

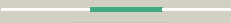
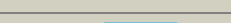
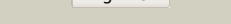
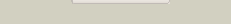
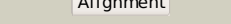
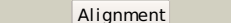
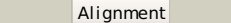
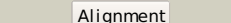
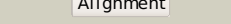
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1ag9a_	 Alignment		100.0	100	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
2	d1lobo_	 Alignment		100.0	45	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
3	d1yoba1	 Alignment		100.0	47	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
4	c2wc1A_	 Alignment		100.0	42	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
5	d1czna_	 Alignment		100.0	46	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
6	d2fcra_	 Alignment		100.0	36	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
7	d1fuea_	 Alignment		100.0	45	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
8	c3hr4C_	 Alignment		100.0	21	PDB header: oxidoreductase/metal binding protein Chain: C: PDB Molecule: nitric oxide synthase, inducible; PDBTitle: human inos reductase and calmodulin complex
9	d1tla2	 Alignment		100.0	21	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
10	c2hnbA_	 Alignment		100.0	24	PDB header: electron transport Chain: A: PDB Molecule: protein mioc; PDBTitle: solution structure of a bacterial holo-flavodoxin
11	d1b1ca_	 Alignment		99.9	23	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like

12	c1tHIA_	Alignment		99.9	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.
13	dlykga1	Alignment		99.9	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
14	c1bvvyF_	Alignment		99.9	18	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)
15	d1bvvyf_	Alignment		99.9	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
16	d1ja1a2	Alignment		99.9	23	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
17	c2bpoA_	Alignment		99.9	25	PDB header: reductase Chain: A: PDB Molecule: nadph-cytochrom p450 reductase; PDBTitle: crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
18	c1j9zB_	Alignment		99.9	24	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-cytochrome p450 reductase; PDBTitle: cypor-w677g
19	c3f6sl_	Alignment		99.9	30	PDB header: electron transport Chain: I: PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
20	d1f4pa_	Alignment		99.9	37	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
21	d1vmea1	Alignment	not modelled	99.9	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
22	c1vmeB_	Alignment	not modelled	99.9	20	PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
23	c3klbA_	Alignment	not modelled	99.9	21	PDB header: flavoprotein Chain: A: PDB Molecule: putative flavoprotein; PDBTitle: crystal structure of putative flavoprotein in complex with fnn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
24	d2arka1	Alignment	not modelled	99.9	21	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
25	d2fz5a1	Alignment	not modelled	99.8	25	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
26	dlycga1	Alignment	not modelled	99.8	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
27	d1e5da1	Alignment	not modelled	99.8	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
28	d5nula_	Alignment	not modelled	99.8	23	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
						PDB header: flavoprotein

29	c3hlyA	Alignment	not modelled	99.8	18	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.
30	d1rlja	Alignment	not modelled	99.8	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavoprotein NrdI
31	c2x2oA	Alignment	not modelled	99.8	24	PDB header: flavoprotein Chain: A: PDB Molecule: nrdi protein; PDBTitle: the flavoprotein nrdi from bacillus cereus with the2 initially oxidized fmh cofactor in an intermediate3 radiation reduced state
32	c1ychD	Alignment	not modelled	99.8	14	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
33	c3n39D	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: D: PDB Molecule: protein nrdi; PDBTitle: ribonucleotide reductase di manganese(ii)-nrdf from escherichia coli in2 complex with nrdi
34	c3fniA	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (al13895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
35	d2a5la1	Alignment	not modelled	99.8	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
36	c2ohiB	Alignment	not modelled	99.8	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
37	c3edoA	Alignment	not modelled	99.7	26	PDB header: flavoprotein Chain: A: PDB Molecule: putative trp repressor binding protein; PDBTitle: crystal structure of flavoprotein in complex with fmh2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution
38	c3d7nA	Alignment	not modelled	99.7	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
39	c2zkiH	Alignment	not modelled	99.7	22	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)
40	c3b6iB	Alignment	not modelled	99.7	22	PDB header: flavoprotein Chain: B: PDB Molecule: flavoprotein wrba; PDBTitle: wrba from escherichia coli, native structure
41	d1ydga	Alignment	not modelled	99.7	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
42	c2q9uB	Alignment	not modelled	99.7	11	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
43	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
44	d1t5ba	Alignment	not modelled	99.3	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
45	d1sqsa	Alignment	not modelled	99.1	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein SP1951
46	d1rtta	Alignment	not modelled	99.1	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
47	c2hvpA	Alignment	not modelled	99.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: fmh-dependent nadh-azoreductase; PDBTitle: crystal structure of fmh-dependent azoreductase from enterococcus2 faecalis
48	c2q62A	Alignment	not modelled	99.0	16	PDB header: flavoprotein Chain: A: PDB Molecule: arsh; PDBTitle: crystal structure of arsh from sinorhizobium meliloti
49	d1t0ia	Alignment	not modelled	99.0	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
50	c3lcmB	Alignment	not modelled	99.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of smu.1420 from streptococcus mutans ua159
51	c3k1yE	Alignment	not modelled	99.0	17	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
52	c3p0rA	Alignment	not modelled	99.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: azoreductase; PDBTitle: crystal structure of azoreductase from bacillus anthracis str. Sterne
53	c3fvwA	Alignment	not modelled	99.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative nad(p)h-dependent fmh reductase; PDBTitle: crystal structure of the q8dwd8_strmu protein from2

						streptococcus mutans. northeast structural genomics3 consortium target smr99.
54	c3rpeA	Alignment	not modelled	99.0	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.
55	d2z98a1	Alignment	not modelled	98.9	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
56	d1nni1	Alignment	not modelled	98.9	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
57	c3f2vA	Alignment	not modelled	98.9	13	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.
58	c2fzvC	Alignment	not modelled	98.9	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
59	d1rlia	Alignment	not modelled	98.9	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein YwqN
60	d1qrda	Alignment	not modelled	98.8	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
61	d2qwxal	Alignment	not modelled	98.8	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
62	c2vzhA	Alignment	not modelled	98.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-dependent fmN reductase; PDBTitle: structures of nadh:fmN oxidoreductase (emob)-fmN complex
63	d2fzva1	Alignment	not modelled	98.7	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
64	c2v9cA	Alignment	not modelled	98.7	13	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.
65	d1d4aa	Alignment	not modelled	98.5	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
66	d1dxqa	Alignment	not modelled	98.4	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
67	c2amjD	Alignment	not modelled	98.3	15	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	98.1	12	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
69	c3eywA	Alignment	not modelled	97.4	10	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	c3czcA	Alignment	not modelled	88.8	18	PDB header: transferase Chain: A: PDB Molecule: rmpb; PDBTitle: the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
71	d2c42a3	Alignment	not modelled	80.1	13	Fold: TK C-terminal domain-like Superfamily: TK C-terminal domain-like Family: Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
72	c1tvmA	Alignment	not modelled	78.3	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
73	d1u0ta	Alignment	not modelled	74.4	11	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
74	c1jvnB	Alignment	not modelled	73.5	22	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hishf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
75	d1dlja3	Alignment	not modelled	73.0	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: UDP-glucose/GDP-mannose dehydrogenase C-terminal domain Family: UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
76	d1vkra	Alignment	not modelled	67.7	7	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellulose specific IIB subunit
77	c1vkrA	Alignment	not modelled	67.7	7	PDB header: transferase Chain: A: PDB Molecule: mannitol-specific pts system enzyme iiabc components; PDBTitle: structure of iib domain of the mannitol-specific permease enzyme ii

78	d1jvna2	Alignment	not modelled	66.3	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
79	d2r4qa1	Alignment	not modelled	64.6	12	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
80	c2amlB	Alignment	not modelled	64.6	9	PDB header: transferase Chain: B: PDB Molecule: sis domain protein; PDBTitle: crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
81	d1v9la1	Alignment	not modelled	61.9	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
82	d1ccwa	Alignment	not modelled	59.6	15	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
83	c3dnfB	Alignment	not modelled	58.2	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-3-methylbut-2-enyl diphosphate reductase; PDBTitle: structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
84	c3euaD	Alignment	not modelled	57.0	13	PDB header: isomerase Chain: D: PDB Molecule: putative fructose-aminoacid-6-phosphate deglycase; PDBTitle: crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
85	d3eeqa2	Alignment	not modelled	56.7	13	Fold: CbiG N-terminal domain-like Superfamily: CbiG N-terminal domain-like Family: CbiG N-terminal domain-like
86	d1fmfa	Alignment	not modelled	53.9	15	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
87	d1tlva	Alignment	not modelled	53.9	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: SH3BGR (SH3-binding, glutamic acid-rich protein-like)
88	d1j5xa	Alignment	not modelled	50.9	24	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
89	d1y8la1	Alignment	not modelled	50.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
90	d1vima	Alignment	not modelled	50.1	18	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
91	d1liloa	Alignment	not modelled	48.0	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
92	c3fxaA	Alignment	not modelled	47.1	8	PDB header: sugar binding protein Chain: A: PDB Molecule: sis domain protein; PDBTitle: crystal structure of a putative sugar-phosphate isomerase2 (lmo2365_0531) from listeria monocytogenes str. 4b f2365 at 1.60 a3 resolution
93	c1v9la	Alignment	not modelled	46.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
94	d1jeoa	Alignment	not modelled	45.4	17	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
95	c2jmh	Alignment	not modelled	45.2	12	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.
96	c3knzA	Alignment	not modelled	44.6	9	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar binding protein; PDBTitle: crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
97	c3s40C	Alignment	not modelled	43.3	13	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
98	d1x94a	Alignment	not modelled	42.7	13	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
99	c2a3na	Alignment	not modelled	42.2	15	PDB header: sugar binding protein Chain: A: PDB Molecule: putative glucosamine-fructose-6-phosphate aminotransferase; PDBTitle: crystal structure of a putative glucosamine-fructose-6-phosphate2 aminotransferase (stm4540.s) from salmonella typhimurium lt2 at 1.353 a resolution
100	c3g68A	Alignment	not modelled	42.0	10	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
101	c3aoeC	Alignment	not modelled	41.9	19	PDB header: oxidoreductase Chain: C: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
102	d2nv0a1	Alignment	not modelled	41.6	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)

103	c3eeqB_	 Alignment	not modelled	41.4	14	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
104	d1c1da1	 Alignment	not modelled	41.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
105	c3dhnA_	 Alignment	not modelled	40.5	6	PDB header: isomerase, lyase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
106	d1nu0a_	 Alignment	not modelled	39.6	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
107	d1hwxal	 Alignment	not modelled	39.4	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
108	c2puwA_	 Alignment	not modelled	38.9	15	PDB header: transferase Chain: A: PDB Molecule: isomerase domain of glutamine-fructose-6-phosphate PDBTitle: the crystal structure of isomerase domain of glucosamine-6-phosphate2 synthase from candida albicans
109	d1moqa_	 Alignment	not modelled	37.8	13	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
110	d1bgval	 Alignment	not modelled	36.9	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
111	c3shoA_	 Alignment	not modelled	36.6	9	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, rpir family; PDBTitle: crystal structure of rpir transcription factor from spheroobacter2 thermophilus (sugar isomerase domain)
112	c3etjB_	 Alignment	not modelled	36.0	10	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure e. coli purk in complex with mg, adp, and2 pi
113	c2zj3A_	 Alignment	not modelled	35.6	15	PDB header: transferase Chain: A: PDB Molecule: glucosamine--fructose-6-phosphate PDBTitle: isomerase domain of human glucose:fructose-6-phosphate2 amidotransferase
114	d1tk9a_	 Alignment	not modelled	35.0	10	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
115	c2issF_	 Alignment	not modelled	34.7	21	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
116	c3aogA_	 Alignment	not modelled	34.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
117	c2kyrA_	 Alignment	not modelled	34.1	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
118	c2x3yA_	 Alignment	not modelled	34.0	14	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
119	c1hrdA_	 Alignment	not modelled	33.6	25	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: glutamate dehydrogenase
120	d1iiba_	 Alignment	not modelled	33.0	15	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellulose specific IIB subunit