



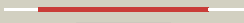










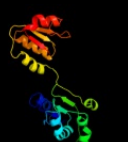



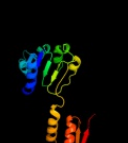











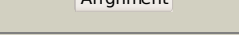






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3re1B_</a>	 Alignment		100.0	27	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> uroporphyrinogen-iii synthetase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen iii synthase from pseudomonas2 syringae pv. tomato dc3000
2	<a href="#">c1jr2A_</a>	 Alignment		100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> uroporphyrinogen-iii synthase; <b>PDBTitle:</b> structure of uroporphyrinogen iii synthase
3	<a href="#">d1jr2a_</a>	 Alignment		100.0	17	<b>Fold:</b> HemD-like <b>Superfamily:</b> HemD-like <b>Family:</b> HemD-like
4	<a href="#">c3mw8A_</a>	 Alignment		100.0	37	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> uroporphyrinogen-iii synthase; <b>PDBTitle:</b> crystal structure of an uroporphyrinogen-iii synthase (sama_3255) from2 shewanella amazonensis sb2b at 1.65 a resolution
5	<a href="#">c3d8tB_</a>	 Alignment		100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> uroporphyrinogen-iii synthase; <b>PDBTitle:</b> thermus thermophilus uroporphyrinogen iii synthase
6	<a href="#">d1wd7a_</a>	 Alignment		100.0	18	<b>Fold:</b> HemD-like <b>Superfamily:</b> HemD-like <b>Family:</b> HemD-like
7	<a href="#">c3p9zA_</a>	 Alignment		100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> uroporphyrinogen iii cosynthase (hemd); <b>PDBTitle:</b> crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695
8	<a href="#">c1ybaC_</a>	 Alignment		96.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> the active form of phosphoglycerate dehydrogenase
9	<a href="#">c3k5pA_</a>	 Alignment		95.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
10	<a href="#">c2eklA_</a>	 Alignment		95.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> structure of st1218 protein from sulfolobus tokodaii
11	<a href="#">c2cukC_</a>	 Alignment		94.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> glycerate dehydrogenase/glyoxylate reductase; <b>PDBTitle:</b> crystal structure of tt0316 protein from thermus thermophilus hb8

12	<a href="#">d1rta_</a>	Alignment		92.8	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
13	<a href="#">c2gcbB_</a>	Alignment		92.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxylate reductase/hydroxypyruvate reductase; <b>PDBTitle:</b> ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
14	<a href="#">c1wwkA_</a>	Alignment		91.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
15	<a href="#">c2o4cB_</a>	Alignment		88.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> erythronate-4-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
16	<a href="#">d7reqa2</a>	Alignment		87.9	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
17	<a href="#">c2yxbA_</a>	Alignment		87.9	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme b12-dependent mutase; <b>PDBTitle:</b> crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
18	<a href="#">c1xdwA_</a>	Alignment		86.7	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad+-dependent (r)-2-hydroxyglutarate <b>PDBTitle:</b> nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
19	<a href="#">c1dxyA_</a>	Alignment		86.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-2-hydroxyisocaproate dehydrogenase; <b>PDBTitle:</b> structure of d-2-hydroxyisocaproate dehydrogenase
20	<a href="#">c3ksmA_</a>	Alignment		86.5	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type sugar transport system, periplasmic component; <b>PDBTitle:</b> crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis
21	<a href="#">d2qwxal</a>	Alignment	not modelled	85.8	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
22	<a href="#">d1lssa_</a>	Alignment	not modelled	83.2	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
23	<a href="#">c3hn0A_</a>	Alignment	not modelled	82.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein; <b>PDBTitle:</b> crystal structure of an abc transporter (bdi_1369) from2 parabacteroides distasonis at 1.75 a resolution
24	<a href="#">c3l7nA_</a>	Alignment	not modelled	82.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of smu.1228c
25	<a href="#">c1lk5C_</a>	Alignment	not modelled	80.7	12	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> d-ribose-5-phosphate isomerase; <b>PDBTitle:</b> structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
26	<a href="#">c3eywA_</a>	Alignment	not modelled	80.1	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal domain of glutathione-regulated potassium-efflux <b>PDBTitle:</b> crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
27	<a href="#">c2g76A_</a>	Alignment	not modelled	79.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of human 3-phosphoglycerate dehydrogenase
28	<a href="#">c3lcmB_</a>	Alignment	not modelled	79.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of smu.1420 from streptococcus mutans ua159

29	<a href="#">d1ccwa_</a>	Alignment	not modelled	79.0	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
30	<a href="#">c3o1hB_</a>	Alignment	not modelled	78.5	12	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic protein tort; <b>PDBTitle:</b> crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
31	<a href="#">c1y80A_</a>	Alignment	not modelled	78.4	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> predicted cobalamin binding protein; <b>PDBTitle:</b> structure of a corrinoid (factor iiii)-binding protein from2 moorella thermoacetica
32	<a href="#">c3e61A_</a>	Alignment	not modelled	77.9	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional repressor of ribose operon; <b>PDBTitle:</b> crystal structure of a putative transcriptional repressor of ribose2 operon from staphylococcus saprophyticus subsp. saprophyticus
33	<a href="#">c2fzvC_</a>	Alignment	not modelled	77.9	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative arsenical resistance protein; <b>PDBTitle:</b> crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
34	<a href="#">d1ydga_</a>	Alignment	not modelled	77.8	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
35	<a href="#">c1k5hB_</a>	Alignment	not modelled	77.8	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-deoxy-d-xylulose-5-phosphate reductoisomerase; <b>PDBTitle:</b> 1-deoxy-d-xylulose-5-phosphate reductoisomerase
36	<a href="#">d2fzva1</a>	Alignment	not modelled	77.6	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
37	<a href="#">d1dxqa_</a>	Alignment	not modelled	77.6	30	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
38	<a href="#">c3orqA_</a>	Alignment	not modelled	76.8	12	<b>PDB header:</b> ligase,biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide synthetase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
39	<a href="#">d1sc6a2</a>	Alignment	not modelled	76.3	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> Formate/glycerate dehydrogenases, substrate-binding domain
40	<a href="#">c2pjuD_</a>	Alignment	not modelled	75.9	13	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> propionate catabolism operon regulatory protein; <b>PDBTitle:</b> crystal structure of propionate catabolism operon2 regulatory protein prpr
41	<a href="#">d1o1ya_</a>	Alignment	not modelled	75.7	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
42	<a href="#">c3pdiB_</a>	Alignment	not modelled	74.7	15	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> nitrogenase mofe cofactor biosynthesis protein nifn; <b>PDBTitle:</b> precursor bound nifen
43	<a href="#">c2f8mB_</a>	Alignment	not modelled	74.4	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose 5-phosphate isomerase; <b>PDBTitle:</b> ribose 5-phosphate isomerase from plasmodium falciparum
44	<a href="#">c3q2oB_</a>	Alignment	not modelled	74.2	9	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, atpase subunit; <b>PDBTitle:</b> crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
45	<a href="#">c2qk4A_</a>	Alignment	not modelled	74.0	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> trifunctional purine biosynthetic protein adenosine-3; <b>PDBTitle:</b> human glycylamide ribonucleotide synthetase
46	<a href="#">c2recB_</a>	Alignment	not modelled	73.5	13	<b>PDB header:</b> helicase <b>PDB COMPND:</b>
47	<a href="#">c3brqA_</a>	Alignment	not modelled	73.1	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator ascg; <b>PDBTitle:</b> crystal structure of the escherichia coli transcriptional repressor2 ascg
48	<a href="#">c3n7uD_</a>	Alignment	not modelled	72.3	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
49	<a href="#">c3qk7C_</a>	Alignment	not modelled	71.1	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulators; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
50	<a href="#">c2yvqA_</a>	Alignment	not modelled	70.7	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase; <b>PDBTitle:</b> crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
51	<a href="#">d1miob_</a>	Alignment	not modelled	70.2	13	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
52	<a href="#">c1lkzB_</a>	Alignment	not modelled	70.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose 5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of d-ribose-5-phosphate isomerase (rpi)2 from escherichia coli.
53	<a href="#">d1t0ia_</a>	Alignment	not modelled	69.8	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase

54	<a href="#">c3d8uA</a>	Alignment	not modelled	69.3	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> purrr transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a purrr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
55	<a href="#">c1kjjA</a>	Alignment	not modelled	69.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase 2; <b>PDBTitle:</b> crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
56	<a href="#">c2zroA</a>	Alignment	not modelled	68.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> msreca adp form iv
57	<a href="#">c2eghA</a>	Alignment	not modelled	68.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
58	<a href="#">c3npgD</a>	Alignment	not modelled	68.6	14	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized duf364 family protein; <b>PDBTitle:</b> crystal structure of a protein with unknown function from duf3642 family (ph1506) from pyrococcus horikoshii at 2.70 a resolution
59	<a href="#">d2a5la1</a>	Alignment	not modelled	68.1	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
60	<a href="#">c3bazA</a>	Alignment	not modelled	67.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyphenylpyruvate reductase; <b>PDBTitle:</b> structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
61	<a href="#">c3ezxA</a>	Alignment	not modelled	67.5	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> monomethylamine corrinoid protein 1; <b>PDBTitle:</b> structure of methanosarcina barkeri monomethylamine2 corrinoid protein
62	<a href="#">c3k4hA</a>	Alignment	not modelled	67.1	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator laci from2 bacillus cereus subsp. cytotoxis nvh 391-98
63	<a href="#">c3gebC</a>	Alignment	not modelled	66.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> eyes absent homolog 2; <b>PDBTitle:</b> crystal structure of edeya2
64	<a href="#">c3g1wB</a>	Alignment	not modelled	65.9	7	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> sugar abc transporter; <b>PDBTitle:</b> crystal structure of sugar abc transporter (sugar-binding protein)2 from bacillus halodurans
65	<a href="#">c3k9cA</a>	Alignment	not modelled	65.9	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, laci family protein; <b>PDBTitle:</b> crystal structure of laci transcriptional regulator from rhodococcus2 species.
66	<a href="#">c2issF</a>	Alignment	not modelled	65.4	32	<b>PDB header:</b> lyase, transferase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> structure of the plp synthase holoenzyme from thermotoga maritima
67	<a href="#">d1o8bb1</a>	Alignment	not modelled	65.2	13	<b>Fold:</b> NagB/RpiA/CoA transferase-like <b>Superfamily:</b> NagB/RpiA/CoA transferase-like <b>Family:</b> D-ribose-5-phosphate isomerase (RpiA), catalytic domain
68	<a href="#">d2nv0a1</a>	Alignment	not modelled	64.8	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
69	<a href="#">d1wl8a1</a>	Alignment	not modelled	64.3	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
70	<a href="#">c3gt7A</a>	Alignment	not modelled	62.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
71	<a href="#">d1qo0a</a>	Alignment	not modelled	62.7	14	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
72	<a href="#">c2zayA</a>	Alignment	not modelled	62.6	9	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator from desulfuromonas2 acetoxidans
73	<a href="#">c3uifA</a>	Alignment	not modelled	62.5	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfonate abc transporter, periplasmic sulfonate-binding <b>PDBTitle:</b> crystal structure of putative sulfonate abc transporter, periplasmic2 sulfonate-binding protein ssua from methylobacillus flagellatus kt
74	<a href="#">c1m0sA</a>	Alignment	not modelled	62.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> northeast structural genomics consortium (nesg id ir21)
75	<a href="#">d1fmfa</a>	Alignment	not modelled	61.5	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
76	<a href="#">d1zesa1</a>	Alignment	not modelled	61.5	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
77	<a href="#">c1bvyf</a>	Alignment	not modelled	61.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> protein (cytochrome p450 bm-3); <b>PDBTitle:</b> complex of the heme and fnn-binding domains of the2 cytochrome p450(bm-3)
78	<a href="#">d1bvyf</a>	Alignment	not modelled	61.3	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related

79	<a href="#">c2dwcB</a>	 Alignment	not modelled	61.2	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 433aa long hypothetical phosphoribosylglycinamide formyl <b>PDBTitle:</b> crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
80	<a href="#">c3fwzA</a>	 Alignment	not modelled	60.9	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> inner membrane protein ybal; <b>PDBTitle:</b> crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
81	<a href="#">c3hheA</a>	 Alignment	not modelled	60.9	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
82	<a href="#">c3clkB</a>	 Alignment	not modelled	60.8	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcription regulator; <b>PDBTitle:</b> crystal structure of a transcription regulator from lactobacillus2 plantarum
83	<a href="#">d1vmea1</a>	 Alignment	not modelled	60.6	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
84	<a href="#">d1p90a</a>	 Alignment	not modelled	60.3	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Nitrogenase accessory factor-like <b>Family:</b> Nitrogenase accessory factor
85	<a href="#">c3e4rA</a>	 Alignment	not modelled	59.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate transport protein; <b>PDBTitle:</b> crystal structure of the alkanesulfonate binding protein2 (ssua) from the phytopathogenic bacteria xanthomonas3 axonopodis pv. citri bound to hepes
86	<a href="#">d2hmv1</a>	 Alignment	not modelled	59.5	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
87	<a href="#">d1mioa</a>	 Alignment	not modelled	59.4	12	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> "Helical backbone" metal receptor <b>Family:</b> Nitrogenase iron-molybdenum protein
88	<a href="#">d1d4aa</a>	 Alignment	not modelled	59.3	30	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
89	<a href="#">c3brsA</a>	 Alignment	not modelled	58.5	5	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic binding protein/laci transcriptional regulator; <b>PDBTitle:</b> crystal structure of sugar transporter from clostridium2 phytofermentans
90	<a href="#">c1uj6A</a>	 Alignment	not modelled	57.9	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose 5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
91	<a href="#">c3gv0A</a>	 Alignment	not modelled	57.8	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of laci family transcription regulator from2 agrobacterium tumefaciens
92	<a href="#">c3l6uA</a>	 Alignment	not modelled	57.8	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type sugar transport system periplasmic <b>PDBTitle:</b> crystal structure of abc-type sugar transport system,2 periplasmic component from exiguobacterium sibiricum
93	<a href="#">c3a0rB</a>	 Alignment	not modelled	57.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
94	<a href="#">d1qrda</a>	 Alignment	not modelled	57.1	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
95	<a href="#">c1xtzA</a>	 Alignment	not modelled	56.7	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase; <b>PDBTitle:</b> crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
96	<a href="#">d1xi8a3</a>	 Alignment	not modelled	56.0	11	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
97	<a href="#">c3l7oB</a>	 Alignment	not modelled	55.7	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
98	<a href="#">c2zkiH</a>	 Alignment	not modelled	55.1	15	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> 199aa long hypothetical trp repressor binding <b>PDBTitle:</b> crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
99	<a href="#">c3u7jA</a>	 Alignment	not modelled	54.9	9	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
100	<a href="#">c2rjoA</a>	 Alignment	not modelled	54.5	8	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> twin-arginine translocation pathway signal protein; <b>PDBTitle:</b> crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
101	<a href="#">c2xdqA</a>	Alignment	not modelled	54.2	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit n; <b>PDBTitle:</b> dark operative protochlorophyllide oxidoreductase (chlN-2 chlB)2 complex
102	<a href="#">c2q5cA</a>	Alignment	not modelled	54.2	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ntrc family transcriptional regulator; <b>PDBTitle:</b> crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum



103	<a href="#">d2a9va1</a>	Alignment	not modelled	53.3	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
104	<a href="#">d1a9xa2</a>	Alignment	not modelled	52.6	18	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
105	<a href="#">c3h5oB_</a>	Alignment	not modelled	52.5	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator gntR; <b>PDBTitle:</b> the crystal structure of transcription regulator gntR from2 chromobacterium violaceum
106	<a href="#">c3d3jA_</a>	Alignment	not modelled	52.4	9	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
107	<a href="#">c2ioyB_</a>	Alignment	not modelled	52.4	12	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> periplasmic sugar-binding protein; <b>PDBTitle:</b> crystal structure of thermoanaerobacter tengcongensis2 ribose binding protein
108	<a href="#">c1xp8A_</a>	Alignment	not modelled	52.0	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> reca protein; <b>PDBTitle:</b> "deinococcus radiodurans reca in complex with atp-gamma-s"
109	<a href="#">c3l4bG_</a>	Alignment	not modelled	50.3	8	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> trka k+ channel protien tm1088b; <b>PDBTitle:</b> crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
110	<a href="#">c1vkzA_</a>	Alignment	not modelled	49.6	7	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylamine--glycine ligase; <b>PDBTitle:</b> crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
111	<a href="#">c1e1cA_</a>	Alignment	not modelled	49.6	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> methylmalonyl-coa mutase alpha chain; <b>PDBTitle:</b> methylmalonyl-coa mutase h244a mutant
112	<a href="#">c3kwmC_</a>	Alignment	not modelled	49.3	16	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> ribose-5-phosphate isomerase a; <b>PDBTitle:</b> crystal structure of ribose-5-isomerase a
113	<a href="#">d1dxya2</a>	Alignment	not modelled	48.7	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> Formate/glycerate dehydrogenases, substrate-binding domain
114	<a href="#">c3icpA_</a>	Alignment	not modelled	48.4	31	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent epimerase/dehydratase; <b>PDBTitle:</b> crystal structure of udp-galactose 4-epimerase
115	<a href="#">c3f2vA_</a>	Alignment	not modelled	48.3	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> general stress protein 14; <b>PDBTitle:</b> crystal structure of the general stress protein 142 (tde0354) in complex with fmh from treponema denticola,3 northeast structural genomics consortium target tdr58.
116	<a href="#">d1vkza2</a>	Alignment	not modelled	48.0	7	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
117	<a href="#">c2rgyA_</a>	Alignment	not modelled	47.9	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, laci family; <b>PDBTitle:</b> crystal structure of transcriptional regulator of laci family from2 burkholderia phymatum
118	<a href="#">d1kjqA2</a>	Alignment	not modelled	47.8	11	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
119	<a href="#">c2ywjA_</a>	Alignment	not modelled	47.4	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
120	<a href="#">c2p5uC_</a>	Alignment	not modelled	47.4	24	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of thermus thermophilus hb8 udp-glucose 4-2 epimerase complex with nad