Phyre2

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Description	RVBD3844_(-)_4318953_4319444
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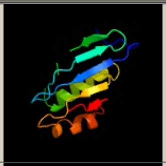
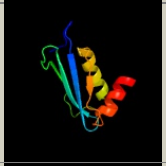
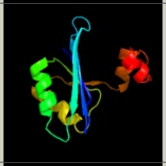
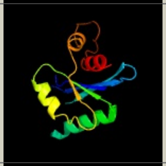
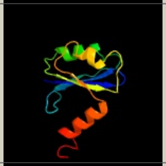
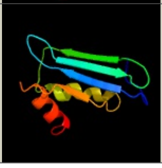
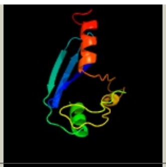
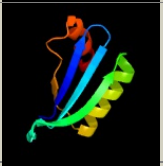
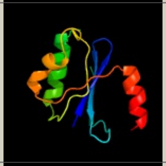
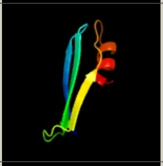
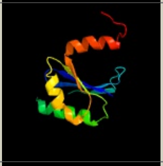
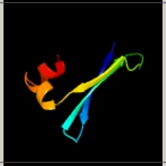
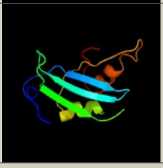
Unique Job ID	1ce276bbc62eca1b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5m1oA_	Alignment		96.9	8	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**phage terminase large subunit; **PDBTitle:** crystal structure of the large terminase nuclease from thermophilic2 phage g20c with bound cobalt
2	c3c6aA_	Alignment		96.7	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**terminase large subunit; **PDBTitle:** crystal structure of the rb49 gp17 nuclease domain
3	d1hjra_	Alignment		96.6	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**RuvC resolvase
4	c4ep5A_	Alignment		96.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**crossover junction endodeoxyribonuclease ruvc; **PDBTitle:** thermus thermophilus ruvc structure
5	c2e2pA_	Alignment		96.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
6	d1xc3a1	Alignment		95.2	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
7	d2ap1a2	Alignment		94.5	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
8	c2ap1A_	Alignment		94.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
9	c3psfA_	Alignment		94.2	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(236-1259)
10	c1xc3A_	Alignment		94.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructokinase; **PDBTitle:** structure of a putative fructokinase from bacillus subtilis
11	c3ezkB_	Alignment		94.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dna packaging protein gp17; **PDBTitle:** bacteriophage t4 gp17 motor assembly based on crystal structures and2 cryo-em reconstructions

12	d1z05a3	Alignment		93.9	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
13	c3eo3B_	Alignment		93.9	16	**PDB header:**isomerase, transferase **Chain:** B: **PDB Molecule:**bifunctional udp-n-acetylglucosamine 2-epimerase/n- **PDBTitle:** crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
14	d3bzka5	Alignment		93.6	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Tex RuvX-like domain-like
15	d2gupa1	Alignment		92.7	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
16	c1zc6A_	Alignment		92.3	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable n-acetylglucosamine kinase; **PDBTitle:** crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics target3 cvr23.
17	c2gupA_	Alignment		90.4	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rok family protein; **PDBTitle:** structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose
18	c4ijaA_	Alignment		90.2	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**xylr protein; **PDBTitle:** structure of s. aureus methicillin resistance factor mecr2
19	c3htvA_	Alignment		90.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**d-allose kinase; **PDBTitle:** crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution
20	c3h1qB_	Alignment		89.9	19	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**ethanolamine utilization protein eutj; **PDBTitle:** crystal structure of ethanolamine utilization protein eutj from2 carboxydothermus hydrogenoformans
21	c4db3A_	Alignment	not modelled	89.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyl-d-glucosamine kinase; **PDBTitle:** 1.95 angstrom resolution crystal structure of n-acetyl-d-glucosamine2 kinase from vibrio vulnificus.
22	c2ch5D_	Alignment	not modelled	88.8	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nagk protein; **PDBTitle:** crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
23	c4htlA_	Alignment	not modelled	87.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-glucoside kinase; **PDBTitle:** lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
24	d2aa4a1	Alignment	not modelled	87.0	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
25	c3vovC_	Alignment	not modelled	86.7	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of rok hexokinase from thermus thermophilus
26	c2aa4B_	Alignment	not modelled	86.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative n-acetylmannosamine kinase; **PDBTitle:** crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
27	c5nckA_	Alignment	not modelled	85.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetylmannosamine kinase; **PDBTitle:** the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum
28	c5f7pA_	Alignment	not modelled	85.6	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lmo0178 protein; **PDBTitle:** rok repressor lmo0178 from listeria monocytogenes

29	d1g8ma1	Alignment	not modelled	85.6	20	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
30	c2w40C_	Alignment	not modelled	85.1	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
31	c6nkoA_	Alignment	not modelled	84.6	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**forh; **PDBTitle:** crystal structure of forh
32	d2ch5a2	Alignment	not modelled	84.5	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
33	c3gbtA_	Alignment	not modelled	84.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus
34	d1zcza1	Alignment	not modelled	84.1	11	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
35	c2qm1D_	Alignment	not modelled	83.4	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase from enterococcus faecalis
36	d1z6ra2	Alignment	not modelled	83.4	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
37	d1nu0a_	Alignment	not modelled	83.1	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
38	c1zczA_	Alignment	not modelled	83.0	11	**PDB header:**transferase/hydrolase **Chain:** A: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
39	d1pkxa1	Alignment	not modelled	82.2	18	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
40	d1zc6a1	Alignment	not modelled	82.1	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
41	c1z05A_	Alignment	not modelled	82.0	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, rok family; **PDBTitle:** crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
42	d1woqa1	Alignment	not modelled	81.7	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
43	c3lm2B_	Alignment	not modelled	81.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative kinase; **PDBTitle:** crystal structure of putative kinase. (17743352) from agrobacterium2 tumefaciens str. c58 (dupont) at 1.70 a resolution
44	c4ehtA_	Alignment	not modelled	81.5	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**activator of 2-hydroxyisocaproyl-coa dehydratase; **PDBTitle:** activator of the 2-hydroxyisocaproyl-coa dehydratase from clostridium2 difficile with bound adp
45	c1thzA_	Alignment	not modelled	81.4	20	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
46	d2p3ra1	Alignment	not modelled	81.4	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
47	c5f7rA_	Alignment	not modelled	81.1	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lmo0178 protein; **PDBTitle:** rok repressor lmo0178 from listeria monocytogenes bound to inducer
48	c4a1oB_	Alignment	not modelled	80.3	18	**PDB header:**transferase-hydrolase **Chain:** B: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
49	c3wxiB_	Alignment	not modelled	80.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
50	c6gmhM_	Alignment	not modelled	78.4	18	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription elongation factor spt6,transcription **PDBTitle:** structure of activated transcription complex pol ii-dsif-paf-spt6
51	c3ifrB_	Alignment	not modelled	77.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
52	c3g25B_	Alignment	not modelled	76.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
53	c2nlxA_	Alignment	not modelled	76.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase;

						PDBTitle: crystal structure of the apo e. coli xylulose kinase
54	c5m45K_	Alignment	not modelled	76.1	24	**PDB header:**ligase **Chain:** K: **PDB Molecule:**acetone carboxylase beta subunit; **PDBTitle:** structure of acetone carboxylase purified from xanthobacter2 autotrophicus
55	c5vm1A_	Alignment	not modelled	76.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of a xyloylose kinase from brucella ovis
56	c5htxA_	Alignment	not modelled	75.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative xylulose kinase; **PDBTitle:** putative sugar kinases from arabidopsis thaliana in complex with adp
57	d2ewsa1	Alignment	not modelled	75.6	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
58	d1huxa_	Alignment	not modelled	73.8	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
59	c2hoeA_	Alignment	not modelled	73.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetylglucosamine kinase; **PDBTitle:** crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
60	c3hz6A_	Alignment	not modelled	73.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
61	c3flcX_	Alignment	not modelled	72.5	20	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol
62	c2duwA_	Alignment	not modelled	72.2	8	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**putative coa-binding protein; **PDBTitle:** solution structure of putative coa-binding protein of2 klebsiella pneumoniae
63	c3t69A_	Alignment	not modelled	72.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative 2-dehydro-3-deoxygalactonokinase; **PDBTitle:** crystal structure of a putative 2-dehydro-3-deoxygalactonokinase2 protein from sinorhizobium meliloti
64	d1q18a1	Alignment	not modelled	71.9	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
65	c3r8eA_	Alignment	not modelled	71.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical sugar kinase; **PDBTitle:** crystal structure of a putative sugar kinase (chu_1875) from cytophaga2 hutchinsonii atcc 33406 at 1.65 a resolution
66	d1vhxa_	Alignment	not modelled	70.6	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
67	c5ya2A_	Alignment	not modelled	70.2	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**autoinducer-2 kinase; **PDBTitle:** crystal structure of lsrk-hpr complex with adp
68	c2oceA_	Alignment	not modelled	70.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa5201; **PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
69	d1y81a1	Alignment	not modelled	69.7	4	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
70	c2d4wA_	Alignment	not modelled	69.4	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
71	d2pgda2	Alignment	not modelled	69.3	5	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
72	c4c23A_	Alignment	not modelled	68.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**l-fuculose kinase fuck; **PDBTitle:** l-fuculose kinase
73	c1woqB_	Alignment	not modelled	68.7	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**inorganic polyphosphate/atp-glucomannokinase; **PDBTitle:** crystal structure of inorganic polyphosphate/atp-glucomannokinase from2 arthrobacter sp. strain km at 1.8 a resolution
74	c3ff4A_	Alignment	not modelled	68.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein chu_1412
75	c4bc2A_	Alignment	not modelled	68.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** crystal structure of human d-xylulokinase in complex with d-2 xylulose and adenosine diphosphate
76	d2d59a1	Alignment	not modelled	67.6	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
77	c4e1jA_	Alignment	not modelled	67.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021
78	c5hv7A_	Alignment	not modelled	66.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable sugar kinase; **PDBTitle:** putative sugar kinases from synechococcus elongatus pcc7942 in complex2 with d-ribulose
79	c3psiA_	Alignment	not modelled	65.2	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt6;

79	c3psiA_	Alignment	not modelled	65.2	6	**PDBTitle:** crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
80	d2hoea3	Alignment	not modelled	64.9	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
81	c3vgkB_	Alignment	not modelled	64.2	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of a rok family glucokinase from streptomyces2 griseus
82	c1glbG_	Alignment	not modelled	64.1	18	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
83	c3mcpA_	Alignment	not modelled	62.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase (bdi_1628) from parabacteroides2 distasonis atcc 8503 at 3.00 a resolution
84	d1iv0a_	Alignment	not modelled	62.0	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
85	c3h6eB_	Alignment	not modelled	61.5	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
86	c3ezwD_	Alignment	not modelled	61.0	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
87	c1z6rC_	Alignment	not modelled	60.3	19	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
88	c4ehiB_	Alignment	not modelled	58.3	13	**PDB header:**hydrolase,transferase **Chain:** B: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** an x-ray crystal structure of a putative bifunctional2 phosphoribosylaminoimidazolecarboxamide formyltransferase/imp3 cyclohydrolase
89	d1iuka_	Alignment	not modelled	58.2	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
90	c2dpnB_	Alignment	not modelled	58.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
91	d1r59o1	Alignment	not modelled	57.0	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
92	c2rkbE_	Alignment	not modelled	55.9	6	**PDB header:**lyase **Chain:** E: **PDB Molecule:**serine dehydratase-like; **PDBTitle:** serine dehydratase like-1 from human cancer cells
93	c3gg4B_	Alignment	not modelled	55.7	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
94	c3i8bA_	Alignment	not modelled	54.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
95	c3fwzA_	Alignment	not modelled	53.9	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**inner membrane protein ybal; **PDBTitle:** crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
96	c2zf5O_	Alignment	not modelled	53.8	15	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
97	c2cgkB_	Alignment	not modelled	52.8	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l-rhamnulose kinase; **PDBTitle:** crystal structure of l-rhamnulose kinase from escherichia coli in an2 open uncomplexed conformation.
98	d1yt8a4	Alignment	not modelled	52.4	11	**Fold:**Rhodanese/Cell cycle control phosphatase **Superfamily:**Rhodanese/Cell cycle control phosphatase **Family:**Multidomain sulfurtransferase (rhodanese)
99	c6hulB_	Alignment	not modelled	49.9	4	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase beta chain 1; **PDBTitle:** sulfolobus solfataricus tryptophan synthase ab complex
100	d1pwha_	Alignment	not modelled	49.7	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
101	c5l9wb_	Alignment	not modelled	49.5	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetophenone carboxylase gamma subunit; **PDBTitle:** crystal structure of the apc core complex
102	d1gsoa2	Alignment	not modelled	49.4	15	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
103	c1xupO_	Alignment	not modelled	48.5	23	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** enterococcus casseliflavus glycerol kinase complexed with glycerol
104	c3od1A_	Alignment	not modelled	47.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase regulatory subunit; **PDBTitle:** the crystal structure of an atp phosphoribosyltransferase

						regulatory2 subunit/histidyl-trna synthetase from bacillus halodurans c
105	c2d1fA_	Alignment	not modelled	46.8	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine synthase; **PDBTitle:** structure of mycobacterium tuberculosis threonine synthase
106	c6cgqA_	Alignment	not modelled	45.3	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine synthase; **PDBTitle:** threonine synthase from bacillus subtilis atcc 6633 with plp and plp-2 ala
107	c5ybwA_	Alignment	not modelled	44.5	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**aspartate racemase; **PDBTitle:** crystal structure of pyridoxal 5'-phosphate-dependent aspartate2 racemase
108	d1jaya_	Alignment	not modelled	43.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
109	d1f0ya2	Alignment	not modelled	43.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
110	d1v7ca_	Alignment	not modelled	42.7	13	**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
111	c3nglA_	Alignment	not modelled	42.3	16	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
112	c4a26B_	Alignment	not modelled	41.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative c-1-tetrahydrofolate synthase, cytoplasmic; **PDBTitle:** the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
113	d2csua1	Alignment	not modelled	40.9	0	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
114	d1a9xa2	Alignment	not modelled	40.4	17	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
115	c5i4aC_	Alignment	not modelled	39.7	22	**PDB header:**rna binding protein/rna **Chain:** C: **PDB Molecule:**argonaute protein; **PDBTitle:** x-ray crystal structure of marinitoga piezophila argonaute in complex2 with 5' oh guide rna
116	c4negA_	Alignment	not modelled	39.2	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** the crystal structure of tryptophan synthase subunit beta from2 bacillus anthracis str. 'ames ancestor'
117	d1b0aa1	Alignment	not modelled	38.4	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
118	c2o2jA_	Alignment	not modelled	38.4	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** mycobacterium tuberculosis tryptophan synthase beta chain dimer2 (apoform)
119	c4j7cA_	Alignment	not modelled	38.1	5	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ktr system potassium uptake protein a; **PDBTitle:** ktrab potassium transporter from bacillus subtilis
120	c1np3B_	Alignment	not modelled	38.0	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa