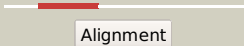



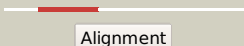

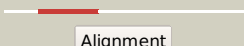

















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2974c_(-)_3329959_3331371
Date	Thu Aug 8 16:20:13 BST 2019
Unique Job ID	436e82600363152c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2btdA_	 Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: pts-dependent dihydroxyacetone kinase; PDBTitle: crystal structure of dhal from e. coli
2	d3cr3a1	 Alignment		99.8	17	Fold: DhaL-like Superfamily: DhaL-like Family: DhaL-like
3	d1un8a1	 Alignment		99.8	24	Fold: DhaL-like Superfamily: DhaL-like Family: DhaL-like
4	c1un9B_	 Alignment		99.7	24	PDB header: kinase Chain: B: PDB Molecule: dihydroxyacetone kinase; PDBTitle: crystal structure of the dihydroxyacetone kinase from c.2 freundii in complex with amp-pnp and mg2+
5	c4x9xA_	 Alignment		99.0	8	PDB header: transferase Chain: A: PDB Molecule: degv domain-containing protein mw1315; PDBTitle: biochemical roles for conserved residues in the bacterial fatty acid2 binding protein family
6	d1mgpa_	 Alignment		98.9	15	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DegV-like
7	c1mgpA_	 Alignment		98.9	15	PDB header: lipid binding protein Chain: A: PDB Molecule: hypothetical protein tm841; PDBTitle: hypothetical protein tm841 from thermotoga maritima reveals2 fatty acid binding function
8	c6cngA_	 Alignment		98.8	13	PDB header: transferase Chain: A: PDB Molecule: fatty acid kinase (fak) b3 protein; PDBTitle: the x-ray crystal structure of the streptococcus pneumoniae fatty acid2 kinase (fak) b3 protein loaded with linoleic acid to 1.47 angstrom3 resolution
9	c2g7zB_	 Alignment		98.7	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein spy1493; PDBTitle: conserved degv-like protein of unknown function from streptococcus2 pyogenes m1 gas binds long-chain fatty acids
10	d1pzxA_	 Alignment		98.2	10	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DegV-like
11	c3fysA_	 Alignment		98.1	14	PDB header: fatty acid-binding protein Chain: A: PDB Molecule: protein degv; PDBTitle: crystal structure of degv, a fatty acid binding protein2 from bacillus subtilis

12	c3lupA_	Alignment		98.1	13	PDB header: structure genomics, unknown function Chain: A; PDB Molecule: degv family protein; PDBTitle: crystal structure of fatty acid binding degv family protein sag13422 from streptococcus agalactiae
13	c6dj6B_	Alignment		98.1	14	PDB header: transferase Chain: B; PDB Molecule: fatty acid kinase (fak) b2 protein (spr1019); PDBTitle: the x-ray crystal structure of the streptococcus pneumoniae fatty acid2 kinase (fak) b2 protein loaded with cis-oleic acid to 1.9 angstrom3 resolution
14	c3pl5A_	Alignment		98.0	13	PDB header: lipid binding protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: fatty acid binding protein
15	c5utoB_	Alignment		98.0	12	PDB header: transport protein Chain: B; PDB Molecule: edd domain protein, degv family; PDBTitle: the crystal structure of the staphylococcus aureus fatty acid kinase2 (fak) b1 protein loaded with palmitic acid to 1.83 angstrom3 resolution
16	c3jr7A_	Alignment		98.0	12	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized egv family protein cog1307; PDBTitle: the crystal structure of the protein of degv family cog1307 with2 unknown function from ruminococcus gnavus atcc 29149
17	c2dt8A_	Alignment		97.9	18	PDB header: lipid binding protein Chain: A; PDB Molecule: degv family protein; PDBTitle: fatty acid binding of a degv family protein from thermus thermophilus
18	c3fdjA_	Alignment		97.9	11	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: degv family protein; PDBTitle: the structure of a degv family protein from eubacterium eligens.
19	c6dkeA_	Alignment		97.9	17	PDB header: transferase Chain: A; PDB Molecule: fatty acid kinase (fak) b1 protein; PDBTitle: the x-ray crystal structure of streptococcus pneumoniae fatty acid2 kinase (fak) b1 protein loaded with palmitic acid (c16:0) to 1.763 angstrom resolution
20	c3nyiA_	Alignment		97.4	9	PDB header: lipid binding protein Chain: A; PDB Molecule: fat acid-binding protein; PDBTitle: the crystal structure of a fat acid (stearic acid)-binding protein2 from eubacterium ventriosum atcc 27560.
21	c3eglC_	Alignment	not modelled	96.1	14	PDB header: structural genomics, unknown function Chain: C; PDB Molecule: degv family protein; PDBTitle: crystal structure of degv family protein cg2579 from corynebacterium2 glutamicum
22	d3ct6a1	Alignment	not modelled	95.7	11	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: DhaM-like
23	c4wzzA_	Alignment	not modelled	94.6	15	PDB header: transport protein Chain: A; PDB Molecule: putative sugar abc transporter, substrate-binding protein; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentas (cphy_0583, target efi-3 511148) with bound l-rhamnose
24	d1ccwa_	Alignment	not modelled	94.2	19	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
25	c6dspB_	Alignment	not modelled	91.5	10	PDB header: signaling protein Chain: B; PDB Molecule: autoinducer 2-binding protein lsrb; PDBTitle: lsrb from clostridium saccharobutylicum in complex with ai-2
26	c4pz0A_	Alignment	not modelled	91.5	13	PDB header: sugar binding protein Chain: A; PDB Molecule: sugar abc transporter, sugar-binding protein; PDBTitle: the crystal structure of a solute binding protein from bacillus2 anthracis str. ames in complex with quorum-sensing signal3 autoinducer-2 (ai-2)
27	c1y80A_	Alignment	not modelled	90.2	26	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
						Fold: Flavodoxin-like

28	d1fmfa_	Alignment	not modelled	88.8	21	Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
29	d7reqa2	Alignment	not modelled	87.2	15	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
30	c5braA_	Alignment	not modelled	86.9	16	PDB header: solute-binding protein Chain: A: PDB Molecule: putative periplasmic binding protein with substrate ribose; PDBTitle: crystal structure of a putative periplasmic solute binding protein2 (ipr025997) from ochrobactrum anthropi atcc49188 (oant_2843, target3 efi-511085)
31	c2yxbA_	Alignment	not modelled	85.9	16	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
32	c6fjID_	Alignment	not modelled	81.3	22	PDB header: metal binding protein Chain: D: PDB Molecule: abc-type fe3+ transport system, periplasmic component; PDBTitle: structure of ibps from dickeya dadantii
33	d1xvla1	Alignment	not modelled	81.3	10	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
34	c1w5fA_	Alignment	not modelled	80.3	12	PDB header: cell division Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz, t7 mutated, domain swapped (t. maritima)
35	d3b48a1	Alignment	not modelled	80.0	7	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: DhaM-like
36	c3hjtB_	Alignment	not modelled	79.7	13	PDB header: cell adhesion, transport protein Chain: B: PDB Molecule: lmb; PDBTitle: structure of laminin binding protein (lmb) of streptococcus agalactiae2 a bifunctional protein with adhesin and metal transporting activity
37	c3ezxA_	Alignment	not modelled	76.5	16	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
38	d1psza_	Alignment	not modelled	75.2	7	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
39	c4kvfA_	Alignment	not modelled	74.7	13	PDB header: transport protein Chain: A: PDB Molecule: rhamnose abc transporter, periplasmic rhamnose-binding PDBTitle: the crystal structure of a rhamnose abc transporter, periplasmic2 rhamnose-binding protein from kribbella flavida dsm 17836
40	c1bmtB_	Alignment	not modelled	73.3	19	PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
41	c5c8eC_	Alignment	not modelled	72.6	28	PDB header: transcription regulator/dna Chain: C: PDB Molecule: light-dependent transcriptional regulator carh; PDBTitle: crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
42	c2i2xD_	Alignment	not modelled	72.4	26	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
43	c3gx1A_	Alignment	not modelled	71.4	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1832 protein; PDBTitle: crystal structure of a domain of lin1832 from listeria innocua
44	d3bula2	Alignment	not modelled	70.7	19	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
45	d1wh9a_	Alignment	not modelled	68.7	16	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
46	c4pe6B_	Alignment	not modelled	68.3	15	PDB header: solute-binding protein Chain: B: PDB Molecule: putative abc transporter; PDBTitle: crystal structure of abc transporter solute binding protein from2 thermobispora bispora dsm 43833
47	c2vxyA_	Alignment	not modelled	67.5	17	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: the structure of ftsz from bacillus subtilis at 1.7a2 resolution
48	c4bloC_	Alignment	not modelled	67.1	12	PDB header: hydrolase Chain: C: PDB Molecule: packaging enzyme p4; PDBTitle: p4 protein from bacteriophage phi6 in complex with adp
49	d1jha2	Alignment	not modelled	66.8	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidylyl transferase Family: ATP sulfurylase catalytic domain
50	c3whpA_	Alignment	not modelled	66.8	28	PDB header: gene regulation Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of the c-terminal domain of themus thermophilus litr2 in complex with cobalamin
51	d1lssa_	Alignment	not modelled	65.4	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
52	d1oi2a_	Alignment	not modelled	65.3	16	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DAK1
						PDB header: sugar binding protein Chain: A: PDB Molecule: putative lacI-type transcriptional regulator;

53	c3d02A_	Alignment	not modelled	65.1	14	PDBTitle: crystal structure of periplasmic sugar-binding protein2 (yp_001338366.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 1.30 a resolution
54	c2iu6B_	Alignment	not modelled	64.9	17	PDB header: transferase Chain: B: PDB Molecule: dihydroxyacetone kinase; PDBTitle: regulation of the dha operon of lactococcus lactis
55	c4jgiB_	Alignment	not modelled	63.8	23	PDB header: protein binding Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfitobacterium hafniense dcb-2
56	c2cw6B_	Alignment	not modelled	63.5	13	PDB header: lyase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa lyase, mitochondrial; PDBTitle: crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
57	c2vavA_	Alignment	not modelled	62.4	16	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz pseudomonas aeruginosa gdp
58	c4xrvB_	Alignment	not modelled	61.9	13	PDB header: metal binding protein Chain: B: PDB Molecule: periplasmic solute binding protein; PDBTitle: structure of a zn abc transporter substrate binding protein from2 paracoccus denitrificans
59	c2o1eB_	Alignment	not modelled	61.1	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ycdh; PDBTitle: crystal structure of the metal-dependent lipoprotein ycdh2 from bacillus subtilis, northeast structural genomics3 target sr583
60	c6mspA_	Alignment	not modelled	61.0	16	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed protein foldit3; PDBTitle: de novo designed protein foldit3
61	c3llvA_	Alignment	not modelled	60.5	19	PDB header: nad(p) binding protein Chain: A: PDB Molecule: exopolyphosphatase-related protein; PDBTitle: the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
62	d1tjya_	Alignment	not modelled	59.2	14	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
63	c4blpD_	Alignment	not modelled	59.0	16	PDB header: hydrolase Chain: D: PDB Molecule: packaging enzyme p4; PDBTitle: p4 protein from bacteriophage phi13
64	c3c9hB_	Alignment	not modelled	58.8	10	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, substrate binding protein; PDBTitle: crystal structure of the substrate binding protein of the abc2 transporter from agrobacterium tumefaciens
65	c3e6sD_	Alignment	not modelled	57.9	18	PDB header: oxidoreductase Chain: D: PDB Molecule: ferritin; PDBTitle: crystal structure of ferritin soaked with iron from pseudo-nitzschia2 multiseris
66	c1ofuB_	Alignment	not modelled	56.8	16	PDB header: bacterial cell division inhibitor Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of sula:fts from pseudomonas aeruginosa
67	c2kz0A_	Alignment	not modelled	56.8	13	PDB header: transcription Chain: A: PDB Molecule: bola family protein; PDBTitle: solution structure of a bola protein (ech_0303) from ehrlichia2 chaffeensis. seattle structural genomics center for infectious3 disease target ehcha.10365.a
68	d1pjwa_	Alignment	not modelled	56.5	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
69	c3tr3A_	Alignment	not modelled	56.3	3	PDB header: unknown function Chain: A: PDB Molecule: bola; PDBTitle: structure of a bola protein homologue from coxiella burnetii
70	d1q77a_	Alignment	not modelled	56.3	10	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
71	c4hh3C_	Alignment	not modelled	56.2	21	PDB header: flavoprotein/transcription Chain: C: PDB Molecule: appa protein; PDBTitle: structure of the appa-ppsr2 core complex from rb. sphaeroides
72	c1jhdA_	Alignment	not modelled	56.1	13	PDB header: transferase Chain: A: PDB Molecule: sulfate adenylyltransferase; PDBTitle: crystal structure of bacterial atp sulfurylase from the2 riftia pachyptila symbiont
73	c3rf7A_	Alignment	not modelled	56.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: iron-containing alcohol dehydrogenase; PDBTitle: crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
74	c4r3uD_	Alignment	not modelled	55.2	19	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
75	c2q1yB_	Alignment	not modelled	55.0	20	PDB header: cell cycle, signaling protein Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis in complex with gtp-gamma-s
76	c2odaB_	Alignment	not modelled	54.9	18	PDB header: protein binding Chain: B: PDB Molecule: hypothetical protein pspto_2114; PDBTitle: crystal structure of pspto_2114
77	c1xrsB_	Alignment	not modelled	54.6	15	PDB header: isomerase Chain: B: PDB Molecule: d-lysine 5,6-aminomutase beta subunit; PDBTitle: crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine

78	c2fqxA	Alignment	not modelled	54.4	15	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
79	c3okfA	Alignment	not modelled	53.9	18	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: 2.5 angstrom resolution crystal structure of 3-dehydroquinase synthase2 (arob) from vibrio cholerae
80	c3ct4B	Alignment	not modelled	53.2	13	PDB header: transferase Chain: B: PDB Molecule: pts-dependent dihydroxyacetone kinase, dihydroxyacetone- PDBTitle: structure of dha-kinase subunit dhak from I. lactis
81	d1zbsa2	Alignment	not modelled	52.9	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
82	c3clhA	Alignment	not modelled	52.6	15	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of 3-dehydroquinase synthase (dhqs)from2 helicobacter pylori
83	c3mfqB	Alignment	not modelled	52.4	13	PDB header: metal binding protein Chain: B: PDB Molecule: high-affinity zinc uptake system protein znua; PDBTitle: a glance into the metal binding specificity of troa: where elaborate2 behaviors occur in the active center
84	c5wb4H	Alignment	not modelled	49.4	24	PDB header: transferase Chain: H: PDB Molecule: n-acetylglucosaminylidiphosphoundecaprenol n-acetyl-beta-d- PDBTitle: crystal structure of the tara wall teichoic acid glycosyltransferase
85	c2rjoA	Alignment	not modelled	48.5	13	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal protein; PDBTitle: crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
86	d1ztxe1	Alignment	not modelled	48.3	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
87	c1s1hC	Alignment	not modelled	48.3	16	PDB header: ribosome Chain: C: PDB Molecule: 40s ribosomal protein s3; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i.
88	c3uzeC	Alignment	not modelled	47.8	12	PDB header: immune system Chain: C: PDB Molecule: envelope protein; PDBTitle: crystal structure of the dengue virus serotype 3 envelope protein2 domain iii in complex with the variable domains of mab 4e11
89	c2mcqA	Alignment	not modelled	47.8	23	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein rp812; PDBTitle: nmr structure of a bola-like hypothetical protein rp812 from2 rickettsia prowazekii, seattle structural genomics center for3 infectious disease (ssgid)
90	d1s6na	Alignment	not modelled	47.7	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
91	c2ftpA	Alignment	not modelled	47.7	16	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
92	d2uubc1	Alignment	not modelled	46.7	22	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
93	c3egpA	Alignment	not modelled	45.5	19	PDB header: viral protein Chain: A: PDB Molecule: envelope protein; PDBTitle: crystal structure analysis of dengue-1 envelope protein2 domain iii
94	c2jqmA	Alignment	not modelled	44.4	19	PDB header: transferase Chain: A: PDB Molecule: envelope protein e; PDBTitle: yellow fever envelope protein domain iii nmr structure2 (s288-k398)
95	d1pvda2	Alignment	not modelled	44.2	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
96	d1ok8a1	Alignment	not modelled	44.1	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
97	c3h75A	Alignment	not modelled	43.9	13	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic sugar-binding domain protein; PDBTitle: crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
98	c3gdwA	Alignment	not modelled	43.8	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sigma-54 interaction domain protein; PDBTitle: crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
99	c2ps3A	Alignment	not modelled	43.4	16	PDB header: metal transport Chain: A: PDB Molecule: high-affinity zinc uptake system protein znua; PDBTitle: structure and metal binding properties of znua, a periplasmic zinc2 transporter from escherichia coli
100	d2qalc1	Alignment	not modelled	43.1	24	Fold: Alpha-lytic protease prodomain-like Superfamily: Prokaryotic type KH domain (KH-domain type II) Family: Prokaryotic type KH domain (KH-domain type II)
101	d2ptza1	Alignment	not modelled	42.9	14	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
						PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci

102	c6hyhA_	Alignment	not modelled	42.4	13	transcriptional regulator; PDBTitle: crystal structure of msmeg_1712 from mycobacterium smegmatis in2 complex with beta-d-fucufuranose
103	c5xyiD_	Alignment	not modelled	42.2	14	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s3, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
104	c2h0pA_	Alignment	not modelled	41.9	14	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: nmr structure of the dengue-4 virus envelope protein domain2 iii
105	c6r6kB_	Alignment	not modelled	40.8	16	PDB header: protein transport Chain: B: PDB Molecule: abc transporter substrate-binding protein; PDBTitle: structure of a fpvc mutant from pseudomonas aeruginosa
106	c4av2P_	Alignment	not modelled	40.6	22	PDB header: protein transport Chain: P: PDB Molecule: pilp protein; PDBTitle: single particle electron microscopy of pilq dodecameric complexes from2 neisseria meningitidis.
107	d1un8a4	Alignment	not modelled	40.2	18	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DAK1
108	c2xznC_	Alignment	not modelled	39.9	8	PDB header: ribosome Chain: C: PDB Molecule: kh domain containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
109	d1ad1a_	Alignment	not modelled	39.7	18	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
110	c2r6r1_	Alignment	not modelled	38.4	18	PDB header: cell cycle Chain: 1: PDB Molecule: cell division protein ftsz; PDBTitle: aquifex aeolicus ftsz
111	c3zeyX_	Alignment	not modelled	38.1	11	PDB header: ribosome Chain: X: PDB Molecule: 40s ribosomal protein s3, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
112	c4af1A_	Alignment	not modelled	37.9	20	PDB header: hydrolase Chain: A: PDB Molecule: peptide chain release factor subunit 1; PDBTitle: archeal release factor arf1
113	c3eq5G_	Alignment	not modelled	36.9	28	PDB header: signaling protein Chain: G: PDB Molecule: ski-like protein; PDBTitle: crystal structure of fragment 137 to 238 of the human ski-like protein
114	c4yajA_	Alignment	not modelled	36.4	12	PDB header: ligase Chain: A: PDB Molecule: alpha subunit of acetyl-coenzyme a synthetase PDBTitle: ca. korarchaeum cryptofilum dinucleotide forming acetyl-coenzyme a2 synthetase 1 (apo form)
115	c3ewbX_	Alignment	not modelled	36.3	12	PDB header: transferase Chain: X: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from listeria monocytogenes
116	c2h9aB_	Alignment	not modelled	36.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase, iron-sulfur protein; PDBTitle: corrinoid iron-sulfur protein
117	d1ovma2	Alignment	not modelled	36.1	22	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
118	d1xrsb1	Alignment	not modelled	35.9	15	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
119	c1xs3A_	Alignment	not modelled	35.8	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein xc975; PDBTitle: solution structure analysis of the xc975 protein
120	c3izbB_	Alignment	not modelled	35.2	16	PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein rps3 (s3p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome