


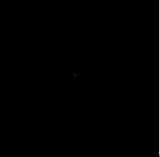



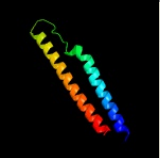

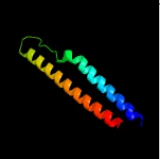

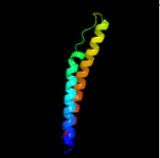

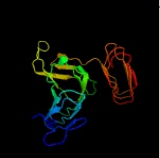

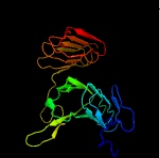

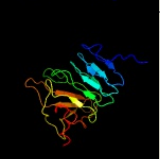

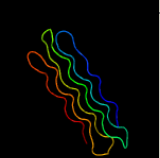

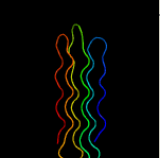
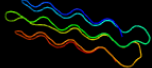
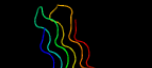

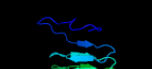


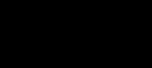
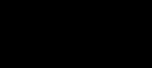



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1450c_PE_PGRS27)_1630644_1634633
 Date Fri Aug 2 13:30:02 BST 2019
 Unique Job ID a7e11fe1aed2379a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ygvA_	 Alignment		100.0	28	PDB header: structural protein/contractile protein Chain: A; PDB Molecule: collagen i alpha 1; PDBTitle: the structure of collagen type i. single type i collagen2 molecule: rigid refinement
2	c1y0fB_	 Alignment		100.0	33	PDB header: structural protein/contractile protein Chain: B; PDB Molecule: collagen i alpha 2; PDBTitle: the structure of collagen type i. single type i collagen2 molecule
3	c3hqvB_	 Alignment		100.0	27	PDB header: structural protein, contractile protein Chain: B; PDB Molecule: collagen alpha-2(i) chain; PDBTitle: low resolution, molecular envelope structure of type i2 collagen in situ determined by fiber diffraction. single3 type i collagen molecule, rigid body refinement
4	c2g38A_	 Alignment		98.6	33	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
5	d2g38a1	 Alignment		98.6	33	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
6	c5xfA_	 Alignment		98.6	44	PDB header: protein transport Chain: A; PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-pep15 in complex with espg5 from m.2 tuberculosis
7	c2zj6A_	 Alignment		97.9	18	PDB header: hydrolase Chain: A; PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
8	c2qubG_	 Alignment		97.8	16	PDB header: hydrolase Chain: G; PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serratia2 marcescens
9	c2ml3A_	 Alignment		96.9	16	PDB header: isomerase Chain: A; PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 6; PDBTitle: solution structure of alge6r3 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
10	c3bogB_	 Alignment		96.9	37	PDB header: antifreeze protein Chain: B; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
11	c3bogA_	 Alignment		96.9	37	PDB header: antifreeze protein Chain: A; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate

12	c2pneA	Alignment		96.6	37	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: crystal structure of the snow flea antifreeze protein
13	c3boiB	Alignment		96.6	37	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
14	c3boiA	Alignment		96.6	37	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
15	c1satA	Alignment		96.0	17	PDB header: hydrolase (serine protease) Chain: A: PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2 marcescens
16	d1kapp1	Alignment		95.9	17	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
17	c5ctdA	Alignment		95.9	38	PDB header: structural protein Chain: A: PDB Molecule: collagen alpha-1(i) chain,collagen alpha-1(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
18	c5ctdB	Alignment		95.8	33	PDB header: structural protein Chain: B: PDB Molecule: collagen alpha-2(i) chain,collagen alpha-2(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
19	c5ctiC	Alignment		95.8	35	PDB header: structural protein Chain: C: PDB Molecule: collagen alpha-1(i) chain,collagen alpha-3(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen (native form)
20	d1sata1	Alignment		95.7	18	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
21	d1g9ka1	Alignment	not modelled	95.7	17	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
22	c1k7qA	Alignment	not modelled	95.4	17	PDB header: hydrolase Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtc from erwinia chrysanthemi: e189a mutant
23	d1k7ia1	Alignment	not modelled	95.1	19	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
24	c1nayC	Alignment	not modelled	95.0	21	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
25	c2ml2A	Alignment	not modelled	93.3	21	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 6; PDBTitle: solution structure of alge6r2 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
26	c2agmA	Alignment	not modelled	91.4	24	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
27	c1jiwP	Alignment	not modelled	90.8	22	PDB header: hydrolase/hyrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
28	c1om8A	Alignment	not modelled	89.1	23	PDB header: hydrolase Chain: A: PDB Molecule: serralysin; PDBTitle: crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta

29	d8ruca2	Alignment	not modelled	87.8	22	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
30	d1rbla2	Alignment	not modelled	87.3	20	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
31	d1svda2	Alignment	not modelled	87.2	22	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
32	c2klwA_	Alignment	not modelled	86.5	27	PDB header: de novo protein Chain: A: PDB Molecule: (pkg)10; PDBTitle: solution structure of an abc collagen heterotrimer reveals a2 single-register helix stabilized by electrostatic3 interactions
33	d1bxna2	Alignment	not modelled	84.5	19	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
34	c5macD_	Alignment	not modelled	82.5	25	PDB header: lyase Chain: D: PDB Molecule: ribulose-1,5-bisphosphate carboxylase-oxygenase type iii; PDBTitle: crystal structure of decameric methanococcoides burtonii rubisco2 complexed with 2-carboxyarabinitol biphosphate
35	c5cxlA_	Alignment	not modelled	82.5	28	PDB header: toxin Chain: A: PDB Molecule: bifunctional hemolysin/adenylate cyclase; PDBTitle: crystal structure of rtx domain block v of adenylate cyclase toxin2 from bordetella pertussis
36	d1gk8a2	Alignment	not modelled	81.7	19	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
37	d1wdda2	Alignment	not modelled	80.9	24	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
38	c2cuoF_	Alignment	not modelled	80.8	30	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
39	c2cuoC_	Alignment	not modelled	80.8	30	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
40	d2d69a2	Alignment	not modelled	79.6	15	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
41	c1k6fC_	Alignment	not modelled	76.9	31	PDB header: structural protein Chain: C: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
42	c1k6fE_	Alignment	not modelled	76.9	31	PDB header: structural protein Chain: E: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
43	c1k6fB_	Alignment	not modelled	76.9	31	PDB header: structural protein Chain: B: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
44	c1k6fF_	Alignment	not modelled	76.9	31	PDB header: structural protein Chain: F: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
45	c1k6fA_	Alignment	not modelled	76.9	31	PDB header: structural protein Chain: A: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
46	c1k6fD_	Alignment	not modelled	76.9	31	PDB header: structural protein Chain: D: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
47	c2cuoB_	Alignment	not modelled	73.7	27	PDB header: structural protein Chain: B: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
48	c2cuoE_	Alignment	not modelled	73.7	27	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
49	c2cuoA_	Alignment	not modelled	73.7	27	PDB header: structural protein Chain: A: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
50	c2cuoD_	Alignment	not modelled	73.7	27	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
51	c3ah9A_	Alignment	not modelled	73.7	29	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
52	c3ah9C_	Alignment	not modelled	73.0	28	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
53	c3ah9E_	Alignment	not modelled	73.0	28	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
54	c3ah9B_	Alignment	not modelled	73.0	28	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
55	d1bwva2	Alignment	not modelled	72.8	22	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase

56	c3ah9F_	Alignment	not modelled	72.6	29	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
57	d1ej7I2	Alignment	not modelled	70.8	24	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
58	c3ah9D_	Alignment	not modelled	70.3	29	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
59	c3p4gD_	Alignment	not modelled	69.9	9	PDB header: antifreeze protein Chain: D: PDB Molecule: antifreeze protein; PDBTitle: x-ray crystal structure of a hyperactive, ca2+-dependent, beta-helical2 antifreeze protein from an antarctic bacterium
60	c2zviB_	Alignment	not modelled	63.7	21	PDB header: isomerase Chain: B: PDB Molecule: 2,3-diketo-5-methylthiopentyl-1-phosphate PDBTitle: crystal structure of 2,3-diketo-5-methylthiopentyl-1-2 phosphate enolase from bacillus subtilis
61	c1telA_	Alignment	not modelled	62.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ribulose bisphosphate carboxylase, large subunit; PDBTitle: crystal structure of a rubisco-like protein from chlorobium2 tepidum
62	c1bwvA_	Alignment	not modelled	61.9	21	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
63	c3a0mF_	Alignment	not modelled	61.3	28	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
64	c2d69B_	Alignment	not modelled	59.5	16	PDB header: lyase Chain: B: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
65	c5c2gD_	Alignment	not modelled	58.6	24	PDB header: lyase Chain: D: PDB Molecule: form ii rubisco; PDBTitle: gws1b rubisco: form ii rubisco derived from uncultivated2 gallionellacea species (cabp-bound).
66	c2oemA_	Alignment	not modelled	57.9	23	PDB header: isomerase Chain: A: PDB Molecule: 2,3-diketo-5-methylthiopentyl-1-phosphate enolase; PDBTitle: crystal structure of a rubisco-like protein from geobacillus2 kaustophilus liganded with mg2+ and 2,3-diketohehexane 1-phosphate
67	c6hunA_	Alignment	not modelled	55.5	19	PDB header: photosynthesis Chain: A: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: dimeric archeal rubisco from hyperthermus butylicus
68	c2qygC_	Alignment	not modelled	53.7	14	PDB header: unknown function Chain: C: PDB Molecule: ribulose bisphosphate carboxylase-like protein 2; PDBTitle: crystal structure of a rubisco-like protein rlp2 from rhodopseudomonas2 palustris
69	c1wwyA_	Alignment	not modelled	50.9	11	PDB header: apoptosis Chain: A: PDB Molecule: thioredoxin-like protein 1; PDBTitle: solution structure of the duf1000 domain of a thioredoxin-like protein2 1
70	d5ruba2	Alignment	not modelled	50.9	24	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
71	d1geha2	Alignment	not modelled	49.9	24	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
72	c1gehE_	Alignment	not modelled	49.6	22	PDB header: lyase Chain: E: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase; PDBTitle: crystal structure of archaeal rubisco (ribulose 1,5-bisphosphate2 carboxylase/oxygenase)
73	d1vjha_	Alignment	not modelled	43.7	15	Fold: TBP-like Superfamily: Bet v1-like Family: Pathogenesis-related protein 10 (PR10)-like
74	c4fe9A_	Alignment	not modelled	43.5	10	PDB header: carbohydrate-binding protein Chain: A: PDB Molecule: outer membrane protein susf; PDBTitle: crystal structure of susf from bacteroides thetaiotaomicron
75	c2qmxB_	Alignment	not modelled	42.6	16	PDB header: ligase Chain: B: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum tis
76	c3admC_	Alignment	not modelled	40.2	32	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
77	c3admF_	Alignment	not modelled	39.2	31	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
78	c3admA_	Alignment	not modelled	39.2	31	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
79	c3admB_	Alignment	not modelled	39.2	31	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
						PDB header: structural protein

80	c3admE_	Alignment	not modelled	39.2	31	Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
81	c4ojpC_	Alignment	not modelled	39.0	25	PDB header: viral protein Chain: C: PDB Molecule: tailspike protein; PDBTitle: crystal structure of putative tailspike protein (tsp1, orf210) from <i>escherichia coli</i> o157:h7 bacteriophage cba120 in complex with maltose
82	c6gzuA_	Alignment	not modelled	37.0	13	PDB header: transferase Chain: A: PDB Molecule: conserved membrane protein; PDBTitle: structure of chlamydia abortus effector protein chladub
83	c3a19D_	Alignment	not modelled	34.3	36	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
84	d2i5nc1	Alignment	not modelled	33.1	29	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Photosynthetic reaction centre (cytochrome subunit)
85	c3abnA_	Alignment	not modelled	32.2	31	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
86	c1x1kB_	Alignment	not modelled	32.0	31	PDB header: structural protein Chain: B: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
87	c2d3fE_	Alignment	not modelled	32.0	31	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
88	c2d3fD_	Alignment	not modelled	32.0	31	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
89	c2d3fF_	Alignment	not modelled	32.0	31	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
90	c1x1kA_	Alignment	not modelled	32.0	31	PDB header: structural protein Chain: A: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
91	c1x1kD_	Alignment	not modelled	32.0	31	PDB header: structural protein Chain: D: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
92	c1x1kC_	Alignment	not modelled	32.0	31	PDB header: structural protein Chain: C: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
93	c6q5uQ_	Alignment	not modelled	31.7	14	PDB header: virus Chain: Q: PDB Molecule: spike protein; PDBTitle: high resolution electron cryo-microscopy structure of the ϕ 2 bacteriophage p772
94	c9rubB_	Alignment	not modelled	31.3	17	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribose-1,5-bisphosphate carboxylase; PDBTitle: crystal structure of activated ribose-1,5-bisphosphate carboxylase2 complexed with its substrate, ribose-1,5-bisphosphate
95	c3a0mC_	Alignment	not modelled	31.2	33	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
96	c5yq7C_	Alignment	not modelled	30.9	22	PDB header: photosynthesis Chain: C: PDB Molecule: cytochrome subunit of photosynthetic reaction center; PDBTitle: cryo-em structure of the rc-lh core complex from <i>roseiflexus</i> 2 castenholzii
97	d1h7za_	Alignment	not modelled	30.7	11	Fold: Virus attachment protein globular domain Superfamily: Virus attachment protein globular domain Family: Adenovirus fiber protein "knob" domain
98	c3rkiB_	Alignment	not modelled	30.2	27	PDB header: viral protein Chain: B: PDB Molecule: fusion glycoprotein f0; PDBTitle: structural basis for immunization with post-fusion rsv f to elicit2 high neutralizing antibody titers
99	c2jblC_	Alignment	not modelled	29.5	29	PDB header: electron transport Chain: C: PDB Molecule: photosynthetic reaction center cytochrome c subunit; PDBTitle: photosynthetic reaction center from <i>blastochloris viridis</i>
100	c2e8mA_	Alignment	not modelled	29.0	27	PDB header: signaling protein Chain: A: PDB Molecule: epidermal growth factor receptor kinase PDBTitle: solution structure of the c-terminal sam-domain of2 epidermal growth receptor pathway substrate 8
101	c3nwrA_	Alignment	not modelled	28.6	7	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from <i>burkholderia fungorum</i>
102	c1eysC_	Alignment	not modelled	26.9	14	PDB header: electron transport Chain: C: PDB Molecule: photosynthetic reaction center; PDBTitle: crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, <i>thermochromatium tepidum</i>
103	d1eysc_	Alignment	not modelled	26.9	14	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Photosynthetic reaction centre (cytochrome subunit)

104	c4r33A_	Alignment	not modelled	26.0	19	PDB header: lyase Chain: A: PDB Molecule: nosl; PDBTitle: x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
105	c2y9xG_	Alignment	not modelled	26.0	27	PDB header: oxidoreductase Chain: G: PDB Molecule: lectin-like fold protein; PDBTitle: crystal structure of ppo3, a tyrosinase from agaricus bisporus, in2 deoxy-form that contains additional unknown lectin-like subunit,3 with inhibitor tropolone
106	d2czvc1	Alignment	not modelled	25.8	8	Fold: Ferredoxin-like Superfamily: Rnp2-like Family: Rpp14/Pop5-like
107	c5e68A_	Alignment	not modelled	25.8	13	PDB header: lyase Chain: A: PDB Molecule: s-ribosylhomocysteine lyase; PDBTitle: high resolution crystal structure of luxs - quorum sensor molecular2 complex from salmonella typhi at 1.58 angstroms
108	c4twmA_	Alignment	not modelled	24.9	9	PDB header: plant protein Chain: A: PDB Molecule: dioscorin 5; PDBTitle: crystal structure of dioscorin from dioscorea japonica
109	c2p5xB_	Alignment	not modelled	24.7	16	PDB header: cell cycle Chain: B: PDB Molecule: n-acetylserotonin o-methyltransferase-like protein; PDBTitle: crystal structure of maf domain of human n-acetylserotonin o-2 methyltransferase-like protein
110	c3a19F_	Alignment	not modelled	24.5	38	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
111	c2d3hD_	Alignment	not modelled	24.5	38	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
112	c3a08D_	Alignment	not modelled	24.5	38	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
113	c3ozhA_	Alignment	not modelled	24.2	14	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase/d-alanine carboxypeptidase; PDBTitle: crystal structure of beta-lactamase/d-alanine carboxypeptidase from2 yersinia pestis
114	d2j2ja1	Alignment	not modelled	24.0	11	Fold: Virus attachment protein globular domain Superfamily: Virus attachment protein globular domain Family: Adenovirus fiber protein "knob" domain
115	d1xoya_	Alignment	not modelled	23.6	10	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Hypothetical protein AT3g04780/F7O18 27
116	d1gp0a_	Alignment	not modelled	23.2	7	Fold: Mannose 6-phosphate receptor domain Superfamily: Mannose 6-phosphate receptor domain Family: Mannose 6-phosphate receptor domain
117	c1gp0A_	Alignment	not modelled	23.2	7	PDB header: receptor Chain: A: PDB Molecule: cation-independent mannose-6-phosphate receptor; PDBTitle: human igf2r domain 11
118	d1v2ba_	Alignment	not modelled	23.2	12	Fold: Mog1p/PsbP-like Superfamily: Mog1p/PsbP-like Family: PsbP-like
119	c5juhA_	Alignment	not modelled	22.8	33	PDB header: cell adhesion Chain: A: PDB Molecule: antifreeze protein; PDBTitle: crystal structure of c-terminal domain (rv) of mpafp
120	c3admD_	Alignment	not modelled	22.5	28	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4