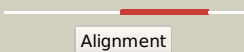

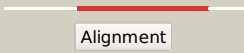



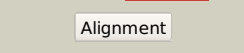



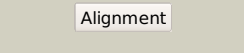

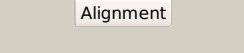



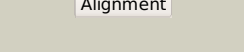

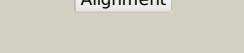

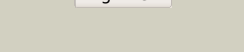
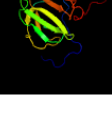











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0950c_(-)_1060660_1061658
Date	Fri Jul 26 01:50:54 BST 2019
Unique Job ID	2afe2571e827f560

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sluB_	 Alignment		100.0	38	PDB header: hydrolase Chain: B: PDB Molecule: m23 peptidase domain protein; PDBTitle: crystal structure of nmb0315
2	c2gu1A_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
3	c2hsiB_	 Alignment		100.0	33	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
4	c4rnzA_	 Alignment		100.0	33	PDB header: hydrolase Chain: A: PDB Molecule: conserved hypothetical secreted protein; PDBTitle: structure of helicobacter pylori csd3 from the hexagonal crystal
5	d1qwya_	 Alignment		100.0	38	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Peptidoglycan hydrolase LytM
6	c4bh5B_	 Alignment		100.0	35	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
7	c4lxcA_	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: lysostaphin; PDBTitle: the antimicrobial peptidase lysostaphin from staphylococcus simulans
8	c3nyyA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: putative glycyl-glycine endopeptidase lytm; PDBTitle: crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
9	c2b44A_	 Alignment		100.0	40	PDB header: hydrolase Chain: A: PDB Molecule: glycyl-glycine endopeptidase lytm; PDBTitle: truncated s. aureus lytm, p 32 2 1 crystal form
10	c5j1mD_	 Alignment		100.0	31	PDB header: hydrolase Chain: D: PDB Molecule: tox-activated gene (tage); PDBTitle: crystal structure of csd1-csd2 dimer ii
11	c5kvpA_	 Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: zoocin a endopeptidase; PDBTitle: solution structure of the catalytic domain of zoocin a

12	c5kqbA	Alignment		100.0	35	PDB header: hydrolase Chain: A: PDB Molecule: peptidase m23; PDBTitle: identification and structural characterization of lytu
13	c4qpbB	Alignment		100.0	35	PDB header: hydrolase Chain: B: PDB Molecule: lysostaphin; PDBTitle: catalytic domain of the antimicrobial peptidase lysostaphin from <i>Staphylococcus simulans</i> crystallized in the absence of phosphate
14	c3tufB	Alignment		100.0	30	PDB header: signaling protein Chain: B: PDB Molecule: stage ii sporulation protein q; PDBTitle: structure of the spoIIQ-spoIIIAH pore forming complex.
15	c5j1IA	Alignment		100.0	43	PDB header: hydrolase Chain: A: PDB Molecule: toxR-activated gene (tage); PDBTitle: crystal structure of Csd1-Csd2 dimer I
16	c3uz0D	Alignment		100.0	24	PDB header: transport protein Chain: D: PDB Molecule: stage ii sporulation protein q; PDBTitle: crystal structure of spoIIAH and spoIIQ complex
17	c5gt1A	Alignment		100.0	21	PDB header: choline-binding protein Chain: A: PDB Molecule: choline binding protein a; PDBTitle: crystal structure of Cbpa from <i>L. salivarius</i> ren
18	c3it5B	Alignment		99.9	23	PDB header: hydrolase Chain: B: PDB Molecule: protease lasa; PDBTitle: crystal structure of the lasa virulence factor from <i>Pseudomonas aeruginosa</i>
19	c5b0hB	Alignment		99.9	18	PDB header: metal binding protein Chain: B: PDB Molecule: leukocyte cell-derived chemotaxin-2; PDBTitle: crystal structure of human leukocyte cell-derived chemotaxin 2
20	c3csqC	Alignment		99.9	21	PDB header: hydrolase Chain: C: PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall-degrading enzyme in the bacteriophage phi29 tail
21	c4cgkA	Alignment	not modelled	97.2	15	PDB header: cell cycle Chain: A: PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from <i>Streptococcus pneumoniae</i>
22	d2f3ga	Alignment	not modelled	96.9	22	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
23	d1glaf	Alignment	not modelled	96.7	24	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
24	d2gpRA	Alignment	not modelled	96.4	24	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
25	d1gpRA	Alignment	not modelled	96.3	22	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
26	d1ci3m2	Alignment	not modelled	94.6	29	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
27	c2aukA	Alignment	not modelled	93.4	19	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert
28	d1brwa3	Alignment	not modelled	93.3	31	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
29	c2lmcB	Alignment	not modelled	93.1	28	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase subunit beta;

29	c2m1cB	Alignment	not modelled	93.1	20	PDBTitle: structure of t7 transcription factor gp2-e. coli rnap jaw domain2 complex
30	d1e2wa2	Alignment	not modelled	92.8	21	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
31	c4iqzD	Alignment	not modelled	92.7	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 (rroc)2 subunit from e. coli
32	d2tpt3	Alignment	not modelled	91.9	22	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
33	c3n6rK	Alignment	not modelled	91.8	28	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
34	c1e2vB	Alignment	not modelled	91.7	21	PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: n153q mutant of cytochrome f from chlamydomonas reinhardtii
35	c2j0fC	Alignment	not modelled	91.3	30	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
36	c1otpA	Alignment	not modelled	90.8	24	PDB header: phosphorylase Chain: A: PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
37	c3h5qA	Alignment	not modelled	90.2	26	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
38	c4xcmB	Alignment	not modelled	89.4	10	PDB header: hydrolase Chain: B: PDB Molecule: cell wall-binding endopeptidase-related protein; PDBTitle: crystal structure of the putative nlpc/p60 d,l endopeptidase from t.2 thermophilus
39	c1ctmA	Alignment	not modelled	89.3	17	PDB header: electron transport(cytochrome) Chain: A: PDB Molecule: cytochrome f; PDBTitle: crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
40	c2jxmB	Alignment	not modelled	89.3	24	PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
41	c2ejgD	Alignment	not modelled	88.6	22	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
42	c1q90A	Alignment	not modelled	88.3	20	PDB header: photosynthesis Chain: A: PDB Molecule: apocytochrome f; PDBTitle: structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
43	c5c22A	Alignment	not modelled	87.7	30	PDB header: protein transport Chain: A: PDB Molecule: chromosomal hemolysin d; PDBTitle: crystal structure of zn-bound hlyd from e. coli
44	c4hmvB	Alignment	not modelled	87.7	45	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of r54e mutant of s. aureus pyruvate carboxylase
45	d1bdoa	Alignment	not modelled	87.6	16	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
46	c3hblA	Alignment	not modelled	87.1	45	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of s. aureus pyruvate carboxylase t908a mutant
47	c5ks8D	Alignment	not modelled	87.1	31	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
48	c3bg5B	Alignment	not modelled	86.9	45	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate carboxylase
49	c5vz0D	Alignment	not modelled	86.9	29	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
50	c2dsjA	Alignment	not modelled	86.6	33	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
51	c5xu0B	Alignment	not modelled	85.9	35	PDB header: transport protein Chain: B: PDB Molecule: membrane-fusion protein; PDBTitle: structure of the membrane fusion protein spr0693 from streptococcus2 pneumoniae r6
52	c1brwB	Alignment	not modelled	85.9	34	PDB header: transferase Chain: B: PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
53	c4qskB	Alignment	not modelled	85.7	39	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of l. monocytogenes pyruvate

						carboxylase in complex2 with cyclic-di-amp
54	d1dcza_	Alignment	not modelled	84.9	20	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
55	c5ks8F_	Alignment	not modelled	83.8	31	PDB header: ligase Chain: F: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
56	c1tu2B_	Alignment	not modelled	83.5	27	PDB header: electron transport Chain: B: PDB Molecule: apocytochrome f; PDBTitle: the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
57	d1o78a_	Alignment	not modelled	83.2	35	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
58	c4ga5H_	Alignment	not modelled	83.0	30	PDB header: transferase Chain: H: PDB Molecule: putative thymidine phosphorylase; PDBTitle: crystal structure of amp phosphorylase c-terminal deletion mutant in2 the apo-form
59	c3lnnB_	Alignment	not modelled	82.9	30	PDB header: metal transport Chain: B: PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans
60	c3bg3A_	Alignment	not modelled	82.8	37	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)
61	c1t5eB_	Alignment	not modelled	82.8	30	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance protein mexa; PDBTitle: the structure of mexa
62	c3va7A_	Alignment	not modelled	82.8	28	PDB header: ligase Chain: A: PDB Molecule: klla0e08119p; PDBTitle: crystal structure of the kluyveromyces lactis urea carboxylase
63	c2kccA_	Alignment	not modelled	82.8	17	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
64	c2q8iB_	Alignment	not modelled	82.7	26	PDB header: transferase Chain: B: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase component of PDBTitle: pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
65	c4l8jA_	Alignment	not modelled	82.7	35	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
66	c4tkoB_	Alignment	not modelled	82.5	26	PDB header: membrane protein Chain: B: PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra
67	c2f1mA_	Alignment	not modelled	82.0	17	PDB header: transport protein Chain: A: PDB Molecule: acriflavine resistance protein a; PDBTitle: conformational flexibility in the multidrug efflux system protein acra
68	c3tw6B_	Alignment	not modelled	81.6	14	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
69	c2dn8A_	Alignment	not modelled	81.4	35	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
70	d1laba_	Alignment	not modelled	81.0	22	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
71	c2zbc_	Alignment	not modelled	80.9	19	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of uncharacterized conserved protein from thermotoga2 maritima
72	c2ejmA_	Alignment	not modelled	80.8	35	PDB header: ligase Chain: A: PDB Molecule: methylcrotonoyl-coa carboxylase subunit alpha; PDBTitle: solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase
73	c4p6vA_	Alignment	not modelled	80.7	28	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
74	c2k33A_	Alignment	not modelled	80.5	22	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: acra; PDBTitle: solution structure of an n-glycosylated protein using in2 vitro glycosylation
75	d1vf7a_	Alignment	not modelled	79.6	30	Fold: HlyD-like secretion proteins Superfamily: HlyD-like secretion proteins Family: HlyD-like secretion proteins
76	c5v5sH_	Alignment	not modelled	79.6	17	PDB header: membrane protein Chain: H: PDB Molecule: multidrug efflux pump subunit acra; PDBTitle: multi-drug efflux; membrane transport; rnd superfamily; drug2 resistance
77	c3lnnA_	Alignment	not modelled	78.9	31	PDB header: metal transport Chain: A: PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans
78	d1y8ob1	Alignment	not modelled	78.5	35	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif

						Family: Biotinyl/lipoyl-carrier proteins and domains
79	c4dk1B_	Alignment	not modelled	78.4	30	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.
80	c2l5tA_	Alignment	not modelled	77.6	17	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase; PDBTitle: solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
81	c3fppB_	Alignment	not modelled	77.6	22	PDB header: membrane protein Chain: B: PDB Molecule: macrolide-specific efflux protein maca; PDBTitle: crystal structure of e.coli maca
82	c2b8gA_	Alignment	not modelled	77.3	15	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)
83	d1k8ma_	Alignment	not modelled	77.2	26	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
84	c2v4dM_	Alignment	not modelled	77.1	30	PDB header: membrane protein Chain: M: PDB Molecule: multidrug resistance protein mexa; PDBTitle: re-refinement of mexa adaptor protein
85	c2dneA_	Alignment	not modelled	76.8	26	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
86	c1rqrA_	Alignment	not modelled	76.5	17	PDB header: transferase Chain: A: PDB Molecule: 5'-fluoro-5'-deoxyadenosine synthase; PDBTitle: crystal structure and mechanism of a bacterial fluorinating enzyme,2 product complex
87	d1tu2b2	Alignment	not modelled	76.3	25	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
88	d1qjoa_	Alignment	not modelled	75.0	21	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
89	d2pnrc1	Alignment	not modelled	74.6	35	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
90	c5nenA_	Alignment	not modelled	74.4	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
91	c2dncA_	Alignment	not modelled	73.8	35	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
92	d1ghja_	Alignment	not modelled	73.1	15	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
93	d1uoua3	Alignment	not modelled	72.8	32	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
94	c4dk0A_	Alignment	not modelled	71.8	30	PDB header: membrane protein Chain: A: PDB Molecule: putative maca; PDBTitle: crystal structure of maca from actinobacillus actinomycetemcomitans
95	c6g2dC_	Alignment	not modelled	71.5	28	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
96	c4kkuD_	Alignment	not modelled	70.5	26	PDB header: membrane protein Chain: D: PDB Molecule: membrane fusion protein; PDBTitle: structure of besa (selenomethionone derivative - p212121)
97	d1gjxa_	Alignment	not modelled	70.5	26	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
98	c2qj8B_	Alignment	not modelled	70.2	16	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
99	c2aujD_	Alignment	not modelled	70.1	29	PDB header: transferase Chain: D: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of thermus aquaticus rna polymerase beta'-subunit2 insert
100	c5nilG_	Alignment	not modelled	68.8	22	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
101	d1pmra_	Alignment	not modelled	68.5	17	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
102	c2q6oB_	Alignment	not modelled	67.5	19	PDB header: biosynthetic protein Chain: B: PDB Molecule: hypothetical protein; PDBTitle: sall-y70t with sam and cl
103	c2qf7A_	Alignment	not modelled	66.9	19	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli PDB header: photosynthesis

104	c2e75C_	Alignment	not modelled	66.4	21	Chain: C; PDB Molecule: apocytochrome f; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
105	c3fmcC_	Alignment	not modelled	65.9	17	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
106	d1iyua_	Alignment	not modelled	64.5	23	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
107	c3camB_	Alignment	not modelled	63.2	23	PDB header: gene regulation Chain: B; PDB Molecule: cold-shock domain family protein; PDBTitle: crystal structure of the cold shock domain protein from neisseria2 meningitidis
108	d1h95a_	Alignment	not modelled	63.2	28	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
109	c3h9iB_	Alignment	not modelled	62.8	22	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
110	c2jkuA_	Alignment	not modelled	62.6	30	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
111	c5cslA_	Alignment	not modelled	60.8	18	PDB header: ligase Chain: A; PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of the 500 kd yeast acetyl-coa carboxylase2 holoenzyme dimer
112	c3na6A_	Alignment	not modelled	57.4	35	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
113	c3u9sA_	Alignment	not modelled	56.6	30	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
114	c5o6fA_	Alignment	not modelled	55.0	16	PDB header: dna binding protein Chain: A; PDB Molecule: cold-shock protein; PDBTitle: nmr structure of cold shock protein a from corynebacterium2 pseudotuberculosis
115	c3t51C_	Alignment	not modelled	53.6	22	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
116	c1wu8B_	Alignment	not modelled	53.3	17	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: hypothetical protein ph0463; PDBTitle: crystal structure of project ph0463 from pyrococcus horikoshii ot3
117	c4ivvA_	Alignment	not modelled	52.8	50	PDB header: hydrolase Chain: A; PDB Molecule: autolysin; PDBTitle: catalytic amidase domain of the major autolysin lyta from2 streptococcus pneumoniae
118	c3a0jB_	Alignment	not modelled	51.1	23	PDB header: transcription Chain: B; PDB Molecule: cold shock protein; PDBTitle: crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
119	c2k5nA_	Alignment	not modelled	50.5	23	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative cold-shock protein; PDBTitle: solution nmr structure of the n-terminal domain of protein eca15802 from erwinia carotovora, northeast structural genomics consortium3 target ewr156a
120	c3cdxB_	Alignment	not modelled	50.3	12	PDB header: hydrolase Chain: B; PDB Molecule: succinylglutamatedesuccinylase/aspartoacylase; PDBTitle: crystal structure of succinylglutamatedesuccinylase/aspartoacylase2 from rhodobacter sphaeroides