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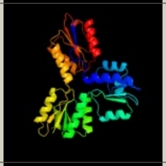
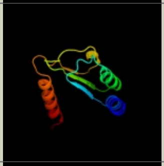
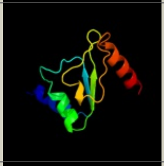
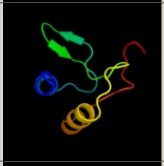
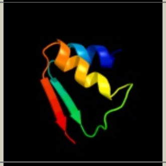
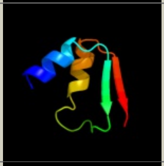
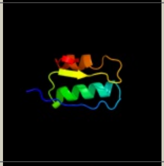
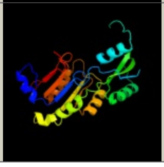
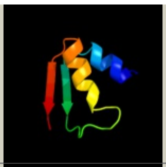
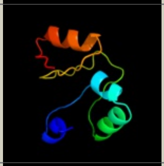
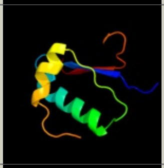
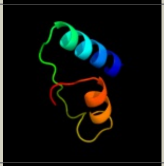
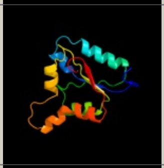
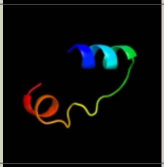
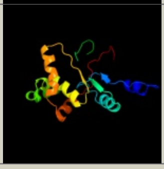
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ke8A_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
2	c3dnfB_	Alignment		100.0	33	**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
3	c3j09A_	Alignment		86.1	13	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
4	d1ma3a_	Alignment		84.9	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
5	d1m2ka_	Alignment		84.7	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
6	c3ff4A_	Alignment		84.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein chu_1412
7	c3pkiF_	Alignment		79.1	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
8	d1s5pa_	Alignment		76.5	9	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
9	c3h5lB_	Alignment		76.3	16	**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
10	c1kblA_	Alignment		75.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase
11	c3j08A_	Alignment		75.1	12	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa

12	d1yc5a1	Alignment		74.8	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
13	d1j6ua1	Alignment		74.5	12	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
14	c2bg5C_	Alignment		72.6	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphoenolpyruvate-protein kinase; **PDBTitle:** crystal structure of the phosphoenolpyruvate-binding enzyme2 i-domain from the thermoanaerobacter tengcongensis pep:3 sugar phosphotransferase system (pts)
15	c3afoB_	Alignment		72.3	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nadh kinase pos5; **PDBTitle:** crystal structure of yeast nadh kinase complexed with nadh
16	c2olsA_	Alignment		71.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate synthase; **PDBTitle:** the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
17	c3l4eA_	Alignment		69.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized peptidase lmo0363; **PDBTitle:** 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
18	c3d22A_	Alignment		69.8	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h-type; **PDBTitle:** crystal structure of a poplar thioredoxin h mutant,2 pttrxh4c61s
19	d1xmta_	Alignment		69.7	20	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
20	d1s1pa_	Alignment		69.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
21	d1fyea_	Alignment	not modelled	68.2	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Aspartyl dipeptidase PepE
22	c3rfuC_	Alignment	not modelled	67.1	15	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
23	d1qo0a_	Alignment	not modelled	65.5	16	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
24	c3cumA_	Alignment	not modelled	65.4	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
25	c3h75A_	Alignment	not modelled	65.1	10	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**periplasmic sugar-binding domain protein; **PDBTitle:** crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
26	d1kbla1	Alignment	not modelled	64.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
27	d1oj7a_	Alignment	not modelled	63.7	10	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
28	d2dlxa1	Alignment	not modelled	62.8	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**UAS domain

29	d1oboa_	Alignment	not modelled	62.2	7	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
30	d2j13a1	Alignment	not modelled	61.8	12	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
31	c3k35D_	Alignment	not modelled	60.0	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
32	c2iz6A_	Alignment	not modelled	59.3	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**molybdenum cofactor carrier protein; **PDBTitle:** structure of the chlamydomonas rheinhardtii moco carrier2 protein
33	c1j6uA_	Alignment	not modelled	59.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-alanine ligase murc; **PDBTitle:** crystal structure of udp-n-acetylmuramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
34	d1e0ta2	Alignment	not modelled	57.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
35	d1pkla2	Alignment	not modelled	57.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
36	c3ej6D_	Alignment	not modelled	57.3	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**catalase-3; **PDBTitle:** neurospora crassa catalase-3 crystal structure
37	c2vlvA_	Alignment	not modelled	56.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h isoform 2.; **PDBTitle:** crystal structure of barley thioredoxin h isoform 2 in2 partially radiation-reduced state
38	d1w5fa1	Alignment	not modelled	56.3	23	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
39	c1jzdA_	Alignment	not modelled	55.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
40	c3mw8A_	Alignment	not modelled	54.8	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** crystal structure of an uroporphyrinogen-iii synthase (sama_3255) from2 shewanella amazonensis sb2b at 1.65 a resolution
41	c2hroA_	Alignment	not modelled	54.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
42	d1ep7a_	Alignment	not modelled	54.3	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
43	d1ag9a_	Alignment	not modelled	54.0	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
44	c3snrA_	Alignment	not modelled	53.7	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
45	c3oa3A_	Alignment	not modelled	53.1	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
46	c3s40C_	Alignment	not modelled	52.9	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
47	d1ofua1	Alignment	not modelled	52.8	23	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
48	c1t00A_	Alignment	not modelled	52.5	10	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** the structure of thioredoxin from s. coelicolor
49	d1h6za1	Alignment	not modelled	52.3	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
50	d1r57a_	Alignment	not modelled	52.2	22	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
51	d2d59a1	Alignment	not modelled	51.6	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
52	d2hk6a1	Alignment	not modelled	51.6	17	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
53	d1vbga1	Alignment	not modelled	51.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
54	c1vbhA_	Alignment	not modelled	51.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate,orthophosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase with bound mg-pep from maize
						PDB header:membrane protein

55	c3h6hB_	Alignment	not modelled	50.5	13	**Chain:** B: **PDB Molecule:**glutamate receptor, ionotropic kainate 2; **PDBTitle:** crystal structure of the glur6 amino terminal domain dimer assembly2 mpd form
56	c3i09A_	Alignment	not modelled	50.4	20	**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
57	d1yq2a5	Alignment	not modelled	49.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
58	c2h9aA_	Alignment	not modelled	49.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase corrinoid/iron- **PDBTitle:** corrinoid iron-sulfur protein
59	c1zxxA_	Alignment	not modelled	49.2	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase; **PDBTitle:** the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
60	c2hwgA_	Alignment	not modelled	49.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
61	d2g17a1	Alignment	not modelled	48.9	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
62	c2vpiA_	Alignment	not modelled	48.8	2	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase; **PDBTitle:** human gmp synthetase - glutaminase domain
63	c1w89E_	Alignment	not modelled	48.6	16	**PDB header:**electron transport **Chain:** E: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of the reduced form of human thioredoxin 2
64	d1j6ua2	Alignment	not modelled	48.5	14	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
65	c1t3bA_	Alignment	not modelled	48.4	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
66	d2b4ya1	Alignment	not modelled	48.0	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
67	c3pfnB_	Alignment	not modelled	46.1	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nad kinase; **PDBTitle:** crystal structure of human nad kinase
68	c3tcoA_	Alignment	not modelled	45.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin (trxa-1); **PDBTitle:** crystallographic and spectroscopic characterization of sulfolobus2 solfataricus trxa1 provide insights into the determinants of3 thioredoxin fold stability
69	c3hutA_	Alignment	not modelled	45.1	15	**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
70	d2jfga1	Alignment	not modelled	44.8	17	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
71	d2je8a5	Alignment	not modelled	44.7	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
72	d1qwka_	Alignment	not modelled	44.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
73	d1a3xa2	Alignment	not modelled	43.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
74	d1t3ba1	Alignment	not modelled	41.7	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
75	c3k2qA_	Alignment	not modelled	41.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrophosphate-dependent phosphofructokinase; **PDBTitle:** crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
76	c3gnjD_	Alignment	not modelled	40.4	13	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**thioredoxin domain protein; **PDBTitle:** the crystal structure of a thioredoxin-related protein from2 desulfitobacterium hafniense dcb
77	c3la6P_	Alignment	not modelled	40.0	10	**PDB header:**transferase **Chain:** P: **PDB Molecule:**tyrosine-protein kinase wzc; **PDBTitle:** octameric kinase domain of the e. coli tyrosine kinase wzc with bound2 adp
78	d1j96a_	Alignment	not modelled	39.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
79	c3p9zA_	Alignment	not modelled	39.9	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**uroporphyrinogen iii cosynthase (hemd); **PDBTitle:** crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695
80	d1jhfa1	Alignment	not modelled	39.8	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain

81	d1p3da1	Alignment	not modelled	39.8	19	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
82	c2qsiB_	Alignment	not modelled	39.5	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative hydrogenase expression/formation protein hupg; **PDBTitle:** crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009
83	c3n0xA_	Alignment	not modelled	39.1	18	**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
84	d1jvna2	Alignment	not modelled	38.9	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
85	d1vqof1	Alignment	not modelled	38.7	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
86	c3canA_	Alignment	not modelled	38.7	12	**PDB header:**lyase activator **Chain:** A: **PDB Molecule:**pyruvate-formate lyase-activating enzyme; **PDBTitle:** crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
87	d1hw6a_	Alignment	not modelled	38.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
88	c1v57A_	Alignment	not modelled	38.6	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbg; **PDBTitle:** crystal structure of the disulfide bond isomerase dsbg
89	d1rlga_	Alignment	not modelled	38.5	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
90	c3g1wB_	Alignment	not modelled	38.3	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**sugar abc transporter; **PDBTitle:** crystal structure of sugar abc transporter (sugar-binding protein)2 from bacillus halodurans
91	d1xwaa_	Alignment	not modelled	38.2	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
92	d1lbqa_	Alignment	not modelled	37.7	16	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
93	c3h7uA_	Alignment	not modelled	37.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c9
94	c3cvjB_	Alignment	not modelled	37.5	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
95	c3fn9B_	Alignment	not modelled	37.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
96	c3hz4A_	Alignment	not modelled	36.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from methanosarcina mazei
97	c2xhzC_	Alignment	not modelled	36.3	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**arabinose 5-phosphate isomerase; **PDBTitle:** probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
98	d2f48a1	Alignment	not modelled	35.8	18	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
99	d4pfka_	Alignment	not modelled	35.4	11	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
100	c3lkbB_	Alignment	not modelled	35.1	15	**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
101	c3koxA_	Alignment	not modelled	34.8	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**d-ornithine aminomutase e component; **PDBTitle:** crystal structure of ornithine 4,5 aminomutase in complex with 2,4-2 diaminobutyrate (anaerobic)
102	d1vp5a_	Alignment	not modelled	34.1	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
103	c3p3wC_	Alignment	not modelled	33.9	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**glutamate receptor 3; **PDBTitle:** structure of a dimeric glua3 n-terminal domain (ntd) at 4.2 a2 resolution
104	c3glsC_	Alignment	not modelled	33.7	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
105	c3mn1B_	Alignment	not modelled	33.5	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable yrbi family phosphatase; **PDBTitle:** crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a

106	d1vhca_	Alignment	not modelled	33.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
107	d1thxa_	Alignment	not modelled	32.9	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
108	c3ngjC_	Alignment	not modelled	32.7	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
109	c3s99A_	Alignment	not modelled	32.7	9	**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
110	c2r8zC_	Alignment	not modelled	32.7	9	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; **PDBTitle:** crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
111	c3p2yA_	Alignment	not modelled	32.6	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alanine dehydrogenase/pyridine nucleotide transhydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
112	c3cmgA_	Alignment	not modelled	32.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
113	d1nria_	Alignment	not modelled	32.0	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
114	c1nriA_	Alignment	not modelled	32.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
115	d1pfka_	Alignment	not modelled	31.9	14	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
116	c1h6zA_	Alignment	not modelled	31.7	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase; **PDBTitle:** 3.0 a resolution crystal structure of glycosomal pyruvate2 phosphate dikinase from trypanosoma brucei
117	c3cyvA_	Alignment	not modelled	31.6	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** crystal structure of uroporphyrinogen decarboxylase from2 shigella flexineri: new insights into its catalytic3 mechanism
118	d1z2wa1	Alignment	not modelled	31.4	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
119	d1o5za1	Alignment	not modelled	31.3	23	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**Folylpolyglutamate synthetase, C-terminal domain
120	d2alra_	Alignment	not modelled	31.3	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)