7	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
						PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3;

28	c3fniA_	Alignment	not modelled	99.7	10	PDBTitle: crystal structure of a diflavin flavoprotein a3 (al13895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
29	c1bvyF_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: F: PDB Molecule: protein (cytochrome p450 bm-3); PDBTitle: complex of the heme and fnm-binding domains of the2 cytochrome p450(bm-3)
30	d1bvyf_	Alignment	not modelled	99.7	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
31	c3hr4C_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase/metal binding protein Chain: C: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: human inos reductase and calmodulin complex
32	d1b1ca_	Alignment	not modelled	99.7	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
33	c2hnbA_	Alignment	not modelled	99.7	12	PDB header: electron transport Chain: A: PDB Molecule: protein mioc; PDBTitle: solution structure of a bacterial holo-flavodoxin
34	c3edoA_	Alignment	not modelled	99.7	19	PDB header: flavoprotein Chain: A: PDB Molecule: putative trp repressor binding protein; PDBTitle: crystal structure of flavoprotein in complex with fnm2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution
35	d1ja1a2_	Alignment	not modelled	99.7	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
36	c1e5dA_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin:;oxygen oxidoreductase; PDBTitle: rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
37	c1tlIA_	Alignment	not modelled	99.7	19	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.
38	d1f4pa_	Alignment	not modelled	99.6	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
39	c2bpoA_	Alignment	not modelled	99.5	14	PDB header: reductase Chain: A: PDB Molecule: nadph-cytochrom p450 reductase; PDBTitle: crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
40	c1j9zB_	Alignment	not modelled	99.5	12	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-cytochrome p450 reductase; PDBTitle: cypor-w677g
41	c3lcmB_	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of smu.1420 from streptococcus mutans ua159
42	d1rtta_	Alignment	not modelled	99.4	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
43	d1t0ia_	Alignment	not modelled	99.4	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
44	c2x2oA_	Alignment	not modelled	99.3	15	PDB header: flavoprotein Chain: A: PDB Molecule: nrdi protein; PDBTitle: the flavoprotein nrdi from bacillus cereus with the2 initially oxidized fnm cofactor in an intermediate3 radiation reduced state
45	c3p0rA_	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: azoreductase; PDBTitle: crystal structure of azoreductase from bacillus anthracis str. Sterne
46	d1sqsa_	Alignment	not modelled	99.3	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein SP1951
47	d1rlja_	Alignment	not modelled	99.3	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavoprotein Nrdl
48	c2q62A_	Alignment	not modelled	99.2	15	PDB header: flavoprotein Chain: A: PDB Molecule: arsh; PDBTitle: crystal structure of arsh from sinorhizobium meliloti
49	c3f2vA_	Alignment	not modelled	99.2	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: general stress protein 14; PDBTitle: crystal structure of the general stress protein 142 (tde0354) in complex with fnm from treponema denticola,3 northeast structural genomics consortium target tdr58.
50	c3k1yE_	Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: E: PDB Molecule: oxidoreductase; PDBTitle: x-ray structure of oxidoreductase from corynebacterium2 diphtheriae. orthorhombic crystal form, northeast structural3 genomics consortium target cdr100d
51	c2hpyA_	Alignment	not modelled	99.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: fnm-dependent nadh-azoreductase; PDBTitle: crystal structure of fnm-dependent azoreductase from enterococcus2 faecalis
52	d2qwxal_	Alignment	not modelled	99.2	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
53	d1rlia_	Alignment	not modelled	99.2	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein YwqN

54	c3n39D_	Alignment	not modelled	99.1	14	PDB header: oxidoreductase Chain: D: PDB Molecule: protein nrdr; PDBTitle: ribonucleotide reductase dimanganese(ii)-nrdf from escherichia coli in2 complex with nrdr
55	d1dxqa_	Alignment	not modelled	99.1	9	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
56	d1t5ba_	Alignment	not modelled	99.1	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
57	c2v9cA_	Alignment	not modelled	99.1	14	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.
58	c3rpeA_	Alignment	not modelled	99.1	12	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.
59	d1qrda_	Alignment	not modelled	99.1	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
60	d1nni1_	Alignment	not modelled	99.1	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
61	d1d4aa_	Alignment	not modelled	99.1	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
62	c2vzhA_	Alignment	not modelled	99.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-dependent fmn reductase; PDBTitle: structures of nadh:fmn oxidoreductase (emob)-fmn complex
63	d2z98a1	Alignment	not modelled	99.0	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
64	c2fzvC_	Alignment	not modelled	99.0	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
65	c3fvwA_	Alignment	not modelled	98.9	12	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 from2 streptococcus mutans. northeast structural genomics3 consortium target smr99.
66	d2fzva1	Alignment	not modelled	98.9	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
67	c2amjD_	Alignment	not modelled	98.8	12	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
68	c3ha2B_	Alignment	not modelled	98.5	11	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
69	c3eywA_	Alignment	not modelled	98.0	7	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
70	c2zklA_	Alignment	not modelled	95.0	13	PDB header: isomerase Chain: A: PDB Molecule: capsular polysaccharide synthesis enzyme cap5f; PDBTitle: crystal structure of capsular polysaccharide assembling protein capf2 from staphylococcus aureus
71	c3kk1A_	Alignment	not modelled	94.6	15	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
72	d2a9va1	Alignment	not modelled	94.4	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
73	d1o1ya_	Alignment	not modelled	94.1	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
74	c3l7nA_	Alignment	not modelled	94.1	12	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
75	d1qvwa_	Alignment	not modelled	93.3	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
76	c1tvmA_	Alignment	not modelled	93.1	10	PDB header: transferase Chain: A: PDB Molecule: pts system, galactitol-specific iib component; PDBTitle: nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
77	d1k9vf_	Alignment	not modelled	92.8	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
78	d1t0ba_	Alignment	not modelled	92.1	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: ThuA-like
						PDB header: transferase

79	c3czcA	Alignment	not modelled	92.0	25	Chain: A: PDB Molecule: rmrb; PDBTitle: the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
80	c3l3bA	Alignment	not modelled	91.0	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: es1 family protein; PDBTitle: crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
81	d1wd7a	Alignment	not modelled	90.6	17	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
82	d1ka9h	Alignment	not modelled	89.4	28	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
83	c3r74B	Alignment	not modelled	88.9	21	PDB header: lyase, biosynthetic protein Chain: B: PDB Molecule: anthranilate/para-aminobenzoate synthases component i; PDBTitle: crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
84	c3nbmA	Alignment	not modelled	88.7	13	PDB header: transferase Chain: A: PDB Molecule: pts system, lactose-specific iibc components; PDBTitle: the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
85	c2jjmH	Alignment	not modelled	88.4	10	PDB header: transferase Chain: H: PDB Molecule: glycosyl transferase, group 1 family protein; PDBTitle: crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.
86	d1jvna2	Alignment	not modelled	88.2	10	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
87	d1rzua	Alignment	not modelled	88.2	20	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
88	d1u9ca	Alignment	not modelled	88.0	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
89	c2issF	Alignment	not modelled	88.0	24	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
90	c2qzsA	Alignment	not modelled	87.2	23	PDB header: transferase Chain: A: PDB Molecule: glycogen synthase; PDBTitle: crystal structure of wild-type e.coli gs in complex with adp2 and glucose(wtgsb)
91	d1jaya	Alignment	not modelled	86.9	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
92	c3uk7B	Alignment	not modelled	85.5	22	PDB header: transferase Chain: B: PDB Molecule: class i glutamine amidotransferase-like domain-containing PDBTitle: crystal structure of arabidopsis thaliana dj-1d
93	d2bisa1	Alignment	not modelled	85.5	29	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
94	c3d54D	Alignment	not modelled	85.4	13	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: structure of purlqs from thermotoga maritima
95	d2gk3a1	Alignment	not modelled	85.1	28	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: STM3548-like
96	c2iv3B	Alignment	not modelled	83.9	14	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
97	c2gejA	Alignment	not modelled	83.2	20	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannosyltransferase (pima); PDBTitle: crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
98	c1ks9A	Alignment	not modelled	83.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: ketopantoate reductase from escherichia coli
99	c3oh8A	Alignment	not modelled	83.0	10	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate sugar epimerase (sula family); PDBTitle: crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
100	c3c7cB	Alignment	not modelled	82.6	15	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)
101	c3l83A	Alignment	not modelled	82.5	6	PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
102	c3oy2A	Alignment	not modelled	82.5	14	PDB header: viral protein,transferase Chain: A: PDB Molecule: glycosyltransferase b736l; PDBTitle: crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
						Fold: Flavodoxin-like

103	d1wl8a1	Alignment	not modelled	82.4	15	Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
104	d1rrva	Alignment	not modelled	82.3	29	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
105	d1txga2	Alignment	not modelled	82.1	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
106	c2l2qa	Alignment	not modelled	82.1	15	PDB header: transferase Chain: A: PDB Molecule: pts system, cellobiose-specific iib component (cela); PDBTitle: solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
107	d2r4qa1	Alignment	not modelled	82.0	25	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
108	d1iiba	Alignment	not modelled	81.8	18	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
109	d1n57a	Alignment	not modelled	80.9	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
110	c3rhtB	Alignment	not modelled	80.8	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
111	d1z0sa1	Alignment	not modelled	80.2	18	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
112	c1z0zC	Alignment	not modelled	80.2	18	PDB header: transferase Chain: C: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
113	d2abwa1	Alignment	not modelled	80.1	9	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
114	c2pv7B	Alignment	not modelled	80.0	13	PDB header: isomerase, oxidoreductase Chain: B: PDB Molecule: t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) PDBTitle: crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
115	c3d8tB	Alignment	not modelled	80.0	16	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: thermus thermophilus uroporphyrinogen iii synthase
116	c3c4vB	Alignment	not modelled	80.0	29	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	c3eeqB	Alignment	not modelled	78.9	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative cobalamin biosynthesis protein g PDBTitle: crystal structure of a putative cobalamin biosynthesis2 protein g homolog from sulfolobus solfataricus
118	d1pn3a	Alignment	not modelled	78.8	35	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Gtf glycosyltransferase
119	d1u0ta	Alignment	not modelled	78.8	16	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
120	d1p80a1	Alignment	not modelled	78.5	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain