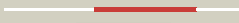
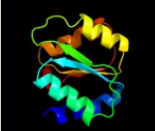
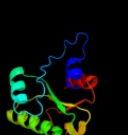
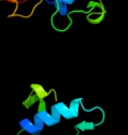


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3i09A_	 Alignment		95.8	11	PDB header: transport protein Chain: A: PDB Molecule: periplasmic branched-chain amino acid-binding protein; PDBTitle: crystal structure of a periplasmic binding protein (bma2936) from2 burkholderia mallei at 1.80 a resolution
2	c3sg0A_	 Alignment		95.0	11	PDB header: signaling protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
3	d1t1ra2	 Alignment		93.2	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
4	c3lopA_	 Alignment		93.0	8	PDB header: substrate binding protein Chain: A: PDB Molecule: substrate binding periplasmic protein; PDBTitle: crystal structure of substrate-binding periplasmic protein2 (pbp) from ralstonia solanacearum
5	c3n0wA_	 Alignment		91.9	18	PDB header: transport protein Chain: A: PDB Molecule: abc branched chain amino acid family transporter, PDBTitle: crystal structure of a branched chain amino acid abc transporter2 periplasmic ligand-binding protein (bx_e_c0949) from burkholderia3 xenovorans lb400 at 1.88 a resolution
6	c3lkbB_	 Alignment		91.8	18	PDB header: transport protein Chain: B: PDB Molecule: probable branched-chain amino acid abc PDBTitle: crystal structure of a branched chain amino acid abc2 transporter from thermus thermophilus with bound valine
7	c3h5lB_	 Alignment		89.3	6	PDB header: transport protein Chain: B: PDB Molecule: putative branched-chain amino acid abc PDBTitle: crystal structure of a putative branched-chain amino acid2 abc transporter from silicibacter pomeroyi
8	c3nklA_	 Alignment		89.1	15	PDB header: oxidoreductase/lyase Chain: A: PDB Molecule: udp-d-quinovosamine 4-dehydrogenase; PDBTitle: crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
9	c3snrA_	 Alignment		86.8	12	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
10	d2eyqa5	 Alignment		86.8	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
11	d1usga_	 Alignment		86.7	12	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like

12	c3ip5A_	Alignment		86.1	14	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein (amino acid); PDBTitle: structure of atu2422-gaba receptor in complex with alanine
13	c1a2oB_	Alignment		85.2	11	PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
14	c1k5hB_	Alignment		83.5	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose-5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose-5-phosphate reductoisomerase
15	c1y80A_	Alignment		83.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from2 moorella thermoacetica
16	c2ozpA_	Alignment		82.1	9	PDB header: oxidoreductase Chain: A: PDB Molecule: n-acetyl-gamma-glutamyl-phosphate reductase; PDBTitle: crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (ttha1904) from thermus thermophilus
17	d2q49a1	Alignment		81.7	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
18	d1vkna1	Alignment		80.0	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
19	d1qo0a_	Alignment		79.6	14	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
20	c1ys4A_	Alignment		79.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: structure of aspartate-semialdehyde dehydrogenase from2 methanococcus jannaschii
21	d2liva_	Alignment	not modelled	79.0	15	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
22	c3hskB_	Alignment		78.7	9	PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of aspartate semialdehyde dehydrogenase2 with nadp from candida albicans
23	d3bula2	Alignment	not modelled	78.2	8	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
24	c2gwrA_	Alignment	not modelled	77.7	12	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator mtra; PDBTitle: crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
25	c3hutA_	Alignment	not modelled	76.8	13	PDB header: transport protein Chain: A: PDB Molecule: putative branched-chain amino acid abc PDBTitle: crystal structure of a putative branched-chain amino acid2 abc transporter from rhodospirillum rubrum
26	c2eyqA_	Alignment	not modelled	76.6	11	PDB header: hydrolase Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of escherichia coli transcription-repair2 coupling factor
27	c2g17A_	Alignment	not modelled	74.9	10	PDB header: oxidoreductase Chain: A: PDB Molecule: n-acetyl-gamma-glutamyl-phosphate reductase; PDBTitle: the structure of n-acetyl-gamma-glutamyl-phosphate reductase from2 salmonella typhimurium. PDB header: transcription

28	c3eulB_	Alignment	not modelled	74.7	18	Chain: B: PDB Molecule: possible nitrate/nitrite response transcriptional PDBTitle: structure of the signal receiver domain of the putative2 response regulator narl from mycobacterium tuberculosis
29	d2a9pa1	Alignment	not modelled	74.5	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
30	c3f6cB_	Alignment	not modelled	74.0	13	PDB header: dna binding protein Chain: B: PDB Molecule: positive transcription regulator evga; PDBTitle: crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
31	c2eghA_	Alignment	not modelled	72.7	11	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
32	c2zwmA_	Alignment	not modelled	72.1	14	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
33	c3eafA_	Alignment	not modelled	72.1	14	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein; PDBTitle: crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
34	d1r0ka2	Alignment	not modelled	71.8	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
35	c3rfuC_	Alignment	not modelled	71.4	13	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
36	c1t4bB_	Alignment	not modelled	70.9	11	PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: 1.6 angstrom structure of esherichia coli aspartate-2 semialdehyde dehydrogenase.
37	c2gz3D_	Alignment	not modelled	70.6	15	PDB header: oxidoreductase Chain: D: PDB Molecule: aspartate beta-semialdehyde dehydrogenase; PDBTitle: structure of aspartate semialdehyde dehydrogenase (asadh) from2 streptococcus pneumoniae complexed with nadp and aspartate-3 semialdehyde
38	c3b2nA_	Alignment	not modelled	70.1	10	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
39	c3n0xA_	Alignment	not modelled	70.0	7	PDB header: transport protein Chain: A: PDB Molecule: possible substrate binding protein of abc transporter PDBTitle: crystal structure of an abc-type branched-chain amino acid transporter2 (rpa4397) from rhodopseudomonas palustris cga009 at 1.50 a resolution
40	d2gz1a1	Alignment	not modelled	69.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
41	c2yxbA_	Alignment	not modelled	68.2	9	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
42	c3nhzA_	Alignment	not modelled	67.7	13	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
43	c2q5cA_	Alignment	not modelled	67.5	10	PDB header: transcription Chain: A: PDB Molecule: ntrc family transcriptional regulator; PDBTitle: crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
44	d2hjsa1	Alignment	not modelled	67.4	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
45	d1u0sy_	Alignment	not modelled	67.2	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
46	c1r0lD_	Alignment	not modelled	66.7	11	PDB header: oxidoreductase Chain: D: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate reductoisomerase from2 zymomonas mobilis in complex with nadph
47	d2pjua1	Alignment	not modelled	66.7	19	Fold: Chelatase-like Superfamily: PrpR receptor domain-like Family: PrpR receptor domain-like
48	d2g17a1	Alignment	not modelled	65.5	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
49	c1mb4B_	Alignment	not modelled	65.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of aspartate semialdehyde dehydrogenase2 from vibrio cholerae with nadp and s-methyl-l-cysteine3 sulfoxide
50	d1dz3a_	Alignment	not modelled	65.4	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
51	c3sajB_	Alignment	not modelled	64.3	11	PDB header: transport protein Chain: B: PDB Molecule: glutamate receptor 1; PDBTitle: crystal structure of glutamate receptor glua1 amino terminal domain

52	dlxhfa1	Alignment	not modelled	63.9	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
53	dlvl0a_	Alignment	not modelled	62.8	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
54	c2pjuD_	Alignment	not modelled	62.3	18	PDB header: transcription Chain: D: PDB Molecule: propionate catabolism operon regulatory protein; PDBTitle: crystal structure of propionate catabolism operon2 regulatory protein prpr
55	dlxfia_	Alignment	not modelled	61.3	11	Fold: AF1104-like Superfamily: AF1104-like Family: AF1104-like
56	c2zsjB_	Alignment	not modelled	60.8	17	PDB header: lyase Chain: B: PDB Molecule: threonine synthase; PDBTitle: crystal structure of threonine synthase from aquifex aeolicus vf5
57	dljw9b_	Alignment	not modelled	60.7	11	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Molybdenum cofactor biosynthesis protein MoeB
58	c3ox4D_	Alignment	not modelled	60.6	14	PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 2; PDBTitle: structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
59	c3t8yA_	Alignment	not modelled	60.5	14	PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of the response regulator domain of thermotoga2 maritima cheb
60	dl1uaa1	Alignment	not modelled	60.2	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
61	dlv71a1	Alignment	not modelled	59.3	10	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
62	c2qioA_	Alignment	not modelled	59.2	11	PDB header: unknown function Chain: A: PDB Molecule: enoyl-(acyl-carrier-protein) reductase; PDBTitle: x-ray structure of enoyl-acyl carrier protein reductase from bacillus2 anthracis with triclosan
63	c3au9A_	Alignment	not modelled	59.0	14	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of the quaternary complex-1 of an isomerase
64	c2hjsA_	Alignment	not modelled	58.9	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: usg-1 protein homolog; PDBTitle: the structure of a probable aspartate-semialdehyde dehydrogenase from2 pseudomonas aeruginosa
65	d1a04a2	Alignment	not modelled	57.7	9	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
66	dlxrsb1	Alignment	not modelled	57.7	14	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
67	d3ckma1	Alignment	not modelled	57.6	8	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
68	c3q41B_	Alignment	not modelled	56.9	10	PDB header: transport protein Chain: B: PDB Molecule: glutamate [nmda] receptor subunit zeta-1; PDBTitle: crystal structure of the glun1 n-terminal domain (ntd)
69	c1luaA_	Alignment	not modelled	56.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: methylene tetrahydromethanopterin dehydrogenase; PDBTitle: structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
70	c3c3wB_	Alignment	not modelled	55.9	20	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
71	dlv7ca_	Alignment	not modelled	55.7	14	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
72	c3e7dC_	Alignment	not modelled	55.5	11	PDB header: isomerase Chain: C: PDB Molecule: cobh, precorrin-8x methylmutase; PDBTitle: crystal structure of precorrin-8x methyl mutase cbic/cobh from2 brucella melitensis
73	c3nglA_	Alignment	not modelled	54.9	20	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
74	dlf2va_	Alignment	not modelled	54.5	14	Fold: Flavodoxin-like Superfamily: Precorrin-8X methylmutase CbiC/CobH Family: Precorrin-8X methylmutase CbiC/CobH
75	d1a9xa4	Alianment	not modelled	54.4	21	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain

						Family: BC N-terminal domain-like
76	c1rn1A_	Alignment	not modelled	54.2	10	PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl; PDBTitle: the nitrate/nitrite response regulator protein narl from narl
77	d1tjya_	Alignment	not modelled	54.0	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
78	d1w6ua_	Alignment	not modelled	53.9	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
79	c3a14B_	Alignment	not modelled	53.5	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of dxr from thermotoga maritima, in complex with2 nadph
80	d1jbea_	Alignment	not modelled	53.2	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
81	d1zh2a1	Alignment	not modelled	53.0	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
82	c3uw3A_	Alignment	not modelled	52.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of an aspartate-semialdehyde dehydrogenase from2 burkholderia thailandensis
83	c3s99A_	Alignment	not modelled	51.3	12	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
84	d1txga2	Alignment	not modelled	51.3	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
85	c3a0rB_	Alignment	not modelled	51.1	13	PDB header: transferase Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
86	d1fmfa_	Alignment	not modelled	51.0	12	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
87	c3iauA_	Alignment	not modelled	50.2	11	PDB header: lyase Chain: A: PDB Molecule: threonine deaminase; PDBTitle: the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
88	d1i3ca_	Alignment	not modelled	50.0	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
89	d2g8la1	Alignment	not modelled	49.7	13	Fold: AF1104-like Superfamily: AF1104-like Family: AF1104-like
90	d1zgza1	Alignment	not modelled	49.6	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
91	c3cz5B_	Alignment	not modelled	49.5	14	PDB header: transcription regulator Chain: B: PDB Molecule: two-component response regulator, luxr family; PDBTitle: crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
92	d1q0qa2	Alignment	not modelled	49.5	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
93	d1krwa_	Alignment	not modelled	49.1	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
94	d2ffja1	Alignment	not modelled	48.7	22	Fold: AF1104-like Superfamily: AF1104-like Family: AF1104-like
95	d1jq5a_	Alignment	not modelled	48.2	8	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
96	c1vknC_	Alignment	not modelled	48.1	14	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
97	c3bfjK_	Alignment	not modelled	47.5	20	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
98	c1bmtB_	Alignment	not modelled	46.7	8	PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
99	c2afvB_	Alignment	not modelled	46.1	16	PDB header: isomerase Chain: B: PDB Molecule: cobalamin biosynthesis precorrin isomerase; PDBTitle: the crystal structure of putative precorrin isomerase cbic2 in cobalamin biosynthesis
100	c2rkbE_	Alignment	not modelled	45.9	19	PDB header: lyase Chain: E: PDB Molecule: serine dehydratase-like; PDBTitle: serine dehydratase like-1 from human cancer cells

101	clzfnA_	Alignment	not modelled	45.5	9	PDB header: transferase Chain: A: PDB Molecule: adenylyltransferase thif; PDBTitle: structural analysis of escherichia coli thif
102	c2d1fA_	Alignment	not modelled	45.0	9	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: structure of mycobacterium tuberculosis threonine synthase
103	dlve5a1	Alignment	not modelled	44.8	12	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
104	d3dc7a1	Alignment	not modelled	44.3	13	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: BT2961-like
105	dls8na_	Alignment	not modelled	44.0	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
106	c2gn0A_	Alignment	not modelled	44.0	12	PDB header: lyase Chain: A: PDB Molecule: threonine dehydratase catabolic; PDBTitle: crystal structure of dimeric biodegradative threonine deaminase (tdcb)2 from salmonella typhimurium at 1.7 a resolution (triclinic form with3 one complete subunit built in alternate conformation)
107	c3sc6F_	Alignment	not modelled	43.9	10	PDB header: oxidoreductase Chain: F: PDB Molecule: ddtp-4-dehydrorhamnose reductase; PDBTitle: 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfd) from bacillus anthracis str. ames in complex with3 nadp
108	dlxsea_	Alignment	not modelled	43.5	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
109	c3bolB_	Alignment	not modelled	43.5	12	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
110	dlpqua1	Alignment	not modelled	43.1	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
111	c3l6cA_	Alignment	not modelled	43.0	7	PDB header: isomerase Chain: A: PDB Molecule: serine racemase; PDBTitle: x-ray crystal structure of rat serine racemase in complex with2 malonate a potent inhibitor
112	c2q49B_	Alignment	not modelled	42.8	14	PDB header: oxidoreductase Chain: B: PDB Molecule: probable n-acetyl-gamma-glutamyl-phosphate reductase; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at2g19940
113	c3t0nA_	Alignment	not modelled	42.2	12	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal; PDBTitle: crystal structure of twin-arginine translocation pathway signal from2 rhodopseudomonas palustris bisb5
114	dlvjga_	Alignment	not modelled	42.1	14	Fold: Flavodoxin-like Superfamily: SGNH hydrolase Family: Hypothetical protein alr1529
115	c2qv0A_	Alignment	not modelled	41.5	10	PDB header: transcription Chain: A: PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
116	c2qz9B_	Alignment	not modelled	41.5	11	PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of aspartate semialdehyde dehydrogenase2 ii from vibrio cholerae
117	dlxcfa_	Alignment	not modelled	41.4	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
118	dlkq3a_	Alignment	not modelled	41.1	14	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
119	dla2oa1	Alignment	not modelled	41.0	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
120	c2yyaB_	Alignment	not modelled	40.1	18	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus