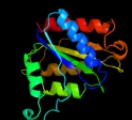


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fzvC_	 Alignment		100.0	19	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: putative arsenical resistance protein; PDBTitle: crystal structure of an apo form of a flavin-binding protein from <i>Shigella flexneri</i>
2	c2vzhA_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-dependent fmN reductase; PDBTitle: structures of nadh:fmN oxidoreductase (emob)-fmN complex
3	c2q62A_	 Alignment		100.0	19	PDB header: flavoprotein Chain: A: PDB Molecule: arsh; PDBTitle: crystal structure of arsh from <i>Sinorhizobium meliloti</i>
4	d2fzva1	 Alignment		100.0	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
5	c3k1yE_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: E: PDB Molecule: oxidoreductase; PDBTitle: x-ray structure of oxidoreductase from <i>Corynebacterium diphtheriae</i> . orthorhombic crystal form, northeast structural genomics consortium target cdr100d
6	d1rtta_	 Alignment		100.0	22	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
7	d1nni1_	 Alignment		100.0	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
8	c3fvwA_	 Alignment		100.0	19	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 <i>Streptococcus mutans</i> . northeast structural genomics3 consortium target smr99.
9	d1t0ia_	 Alignment		100.0	22	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
10	d1sqsa_	 Alignment		100.0	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein SP1951
11	c3lcmB_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of smu.1420 from <i>Streptococcus mutans</i> ua159

12	d2qwa1	Alignment		100.0	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
13	d1d4aa	Alignment		100.0	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
14	d1qrda	Alignment		100.0	22	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
15	d1dxqa	Alignment		100.0	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
16	d1t5ba	Alignment		100.0	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
17	d1ydg	Alignment		100.0	12	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
18	c3p0rA	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: azoreductase; PDBTitle: crystal structure of azoreductase from bacillus anthracis str. Sterne
19	d2z98a1	Alignment		99.9	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
20	c2hpa	Alignment		99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn-dependent nadh-azoreductase; PDBTitle: crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
21	c2v9cA	Alignment	not modelled	99.9	25	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.
22	c2zkiH	Alignment	not modelled	99.9	15	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	c3b6iB	Alignment	not modelled	99.9	18	PDB header: flavoprotein Chain: B: PDB Molecule: flavoprotein wrba; PDBTitle: wrba from escherichia coli, native structure
24	c3f2vA	Alignment	not modelled	99.9	14	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 fmn from treponema denticola,3 northeast structural genomics consortium target tdr58.
25	d2a5la1	Alignment	not modelled	99.9	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
26	d1rlia	Alignment	not modelled	99.9	21	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein YwqN
27	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.
28	c2amjD	Alignment	not modelled	99.8	19	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 PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-quinone reductase; PDBTitle: crystal structure of protein (nadh-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a
29	c3ha2B_	Alignment	not modelled	99.8	18
30	d1e5da1	Alignment	not modelled	99.8	14
31	c3d7nA_	Alignment	not modelled	99.8	14
32	d2arka1	Alignment	not modelled	99.8	14
33	d1ycga1	Alignment	not modelled	99.8	16
34	c3eywA_	Alignment	not modelled	99.8	21
35	c1ychD_	Alignment	not modelled	99.8	16
36	c1e5dA_	Alignment	not modelled	99.7	14
37	d1vmea1	Alignment	not modelled	99.7	14
38	c2ohiB_	Alignment	not modelled	99.7	13
39	c2q9uB_	Alignment	not modelled	99.7	9
40	c3fniA_	Alignment	not modelled	99.7	17
41	c3hlyA_	Alignment	not modelled	99.6	22
42	c1vmeB_	Alignment	not modelled	99.5	13
43	c3klbA_	Alignment	not modelled	99.5	19
44	c3edoA_	Alignment	not modelled	99.5	17
45	d2fz5a1	Alignment	not modelled	99.4	13
46	c3f6sl_	Alignment	not modelled	99.3	18
47	d5nula_	Alignment	not modelled	99.3	10
48	d1loboa_	Alignment	not modelled	99.2	14
49	d1ag9a_	Alignment	not modelled	99.2	18
50	d1czna_	Alignment	not modelled	99.2	17
51	d1tlla2	Alignment	not modelled	99.1	13
52	d1f4pa_	Alignment	not modelled	99.1	16
53	c2wv1A_	Alignment	not modelled	99.1	14

53	c2wclA	Alignment	not modelled	99.1	14	PDBTitle: three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
54	dlykga1	Alignment	not modelled	99.1	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
55	dlyoba1	Alignment	not modelled	99.0	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
56	d1fuea	Alignment	not modelled	99.0	10	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
57	d1bvyf	Alignment	not modelled	99.0	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
58	c1bvyF	Alignment	not modelled	99.0	19	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)
59	c2hnbA	Alignment	not modelled	98.9	16	PDB header: electron transport Chain: A: PDB Molecule: protein mioc; PDBTitle: solution structure of a bacterial holo-flavodoxin
60	c3hr4C	Alignment	not modelled	98.9	16	PDB header: oxidoreductase/metal binding protein Chain: C: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: human inos reductase and calmodulin complex
61	d1b1ca	Alignment	not modelled	98.9	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
62	d2fcra	Alignment	not modelled	98.8	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
63	d1ja1a2	Alignment	not modelled	98.8	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
64	c1t1IA	Alignment	not modelled	98.4	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.
65	c2bpoA	Alignment	not modelled	98.2	15	PDB header: reductase Chain: A: PDB Molecule: nadh-cytochrom p450 reductase; PDBTitle: crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
66	c1j9zB	Alignment	not modelled	98.1	18	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-cytochrome p450 reductase; PDBTitle: cypor-w677g
67	c2x2oA	Alignment	not modelled	96.7	13	PDB header: flavoprotein Chain: A: PDB Molecule: nrld protein; PDBTitle: the flavoprotein nrld from bacillus cereus with the2 initially oxidized fnn cofactor in an intermediate3 radiation reduced state
68	d1cfza	Alignment	not modelled	96.3	17	Fold: Phosphorylase/hydrolase-like Superfamily: HybD-like Family: Hydrogenase maturing endopeptidase HybD
69	c3n39D	Alignment	not modelled	95.8	17	PDB header: oxidoreductase Chain: D: PDB Molecule: protein nrld; PDBTitle: ribonucleotide reductase di manganese(ii)-nrdf from escherichia coli in2 complex with nrld
70	d1rlja	Alignment	not modelled	95.3	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavoprotein Nrld
71	d2a9va1	Alignment	not modelled	95.2	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
72	d1o1ya	Alignment	not modelled	94.7	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
73	d2r4qa1	Alignment	not modelled	94.2	20	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
74	c2kyrA	Alignment	not modelled	94.0	13	PDB header: transferase Chain: A: PDB Molecule: fructose-like phosphotransferase enzyme iib component 1; PDBTitle: solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
75	d2r48a1	Alignment	not modelled	92.9	18	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
76	c3l7nA	Alignment	not modelled	92.1	14	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
77	c2e85B	Alignment	not modelled	91.5	10	PDB header: hydrolase Chain: B: PDB Molecule: hydrogenase 3 maturation protease; PDBTitle: crystal structure of the hydrogenase 3 maturation protease
78	d1qdlb	Alignment	not modelled	91.3	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
79	c3d8tB	Alignment	not modelled	90.6	18	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen-iii synthase;

					PDBTitle: thermus thermophilus uroporphyrinogen iii synthase
80	d1mkza_	Alignment	not modelled	90.1	13 Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
81	c3lwzC_	Alignment	not modelled	90.0	20 PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinatate dehydratase; PDBTitle: 1.65 angstrom resolution on crystal structure of type ii 3-2 dehydroquinatate dehydratase (aroq) from yersinia pestis
82	d1n57a_	Alignment	not modelled	89.9	13 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
83	c3nbmA_	Alignment	not modelled	89.8	21 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.
84	c3orsD_	Alignment	not modelled	89.5	14 PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
85	d1txga2	Alignment	not modelled	89.3	15 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
86	c2ofpB_	Alignment	not modelled	89.1	16 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
87	c3kkIA_	Alignment	not modelled	88.8	13 PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
88	c3c4vB_	Alignment	not modelled	88.7	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.
89	c3oy2A_	Alignment	not modelled	88.6	17 PDB header: viral protein,transferase Chain: A: PDB Molecule: glycosyltransferase b736l; PDBTitle: crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
90	d1u7za_	Alignment	not modelled	88.5	12 Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
91	c2l2qA_	Alignment	not modelled	88.3	13 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
92	c3c7cB_	Alignment	not modelled	87.3	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)
93	d1ks9a2	Alignment	not modelled	87.2	16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
94	c1p74B_	Alignment	not modelled	87.0	18 PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroE) from2 haemophilus influenzae
95	d2bisa1	Alignment	not modelled	86.8	22 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
96	c2qzsA_	Alignment	not modelled	86.5	8 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)
97	c1ks9A_	Alignment	not modelled	86.4	16 PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: ketopantoate reductase from escherichia coli
98	c3l83A_	Alignment	not modelled	86.0	19 PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
99	d1n1ea2	Alignment	not modelled	85.9	17 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
100	d1rzua_	Alignment	not modelled	85.6	11 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: Glycosyl transferases group 1
101	c3czcA_	Alignment	not modelled	85.4	14 PDB header: transferase Chain: A: PDB Molecule: rmpb; PDBTitle: the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
102	c1tvmA_	Alignment	not modelled	85.2	16 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
103	d1jaya_	Alignment	not modelled	85.2	19 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain

104	d2d1pa1	Alignment	not modelled	84.1	12	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
105	d1wl8a1	Alignment	not modelled	84.1	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
106	d1u9ca	Alignment	not modelled	83.6	9	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
107	c3l4bG	Alignment	not modelled	82.9	19	PDB header: transport protein Chain: G: PDB Molecule: trka k+ channel protien tm1088b; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
108	c2z04A	Alignment	not modelled	82.7	16	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
109	d1ka9h	Alignment	not modelled	82.4	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
110	c2z2vA	Alignment	not modelled	81.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
111	d1y5ea1	Alignment	not modelled	81.8	10	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
112	d1iowa1	Alignment	not modelled	81.6	15	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
113	c3l4eA	Alignment	not modelled	80.8	21	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized peptidase lmo0363; PDBTitle: 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
114	d1lssa	Alignment	not modelled	80.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
115	d2hy5a1	Alignment	not modelled	80.3	11	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
116	c2gejA	Alignment	not modelled	80.3	17	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
117	c1jr2A	Alignment	not modelled	80.1	17	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: structure of uroporphyrinogen iii synthase
118	d1jr2a	Alignment	not modelled	80.1	17	Fold: HemD-like Superfamily: HemD-like Family: HemD-like
119	c1vkzA	Alignment	not modelled	79.9	11	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
120	d1h05a	Alignment	not modelled	79.5	13	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinate dehydratase Family: Type II 3-dehydroquinate dehydratase