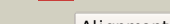
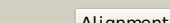
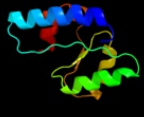


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2r48a1	 Alignment		100.0	41	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
2	c2kyrA	 Alignment		100.0	40	PDB header: transferase 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
3	c3qngD	 Alignment		100.0	14	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
4	d2r4qa1	 Alignment		100.0	35	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Fructose specific IIB subunit-like
5	c1tvmA	 Alignment		97.0	13	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
6	d1ydga	 Alignment		96.7	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
7	d2a5la1	 Alignment		96.5	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
8	c3nbmA	 Alignment		96.0	12	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.
9	d1iiba	 Alignment		95.9	16	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
10	c3czcA	 Alignment		95.7	19	PDB header: transferase Chain: A: PDB Molecule: rmpb; PDBTitle: the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
11	c2l2qa	 Alignment		95.7	18	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

12	d1vkra_	Alignment		95.7	18	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: PTS system IIB component-like Family: PTS system, Lactose/Cellobiose specific IIB subunit
13	c1vkra_	Alignment		95.7	18	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
14	c3fniA_	Alignment		95.1	11	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
15	d2arka1	Alignment		94.8	24	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
16	d1ycga1	Alignment		93.6	21	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
17	d1vmea1	Alignment		91.4	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
18	c3p0rA_	Alignment		90.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: azoreductase; PDBTitle: crystal structure of azoreductase from bacillus anthracis str. Sterne
19	c3b6iB_	Alignment		88.2	20	PDB header: flavoprotein Chain: B: PDB Molecule: flavoprotein wrba; PDBTitle: wrba from escherichia coli, native structure
20	c3lcmB_	Alignment		88.1	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of smu.1420 from streptococcus mutans ua159
21	c3d7nA_	Alignment	not modelled	87.5	29	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
22	d1e5da1	Alignment	not modelled	86.1	22	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
23	c2zkiH_	Alignment	not modelled	85.9	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)
24	c3fmfA_	Alignment	not modelled	85.3	31	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
25	c2q62A_	Alignment	not modelled	85.1	13	PDB header: flavoprotein Chain: A: PDB Molecule: arsh; PDBTitle: crystal structure of arsh from sinorhizobium meliloti
26	c1zggA_	Alignment	not modelled	84.5	23	PDB header: hydrolase Chain: A: PDB Molecule: putative low molecular weight protein-tyrosine- PDBTitle: solution structure of a low molecular weight protein2 tyrosine phosphatase from bacillus subtilis
27	c3f2vA_	Alignment	not modelled	84.1	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. PDB header: oxidoreductase

28	c2v9cA	Alignment	not modelled	82.3	24	Chain: A: PDB Molecule: fmn-dependent nadh-azoreductase 1; PDBTitle: x-ray crystallographic structure of a pseudomonas2 aeruginosa azoreductase in complex with methyl red.
29	c1ychD	Alignment	not modelled	80.8	13	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
30	d1sqsa	Alignment	not modelled	80.2	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein SP1951
31	d2qwa1	Alignment	not modelled	80.0	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
32	d1t0ba	Alignment	not modelled	79.5	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: ThuA-like
33	c2ohiB	Alignment	not modelled	79.0	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
34	c2kncA	Alignment	not modelled	78.5	14	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
35	d1rtta	Alignment	not modelled	77.9	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
36	c3snoA	Alignment	not modelled	77.6	28	PDB header: transferase Chain: A: PDB Molecule: hypothetical aminotransferase; PDBTitle: crystal structure of a hypothetical aminotransferase (ncgl2491) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.60 a resolution
37	c2cwaA	Alignment	not modelled	77.2	24	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight phosphotyrosine protein phosphatase; PDBTitle: crystal structure of tt1001 protein from thermophilus hb8
38	d1qrda	Alignment	not modelled	75.5	25	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
39	c2gi4A	Alignment	not modelled	75.0	23	PDB header: hydrolase Chain: A: PDB Molecule: possible phosphotyrosine protein phosphatase; PDBTitle: solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
40	c3klbA	Alignment	not modelled	74.6	16	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
41	c3jviA	Alignment	not modelled	74.0	11	PDB header: hydrolase Chain: A: PDB Molecule: protein tyrosine phosphatase; PDBTitle: product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
42	c1vmeB	Alignment	not modelled	73.6	11	PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
43	c3rh0A	Alignment	not modelled	71.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: corynebacterium glutamicum mycothiol/mycoredoxin1-dependent arsenate2 reductase cg_arsc2
44	c3k9cA	Alignment	not modelled	71.5	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, laci family protein; PDBTitle: crystal structure of laci transcriptional regulator from rhodococcus2 species.
45	c2hpaA	Alignment	not modelled	70.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: fmn-dependent nadh-azoreductase; PDBTitle: crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
46	c3rpeA	Alignment	not modelled	70.1	22	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.
47	d1dxqa	Alignment	not modelled	67.4	23	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
48	d2z98a1	Alignment	not modelled	66.7	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
49	d2fzva1	Alignment	not modelled	66.2	8	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
50	d1acoa2	Alignment	not modelled	64.9	17	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
51	d1duvg1	Alignment	not modelled	64.4	15	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
52	c2fzvC	Alignment	not modelled	61.2	7	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
						PDB header: transferase/antibiotic

53	c3h9gA_	Alignment	not modelled	60.6	10	Chain: A: PDB Molecule: mccb protein; PDBTitle: crystal structure of e. coli mccb + mcca-n7isoasn
54	d1d1qa_	Alignment	not modelled	60.6	17	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
55	c5acnA_	Alignment	not modelled	57.8	17	PDB header: lyase(carbon-oxygen) Chain: A: PDB Molecule: aconitase; PDBTitle: structure of activated aconitase. formation of the (4fe-4s)2 cluster in the crystal
56	c3fvwA_	Alignment	not modelled	57.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative nad(p)h-dependent fmnr reductase; PDBTitle: crystal structure of the q8dwd8_strmu protein from2 streptococcus mutans. northeast structural genomics3 consortium target smr99.
57	d2fz5a1	Alignment	not modelled	57.4	15	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
58	d1t5ba_	Alignment	not modelled	57.3	11	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
59	c1wrvB_	Alignment	not modelled	56.8	14	PDB header: transferase Chain: B: PDB Molecule: branched-chain amino acid aminotransferase; PDBTitle: crystal structure of t.th.hb8 branched-chain amino acid2 aminotransferase
60	d1u7ga_	Alignment	not modelled	56.3	13	Fold: Ammonium transporter Superfamily: Ammonium transporter Family: Ammonium transporter
61	c3hlyA_	Alignment	not modelled	56.0	14	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.
62	d2b3ya2	Alignment	not modelled	53.3	32	Fold: Aconitase iron-sulfur domain Superfamily: Aconitase iron-sulfur domain Family: Aconitase iron-sulfur domain
63	c2q9uB_	Alignment	not modelled	53.1	21	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiiron protein from giardia2 intestinalis
64	d5nula_	Alignment	not modelled	52.9	21	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
65	d1otha1	Alignment	not modelled	52.3	21	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
66	d2oara1	Alignment	not modelled	51.2	13	Fold: Gated mechanosensitive channel Superfamily: Gated mechanosensitive channel Family: Gated mechanosensitive channel
67	d1vkna1	Alignment	not modelled	51.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
68	d1b1ca_	Alignment	not modelled	50.3	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
69	c3cswB_	Alignment	not modelled	48.8	22	PDB header: transferase Chain: B: PDB Molecule: putative branched-chain-amino-acid aminotransferase; PDBTitle: crystal structure of a putative branched-chain amino acid2 aminotransferase (tm0831) from thermotoga maritima at 2.15 a3 resolution
70	d1iyea_	Alignment	not modelled	48.6	29	Fold: D-aminoacid aminotransferase-like PLP-dependent enzymes Superfamily: D-aminoacid aminotransferase-like PLP-dependent enzymes Family: D-aminoacid aminotransferase-like PLP-dependent enzymes
71	d1vlva1	Alignment	not modelled	47.7	18	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
72	d1dxha1	Alignment	not modelled	47.5	21	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
73	c2oarA_	Alignment	not modelled	46.8	13	PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: mechanosensitive channel of large conductance (mscl)
74	c2b2hA_	Alignment	not modelled	46.7	11	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter; PDBTitle: ammonium transporter amt-1 from a. fulgidus (as)
75	c2p2gD_	Alignment	not modelled	45.5	21	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
76	c3s99A_	Alignment	not modelled	45.5	19	PDB header: lipid binding protein Chain: A: PDB Molecule: basic membrane lipoprotein; PDBTitle: crystal structure of a basic membrane lipoprotein from brucella2 melitensis, iodide soak
77	c2ef0A_	Alignment	not modelled	45.3	21	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
						Fold: Activating enzymes of the ubiquitin-like proteins

78	d1jw9b_	Alignment	not modelled	44.7	16	Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Molybdenum cofactor biosynthesis protein MoeB
79	c2b3yB_	Alignment	not modelled	44.3	29	PDB header: lyase Chain: B: PDB Molecule: iron-responsive element binding protein 1; PDBTitle: structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
80	d1h05a_	Alignment	not modelled	44.1	26	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinase dehydratase Family: Type II 3-dehydroquinase dehydratase
81	c1zfnA_	Alignment	not modelled	42.5	13	PDB header: transferase Chain: A: PDB Molecule: adenyltransferase thif; PDBTitle: structural analysis of escherichia coli thif
82	c3kydB_	Alignment	not modelled	42.4	14	PDB header: ligase Chain: B: PDB Molecule: sumo-activating enzyme subunit 2; PDBTitle: human sumo e1~sumo1-amp tetrahedral intermediate mimic
83	c3o1hB_	Alignment	not modelled	42.4	23	PDB header: signaling protein Chain: B: PDB Molecule: periplasmic protein tort; PDBTitle: crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
84	c1y8qD_	Alignment	not modelled	40.9	11	PDB header: ligase Chain: D: PDB Molecule: ubiquitin-like 2 activating enzyme e1b; PDBTitle: sumo e1 activating enzyme sae1-sae2-mg-atp complex
85	d1dg9a_	Alignment	not modelled	40.5	17	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
86	c2eq8C_	Alignment	not modelled	40.0	24	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
87	d1q6za1	Alignment	not modelled	39.3	11	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
88	d5pnta_	Alignment	not modelled	39.0	19	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
89	c2vzhA_	Alignment	not modelled	39.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-dependent fmN reductase; PDBTitle: structures of nadh:fmN oxidoreductase (emob)-fmN complex
90	d2gk3a1	Alignment	not modelled	37.7	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: STM3548-like
91	d1gqoa_	Alignment	not modelled	37.6	18	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinase dehydratase Family: Type II 3-dehydroquinase dehydratase
92	c3djeA_	Alignment	not modelled	37.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl amine: oxygen oxidoreductase; PDBTitle: crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
93	d1ja1a2	Alignment	not modelled	36.6	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
94	d1rlia_	Alignment	not modelled	36.2	21	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein YwqN
95	c3orsD_	Alignment	not modelled	36.0	11	PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
96	c3n8kG_	Alignment	not modelled	36.0	26	PDB header: lyase Chain: G: PDB Molecule: 3-dehydroquinase dehydratase; PDBTitle: type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
97	c3d0oA_	Alignment	not modelled	35.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase 1; PDBTitle: crystal structure of lactate dehydrogenase from2 staphylococcus aureus
98	c2hqba_	Alignment	not modelled	35.4	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator of comK gene; PDBTitle: crystal structure of a transcriptional activator of comK2 gene from bacillus halodurans
99	c1vknC_	Alignment	not modelled	34.9	16	PDB header: oxidoreductase Chain: C: PDB Molecule: n-acetyl-gamma-glutamyl-phosphate reductase; PDBTitle: crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (tm1782) from thermotoga maritima at 1.80 a resolution
100	d5ldha1	Alignment	not modelled	34.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
101	c1ojua_	Alignment	not modelled	33.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: 2.8 a resolution structure of malate dehydrogenase from2 archaeoglobus fulgidus in complex with etheno-nad.
102	c2an1D_	Alignment	not modelled	33.1	21	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
103	c3lwzC_	Alignment	not modelled	33.0	15	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinase dehydratase;

103	c3rw2C_	Alignment	not modelled	33.0	13	PDBTitle: 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinase dehydratase (aroq) from yersinia pestis PDB header: oxidoreductase
104	c2eq9C_	Alignment	not modelled	32.3	36	Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
105	d1jvna2	Alignment	not modelled	31.6	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
106	c2ad5B_	Alignment	not modelled	31.5	20	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
107	d1pvva1	Alignment	not modelled	31.1	14	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
108	d1s1ma1	Alignment	not modelled	30.9	19	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
109	c1wziA_	Alignment	not modelled	30.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: structural basis for alteration of cofactor specificity of2 malate dehydrogenase from thermus flavus
110	d1qzua_	Alignment	not modelled	30.0	21	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
111	d1d4aa_	Alignment	not modelled	29.6	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Quinone reductase
112	d1jf8a_	Alignment	not modelled	29.5	8	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
113	c2fqxA_	Alignment	not modelled	29.5	16	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
114	c3f6sl_	Alignment	not modelled	29.0	20	PDB header: electron transport Chain: I: PDB Molecule: flavodoxin; PDBTitle: desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
115	d1t0ia_	Alignment	not modelled	28.5	19	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
116	c1vlvA_	Alignment	not modelled	28.2	18	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
117	d1lobo_	Alignment	not modelled	27.7	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
118	d1i0za1	Alignment	not modelled	27.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
119	c1z0zC_	Alignment	not modelled	26.6	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
120	d1z0sa1	Alignment	not modelled	26.6	18	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like