



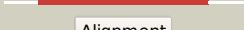

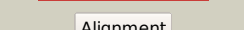



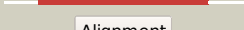





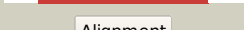


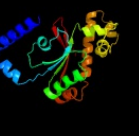
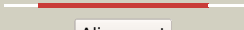

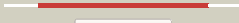

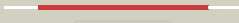












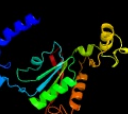





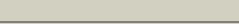
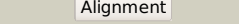





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3588c_(- )_4030050_4030673
Date	Fri Aug 9 18:20:27 BST 2019
Unique Job ID	17ffb9bf666da581

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2a5vB_</a>	 Alignment		100.0	100	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carbonic anhydrase (carbonate dehydratase) (carbonic <b>PDBTitle:</b> crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c,2 tetrameric form
2	<a href="#">d1ekja_</a>	 Alignment		100.0	27	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
3	<a href="#">d1ddza1</a>	 Alignment		100.0	29	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
4	<a href="#">d1ddza2</a>	 Alignment		100.0	27	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
5	<a href="#">c5swcE_</a>	 Alignment		100.0	26	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> the structure of the beta-carbonic anhydrase ccaa
6	<a href="#">c5cxkG_</a>	 Alignment		100.0	31	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> crystal structure of beta carbonic anhydrase from vibrio cholerae
7	<a href="#">c2w3nA_</a>	 Alignment		100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carbonic anhydrase 2; <b>PDBTitle:</b> structure and inhibition of the co2-sensing carbonic anhydrase can22 from the pathogenic fungus cryptococcus neoformans
8	<a href="#">c4o1kA_</a>	 Alignment		100.0	28	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> crystal structures of two tetrameric beta-carbonic anhydrases from the2 filamentous ascomycete sordaria macrospora.
9	<a href="#">c1ddzA_</a>	 Alignment		100.0	29	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1
10	<a href="#">c4o1jB_</a>	 Alignment		100.0	28	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> crystal structures of two tetrameric beta-carbonic anhydrases from the2 filamentous ascomycete sordaria macrospora.
11	<a href="#">c2a8cE_</a>	 Alignment		100.0	29	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> carbonic anhydrase 2; <b>PDBTitle:</b> haemophilus influenzae beta-carbonic anhydrase

12	<a href="#">c6gwuB_</a>	 Alignment		100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> carbonic anhydrase cance103p from candida albicans
13	<a href="#">d1i6pa_</a>	 Alignment		100.0	28	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
14	<a href="#">c3ucoB_</a>	 Alignment		100.0	23	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> coccomyxa beta-carbonic anhydrase in complex with iodide
15	<a href="#">c4rxYA_</a>	 Alignment		100.0	30	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> crystal structure of the beta carbonic anhydrase psca3 isolated from2 pseudomonas aeruginosa
16	<a href="#">c3vrkA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carbonyl sulfide hydrolase; <b>PDBTitle:</b> crystal structure of thiobacillus thioparus thi115 carbonyl sulfide2 hydrolase / thiocyanate complex
17	<a href="#">c3eyxB_</a>	 Alignment		100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
18	<a href="#">c3lasA_</a>	 Alignment		100.0	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carbonic anhydrase; <b>PDBTitle:</b> crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution
19	<a href="#">c1ylkA_</a>	 Alignment		100.0	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rv1284/mt1322; <b>PDBTitle:</b> crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate
20	<a href="#">c3tenD_</a>	 Alignment		100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cs2 hydrolase; <b>PDBTitle:</b> holo form of carbon disulfide hydrolase
21	<a href="#">c5ztpB_</a>	 Alignment	not modelled	100.0	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carbonic anhydrase; <b>PDBTitle:</b> carbonic anhydrase from glaciozyma antarctica
22	<a href="#">d1g5ca_</a>	 Alignment	not modelled	100.0	29	<b>Fold:</b> Resolvase-like <b>Superfamily:</b> beta-carbonic anhydrase, cab <b>Family:</b> beta-carbonic anhydrase, cab
23	<a href="#">c2hwkA_</a>	 Alignment	not modelled	62.4	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> helicase nsp2; <b>PDBTitle:</b> crystal structure of venezuelan equine encephalitis alphavirus nsp22 protease domain
24	<a href="#">c1bm4A_</a>	 Alignment	not modelled	49.3	42	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (moloney murine leukemia virus capsid); <b>PDBTitle:</b> momlv capsid protein major homology region peptide analog
25	<a href="#">d1nlNa_</a>	 Alignment	not modelled	42.0	12	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Adenain-like
26	<a href="#">d1lr6a_</a>	 Alignment	not modelled	38.9	22	<b>Fold:</b> DHH phosphoesterases <b>Superfamily:</b> DHH phosphoesterases <b>Family:</b> Exonuclease RecJ
27	<a href="#">c1lr6A_</a>	 Alignment	not modelled	38.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exonuclease recj; <b>PDBTitle:</b> crystal structure of exonuclease recj bound to manganese
28	<a href="#">c5ghrA_</a>	 Alignment	not modelled	37.5	15	<b>PDB header:</b> dna binding protein/replication <b>Chain:</b> A: <b>PDB Molecule:</b> ssdna-specific exonuclease; <b>PDBTitle:</b> dna replication protein

29	<a href="#">c3vr1B_</a>	Alignment	not modelled	37.1	14	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> peptide chain release factor 3; <b>PDBTitle:</b> crystal structure analysis of the translation factor rf3
30	<a href="#">c5ghrC_</a>	Alignment	not modelled	37.1	15	<b>PDB header:</b> dna binding protein/replication <b>Chain:</b> C: <b>PDB Molecule:</b> ssdna-specific exonuclease; <b>PDBTitle:</b> dna replication protein
31	<a href="#">c3d89A_</a>	Alignment	not modelled	36.7	17	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rieske domain-containing protein; <b>PDBTitle:</b> crystal structure of a soluble rieske ferredoxin from mus musculus
32	<a href="#">d1fqta_</a>	Alignment	not modelled	34.6	8	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
33	<a href="#">c2de7E_</a>	Alignment	not modelled	33.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> ferredoxin component of carbazole; <b>PDBTitle:</b> the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
34	<a href="#">d1z01a1</a>	Alignment	not modelled	32.8	38	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
35	<a href="#">c5f56A_</a>	Alignment	not modelled	32.2	24	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded-dna-specific exonuclease; <b>PDBTitle:</b> structure of recj complexed with dna and ssb-ct
36	<a href="#">d2de6a1</a>	Alignment	not modelled	32.0	31	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Ring hydroxylating alpha subunit ISP domain
37	<a href="#">c2zxrA_</a>	Alignment	not modelled	31.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna specific exonuclease recj; <b>PDBTitle:</b> crystal structure of recj in complex with mg2+ from thermus2 thermophilus hb8
38	<a href="#">d2jo6a1</a>	Alignment	not modelled	31.1	25	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> NirD-like
39	<a href="#">c3gceA_</a>	Alignment	not modelled	30.2	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin component of carbazole 1,9a- <b>PDBTitle:</b> ferredoxin of carbazole 1,9a-dioxygenase from nocardioides2 aromaticivorans ic177
40	<a href="#">c3i8sC_</a>	Alignment	not modelled	28.8	27	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> ferrous iron transport protein b; <b>PDBTitle:</b> structure of the cytosolic domain of e. coli feob, nucleotide-free2 form
41	<a href="#">c3degC_</a>	Alignment	not modelled	28.0	21	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> gtp-binding protein lepa; <b>PDBTitle:</b> complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
42	<a href="#">d1nrjb_</a>	Alignment	not modelled	28.0	33	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
43	<a href="#">c3ibyA_</a>	Alignment	not modelled	27.3	25	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ferrous iron transport protein b; <b>PDBTitle:</b> structure of cytosolic domain of I. pneumophila feob
44	<a href="#">c4proD_</a>	Alignment	not modelled	25.8	9	<b>PDB header:</b> serine protease <b>Chain:</b> D: <b>PDB Molecule:</b> alpha-lytic protease; <b>PDBTitle:</b> alpha-lytic protease complexed with pro region
45	<a href="#">c3j25A_</a>	Alignment	not modelled	25.6	36	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> tetracycline resistance protein tetm; <b>PDBTitle:</b> structural basis for tetm-mediated tetracycline resistance
46	<a href="#">d1zo0a1</a>	Alignment	not modelled	25.6	14	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> Ornithine decarboxylase antizyme-like
47	<a href="#">d1n0ua2</a>	Alignment	not modelled	25.6	36	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
48	<a href="#">c2h5eB_</a>	Alignment	not modelled	25.5	14	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> peptide chain release factor rf-3; <b>PDBTitle:</b> crystal structure of e.coli polypeptide release factor rf3
49	<a href="#">c1d2eA_</a>	Alignment	not modelled	25.3	27	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor tu (ef-tu); <b>PDBTitle:</b> crystal structure of mitochondrial ef-tu in complex with gdp
50	<a href="#">c5yh1A_</a>	Alignment	not modelled	25.2	10	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> member of s1p family of ribosomal proteins; <b>PDBTitle:</b> member of s1p family of ribosomal proteins pf0399 dhh domain
51	<a href="#">d2fh5b1</a>	Alignment	not modelled	24.7	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
52	<a href="#">c3w5iB_</a>	Alignment	not modelled	24.6	33	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> ferrous iron transport protein b; <b>PDBTitle:</b> crystal structure of nfeob from gallionella capsiferriformans
53	<a href="#">c4zciA_</a>	Alignment	not modelled	24.1	21	<b>PDB header:</b> gtp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein typa/bipa; <b>PDBTitle:</b> crystal structure of escherichia coli gtpase bipa/typa
54	<a href="#">c6fgzA_</a>	Alignment	not modelled	23.8	40	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dynamin; <b>PDBTitle:</b> cyanidioschyzon merolae dnm1 (cmdnm1)
55	<a href="#">c4hi2B_</a>	Alignment	not modelled	23.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acylphosphatase;

						<b>PDBTitle:</b> crystal structure of an acylphosphatase protein cage
56	<a href="#">c6humO_</a>	Alignment	not modelled	23.8	30	<b>PDB header:</b> proton transport <b>Chain:</b> O: <b>PDB Molecule:</b> nad(p)h-quinone oxidoreductase subunit o; <b>PDBTitle:</b> structure of the photosynthetic complex i from thermosynechococcus2 elongatus
57	<a href="#">c5b5yA_</a>	Alignment	not modelled	23.3	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ptlcib4; <b>PDBTitle:</b> crystal structure of ptlcib4, a homolog of the limiting co2-inducible2 protein lcib
58	<a href="#">c2qpzA_</a>	Alignment	not modelled	23.2	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> naphthalene 1,2-dioxygenase system ferredoxin <b>PDBTitle:</b> naphthalene 1,2-dioxygenase rieske ferredoxin
59	<a href="#">c3p27A_</a>	Alignment	not modelled	23.1	55	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1 alpha-like protein; <b>PDBTitle:</b> crystal structure of s. cerevisiae hbs1 protein (gdp-bound form), a2 translational gtpase involved in rna quality control pathways and3 interacting with dom34/pelota
60	<a href="#">d1s0ua3</a>	Alignment	not modelled	23.1	36	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
61	<a href="#">d1r5ba3</a>	Alignment	not modelled	23.1	45	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
62	<a href="#">c1mj1A_</a>	Alignment	not modelled	22.8	27	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor tu; <b>PDBTitle:</b> fitting the ternary complex of ef-tu/trna/gtp and ribosomal proteins2 into a 13 a cryo-em map of the coli 70s ribosome
63	<a href="#">c2i7fB_</a>	Alignment	not modelled	22.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin component of dioxygenase; <b>PDBTitle:</b> sphingomonas yanoikuyae b1 ferredoxin
64	<a href="#">c2ywfA_</a>	Alignment	not modelled	22.7	29	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein lepa; <b>PDBTitle:</b> crystal structure of gmppnp-bound lepa from aquifex aeolicus
65	<a href="#">c2qu8A_</a>	Alignment	not modelled	22.5	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative nucleolar gtp-binding protein 1; <b>PDBTitle:</b> crystal structure of putative nucleolar gtp-binding protein 1 pff0625w2 from plasmodium falciparum
66	<a href="#">d1e8ca1</a>	Alignment	not modelled	22.4	71	<b>Fold:</b> MurF and HprK N-domain-like <b>Superfamily:</b> MurE/MurF N-terminal domain <b>Family:</b> MurE/MurF N-terminal domain
67	<a href="#">d1apsa_</a>	Alignment	not modelled	22.1	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> Acylphosphatase-like
68	<a href="#">d1vm9a_</a>	Alignment	not modelled	22.1	17	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> Rieske iron-sulfur protein (ISP)
69	<a href="#">c2bvnB_</a>	Alignment	not modelled	22.1	27	<b>PDB header:</b> elongation factor <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor tu; <b>PDBTitle:</b> e. coli ef-tu:gdppnp in complex with the antibiotic enacyloxin iia
70	<a href="#">d2jzaa1</a>	Alignment	not modelled	21.9	25	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> NirD-like
71	<a href="#">d3c0da1</a>	Alignment	not modelled	21.7	18	<b>Fold:</b> ISP domain <b>Superfamily:</b> ISP domain <b>Family:</b> NirD-like
72	<a href="#">c4fn5A_</a>	Alignment	not modelled	21.4	21	<b>PDB header:</b> translation/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g 1; <b>PDBTitle:</b> elongation factor g 1 (pseudomonas aeruginosa) in complex with argyriin2 b
73	<a href="#">c4aivA_</a>	Alignment	not modelled	21.3	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nitrite reductase [nad(p)h] small subunit nird; <b>PDBTitle:</b> crystal structure of putative nadh-dependent nitrite reductase small2 subunit from mycobacterium tuberculosis
74	<a href="#">c5aorA_</a>	Alignment	not modelled	21.2	33	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> A: <b>PDB Molecule:</b> dosage compensation regulator; <b>PDBTitle:</b> structure of mle rna adp alf4 complex
75	<a href="#">c1zunB_</a>	Alignment	not modelled	21.1	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfate adenylate transferase, subunit <b>PDBTitle:</b> crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
76	<a href="#">c3zjcC_</a>	Alignment	not modelled	21.1	40	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> gtpase imap family member 7; <b>PDBTitle:</b> crystal structure of gmppnp-bound human gimap7 I100q variant
77	<a href="#">c2dy1A_</a>	Alignment	not modelled	20.9	21	<b>PDB header:</b> signaling protein, translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> crystal structure of ef-g-2 from thermus thermophilus
78	<a href="#">d1efca3</a>	Alignment	not modelled	20.8	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
79	<a href="#">c3k53B_</a>	Alignment	not modelled	20.6	15	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> ferrous iron transport protein b; <b>PDBTitle:</b> crystal structure of nfeob from p. furiousus
80	<a href="#">c1z01D_</a>	Alignment	not modelled	20.6	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-oxo-1,2-dihydroquinoline 8-monoxygenase, oxygenase <b>PDBTitle:</b> 2-oxoquinoline 8-monoxygenase component: active site modulation by2 rieske-[2fe-2s] center oxidation/reduction <b>PDB header:</b> rna, ribosomal protein

81	<a href="#">c3izyP_</a>	Alignment	not modelled	20.2	33	<b>Chain:</b> P: <b>PDB Molecule:</b> translation initiation factor if-2, mitochondrial; <b>PDBTitle:</b> mammalian mitochondrial translation initiation factor 2
82	<a href="#">c3gkqB_</a>	Alignment	not modelled	20.2	46	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> terminal oxygenase component of carbazole 1,9a-dioxygenase; <b>PDBTitle:</b> terminal oxygenase of carbazole 1,9a-dioxygenase from novosphingobium2 sp. ka1
83	<a href="#">c2qaqC_</a>	Alignment	not modelled	20.0	27	<b>PDB header:</b> cell cycle, structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> septin-7; <b>PDBTitle:</b> crystal structure of human septin trimer 2/6/7
84	<a href="#">c1r5nA_</a>	Alignment	not modelled	20.0	45	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic peptide chain release factor gtp- <b>PDBTitle:</b> crystal structure analysis of sup35 complexed with gdp
85	<a href="#">d2acya_</a>	Alignment	not modelled	19.8	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Acylphosphatase/BLUF domain-like <b>Family:</b> Acylphosphatase-like
86	<a href="#">c5jkjA_</a>	Alignment	not modelled	19.8	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase e22; <b>PDBTitle:</b> crystal structure of esterase e22 I374d mutant
87	<a href="#">c3t5dC_</a>	Alignment	not modelled	19.8	27	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> septin-7; <b>PDBTitle:</b> crystal structure of septin 7 in complex with gdp
88	<a href="#">d1j2ra_</a>	Alignment	not modelled	19.6	16	<b>Fold:</b> Isochorismatase-like hydrolases <b>Superfamily:</b> Isochorismatase-like hydrolases <b>Family:</b> Isochorismatase-like hydrolases
89	<a href="#">c6cl4A_</a>	Alignment	not modelled	19.5	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase c12; <b>PDBTitle:</b> lipc12 - lipase from metagenomics
90	<a href="#">c2kxfA_</a>	Alignment	not modelled	19.5	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of a potential acylphosphatase from giardia2 lamblia, seattle structural genomics center for infectious disease3 target gilaa.01396.a
91	<a href="#">c3tr5C_</a>	Alignment	not modelled	18.9	14	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> peptide chain release factor 3; <b>PDBTitle:</b> structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
92	<a href="#">c4zkeA_</a>	Alignment	not modelled	18.8	27	<b>PDB header:</b> gtp binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> superkiller protein 7; <b>PDBTitle:</b> crystal structure of the s. cerevisiae ski7 gtpase-like domain, bound2 to gtp.
93	<a href="#">c4aayH_</a>	Alignment	not modelled	18.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> arob; <b>PDBTitle:</b> crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
94	<a href="#">c3br8A_</a>	Alignment	not modelled	18.6	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable acylphosphatase; <b>PDBTitle:</b> crystal structure of acylphosphatase from bacillus subtilis
95	<a href="#">c5yozA_</a>	Alignment	not modelled	18.3	50	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> rab5a; <b>PDBTitle:</b> solution structure of truncated rab5a from leishmania donovani
96	<a href="#">c4b3xA_</a>	Alignment	not modelled	18.2	36	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> bacterial translation initiation factor if2 (1-363), apo form
97	<a href="#">c2de7B_</a>	Alignment	not modelled	18.1	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> terminal oxygenase component of carbazole; <b>PDBTitle:</b> the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
98	<a href="#">d1egaa1</a>	Alignment	not modelled	18.1	30	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
99	<a href="#">d1svia_</a>	Alignment	not modelled	17.8	29	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins