Phyre^2

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Description	RVBD3382c_(lytB1)_3796628_3797617
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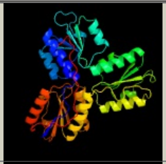
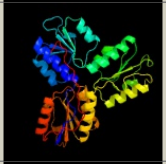
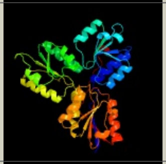
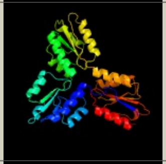
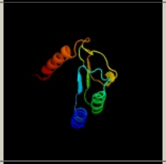
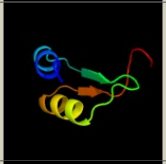
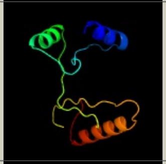
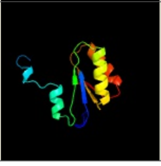
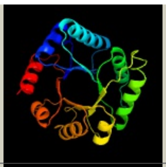
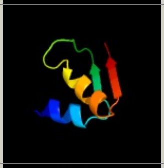
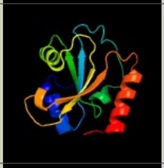
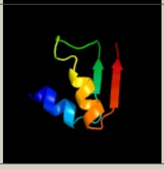
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3urkA_	Alignment		100.0	52	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** isph in complex with propynyl diphosphate (1061)
2	c3ke8A_	Alignment		100.0	52	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** crystal structure of isph:hmbpp-complex
3	c4n7bA_	Alignment		100.0	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lytb; **PDBTitle:** structure of the e-1-hydroxy-2-methyl-but-2-enyl-4-diphosphate2 reductase from plasmodium falciparum
4	c3dnfB_	Alignment		100.0	30	**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
5	c4zhtB_	Alignment		90.7	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**bifunctional udp-n-acetylglucosamine 2-epimerase/n- **PDBTitle:** crystal structure of udp-glcnac 2-epimerase
6	d1m2ka_	Alignment		88.4	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
7	d1ma3a_	Alignment		88.2	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
8	c3ff4A_	Alignment		86.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein chu_1412
9	c5c4nD_	Alignment		86.1	25	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**precorrin-6a reductase; **PDBTitle:** cobk precorrin-6a reductase
10	d2j13a1	Alignment		84.4	16	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
11	c4zo9B_	Alignment		80.9	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lin1840 protein; **PDBTitle:** crystal structure of mutant (d270a) beta-glucosidase from listeria2 innocua in complex with laminaribiose

12	d1e0ta2	Alignment		79.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
13	c3pkiF_	Alignment		78.3	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
14	c3h5lB_	Alignment		77.1	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative branched-chain amino acid abc transporter; **PDBTitle:** crystal structure of a putative branched-chain amino acid abc2 transporter from silicibacter pomeroyi
15	c3zg6A_	Alignment		74.8	14	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**nad-dependent protein deacetylase sirtuin-6; **PDBTitle:** the novel de-long chain fatty acid function of human sirt6
16	c3l4eA_	Alignment		74.7	21	**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
17	d2d59a1	Alignment		73.8	31	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
18	d2dlxa1	Alignment		73.6	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**UAS domain
19	c3hutA_	Alignment		73.4	19	**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
20	d1yc5a1	Alignment		73.3	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
21	c3j09A_	Alignment	not modelled	72.4	17	**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
22	d2hk6a1	Alignment	not modelled	72.2	16	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
23	c4e38A_	Alignment	not modelled	71.7	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate **PDBTitle:** crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibrionales bacterium swat-3 (target efi-502156)
24	d1s5pa_	Alignment	not modelled	70.7	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
25	d1fyea_	Alignment	not modelled	70.5	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Aspartyl dipeptidase PepE
26	d1xmta_	Alignment	not modelled	69.7	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
27	c3afoB_	Alignment	not modelled	69.1	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nadh kinase pos5; **PDBTitle:** crystal structure of yeast nadh kinase complexed with nadh
28	d1oj7a_	Alignment	not modelled	68.9	11	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
						PDB header:signaling protein

29	c5ereA_	Alignment	not modelled	67.8	19	**Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** extracellular ligand binding receptor from desulfohalobium retbaense2 dsm5692
30	c4evsA_	Alignment	not modelled	67.6	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative abc transporter subunit, substrate-binding **PDBTitle:** crystal structure of abc transporter from r. palustris - solute2 binding protein (rpa0985) in complex with 4-hydroxybenzoate
31	d1oboa_	Alignment	not modelled	67.3	7	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
32	c2iz6A_	Alignment	not modelled	67.1	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**molybdenum cofactor carrier protein; **PDBTitle:** structure of the chlamydomonas rheinhardtii moco carrier2 protein
33	c6qkzA_	Alignment	not modelled	66.8	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glua1; **PDBTitle:** full length glua1/2-gamma8 complex
34	d1j6ua2	Alignment	not modelled	65.9	14	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
35	c6oviA_	Alignment	not modelled	64.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**keto-deoxy-phosphogluconate aldolase; **PDBTitle:** crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
36	d1qo0a_	Alignment	not modelled	64.7	11	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
37	c3p9zA_	Alignment	not modelled	64.6	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**uroporphyrinogen iii cosynthase (hemd); **PDBTitle:** crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695
38	c4maaA_	Alignment	not modelled	63.7	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative branched-chain amino acid abc transporter, **PDBTitle:** the crystal structure of amino acid abc transporter substrate-binding2 protein from pseudomonas fluorescens pf-5
39	c3k35D_	Alignment	not modelled	63.4	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
40	c3h75A_	Alignment	not modelled	63.4	15	**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
41	c5i0cA_	Alignment	not modelled	62.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein yjdj; **PDBTitle:** crystal structure of predicted acyltransferase yjdj with acyl-coa n-2 acyltransferase domain from escherichia coli str. k-12
42	c2olsA_	Alignment	not modelled	62.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate synthase; **PDBTitle:** the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
43	c6a4tB_	Alignment	not modelled	62.5	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase e; **PDBTitle:** crystal structure of peptidase e from deinococcus radiodurans r1
44	c3zdrA_	Alignment	not modelled	60.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alcohol dehydrogenase domain of the bifunctional **PDBTitle:** structure of the alcohol dehydrogenase (adh) domain of a2 bifunctional adhe dehydrogenase from geobacillus3 thermoglucosidasius ncimb 11955
45	c3j08A_	Alignment	not modelled	60.8	17	**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
46	d1ag9a_	Alignment	not modelled	60.4	7	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
47	c1kblA_	Alignment	not modelled	59.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase
48	d1w5fa1	Alignment	not modelled	59.5	15	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
49	d1pkla2	Alignment	not modelled	58.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
50	c2bg5C_	Alignment	not modelled	57.9	10	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphoenolpyruvate-protein kinase; **PDBTitle:** crystal structure of the phosphoenolpyruvate-binding enzyme i-domain2 from the thermoanaerobacter tengcongensis pep: sugar3 phosphotransferase system (pts)
51	c5nymA_	Alignment	not modelled	57.8	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-like protein 2.1; **PDBTitle:** crystal structure of the atypical poplar thioredoxin-like2.1 in2 reduced state
52	c3mmzA_	Alignment	not modelled	57.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative had family hydrolase; **PDBTitle:** crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
53	c5wabD_	Alignment	not modelled	57.0	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative beta-glucosidase; **PDBTitle:** crystal structure of bifidobacterium adolescentis gh3 beta-glucosidase

54	d1lbqa_	Alignment	not modelled	56.9	19	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
55	c5hvnA_	Alignment	not modelled	56.7	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** 3.0 angstrom crystal structure of 3-dehydroquinate synthase (arob)2 from francisella tularensis in complex with nad.
56	d1ofua1	Alignment	not modelled	56.2	15	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
57	c3snrA_	Alignment	not modelled	55.7	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.
58	c3d22A_	Alignment	not modelled	55.5	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h-type; **PDBTitle:** crystal structure of a poplar thioredoxin h mutant, pttrxh4c61s
59	c2h9aA_	Alignment	not modelled	55.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase corrinoid/iron-sulfur **PDBTitle:** corrinoid iron-sulfur protein
60	c3h6hB_	Alignment	not modelled	54.1	16	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**glutamate receptor, ionotropic kainate 2; **PDBTitle:** crystal structure of the glur6 amino terminal domain dimer assembly2 mpd form
61	c1jzdA_	Alignment	not modelled	53.1	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
62	c3i09A_	Alignment	not modelled	52.8	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
63	d1rlga_	Alignment	not modelled	51.9	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
64	d1j6ua1	Alignment	not modelled	51.3	14	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
65	d1r57a_	Alignment	not modelled	50.9	27	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
66	c3rfuC_	Alignment	not modelled	50.8	20	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
67	c2mtbA_	Alignment	not modelled	50.2	9	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin-2; **PDBTitle:** solution structure of apo_fldb
68	c3s40C_	Alignment	not modelled	48.9	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
69	c4n03A_	Alignment	not modelled	48.8	2	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc-type branched-chain amino acid transport systems **PDBTitle:** fatty acid abc transporter substrate-binding protein from2 thermomonospora curvata
70	c4kv7A_	Alignment	not modelled	48.5	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**probable leucine/isoleucine/valine-binding protein; **PDBTitle:** the crystal structure of a possible leucine/isoleucine/valine-binding2 protein from rhodopirellula baltica sh 1
71	d1qwka_	Alignment	not modelled	48.2	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
72	c5x2oD_	Alignment	not modelled	47.9	23	**PDB header:**signaling protein/immune system **Chain:** D: **PDB Molecule:**taste receptor, type 1, member 3; **PDBTitle:** crystal structure of the medaka fish taste receptor t1r2a-t1r3 ligand2 binding domains in complex with l-arginine
73	c1t3bA_	Alignment	not modelled	47.8	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
74	d1s1pa_	Alignment	not modelled	47.8	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
75	d1vqof1	Alignment	not modelled	46.9	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
76	c3pfnB_	Alignment	not modelled	46.9	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nad kinase; **PDBTitle:** crystal structure of human nad kinase
77	c4rxuA_	Alignment	not modelled	46.4	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic sugar-binding protein; **PDBTitle:** crystal structure of carbohydrate transporter solute binding protein2 caur_1924 from chloroflexus aurantiacus, target efi-511158, in3 complex with d-glucose
78	c6q7jB_	Alignment	not modelled	46.4	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exo-1,4-beta-xylosidase xlnd; **PDBTitle:** gh3 exo-beta-xylosidase (xlnd) in complex with xylobiose aziridine2 activity based probe
79	c3sq0A	Alignment	not modelled	46.4	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor;

79	c3sg0A_	Alignment	not modelled	46.4	10	**PDBTitle:** the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
80	c4f11A_	Alignment	not modelled	46.4	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**gamma-aminobutyric acid type b receptor subunit 2; **PDBTitle:** crystal structure of the extracellular domain of human gaba(b)2 receptor gbr2
81	c2wjxA_	Alignment	not modelled	45.8	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glutamate receptor 2; **PDBTitle:** crystal structure of the human ionotropic glutamate2 receptor glur2 atd region at 4.1 a resolution
82	d1kbla1	Alignment	not modelled	45.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
83	c3k2qA_	Alignment	not modelled	45.1	14	**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
84	c4npbA_	Alignment	not modelled	45.1	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide isomerase ii; **PDBTitle:** the crystal structure of thiol:disulfide interchange protein dsbc from2 yersinia pestis co92
85	c5kuhB_	Alignment	not modelled	44.7	16	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**glutamate receptor ionotropic, kainate 2; **PDBTitle:** gluk2em with ly466195
86	c5ketA_	Alignment	not modelled	44.3	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase 1; **PDBTitle:** structure of the aldo-keto reductase from coptotermes gestroi
87	c5z6vA_	Alignment	not modelled	44.3	9	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**abc-type uncharacterized transport system periplasmic **PDBTitle:** crystal structure of a substrate-binding protein from rhodothermus2 marinus
88	d1iuka_	Alignment	not modelled	44.2	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
89	c4zdiE_	Alignment	not modelled	44.2	15	**PDB header:**ligase **Chain:** E: **PDB Molecule:**ctp synthase; **PDBTitle:** crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)
90	c4uzzB_	Alignment	not modelled	44.1	19	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**intraflagellar transporter-like protein; **PDBTitle:** crystal structure of the ttift52-46 complex
91	c4n0qD_	Alignment	not modelled	43.8	9	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**leu/ile/val-binding protein homolog 3; **PDBTitle:** crystal structure of an abc transporter, substrate-binding protein2 from brucella melitensis 16m in complex with l-leucine using a3 crystal grown in a crystal former (microlytic)
92	c6c2uA_	Alignment	not modelled	43.3	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**phosphate-loop protein; **PDBTitle:** solution structure of a phosphate-loop protein
93	c4ru0B_	Alignment	not modelled	43.1	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative branched-chain amino acid abc transporter, **PDBTitle:** the crystal structure of abc transporter permease from pseudomonas2 fluorescens group
94	c3n0xA_	Alignment	not modelled	43.0	13	**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
95	c2vlvA_	Alignment	not modelled	41.9	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h isoform 2.; **PDBTitle:** crystal structure of barley thioredoxin h isoform 2 in partially2 radiation-reduced state
96	c3td9A_	Alignment	not modelled	41.9	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**branched chain amino acid abc transporter, periplasmic **PDBTitle:** crystal structure of a leucine binding protein livk (tm1135) from2 thermotoga maritima msb8 at 1.90 a resolution
97	c2vpiA_	Alignment	not modelled	41.8	7	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase; **PDBTitle:** human gmp synthetase - glutaminase domain
98	c1j6uA_	Alignment	not modelled	41.7	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-alanine ligase murc; **PDBTitle:** crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution
99	c3qbeA_	Alignment	not modelled	41.6	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate synthase; **PDBTitle:** crystal structure of the 3-dehydroquinate synthase (arob) from2 mycobacterium tuberculosis
100	c4mlcA_	Alignment	not modelled	41.2	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** abc transporter substrate-binding protein fromdesulfitobacterium2 hafniense
101	c3ej6D_	Alignment	not modelled	41.1	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**catalase-3; **PDBTitle:** neurospora crassa catalase-3 crystal structure
102	c6g61A_	Alignment	not modelled	41.0	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin o1, mitochondrial; **PDBTitle:** crystal structure of thioredoxin o1 from arabidopsis thaliana in2 oxidized state
						PDB header:flavoprotein

103	c4j8pA_	Alignment	not modelled	40.9	20	**Chain:** A: **PDB Molecule:**flavodoxin; **PDBTitle:** crystal structure of a putative flavoprotein (bacuni_04544) from2 bacteroides uniformis atcc 8492 at 1.50 a resolution
104	d1t3ba1	Alignment	not modelled	40.8	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
105	d1j96a_	Alignment	not modelled	40.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
106	c3p3wC_	Alignment	not modelled	40.5	15	**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
107	c3eafA_	Alignment	not modelled	40.5	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter, substrate binding protein; **PDBTitle:** crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
108	c4ys6A_	Alignment	not modelled	40.4	14	**PDB header:**solute-binding protein **Chain:** A: **PDB Molecule:**putative solute-binding component of abc transporter; **PDBTitle:** crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentans (cphy_1585, target efi-3 511156) with bound beta-d-glucose
109	c3sm9A_	Alignment	not modelled	40.0	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**metabotropic glutamate receptor 3; **PDBTitle:** crystal structure of metabotropic glutamate receptor 3 precursor in2 presence of ly341495 antagonist
110	c3trjC_	Alignment	not modelled	39.9	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphoheptose isomerase; **PDBTitle:** structure of a phosphoheptose isomerase from francisella tularensis
111	d1xwaa_	Alignment	not modelled	39.9	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
112	c5zy9D_	Alignment	not modelled	39.8	18	**PDB header:**ligase **Chain:** D: **PDB Molecule:**threonyl-trna synthase; **PDBTitle:** structural basis for a trna synthetase
113	c4wwhA_	Alignment	not modelled	39.8	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter; **PDBTitle:** crystal structure of an abc transporter solute binding protein2 (ipr025997) from mycobacterium smegmatis (msmeg_1704, target efi-3 510967) with bound d-galactose
114	d1vbga1	Alignment	not modelled	39.5	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
115	d1jhfa1	Alignment	not modelled	39.0	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
116	d1a3xa2	Alignment	not modelled	38.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
117	c3h7uA_	Alignment	not modelled	38.2	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c9
118	c5u03C_	Alignment	not modelled	38.1	17	**PDB header:**ligase, protein fibril **Chain:** C: **PDB Molecule:**ctp synthase 1; **PDBTitle:** cryo-em structure of the human ctp synthase filament
119	c4l1gB_	Alignment	not modelled	38.1	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidoglycan n-acetylglucosamine deacetylase; **PDBTitle:** crystal structure of the bc1960 peptidoglycan n-acetylglucosamine2 deacetylase from bacillus cereus
120	d2ozba1	Alignment	not modelled	37.7	10	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins