

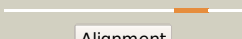
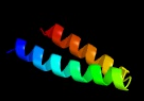
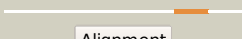






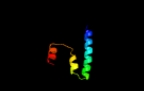




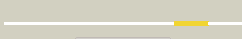


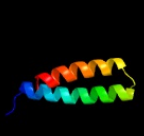


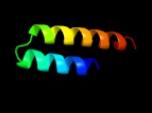

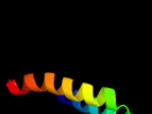




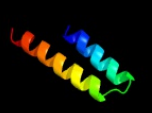



Phyre2

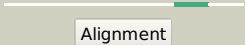

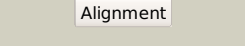
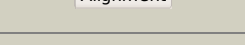
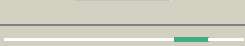
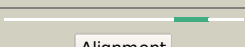
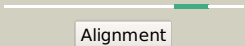

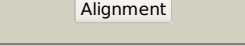
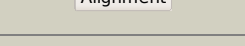
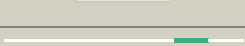
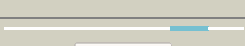


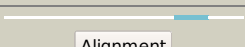
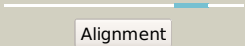
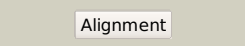
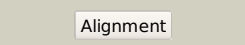
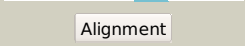
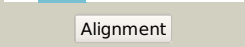


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Description	RVBD3193c_(-)_3560191_3563169
Date	Thu Aug 8 16:20:38 BST 2019
Unique Job ID	2b719bcaa3dcc486

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5gasN_	 Alignment		89.4	15	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
2	c3k17A_	 Alignment		87.3	9	PDB header: transferase Chain: A: PDB Molecule: lin0012 protein; PDBTitle: crystal structure of a lin0012 protein from listeria innocua
3	c1k47F_	 Alignment		87.2	8	PDB header: transferase Chain: F: PDB Molecule: phosphomevalonate kinase; PDBTitle: crystal structure of the streptococcus pneumoniae2 phosphomevalonate kinase (pmk)
4	d1k47a2	 Alignment		86.9	8	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Phosphomevalonate kinase (PMK)
5	c3f0nB_	 Alignment		82.6	18	PDB header: lyase Chain: B: PDB Molecule: mevalonate pyrophosphate decarboxylase; PDBTitle: mus musculus mevalonate pyrophosphate decarboxylase
6	c2oi2A_	 Alignment		82.0	21	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: streptococcus pneumoniae mevalonate kinase in complex with2 diphosphomevalonate
7	c5yysC_	 Alignment		81.1	19	PDB header: transferase Chain: C: PDB Molecule: l-fucokinase, l-fucose-1-p guanylyltransferase; PDBTitle: cryo-em structure of l-fucokinase, gdp-fucose pyrophosphorylase (fkp)2 in bacteroides fragilis
8	c4rksB_	 Alignment		80.7	17	PDB header: transferase Chain: B: PDB Molecule: putative uncharacterized protein ta1305; PDBTitle: crystal structure of mevalonate-3-kinase from thermoplasma acidophilum2 (mevalonate bound)
9	c2gs8A_	 Alignment		75.5	15	PDB header: lyase Chain: A: PDB Molecule: mevalonate pyrophosphate decarboxylase; PDBTitle: structure of mevalonate pyrophosphate decarboxylase from streptococcus2 pyogenes
10	c4ut4B_	 Alignment		74.4	20	PDB header: transferase Chain: B: PDB Molecule: putative sugar kinase; PDBTitle: burkholderia pseudomallei heptokinase wcbl, d-mannose complex.
11	c4n3oB_	 Alignment		73.7	20	PDB header: transferase Chain: B: PDB Molecule: putative d-glycero-d-manno-heptose 7-phosphate kinase; PDBTitle: 2.4 angstrom resolution crystal structure of putative sugar kinase2 from campylobacter jejuni.

12	c3k1sE	Alignment		73.4	21	PDB header: transferase Chain: E; PDB Molecule: pts system, cellobiose-specific iia component; PDBTitle: crystal structure of the pts cellobiose specific enzyme iia from2 bacillus anthracis
13	c5xefA	Alignment		72.8	4	PDB header: chaperone Chain: A; PDB Molecule: flagellar protein flis; PDBTitle: crystal structure of flagellar chaperone from bacteria
14	c3l8rA	Alignment		72.6	18	PDB header: transferase Chain: A; PDB Molecule: putative pts system, cellobiose-specific iia PDBTitle: the crystal structure of ptca from s. mutans
15	d1kvka2	Alignment		72.3	7	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate kinase
16	c3k1iA	Alignment		71.3	12	PDB header: chaperone Chain: A; PDB Molecule: flagellar protein; PDBTitle: crystal strcture of flis-hp1076 complex in h. pylori
17	c2hfuB	Alignment		70.6	21	PDB header: transferase Chain: B; PDB Molecule: mevalonate kinase, putative; PDBTitle: crystal structure of l. major mevalonate kinase in complex2 with r-mevalonate
18	c1wcrA	Alignment		68.5	24	PDB header: transferase Chain: A; PDB Molecule: pts system, n, n'-diacetylchitobiose-specific PDBTitle: trimeric structure of the enzyme iia from escherichia coli2 phosphotransferase system specific for n,n'-3 diacetylchitobiose
19	c6n0yB	Alignment		68.2	14	PDB header: lyase Chain: B; PDB Molecule: diphosphomevalonate decarboxylase; PDBTitle: crystal structure of anaerolinea thermophila mevalonate 5-phosphate2 decarboxylase complexed with (r)-mvapp
20	d2e2aa	Alignment		68.0	21	Fold: Spectrin repeat-like Superfamily: Enzyme Ila from lactose specific PTS, Ila-lac Family: Enzyme Ila from lactose specific PTS, Ila-lac
21	d1vh6a	Alignment	not modelled	67.9	16	Fold: Four-helical up-and-down bundle Superfamily: Flagellar export chaperone FlIS Family: Flagellar export chaperone FlIS
22	c1vh6A	Alignment	not modelled	67.9	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: flagellar protein flis; PDBTitle: crystal structure of a flagellar protein
23	c6n10A	Alignment	not modelled	66.5	21	PDB header: lyase Chain: A; PDB Molecule: diphosphomevalonate decarboxylase mvd1, peroxisomal; PDBTitle: crystal structure of arabidopsis thaliana mevalonate 5-diphosphate2 decarboxylase_1 complexed with (r)-mvapp
24	c4hacA	Alignment	not modelled	66.3	26	PDB header: transferase Chain: A; PDB Molecule: mevalonate kinase; PDBTitle: crystal structure of the mevalonate kinase from an archaeon2 methanosarcina mazi
25	c3dpgE	Alignment	not modelled	63.7	29	PDB header: chaperone, peptide binding protein Chain: E; PDB Molecule: chaperone protein dnaK; PDBTitle: crystal structure of the substrate binding domain of e.2 coli dnaK in complex with a long pyrrolicin-derived3 inhibitor peptide (form b)
26	c5v2IA	Alignment	not modelled	63.2	15	PDB header: lyase Chain: A; PDB Molecule: mevalonate diphosphate decarboxylase; PDBTitle: mevalonate diphosphate mediated atp binding mechanism of the2 mevalonate diphosphate decarboxylase from enterococcus faecalis
27	c4witB	Alignment	not modelled	62.7	14	PDB header: lipid transport Chain: B; PDB Molecule: predicted protein; PDBTitle: tmem16 lipid scramblase in crystal form 2
28	d1piea2	Alignment	not modelled	62.4	16	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Galactokinase

29	c6nrB5_	Alignment	not modelled	61.9	15	PDB header: chaperone Chain: 5: PDB Molecule: prefoldin subunit 5; PDBTitle: htric-hpfd class2
30	c5ir6A_	Alignment	not modelled	60.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: bd-type quinol oxidase subunit i; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
31	c3ltoB_	Alignment	not modelled	58.9	12	PDB header: lyase Chain: B: PDB Molecule: mevalonate diphosphate decarboxylase; PDBTitle: crystal structure of a mevalonate diphosphate decarboxylase2 from legionella pneumophila
32	c2hkeB_	Alignment	not modelled	58.3	20	PDB header: lyase Chain: B: PDB Molecule: diphosphomevalonate decarboxylase, putative; PDBTitle: mevalonate diphosphate decarboxylase from trypanosoma brucei
33	d1fxkc_	Alignment	not modelled	57.9	17	Fold: Long alpha-hairpin Superfamily: Prefoldin Family: Prefoldin
34	c3a7mA_	Alignment	not modelled	57.9	10	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: flagellar protein flit; PDBTitle: structure of flit, the flagellar type iii chaperone for flid
35	c1fi4A_	Alignment	not modelled	57.5	25	PDB header: lyase Chain: A: PDB Molecule: mevalonate 5-diphosphate decarboxylase; PDBTitle: the x-ray crystal structure of mevalonate 5-diphosphate decarboxylase2 at 2.3 angstrom resolution.
36	d1ej7l1	Alignment	not modelled	56.6	18	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
37	d1s4ea2	Alignment	not modelled	56.4	24	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Galactokinase
38	d1h2sa_	Alignment	not modelled	56.1	14	Fold: Family A G protein-coupled receptor-like Superfamily: Family A G protein-coupled receptor-like Family: Bacteriorhodopsin-like
39	c5ig5E_	Alignment	not modelled	52.9	21	PDB header: transferase Chain: E: PDB Molecule: camkii-b hub; PDBTitle: crystal structure of n. vectensis camkii-b hub at ph 4.2
40	d1wuua2	Alignment	not modelled	50.9	21	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Galactokinase
41	c2zdiC_	Alignment	not modelled	50.7	14	PDB header: chaperone Chain: C: PDB Molecule: prefoldin subunit alpha; PDBTitle: crystal structure of prefoldin from pyrococcus horikoshii2 ot3
42	c1bwvA_	Alignment	not modelled	50.3	22	PDB header: lyase Chain: A: PDB Molecule: protein (ribulose bisphosphate carboxylase); PDBTitle: activated ribulose 1,5-bisphosphate carboxylase/oxygenase (rubisco)2 complexed with the reaction intermediate analogue 2-carboxyarabinitol3 1,5-bisphosphate
43	c5tgyA_	Alignment	not modelled	50.2	18	PDB header: unknown function Chain: A: PDB Molecule: ps1; PDBTitle: nmr structure of holo-ps1
44	d1gk8a1	Alignment	not modelled	48.1	22	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
45	d2f1ka1	Alignment	not modelled	48.1	13	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like
46	c5z1fA_	Alignment	not modelled	48.0	11	PDB header: metal transport Chain: A: PDB Molecule: csc1-like protein erd4; PDBTitle: structure of atosca3.1 channel
47	c3t4aG_	Alignment	not modelled	47.3	26	PDB header: immune system Chain: G: PDB Molecule: fibrinogen-binding protein; PDBTitle: structure of a truncated form of staphylococcal complement inhibitor b2 bound to human c3c at 3.4 angstrom resolution
48	c5h7uA_	Alignment	not modelled	46.7	12	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit c; PDBTitle: nmr structure of eif3 36-163
49	d1hkxa_	Alignment	not modelled	46.4	22	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
50	d1kkha2	Alignment	not modelled	46.4	14	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate kinase
51	d1fi4a2	Alignment	not modelled	46.4	17	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate 5-diphosphate decarboxylase
52	c2hk3A_	Alignment	not modelled	46.1	19	PDB header: lyase Chain: A: PDB Molecule: diphosphomevalonate decarboxylase; PDBTitle: crystal structure of mevalonate diphosphate decarboxylase2 from staphylococcus aureus (orthorhombic form)
53	d1bwva1	Alignment	not modelled	46.0	22	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
54	d8ruca1	Alignment	not modelled	45.8	20	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain

55	c3k85B_		Alignment	not modelled	45.8	19	PDB header: transferase Chain: B: PDB Molecule: d-glycero-d-manno-heptose 1-phosphate kinase; PDBTitle: crystal structure of a d-glycero-d-manno-heptose 1-phosphate2 kinase from bacteriodes thetaiotaomicron
56	c2qffA_		Alignment	not modelled	45.0	26	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of staphylococcal complement inhibitor
57	c1u00A_		Alignment	not modelled	43.8	21	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein hsca; PDBTitle: hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc
58	c6oceB_		Alignment	not modelled	43.2	10	PDB header: transport protein Chain: B: PDB Molecule: stress-gated cation channel 1.2; PDBTitle: structure of the rice hyperosmolality-gated ion channel osca1.2
59	c4z7cA_		Alignment	not modelled	43.1	16	PDB header: lyase Chain: A: PDB Molecule: diphosphomevalonate decarboxylase; PDBTitle: diphosphomevalonate decarboxylase from the sulfobolus sulfataricus,2 space group h32
60	c6ch3B_		Alignment	not modelled	43.0	24	PDB header: structural protein Chain: B: PDB Molecule: flagellar secretion chaperone flis,flagellin; PDBTitle: crystal structure of the cytoplasmic domain of flha and flis-flhc2 complex
61	c4g59D_		Alignment	not modelled	42.7	22	PDB header: immune system Chain: D: PDB Molecule: m152 protein; PDBTitle: crystal structure of the murine cytomegalovirus mhc-i homolog m1522 with ligand rae-1 gamma
62	d2g5ca1		Alignment	not modelled	42.7	5	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like
63	c5ir6B_		Alignment	not modelled	42.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: bd-type quinol oxidase subunit ii; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
64	c2k37A_		Alignment	not modelled	42.2	20	PDB header: photosynthesis Chain: A: PDB Molecule: chlorosome protein a; PDBTitle: csma
65	c2mwqA_		Alignment	not modelled	42.2	16	PDB header: plant protein Chain: A: PDB Molecule: oxygen-evolving enhancer protein 3, chloroplastic; PDBTitle: solution structure of psbq from spinacia oleracea
66	d1rbla1		Alignment	not modelled	41.8	24	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
67	d1njra_		Alignment	not modelled	40.8	15	Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain
68	c1pieA_		Alignment	not modelled	40.7	14	PDB header: transferase Chain: A: PDB Molecule: galactokinase; PDBTitle: crystal structure of lactococcus lactis galactokinase2 complexed with galactose
69	c2cz9A_		Alignment	not modelled	40.7	21	PDB header: transferase Chain: A: PDB Molecule: probable galactokinase; PDBTitle: crystal structure of galactokinase from pyrococcus horikoshi
70	d1u00a1		Alignment	not modelled	40.6	21	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Heat shock protein 70kD (HSP70), C-terminal subdomain Family: Heat shock protein 70kD (HSP70), C-terminal subdomain
71	c6nr3_		Alignment	not modelled	39.8	16	PDB header: chaperone Chain: 3: PDB Molecule: prefoldin subunit 3; PDBTitle: htric-hpfd class2
72	c6g7oA_		Alignment	not modelled	39.3	19	PDB header: membrane protein Chain: A: PDB Molecule: alkaline ceramidase 3,soluble cytochrome b562; PDBTitle: crystal structure of human alkaline ceramidase 3 (acer3) at 2.72 angstrom resolution
73	c1nzeA_		Alignment	not modelled	39.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxygen-evolving enhancer protein 3; PDBTitle: crystal structure of psbq polypeptide of photosystem ii2 from higher plants
74	d1nzea_		Alignment	not modelled	39.1	16	Fold: Four-helical up-and-down bundle Superfamily: Oxygen-evolving enhancer protein 3, Family: Oxygen-evolving enhancer protein 3,
75	c4xzsA_		Alignment	not modelled	37.8	33	PDB header: apoptosis Chain: A: PDB Molecule: maltose-binding periplasmic protein,tp53-regulated PDBTitle: crystal structure of triap1-mbp fusion
76	c2vvdA_		Alignment	not modelled	37.6	22	PDB header: viral protein Chain: A: PDB Molecule: spike protein p1; PDBTitle: crystal structure of the receptor binding domain of the2 spike protein p1 from bacteriophage pm2
77	c5woyA_		Alignment	not modelled	37.1	13	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: nmr solution structure of enzyme i (neit) protein using two 4d-spectra
78	c4exrA_		Alignment	not modelled	36.8	21	PDB header: unknown function Chain: A: PDB Molecule: putative lipoprotein; PDBTitle: crystal structure of a putative lipoprotein (cd1622) from clostridium2 difficile 630 at 1.85 a resolution
79	c4zwlA_		Alignment	not modelled	36.4	11	PDB header: signaling protein Chain: A: PDB Molecule: chimera protein of human rhodopsin, mouse s-arrestin, and PDBTitle: crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser

80	c5v88A_	Alignment	not modelled	36.2	16	PDB header: ligase / protein binding Chain: A: PDB Molecule: lysozyme,dcn1-like protein 1; PDBTitle: structure of dcn1 bound to nacm-cov
81	c6p46A_	Alignment	not modelled	35.0	14	PDB header: membrane protein Chain: A: PDB Molecule: anoctamin-6; PDBTitle: cryo-em structure of tmem16f in digitonin with calcium bound
82	c1rcxH_	Alignment	not modelled	34.6	20	PDB header: lyase (carbon-carbon) Chain: H: PDB Molecule: ribulose biphosphate carboxylase/oxygenase; PDBTitle: non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
83	c2rq7A_	Alignment	not modelled	32.7	22	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase epsilon chain; PDBTitle: solution structure of the epsilon subunit chimera combining2 the n-terminal beta-sandwich domain from t. elongatus bp-13 f1 and the c-terminal alpha-helical domain from spinach4 chloroplast f1
84	c4lihG_	Alignment	not modelled	32.4	29	PDB header: oxidoreductase Chain: G: PDB Molecule: gamma-glutamyl-gamma-aminobutyraldehyde dehydrogenase; PDBTitle: the crystal structure of gamma-glutamyl-gamma-aminobutyraldehyde2 dehydrogenase from burkholderia cenocepacia j2315
85	d1sr2a_	Alignment	not modelled	31.6	6	Fold: Four-helical up-and-down bundle Superfamily: Histidine-containing phosphotransfer domain, HPT domain Family: Sensor-like histidine kinase YojN, C-terminal domain
86	c6fkhe_	Alignment	not modelled	30.1	23	PDB header: membrane protein Chain: E: PDB Molecule: atp synthase subunit alpha, chloroplastic; PDBTitle: chloroplast f1fo conformation 2
87	d2d0ta1	Alignment	not modelled	29.9	15	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
88	d1sf9a_	Alignment	not modelled	29.3	17	Fold: SH3-like barrel Superfamily: Hypothetical protein YfhH Family: Hypothetical protein YfhH
89	c2xyxA_	Alignment	not modelled	29.2	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein, gk0453; PDBTitle: crystal structure of hypothetical conserved protein, gk0453
90	c4pt3C_	Alignment	not modelled	29.2	29	PDB header: oxidoreductase Chain: C: PDB Molecule: aldehyde dehydrogenase; PDBTitle: nadph complex structure of aldehyde dehydrogenase from bacillus cereus
91	c4pt2B_	Alignment	not modelled	29.1	24	PDB header: virus like particle Chain: B: PDB Molecule: encapsulin protein; PDBTitle: myxococcus xanthus encapsulin protein (enca)
92	c5x89A_	Alignment	not modelled	28.4	29	PDB header: hydrolase Chain: A: PDB Molecule: enda-like protein,trna-splicing endonuclease; PDBTitle: the x-ray crystal structure of subunit fusion rna splicing2 endonuclease from methanopyrus kandleri
93	c1rldB_	Alignment	not modelled	28.4	20	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose 1,5 bisphosphate carboxylase/oxygenase (large PDBTitle: solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(/slash)oxygenase
94	c1mh3A_	Alignment	not modelled	28.4	24	PDB header: sugar binding, dna binding protein Chain: A: PDB Molecule: maltose binding-a1 homeodomain protein chimera; PDBTitle: maltose binding-a1 homeodomain protein chimera, crystal form i
95	d2ux0a1	Alignment	not modelled	27.9	31	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
96	d3eeqa2	Alignment	not modelled	27.9	4	Fold: CbiG N-terminal domain-like Superfamily: CbiG N-terminal domain-like Family: CbiG N-terminal domain-like
97	d1ykwa1	Alignment	not modelled	27.9	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
98	c1ezaA_	Alignment	not modelled	27.8	17	PDB header: phosphotransferase Chain: A: PDB Molecule: enzyme i; PDBTitle: amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
99	c3l0iA_	Alignment	not modelled	27.5	18	PDB header: protein binding/protein transport Chain: A: PDB Molecule: drra; PDBTitle: complex structure of sidm/drra with the wild type rab1
100	d1bxna1	Alignment	not modelled	26.9	21	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
101	c2jysA_	Alignment	not modelled	26.8	19	PDB header: hydrolase Chain: A: PDB Molecule: protease/reverse transcriptase; PDBTitle: solution structure of simian foamy virus (mac) protease
102	c5t1oB_	Alignment	not modelled	26.6	23	PDB header: transferase Chain: B: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase ptsp; PDBTitle: solution-state nmr and saxs structural ensemble of npr (1-85) in2 complex with ein-ntr (170-424)
103	c2x7iA_	Alignment	not modelled	26.3	11	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: crystal structure of mevalonate kinase from methicillin-2 resistant staphylococcus aureus mrsa252
						PDB header: membrane protein

104	c5nl2A_	Alignment	not modelled	26.0	14	Chain: A; PDB Molecule: anoctamin-1; PDBTitle: cryo-em structure of the mtmem16a ion channel at 6.6 a resolution.
105	c2vveB_	Alignment	not modelled	25.9	22	PDB header: viral protein Chain: B; PDB Molecule: spike protein p1; PDBTitle: crystal structure of the stem and receptor binding domain2 of the spike protein p1 from bacteriophage pm2
106	c5my7A_	Alignment	not modelled	25.6	20	PDB header: cell adhesion Chain: A; PDB Molecule: adhesin; PDBTitle: adhesin complex protein from neisseria meningitidis
107	c3v2uC_	Alignment	not modelled	25.2	11	PDB header: transcription Chain: C; PDB Molecule: protein gal3; PDBTitle: crystal structure of the yeast gal regulon complex of the repressor,2 gal80p, and the transducer, gal3p, with galactose and atp
108	c5l4kZ_	Alignment	not modelled	25.2	15	PDB header: structural protein Chain: Z; PDB Molecule: 26s proteasome non-atpase regulatory subunit 2; PDBTitle: the human 26s proteasome lid
109	d2buqa1	Alignment	not modelled	24.9	28	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tettrapeptide repeat (TPR)
110	c1telA_	Alignment	not modelled	24.8	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: ribulose biphosphate carboxylase, large subunit; PDBTitle: crystal structure of a rubisco-like protein from chlorobium2 tepidum
111	c3eeqB_	Alignment	not modelled	24.8	4	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative cobalamin biosynthesis protein g homolog; PDBTitle: crystal structure of a putative cobalamin biosynthesis protein g2 homolog from sulfobolus solfataricus
112	c3mk7F_	Alignment	not modelled	24.6	15	PDB header: oxidoreductase Chain: F; PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
113	c6iu3A_	Alignment	not modelled	24.4	16	PDB header: metal transport Chain: A; PDB Molecule: vit1; PDBTitle: crystal structure of iron transporter vit1 with zinc ions
114	c5boiA_	Alignment	not modelled	24.4	28	PDB header: unknown function Chain: A; PDB Molecule: germination protein ypeb; PDBTitle: bacillus megaterium ypeb c-terminal domain
115	c5y31B_	Alignment	not modelled	24.1	17	PDB header: cell adhesion Chain: B; PDB Molecule: leucine-rich glioma-inactivated protein 1; PDBTitle: crystal structure of human lgi1-adam22 complex
116	c6jtdB_	Alignment	not modelled	23.7	20	PDB header: transferase Chain: B; PDB Molecule: c-glycosyltransferase; PDBTitle: crystal structure of tccgt1 in complex with udp
117	d2pv7a1	Alignment	not modelled	23.5	10	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like
118	d1dkza1	Alignment	not modelled	23.5	26	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Heat shock protein 70kD (HSP70), C-terminal subdomain Family: Heat shock protein 70kD (HSP70), C-terminal subdomain
119	c2w0cL_	Alignment	not modelled	23.5	22	PDB header: virus Chain: L; PDB Molecule: protein 2; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
120	c4zwcC_	Alignment	not modelled	22.5	8	PDB header: signaling protein Chain: C; PDB Molecule: chimera protein of human rhodopsin, mouse s-arrestin, and PDBTitle: crystal structure of rhodopsin bound to arrestin by femtosecond x-ray2 laser