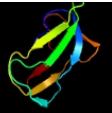







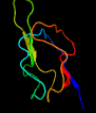


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3221c_(TB7.3)_3597548_3597763
 Date Thu Aug 8 16:20:42 BST 2019
 Unique Job ID f4b183380832bb9e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3n6rK_	Alignment		99.9	26	PDB header: ligase Chain: K; PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
2	d1dcza_	Alignment		99.9	35	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
3	c4hnbV_	Alignment		99.9	33	PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
4	c3hblA_	Alignment		99.9	33	PDB header: ligase Chain: A; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant
5	c3bg5B_	Alignment		99.8	33	PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
6	c5vz0D_	Alignment		99.8	34	PDB header: ligase Chain: D; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of lactococcus lactis pyruvate carboxylase g746a2 mutant in complex with cyclic-di-amp
7	c4qskB_	Alignment		99.8	43	PDB header: ligase Chain: B; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp
8	c5ks8D_	Alignment		99.8	31	PDB header: ligase Chain: D; PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
9	c2ejgD_	Alignment		99.8	29	PDB header: ligase Chain: D; PDB Molecule: 149aa long hypothetical methylmalonyl-coa decarboxylase PDBTitle: crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
10	c2b8gA_	Alignment		99.8	42	PDB header: biosynthetic protein Chain: A; PDB Molecule: biotin/lipoyl attachment protein; PDBTitle: solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
11	c5ks8F_	Alignment		99.8	32	PDB header: ligase Chain: F; PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus

12	c2ejmA	Alignment		99.8	25	PDB header: ligase Chain: A: PDB Molecule: methylcrotonoyl-coa carboxylase subunit alpha; PDBTitle: solution structure of ruh-072, an apo-biotinyl domain form2 human acetyl coenzyme a carboxylase
13	c3u9sA	Alignment		99.8	29	PDB header: ligase Chain: A: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
14	c3bg3A	Alignment		99.8	32	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase, mitochondrial; PDBTitle: crystal structure of human pyruvate carboxylase (missing the biotin2 carboxylase domain at the n-terminus)
15	d1o78a	Alignment		99.8	35	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
16	c2dn8A	Alignment		99.8	21	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
17	c2kccA	Alignment		99.8	23	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
18	c4rcnA	Alignment		99.8	33	PDB header: ligase Chain: A: PDB Molecule: long-chain acyl-coa carboxylase; PDBTitle: structure and function of a single-chain, multi-domain long-chain2 acyl-coa carboxylase
19	c3va7A	Alignment		99.8	39	PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
20	d1qjoa	Alignment		99.8	31	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
21	c5cslA	Alignment	not modelled	99.8	28	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
22	d1bdoa	Alignment	not modelled	99.8	26	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
23	d1iyua	Alignment	not modelled	99.8	35	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
24	c6g2dC	Alignment	not modelled	99.8	21	PDB header: ligase Chain: C: PDB Molecule: acetyl-coa carboxylase 1; PDBTitle: citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
25	c2dncA	Alignment	not modelled	99.8	23	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase protein x component; PDBTitle: solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
26	d1ghja	Alignment	not modelled	99.8	27	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
27	d1k8ma	Alignment	not modelled	99.7	23	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
28	d1y8ob1	Alignment	not modelled	99.7	21	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
						PDB header: transferase Chain: B: PDB Molecule: dihydrolipoyllysine-residue

29	c2q8iB_	Alignment	not modelled	99.7	21	acetyltransferase component of PDBTitle: pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase PDBTitle: solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase PDB header: transferase Chain: A: PDB Molecule: lipoaamide acyltransferase; PDBTitle: solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of domains bt-bccp-ac1-ac5 of yeast acetyl-coa2 carboxylase
30	c2dneA_	Alignment	not modelled	99.7	20	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
31	c2i5tA_	Alignment	not modelled	99.7	21	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
32	c5csaA_	Alignment	not modelled	99.7	28	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
33	d1qjxa_	Alignment	not modelled	99.7	40	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
34	d1laba_	Alignment	not modelled	99.7	18	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
35	d1pmra_	Alignment	not modelled	99.7	23	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
36	c2qf7A_	Alignment	not modelled	99.6	37	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli PDB header: ligase/activator Chain: B: PDB Molecule: pyruvate carboxylase protein; PDBTitle: structure of rhizobium etli pyruvate carboxylase t882a with the2 allosteric activator, acetyl coenzyme-a
37	c3tw6B_	Alignment	not modelled	99.5	44	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
38	d2pnrc1	Alignment	not modelled	99.5	20	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: acra; PDBTitle: solution structure of an n-glycosylated protein using in2 vitro glycosylation
39	c2k33A_	Alignment	not modelled	99.2	19	PDB header: membrane protein Chain: D: PDB Molecule: membrane fusion protein; PDBTitle: structure of besa (selenomethionone derivative - p212121)
40	c4kkuD_	Alignment	not modelled	98.8	23	PDB header: transport protein Chain: B: PDB Molecule: cation efflux system protein cusb; PDBTitle: crystal structure of the membrane fusion protein cusb from escherichia2 coli
41	c3h9iB_	Alignment	not modelled	98.7	29	PDB header: transport protein Chain: C: PDB Molecule: cation efflux system protein cusb; PDBTitle: crystal structures of the pre-extrusion and extrusion states of the2 cusba adaptor-transporter complex
42	c3t51C_	Alignment	not modelled	98.6	29	PDB header: hydrolase Chain: C: PDB Molecule: putative succinylglutamate desuccinylase / aspartoacylase; PDBTitle: crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
43	c3fmcC_	Alignment	not modelled	98.3	12	PDB header: hydrolase Chain: B: PDB Molecule: mlr6093 protein; PDBTitle: crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
44	c2qj8B_	Alignment	not modelled	98.3	22	PDB header: transport protein Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage protein h-like (gcvh-1)2 from streptococcus pyogenes
45	c5a35A_	Alignment	not modelled	98.3	23	PDB header: hydrolase Chain: A: PDB Molecule: succinylglutamate desuccinylase/aspartoacylase; PDBTitle: crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
46	c3na6A_	Alignment	not modelled	98.1	22	PDB header: ligase Chain: A: PDB Molecule: propionyl-coa carboxylase alpha chain, mitochondrial; PDBTitle: crystal structure of the n-terminal region of the biotin acceptor2 domain of human propionyl-coa carboxylase
47	c2jkuA_	Alignment	not modelled	98.1	24	PDB header: protein transport Chain: A: PDB Molecule: chromosomal hemolysin d; PDBTitle: crystal structure of zn-bound hlyd from e. coli
48	c5c22A_	Alignment	not modelled	98.0	29	PDB header: metal transport Chain: A: PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans
49	c3lnnA_	Alignment	not modelled	97.9	21	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance protein mexa; PDBTitle: the structure of mexa
50	c1t5eB_	Alignment	not modelled	97.9	19	PDB header: transport protein Chain: B: PDB Molecule: membrane-fusion protein; PDBTitle: structure of the membrane fusion protein spr0693 from streptococcus2 pneumoniae r6
51	c5xu0B_	Alignment	not modelled	97.9	24	PDB header: membrane protein Chain: B: PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra
52	c4tkoB_	Alignment	not modelled	97.8	22	Fold: HlyD-like secretion proteins Superfamily: HlyD-like secretion proteins Family: HlyD-like secretion proteins
53	d1vf7a_	Alignment	not modelled	97.8	19	PDB header: metal transport Chain: B: PDB Molecule: membrane fusion protein (mfp) heavy
54	c3lnnB_	Alignment	not modelled	97.8	22	

54	c3mnb_	Alignment	not modelled	97.8	22	metal cation efflux PDB header: crystal structure of zneb from cupriavidus metallidurans PDB header: oxidoreductase
55	c3iftA_	Alignment	not modelled	97.8	27	Chain: A; PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
56	d1onla_	Alignment	not modelled	97.8	30	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
57	c2f1mA_	Alignment	not modelled	97.8	22	PDB header: transport protein Chain: A; PDB Molecule: acriflavine resistance protein a; PDBTitle: conformational flexibility in the multidrug efflux system protein acra
58	c3cdxB_	Alignment	not modelled	97.8	18	PDB header: hydrolase Chain: B; PDB Molecule: succinylglutamatedesuccinylase/aspartoacylase; PDBTitle: crystal structure of succinylglutamatedesuccinylase/aspartoacylase2 from rhodobacter sphaeroides
59	d1hpca_	Alignment	not modelled	97.8	27	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
60	c2edgA_	Alignment	not modelled	97.8	20	PDB header: biosynthetic protein Chain: A; PDB Molecule: glycine cleavage system h protein; PDBTitle: solution structure of the gcv_h domain from mouse glycine
61	c3mxuA_	Alignment	not modelled	97.8	25	PDB header: oxidoreductase Chain: A; PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from bartonella2 henselae
62	c4l8jA_	Alignment	not modelled	97.8	16	PDB header: transport protein Chain: A; PDB Molecule: putative efflux transporter; PDBTitle: crystal structure of a putative efflux transporter (bacegg_01895) from2 bacteroides eggerthii dsm 20697 at 2.06 a resolution
63	c5v5sH_	Alignment	not modelled	97.7	22	PDB header: membrane protein Chain: H; PDB Molecule: multidrug efflux pump subunit acra; PDBTitle: multi-drug efflux; membrane transport; rnd superfamily; drug2 resistance
64	c3fppB_	Alignment	not modelled	97.7	22	PDB header: membrane protein Chain: B; PDB Molecule: macrolide-specific efflux protein maca; PDBTitle: crystal structure of e.coli maca
65	c2v4dM_	Alignment	not modelled	97.6	19	PDB header: membrane protein Chain: M; PDB Molecule: multidrug resistance protein mexa; PDBTitle: re-refinement of mexa adaptor protein
66	c5nenA_	Alignment	not modelled	97.6	26	PDB header: hydrolase Chain: A; PDB Molecule: lipase c; PDBTitle: crystal structure of the soluble domain of lipc, a membrane fusion2 protein of a type i secretion system
67	d2f3ga_	Alignment	not modelled	97.4	22	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
68	c2aukA_	Alignment	not modelled	97.4	35	PDB header: transferase Chain: A; PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert
69	d2gprr_	Alignment	not modelled	97.4	24	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
70	d1glaf_	Alignment	not modelled	97.4	22	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
71	c3a8jF_	Alignment	not modelled	97.4	20	PDB header: transferase/transport protein Chain: F; PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of et-ehred complex
72	c4dk0A_	Alignment	not modelled	97.3	31	PDB header: membrane protein Chain: A; PDB Molecule: putative maca; PDBTitle: crystal structure of maca from actinobacillus actinomycetemcomitans
73	c4dk1B_	Alignment	not modelled	97.3	28	PDB header: membrane protein Chain: B; PDB Molecule: putative maca, multidrug resistance protein mexa; PDBTitle: crystal structure of maca-mexa chimeric protein, containing the2 pseudomonas aeruginosa mexa alpha-hairpin domain.
74	c2ka7A_	Alignment	not modelled	97.2	33	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: glycine cleavage system h protein; PDBTitle: nmr solution structure of tm0212 at 40 c
75	c4p6vA_	Alignment	not modelled	97.2	19	PDB header: oxidoreductase Chain: A; PDB Molecule: na(+)-translocating nadh-quinone reductase subunit a; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
76	c5nilG_	Alignment	not modelled	97.1	23	PDB header: transport protein Chain: G; PDB Molecule: macrolide export protein maca; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug efflux pump-2 macb section
77	c2aujD_	Alignment	not modelled	96.6	28	PDB header: transferase Chain: D; PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of thermus aquaticus rna polymerase beta'-subunit2 insert
78	d1gprr_	Alignment	not modelled	96.6	20	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
						PDB header: unknown function

79	c3d4rE_	Alignment	not modelled	96.4	23	Chain: E; PDB Molecule: domain of unknown function from the pfam-b_34464 family; PDBTitle: crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution
80	d1uoua3	Alignment	not modelled	94.9	48	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
81	d1brwa3	Alignment	not modelled	94.6	28	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
82	d2tpta3	Alignment	not modelled	94.2	24	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
83	c2hsiB_	Alignment	not modelled	92.6	27	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative peptidase m23; PDBTitle: crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
84	c4bh5B_	Alignment	not modelled	92.2	29	PDB header: cell cycle Chain: B; PDB Molecule: murein hydrolase activator envc; PDBTitle: lytm domain of envc, an activator of cell wall amidases in2 escherichia coli
85	c2j0fC_	Alignment	not modelled	91.9	43	PDB header: transferase Chain: C; PDB Molecule: thymidine phosphorylase; PDBTitle: structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
86	c3h5qA_	Alignment	not modelled	91.9	28	PDB header: transferase Chain: A; PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
87	c2dsjA_	Alignment	not modelled	91.8	31	PDB header: transferase Chain: A; PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
88	c2gu1A_	Alignment	not modelled	90.8	31	PDB header: hydrolase Chain: A; PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
89	c1otpA_	Alignment	not modelled	90.8	23	PDB header: phosphorylase Chain: A; PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
90	d1qpoa2	Alignment	not modelled	89.7	19	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
91	d1o4ua2	Alignment	not modelled	89.3	19	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
92	c2b44A_	Alignment	not modelled	88.5	23	PDB header: hydrolase Chain: A; PDB Molecule: glycyI-glycine endopeptidase lytm; PDBTitle: truncated s. aureus lytm, p 32 2 1 crystal form
93	c2xhaB_	Alignment	not modelled	88.2	36	PDB header: transcription Chain: B; PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of domain 2 of thermotoga maritima n-utilization2 substance g (nusg)
94	c3tufB_	Alignment	not modelled	88.0	24	PDB header: signaling protein Chain: B; PDB Molecule: stage ii sporulation protein q; PDBTitle: structure of the spoIii-spoIIiAh pore forming complex.
95	c4qpbB_	Alignment	not modelled	87.1	25	PDB header: hydrolase Chain: B; PDB Molecule: lysostaphin; PDBTitle: catalytic domain of the antimicrobial peptidase lysostaphin from2 staphylococcus simulans crystallized in the absence of phosphate
96	c5j1mD_	Alignment	not modelled	86.9	22	PDB header: hydrolase Chain: D; PDB Molecule: toxr-activated gene (tage); PDBTitle: crystal structure of csd1-csd2 dimer ii
97	d1qapa2	Alignment	not modelled	86.8	33	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
98	c4iqzD_	Alignment	not modelled	86.5	23	PDB header: unknown function Chain: D; PDB Molecule: dna-directed rna polymerase subunit beta'; PDBTitle: the crystal structure of a large insert in rna polymerase (rpoC)2 subunit from e. coli
99	c1brwB_	Alignment	not modelled	86.4	21	PDB header: transferase Chain: B; PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
100	c4ga5H_	Alignment	not modelled	85.7	21	PDB header: transferase Chain: H; PDB Molecule: putative thymidine phosphorylase; PDBTitle: crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form
101	c5kqbA_	Alignment	not modelled	84.3	22	PDB header: hydrolase Chain: A; PDB Molecule: peptidase m23; PDBTitle: identification and structural characterization of lytu
102	d1qwya_	Alignment	not modelled	84.1	22	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Peptidoglycan hydrolase LytM
103	c2xhcA_	Alignment	not modelled	83.2	36	PDB header: transcription Chain: A; PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of thermotoga maritima n-utilization

						substance g2 (nusc)
104	c5gt1A_	Alignment	not modelled	82.9	25	PDB header: choline-binding protein Chain: A: PDB Molecule: choline binding protein a; PDBTitle: crystal structure of cbpa from <i>I. salivarius</i> ren
105	d1ci3m2	Alignment	not modelled	82.8	22	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
106	c5j11A_	Alignment	not modelled	82.5	16	PDB header: hydrolase Chain: A: PDB Molecule: toxR-activated gene (tage); PDBTitle: crystal structure of csd1-csd2 dimer i
107	c3gnnA_	Alignment	not modelled	81.3	20	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from <i>2 burkholderi pseudomallei</i>
108	c4lxcA_	Alignment	not modelled	81.0	19	PDB header: hydrolase Chain: A: PDB Molecule: lysostaphin; PDBTitle: the antimicrobial peptidase lysostaphin from <i>staphylococcus simulans</i>
109	c5b0hB_	Alignment	not modelled	80.8	10	PDB header: metal binding protein Chain: B: PDB Molecule: leukocyte cell-derived chemotaxin-2; PDBTitle: crystal structure of human leukocyte cell-derived chemotaxin 2
110	c3uz0D_	Alignment	not modelled	80.4	30	PDB header: transport protein Chain: D: PDB Molecule: stage ii sporulation protein q; PDBTitle: crystal structure of spoIIAH and spoIIQ complex
111	c3pajA_	Alignment	not modelled	79.4	24	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase, carboxylating; PDBTitle: 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from <i>vibrio cholerae</i> o1 biovar eltor str.3 n16961
112	c1o4uA_	Alignment	not modelled	79.2	19	PDB header: transferase Chain: A: PDB Molecule: type ii quinolinic acid phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from <i>thermotoga maritima</i> at 2.50 a resolution
113	d1e2wa2	Alignment	not modelled	78.4	19	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
114	c2lmcB_	Alignment	not modelled	78.0	33	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: structure of t7 transcription factor gp2-e. coli rnap jaw domain2 complex
115	c3it5B_	Alignment	not modelled	77.3	14	PDB header: hydrolase Chain: B: PDB Molecule: protease lasa; PDBTitle: crystal structure of the lasa virulence factor from <i>pseudomonas2 aeruginosa</i>
116	c5kvpA_	Alignment	not modelled	76.0	19	PDB header: hydrolase Chain: A: PDB Molecule: zoocin a endopeptidase; PDBTitle: solution structure of the catalytic domain of zoocin a
117	c1qpoA_	Alignment	not modelled	75.9	19	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apoenzyme from <i>2 mycobacterium tuberculosis</i>
118	c2jbmA_	Alignment	not modelled	75.6	14	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
119	c1qapA_	Alignment	not modelled	75.0	33	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
120	c3tqvA_	Alignment	not modelled	73.8	5	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: structure of the nicotinate-nucleotide pyrophosphorylase from <i>2 francisella tularensis</i> .