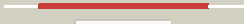



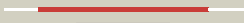



















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1110_(ispH)_1236190_1237197
 Date Wed Jul 31 22:05:19 BST 2019
 Unique Job ID 2cd887ed6b90b14a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3urkA_	 Alignment		100.0	53	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	53	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	41	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	32	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	c5c4nD_	 Alignment		89.2	17	PDB header: oxidoreductase Chain: D: PDB Molecule: precorrin-6a reductase; PDBTitle: cobk precorrin-6a reductase
6	c3rfuC_	 Alignment		87.6	23	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
7	c4zhtB_	 Alignment		86.3	17	PDB header: isomerase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of udp-glnac 2-epimerase
8	c3ff4A_	 Alignment		85.6	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein chu_1412
9	c3j09A_	 Alignment		80.2	16	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
10	c4zo9B_	 Alignment		80.2	15	PDB header: hydrolase Chain: B: PDB Molecule: lin1840 protein; PDBTitle: crystal structure of mutant (d270a) beta-glucosidase from listeria2 innocua in complex with laminaribiose
11	c3h5lB_	 Alignment		78.1	16	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

12	c3j08A_	Alignment		78.0	16	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
13	d1m2ka_	Alignment		77.9	12	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
14	d1j6ua1	Alignment		76.0	16	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
15	c6oviA_	Alignment		75.9	10	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpq aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
16	c4es6A_	Alignment		75.2	10	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen-iii synthase; PDBTitle: crystal structure of hemd (pa5259) from pseudomonas aeruginosa (pao1)2 at 2.22 a resolution
17	c3hutA_	Alignment		73.5	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
18	c3cumA_	Alignment		72.5	22	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
19	c2olsA_	Alignment		71.6	16	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate synthase; PDBTitle: the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
20	c1kblA_	Alignment		71.4	23	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: pyruvate phosphate dikinase
21	d1ma3a_	Alignment	not modelled	71.0	22	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
22	c3afoB_	Alignment	not modelled	70.9	12	PDB header: transferase Chain: B: PDB Molecule: nadh kinase pos5; PDBTitle: crystal structure of yeast nadh kinase complexed with nadh
23	c2bg5C_	Alignment	not modelled	70.2	19	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)
24	d1xmta_	Alignment	not modelled	69.9	20	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
25	d2hk6a1	Alignment	not modelled	65.9	14	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
26	c3l4eA_	Alignment	not modelled	65.2	17	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
27	c4e38A_	Alignment	not modelled	65.1	19	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)
28	c3mw8A_	Alignment	not modelled	65.0	22	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
29	d1fyea_	Alignment	not modelled	64.4	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Aspartyl dipeptidase PepE
30	c5i0cA_	Alignment	not modelled	64.0	15	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
31	c6a4tB_	Alignment	not modelled	62.0	24	PDB header: hydrolase Chain: B: PDB Molecule: peptidase e; PDBTitle: crystal structure of peptidase e from deinococcus radiodurans r1
32	c6q7jB_	Alignment	not modelled	61.8	14	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
33	c3fg9B_	Alignment	not modelled	61.8	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein of universal stress protein uspa family; PDBTitle: the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcf51
34	c3zdrA_	Alignment	not modelled	61.2	10	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
35	c5ereA_	Alignment	not modelled	60.8	16	PDB header: signaling protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: extracellular ligand binding receptor from desulfohalobium retbaense2 dsm5692
36	c4maaA_	Alignment	not modelled	60.7	15	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
37	c5vtoA_	Alignment	not modelled	60.0	23	PDB header: hydrolase Chain: A: PDB Molecule: blasticidin m; PDBTitle: solution structure of blsm
38	c4qccA_	Alignment	not modelled	59.9	16	PDB header: structural protein, lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- PDBTitle: structure of a cube-shaped, highly porous protein cage designed by2 fusing symmetric oligomeric domains
39	d1kbla1	Alignment	not modelled	58.9	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
40	d1qo0a_	Alignment	not modelled	58.4	17	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
41	c4evsA_	Alignment	not modelled	58.2	7	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
42	c1jzdA_	Alignment	not modelled	55.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: dsbc-dsbdalpha complex
43	d2d59a1	Alignment	not modelled	55.8	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
44	c4yt2A_	Alignment	not modelled	55.6	15	PDB header: metal binding protein Chain: A: PDB Molecule: h(2)-forming methylenetetrahydromethanopterin PDBTitle: hmd ii from methanocaldococcus jannaschii
45	c6huxA_	Alignment	not modelled	54.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: h(2)-forming methylenetetrahydromethanopterin PDBTitle: hmdii from methanocaldococcus jannaschii reconstituted with fe-2 guanylylpyridinol (fepg) cofactor and co-crystallized with methenyl-3 tetrahydromethanopterin at 2.5 a resolution
46	c3pkIF_	Alignment	not modelled	54.8	19	PDB header: hydrolase Chain: F: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: human sirt6 crystal structure in complex with adp ribose
47	c3w6uA_	Alignment	not modelled	54.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, nad-binding protein; PDBTitle: crystal structure of nadp bound l-serine 3-dehydrogenase from2 hyperthermophilic archaeon pyrobaculum calidifontis
48	c2iz6A_	Alignment	not modelled	54.5	18	PDB header: metal transport Chain: A: PDB Molecule: molybdenum cofactor carrier protein; PDBTitle: structure of the chlamydomonas reinhardtii moco carrier2 protein
49	c3ac0B_	Alignment	not modelled	54.4	13	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase i; PDBTitle: crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
50	c5mrwF_	Alignment	not modelled	54.3	19	PDB header: hydrolase Chain: F: PDB Molecule: potassium-transporting atpase atp-binding subunit; PDBTitle: structure of the kdpfabc complex
51	c4mlcA_	Alignment	not modelled	54.1	20	PDB header: signaling protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: abc transporter substrate-binding protein fromdesulfitobacterium2 hafniense PDB header: oxidoreductase

52	c4dllB	Alignment	not modelled	53.8	19	Chain: B: PDB Molecule: 2-hydroxy-3-oxopropionate reductase; PDBTitle: crystal structure of a 2-hydroxy-3-oxopropionate reductase from <i>2 polaromonas sp. js666</i>
53	c5i01B	Alignment	not modelled	53.4	22	PDB header: isomerase Chain: B: PDB Molecule: phosphoheptose isomerase; PDBTitle: structure of phosphoheptose isomerase gmha from <i>neisseria gonorrhoeae</i>
54	d2g17a1	Alignment	not modelled	53.2	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
55	c1gqqa	Alignment	not modelled	53.1	22	PDB header: cell wall biosynthesis Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: murc - crystal structure of the apo-enzyme from <i>haemophilus influenzae</i>
56	c3snrA	Alignment	not modelled	52.0	21	PDB header: transport protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: rpd_1889 protein, an extracellular ligand-binding receptor from <i>2 rhodopseudomonas palustris</i> .
57	c4n03A	Alignment	not modelled	51.8	5	PDB header: transport protein Chain: A: PDB Molecule: abc-type branched-chain amino acid transport systems PDBTitle: fatty acid abc transporter substrate-binding protein from <i>2 thermomonospora curvata</i>
58	d1yq2a5	Alignment	not modelled	51.7	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
59	d2jfga1	Alignment	not modelled	50.8	17	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
60	d1h6za1	Alignment	not modelled	50.7	13	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
61	d1yc5a1	Alignment	not modelled	50.7	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
62	d1r57a	Alignment	not modelled	50.5	31	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
63	c3h6hB	Alignment	not modelled	50.3	11	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
64	c1j6uA	Alignment	not modelled	50.0	17	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 <i>thermotoga maritima</i> at 2.3 a resolution
65	d1vbga1	Alignment	not modelled	49.8	26	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
66	c6cauA	Alignment	not modelled	49.7	14	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: udp-n-acetylmuramate--alanine ligase from <i>acinetobacter baumannii2 ab5075-uw</i> with amppnp
67	c3i09A	Alignment	not modelled	49.6	15	PDB header: transport protein Chain: A: PDB Molecule: periplasmic branched-chain amino acid-binding protein; PDBTitle: crystal structure of a periplasmic binding protein (bma2936) from <i>2 burkholderia mallei</i> at 1.80 a resolution
68	c4evrA	Alignment	not modelled	49.5	13	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter subunit, substrate-binding PDBTitle: crystal structure of abc transporter from <i>r. palustris</i> - solute2 binding protein (rpa0668) in complex with benzoate
69	c2hroA	Alignment	not modelled	49.5	19	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of the full-length enzyme i of the pts system from <i>2 staphylococcus carnosus</i>
70	c3s40C	Alignment	not modelled	49.1	24	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from <i>bacillus2 anthracis str. sterne</i>
71	c1t3bA	Alignment	not modelled	48.9	13	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbc; PDBTitle: x-ray structure of dsbc from <i>haemophilus influenzae</i>
72	d2j13a1	Alignment	not modelled	48.7	11	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
73	c4gnrA	Alignment	not modelled	48.3	17	PDB header: transport protein Chain: A: PDB Molecule: abc transporter substrate-binding protein-branched chain PDBTitle: 1.0 angstrom resolution crystal structure of the branched-chain amino2 acid transporter substrate binding protein livj from <i>streptococcus3 pneumoniae str. canada mdr_19a</i> in complex with isoleucine
74	c5f56A	Alignment	not modelled	48.2	15	PDB header: dna binding protein/dna Chain: A: PDB Molecule: single-stranded-dna-specific exonuclease; PDBTitle: structure of recj complexed with dna and ssb-ct
75	c6hpdA	Alignment	not modelled	48.1	11	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase (gh2); PDBTitle: the structure of a beta-glucuronidase from glycoside hydrolase family2 2
76	c3zg6A	Alignment	not modelled	47.8	19	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
77	c3ej6D_	Alignment	not modelled	47.5	15	PDB header: oxidoreductase Chain: D: PDB Molecule: catalase-3; PDBTitle: neurospora crassa catalase-3 crystal structure
78	c4i3gB_	Alignment	not modelled	47.5	14	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of desr, a beta-glucosidase from streptomyces2 venezuelae in complex with d-glucose.
79	c5g6sD_	Alignment	not modelled	47.2	11	PDB header: oxidoreductase Chain: D: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus oryzae in complex with nadp(h) and2 (r)-rasagiline
80	c3sg0A_	Alignment	not modelled	46.6	23	PDB header: signaling protein Chain: A: PDB Molecule: extracellular ligand-binding receptor; PDBTitle: the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
81	c4npbA_	Alignment	not modelled	46.0	17	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
82	d2je8a5	Alignment	not modelled	45.7	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
83	c3eafA_	Alignment	not modelled	44.0	9	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein; PDBTitle: crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
84	c2hwgA_	Alignment	not modelled	43.9	15	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
85	d1uc8a1	Alignment	not modelled	43.8	14	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Lysine biosynthesis enzyme LysX, N-terminal domain
86	c4l1gB_	Alignment	not modelled	43.0	12	PDB header: hydrolase Chain: B: PDB Molecule: peptidoglycan n-acetylglucosamine deacetylase; PDBTitle: crystal structure of the bc1960 peptidoglycan n-acetylglucosamine2 deacetylase from bacillus cereus
87	d1w5fa1	Alignment	not modelled	43.0	14	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
88	d7reqa2	Alignment	not modelled	42.5	16	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
89	c3n0xA_	Alignment	not modelled	42.3	17	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
90	c5nymA_	Alignment	not modelled	42.3	10	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
91	d1t3ba1	Alignment	not modelled	42.3	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
92	c4f11A_	Alignment	not modelled	42.2	17	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
93	c1vbhA_	Alignment	not modelled	42.1	26	PDB header: transferase Chain: A: PDB Molecule: pyruvate,orthophosphate dikinase; PDBTitle: pyruvate phosphate dikinase with bound mg-pep from maize
94	d1vhca_	Alignment	not modelled	42.0	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
95	d1k0ma2	Alignment	not modelled	41.9	13	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
96	c3mn1B_	Alignment	not modelled	41.5	10	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
97	d2hrca1	Alignment	not modelled	41.4	16	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelataase
98	c4umwA_	Alignment	not modelled	41.3	14	PDB header: hydrolase Chain: A: PDB Molecule: zinc-transporting atpase; PDBTitle: crystal structure of a zinc-transporting pib-type atpase in2 e2.pi state
99	d1p3da1	Alignment	not modelled	41.0	24	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
100	c3b8cB_	Alignment	not modelled	40.6	13	PDB header: hydrolase Chain: B: PDB Molecule: atpase 2, plasma membrane-type; PDBTitle: crystal structure of a plasma membrane proton pump
101	c4kv7A_	Alignment	not modelled	40.5	17	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
102	c3fwzA_	Alignment	not modelled	40.2	9	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
103	d1vlja_	Alignment	not modelled	40.1	13	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
104	d2dlxa1	Alignment	not modelled	39.9	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: UAS domain
105	c5kuhB_	Alignment	not modelled	39.7	11	PDB header: signaling protein Chain: B: PDB Molecule: glutamate receptor ionotropic, kainate 2; PDBTitle: gluk2em with lyk466195
106	c6qkzA_	Alignment	not modelled	39.5	8	PDB header: membrane protein Chain: A: PDB Molecule: glua1; PDBTitle: full length glua1/2-gamma8 complex
107	c3cmgA_	Alignment	not modelled	39.1	10	PDB header: hydrolase Chain: A: PDB Molecule: putative beta-galactosidase; PDBTitle: crystal structure of putative beta-galactosidase from bacteroides2 fragilis
108	c2r8zC_	Alignment	not modelled	39.0	13	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
109	d1s5pa_	Alignment	not modelled	38.7	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
110	c2vpiA_	Alignment	not modelled	38.7	3	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
111	c1v57A_	Alignment	not modelled	38.7	17	PDB header: isomerase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsbg; PDBTitle: crystal structure of the disulfide bond isomerase dsbg
112	d1s1pa_	Alignment	not modelled	38.5	11	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
113	c4ru0B_	Alignment	not modelled	38.5	13	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
114	c3f4cA_	Alignment	not modelled	38.4	15	PDB header: hydrolase Chain: A: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of organophosphorus hydrolase from geobacillus2 stearothermophilus strain 10, with glycerol bound
115	d1iuka_	Alignment	not modelled	38.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
116	c3p9zA_	Alignment	not modelled	38.2	17	PDB header: ligase Chain: A: PDB Molecule: uroporphyrinogen iii cosynthase (hemd); PDBTitle: crystal structure of uroporphyrinogen-iii synthetase from helicobacter2 pylori 26695
117	c2mtbA_	Alignment	not modelled	37.8	5	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin-2; PDBTitle: solution structure of apo_fldb
118	c4nqrA_	Alignment	not modelled	37.4	15	PDB header: transport protein Chain: A: PDB Molecule: amino acid/amide abc transporter substrate-binding protein, PDBTitle: the crystal structure of a solute-binding protein (n280d mutant) from2 anabaena variabilis atcc 29413 in complex with alanine
119	d1ofua1	Alignment	not modelled	37.3	16	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
120	d1jhfa1	Alignment	not modelled	37.3	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain