





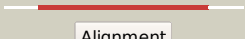

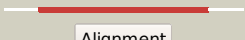

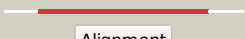







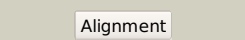



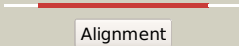

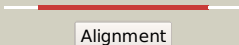

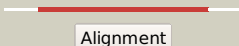



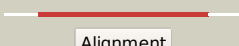

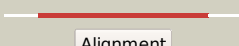

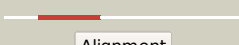







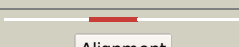

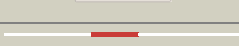
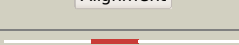
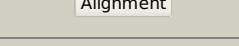
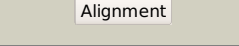
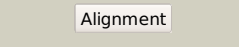


Phyre2

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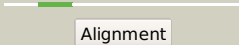
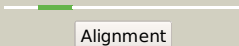



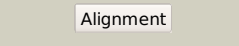
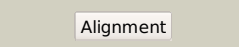



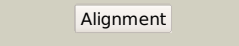
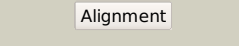

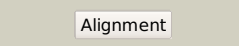

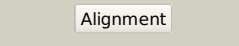
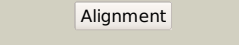
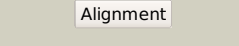

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1c4gB_	 Alignment		100.0	21	PDB header: transferase Chain: B; PDB Molecule: protein (alpha-d-glucose 1-phosphate phosphoglucomutase); PDBTitle: phosphoglucomutase vanadate based transition state analog complex
2	c1kfiA_	 Alignment		100.0	19	PDB header: isomerase Chain: A; PDB Molecule: phosphoglucomutase 1; PDBTitle: crystal structure of the exocytosis-sensitive2 phosphoprotein, pp63/parafusin (phosphoglucomutase) from3 paramecium
3	c2fuvB_	 Alignment		100.0	22	PDB header: isomerase Chain: B; PDB Molecule: phosphoglucomutase; PDBTitle: phosphoglucomutase from salmonella typhimurium.
4	c1wqaB_	 Alignment		100.0	26	PDB header: isomerase Chain: B; PDB Molecule: phospho-sugar mutase; PDBTitle: crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
5	c3c04A_	 Alignment		100.0	20	PDB header: isomerase Chain: A; PDB Molecule: phosphomannomutase/phosphoglucomutase; PDBTitle: structure of the p368g mutant of pmm/pgm from p. aeruginosa
6	c2f7IA_	 Alignment		100.0	24	PDB header: isomerase Chain: A; PDB Molecule: 455aa long hypothetical phospho-sugar mutase; PDBTitle: crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
7	c3uw2A_	 Alignment		100.0	22	PDB header: isomerase Chain: A; PDB Molecule: phosphoglucomutase/phosphomannomutase family protein; PDBTitle: x-ray crystal structure of phosphoglucomutase/phosphomannomutase2 family protein (bth_i1489)from burkholderia thailandensis
8	c4qg5D_	 Alignment		100.0	23	PDB header: isomerase Chain: D; PDB Molecule: putative phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from leishmania major at 3.52 angstrom resolution
9	c5bmpA_	 Alignment		100.0	23	PDB header: isomerase Chain: A; PDB Molecule: phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from xanthomonas citri2 complexed with glucose-1-phosphate
10	c2z0fA_	 Alignment		100.0	27	PDB header: isomerase Chain: A; PDB Molecule: putative phosphoglucomutase; PDBTitle: crystal structure of putative phosphoglucomutase from thermus2 thermophilus hb8
11	c1tuoA_	 Alignment		100.0	28	PDB header: biosynthetic protein Chain: A; PDB Molecule: putative phosphomannomutase; PDBTitle: crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8

12	c3pdkB_	 Alignment		100.0	21	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of phosphoglucosamine mutase from b. anthracis
13	c6gyzB_	 Alignment		100.0	19	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of glmm from staphylococcus aureus
14	c4hjhA_	 Alignment		100.0	22	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase; PDBTitle: iodide sad phased crystal structure of a phosphoglucomutase from2 brucella melitensis complexed with glucose-6-phosphate
15	c3i3wB_	 Alignment		100.0	21	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: structure of a phosphoglucosamine mutase from francisella tularensis
16	c2dkdA_	 Alignment		100.0	20	PDB header: isomerase Chain: A: PDB Molecule: phosphoacetylglucosamine mutase; PDBTitle: crystal structure of n-acetylglucosamine-phosphate mutase,2 a member of the alpha-d-phosphohexomutase superfamily, in3 the product complex
17	c4bjub_	 Alignment		100.0	21	PDB header: isomerase Chain: B: PDB Molecule: n-acetylglucosamine-phosphate mutase; PDBTitle: genetic and structural validation of aspergillus fumigatus2 n-acetylphosphoglucosamine mutase as an antifungal target
18	d1kfia1	 Alignment		100.0	20	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
19	d3pmga1	 Alignment		100.0	22	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
20	d1p5dx1	 Alignment		100.0	24	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
21	d3pmga3	 Alignment	not modelled	99.8	22	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
22	d1kfia3	 Alignment	not modelled	99.8	25	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
23	d1p5dx2	 Alignment	not modelled	99.7	22	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
24	d1p5dx3	 Alignment	not modelled	99.7	17	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
25	d3pmga2	 Alignment	not modelled	99.6	20	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
26	d1kfia2	 Alignment	not modelled	99.6	19	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
27	d1p5dx4	 Alignment	not modelled	99.3	14	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
28	d1wjwa_	 Alignment	not modelled	98.6	23	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
29	d1kfia4	 Alignment	not modelled	97.3	15	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain

						Family: Phosphoglucomutase, C-terminal domain
30	d3pmga4	Alignment	not modelled	97.0	20	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
31	c6ofuC	Alignment	not modelled	89.2	17	PDB header: lyase Chain: C: PDB Molecule: ydji aldolase; PDBTitle: x-ray crystal structure of the ydji aldolase from escherichia coli k12
32	d7reqa2	Alignment	not modelled	87.0	10	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
33	c2i2xD	Alignment	not modelled	85.7	16	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
34	c3pm6B	Alignment	not modelled	85.6	20	PDB header: lyase Chain: B: PDB Molecule: putative fructose-bisphosphate aldolase; PDBTitle: crystal structure of a putative fructose-1,6-biphosphate aldolase from2 coccidioides immitis solved by combined sad mr
35	d3bula2	Alignment	not modelled	85.1	10	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
36	c3he8A	Alignment	not modelled	83.8	26	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase; PDBTitle: structural study of clostridium thermocellum ribose-5-phosphate2 isomerase b
37	d1nn4a	Alignment	not modelled	83.2	25	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
38	c3s5pA	Alignment	not modelled	82.4	22	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
39	d1gvfa	Alignment	not modelled	80.7	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
40	d1rvga	Alignment	not modelled	80.5	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
41	c4jgiB	Alignment	not modelled	80.3	12	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
42	c3c52B	Alignment	not modelled	80.2	18	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: class ii fructose-1,6-bisphosphate aldolase from helicobacter pylori2 in complex with phosphoglycolhydroxamic acid, a competitive3 inhibitor
43	c2iswB	Alignment	not modelled	77.8	22	PDB header: lyase Chain: B: PDB Molecule: putative fructose-1,6-bisphosphate aldolase; PDBTitle: structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolhydroxamate
44	c3ezxA	Alignment	not modelled	76.7	12	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
45	c3nv9A	Alignment	not modelled	75.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: malic enzyme; PDBTitle: crystal structure of entamoeba histolytica malic enzyme
46	c3q94B	Alignment	not modelled	75.2	23	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase, class ii; PDBTitle: the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
47	c3qayC	Alignment	not modelled	74.0	21	PDB header: lyase Chain: C: PDB Molecule: endolysin; PDBTitle: catalytic domain of cd27l endolysin targeting clostridia difficile
48	d1ccwa	Alignment	not modelled	73.2	18	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
49	c3m1pA	Alignment	not modelled	72.4	24	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of ribose 5-phosphate isomerase type b from trypanosoma2 cruzi, soaked with allose-6-phosphate
50	c3hlyA	Alignment	not modelled	71.7	17	PDB header: flavoprotein Chain: A: PDB Molecule: flavodoxin-like domain; PDBTitle: crystal structure of the flavodoxin-like domain from synechococcus sp2 q5mzp6_synp6 protein. northeast structural genomics consortium target3 snr135d.
51	c4m6iA	Alignment	not modelled	69.3	19	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan amidase rv3717; PDBTitle: structure of the reduced, zn-bound form of mycobacterium tuberculosis2 peptidoglycan amidase rv3717
52	c1bmtB	Alignment	not modelled	68.9	11	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
53	c1k98A	Alignment	not modelled	68.6	13	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
54	c3fniA	Alignment	not modelled	68.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a

55	d1dosa_	Alignment	not modelled	67.1	25	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
56	c5ncdA_	Alignment	not modelled	66.6	20	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan n-acetylglucosamine deacetylase; PDBTitle: crystal structure of the polysaccharide deacetylase bc1974 from <i>Bacillus cereus</i> in complex with (2S)-2-amino-5-(diaminomethylideneamino)-n-hydroxypentanamide
57	c3ne8A_	Alignment	not modelled	65.8	33	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase; PDBTitle: the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of <i>Bartonella henselae</i> str. houston-1
58	d1xrsb1	Alignment	not modelled	65.5	10	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
59	c5flzC_	Alignment	not modelled	65.1	14	PDB header: cell cycle Chain: C: PDB Molecule: tubulin gamma chain; PDBTitle: cryo-em structure of gamma-tusc oligomers in a closed conformation
60	c4lfnD_	Alignment	not modelled	64.6	21	PDB header: isomerase Chain: D: PDB Molecule: galactose-6-phosphate isomerase subunit b; PDBTitle: crystal structure of d-galactose-6-phosphate isomerase in complex with 2 d-ribose
61	c3whpA_	Alignment	not modelled	64.5	26	PDB header: gene regulation Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of the c-terminal domain of the <i>Thermophilus litr2</i> in complex with cobalamin
62	c3k7pA_	Alignment	not modelled	64.5	22	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: structure of mutant of ribose 5-phosphate isomerase type b from <i>Trypanosoma cruzi</i> .
63	c2zf8A_	Alignment	not modelled	63.9	12	PDB header: structural protein Chain: A: PDB Molecule: component of sodium-driven polar flagellar motor; PDBTitle: crystal structure of motY
64	d1t6t1_	Alignment	not modelled	63.7	21	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
65	c3qm3C_	Alignment	not modelled	63.6	22	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: 1.85 angstrom resolution crystal structure of fructose-bisphosphate2 aldolase (fba) from <i>Campylobacter jejuni</i>
66	d2vvpA1	Alignment	not modelled	63.2	22	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
67	c4lfmA_	Alignment	not modelled	60.5	23	PDB header: isomerase Chain: A: PDB Molecule: galactose-6-phosphate isomerase subunit a; PDBTitle: crystal structure of d-galactose-6-phosphate isomerase in complex with 2 d-psicose
68	c1y80A_	Alignment	not modelled	60.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from <i>Moorella thermoacetica</i>
69	c6h0cA_	Alignment	not modelled	60.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: flv1 flavodiiron core from <i>Synechocystis</i> sp. pcc6803
70	c2yxbA_	Alignment	not modelled	59.0	22	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from <i>Aeropyrum pernix</i>
71	d1tubb1	Alignment	not modelled	58.2	13	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
72	c4pyrA_	Alignment	not modelled	58.0	15	PDB header: transport protein Chain: A: PDB Molecule: putative branched-chain amino acid abc transporter; PDBTitle: structure of a putative branched-chain amino acid abc transporter from <i>Chromobacterium violaceum</i> atcc 12472
73	c2q9uB_	Alignment	not modelled	56.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: a-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from <i>Giardia intestinalis</i>
74	c2yfkA_	Alignment	not modelled	56.1	23	PDB header: transferase Chain: A: PDB Molecule: aspartate/ornithine carbamoyltransferase; PDBTitle: crystal structure of a putative transcarbamoylase from <i>Enterococcus faecalis</i>
75	c6mu0A_	Alignment	not modelled	55.7	19	PDB header: isomerase Chain: A: PDB Molecule: probable ribose-5-phosphate isomerase b; PDBTitle: crystal structure of ribose-5-phosphate isomerase b from <i>Mycoplasma genitalium</i> with bound ribulose-5-phosphate
76	c3j6vK_	Alignment	not modelled	55.6	30	PDB header: ribosome Chain: K: PDB Molecule: 28s ribosomal protein s11, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial 28s ribosome
77	c2p2gD_	Alignment	not modelled	55.5	18	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from <i>Mycobacterium tuberculosis</i> (rv1656): orthorhombic form
78	c1uarA_	Alignment	not modelled	54.9	10	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: crystal structure of rhodanese from <i>Thermophilus hb8</i>
79	d1b1ca_	Alignment	not modelled	54.8	14	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like

80	c4ne4A	 Alignment	not modelled	53.4	17	PDB header: transport protein Chain: A: PDB Molecule: abc transporter, substrate binding protein PDBTitle: crystal structure of abc transporter substrate binding protein prox2 from agrobacterium tumefaciens cocrystallized with btb
81	c1boiA	 Alignment	not modelled	53.2	12	PDB header: transferase Chain: A: PDB Molecule: rhodanese; PDBTitle: n-terminally truncated rhodanese
82	c3q98A	 Alignment	not modelled	52.5	15	PDB header: transferase Chain: A: PDB Molecule: transcarbamylyase; PDBTitle: structure of ygew encoded protein from e. coli
83	c5ceeA	 Alignment	not modelled	52.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nad-dependent malic enzyme; PDBTitle: malic enzyme from candidatus phytoplasma aywb in complex with nad and2 mg2+
84	d1o0sa1	 Alignment	not modelled	51.7	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
85	c3olhA	 Alignment	not modelled	51.4	16	PDB header: transferase Chain: A: PDB Molecule: 3-mercaptopyruvate sulfurtransferase; PDBTitle: human 3-mercaptopyruvate sulfurtransferase
86	d1ycga1	 Alignment	not modelled	51.2	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
87	c4em8A	 Alignment	not modelled	51.1	17	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase b; PDBTitle: the structure of ribose 5-phosphate isomerase b from anaplasma2 phagocytophilum
88	c1xrsB	 Alignment	not modelled	50.4	9	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
89	c1okgA	 Alignment	not modelled	50.4	13	PDB header: transferase Chain: A: PDB Molecule: possible 3-mercaptopyruvate sulfurtransferase; PDBTitle: 3-mercaptopyruvate sulfurtransferase from leishmania major
90	d1dxha2	 Alignment	not modelled	50.4	16	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
91	c2w37A	 Alignment	not modelled	50.3	15	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase, catabolic; PDBTitle: crystal structure of the hexameric catabolic ornithine2 transcarbamylyase from lactobacillus hilgardii
92	c1e0cA	 Alignment	not modelled	48.8	17	PDB header: sulfurtransferase Chain: A: PDB Molecule: sulfurtransferase; PDBTitle: sulfurtransferase from azotobacter vinelandii
93	d1e5da1	 Alignment	not modelled	48.2	22	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
94	c3r6uA	 Alignment	not modelled	48.1	9	PDB header: transport protein Chain: A: PDB Molecule: choline-binding protein; PDBTitle: crystal structure of choline binding protein opbc from bacillus2 subtilis
95	c1a1sA	 Alignment	not modelled	47.9	18	PDB header: transcarbamylyase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine carbamoyltransferase from pyrococcus furiosus
96	c1o0sB	 Alignment	not modelled	47.6	21	PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent malic enzyme; PDBTitle: crystal structure of ascaris suum malic enzyme complexed with nadh
97	c2p4nB	 Alignment	not modelled	47.5	13	PDB header: transport protein Chain: B: PDB Molecule: tubulin beta chain; PDBTitle: human monomeric kinesin (1bg2) and bovine tubulin (1jff) docked into2 the 9-angstrom cryo-em map of nucleotide-free kinesin complexed to3 the microtubule
98	d1o1xa	 Alignment	not modelled	47.1	22	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB
99	d2qalk1	 Alignment	not modelled	47.0	29	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
100	c4h2dB	 Alignment	not modelled	46.5	11	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-dependent diflavin oxidoreductase 1; PDBTitle: crystal structure of ndor1
101	c2yqrA	 Alignment	not modelled	46.1	26	PDB header: rna binding protein Chain: A: PDB Molecule: kiaa0907 protein; PDBTitle: solution structure of the kh domain in kiaa0907 protein
102	c2pfsA	 Alignment	not modelled	45.1	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
103	c5mp4C	 Alignment	not modelled	45.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: protoplast secreted protein 2; PDBTitle: the structure of pst2p from saccharomyces cerevisiae
104	c1vlvA	 Alignment	not modelled	43.9	18	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
105	c3wjaA	 Alignment	not modelled	43.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nadp-dependent malic enzyme; PDBTitle: the crystal structure of human cytosolic nadp(+)-dependent malic2 enzyme in apo form

106	d2c1ia1	Alignment	not modelled	43.5	13	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
107	d1gq2a1	Alignment	not modelled	43.2	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
108	d1pj3a1	Alignment	not modelled	43.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
109	c2ynmC_	Alignment	not modelled	42.5	13	PDB header: oxidoreductase Chain: C: PDB Molecule: light-independent protochlorophyllide reductase subunit n; PDBTitle: structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
110	c5d88A_	Alignment	not modelled	42.5	14	PDB header: hydrolase Chain: A: PDB Molecule: predicted protease of the collagenase family; PDBTitle: the structure of the u32 peptidase mk0906
111	c3jyvK_	Alignment	not modelled	42.3	24	PDB header: ribosome Chain: K: PDB Molecule: 40s ribosomal protein s14(a); PDBTitle: structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
112	c5jp6A_	Alignment	not modelled	42.3	23	PDB header: hydrolase Chain: A: PDB Molecule: putative polysaccharide deacetylase; PDBTitle: bdellovibrio bacteriovorus peptidoglycan deacetylase bd3279
113	c2aw5A_	Alignment	not modelled	42.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: nadp-dependent malic enzyme; PDBTitle: crystal structure of a human malic enzyme
114	c3edlA_	Alignment	not modelled	42.1	20	PDB header: structural protein Chain: A: PDB Molecule: alpha-tubulin; PDBTitle: kinesin13-microtubule ring complex
115	c1gz3B_	Alignment	not modelled	42.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent malic enzyme, mitochondrial; PDBTitle: molecular mechanism for the regulation of human mitochondrial nad(p)+-2 dependent malic enzyme by atp and fumarate
116	c4xfkA_	Alignment	not modelled	42.0	14	PDB header: transport protein Chain: A: PDB Molecule: putative branched chain amino acid abc transporter, PDBTitle: crystal structure of leucine-, isoleucine-, valine-, threonine-, and2 alanine-binding protein from brucella ovis
117	c2otcA_	Alignment	not modelled	41.8	21	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
118	c1fvoB_	Alignment	not modelled	41.7	17	PDB header: transferase Chain: B: PDB Molecule: ornithine transcarbamylase; PDBTitle: crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
119	d2btoa1	Alignment	not modelled	41.5	16	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
120	d1ykga1	Alignment	not modelled	41.4	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like