
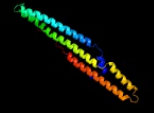



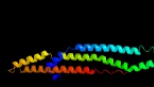

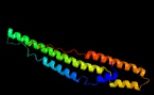



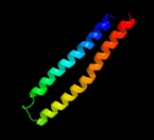

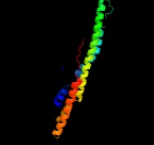

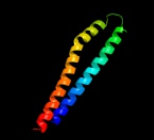



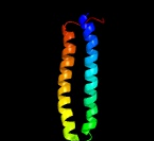

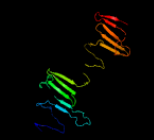

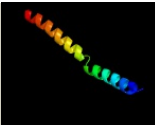



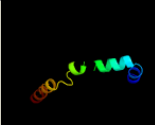
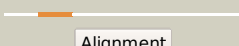

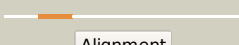
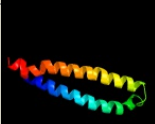
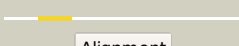


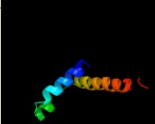



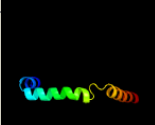




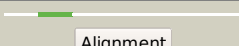


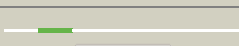


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0355c_(PPE8)_424778_434680
 Date Tue Jul 23 14:50:42 BST 2019
 Unique Job ID d4d863a0037eef76

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	55	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	d2g38b1	 Alignment		100.0	34	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	c2g38B_	 Alignment		100.0	34	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	c4xy3A_	 Alignment		100.0	18	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
5	c2vs0B_	 Alignment		96.8	10	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
6	c4iogD_	 Alignment		96.8	17	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
7	c4wj2A_	 Alignment		96.7	18	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
8	c3gvmA_	 Alignment		96.4	10	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
9	c3zbhC_	 Alignment		96.1	16	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		95.0	20	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c5nxhB_	 Alignment		91.1	12	PDB header: viral protein Chain: B: PDB Molecule: long-tail fiber proximal subunit; PDBTitle: crystal structure of the carboxy-terminal region of the bacteriophage2 t4 proximal long tail fibre protein gp34, residues 744-1289 at 2.93 angstrom resolution

12	c3jywF_	 Alignment		88.1	46	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
13	c4i0xA_	 Alignment		84.5	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
14	c2vsnB_	 Alignment		82.8	21	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
15	c4lwsA_	 Alignment		80.9	19	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
16	d1wa8b1	 Alignment		80.1	21	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
17	d1ui5a2	 Alignment		70.9	18	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	d1rp4a_	 Alignment		64.6	16	Fold: ERO1-like Superfamily: ERO1-like Family: ERO1-like
19	c4lwsB_	 Alignment		61.4	13	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
20	c3pe3D_	 Alignment		60.4	18	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcna2 transferase and its complex with a peptide2 substrate
21	c3lhoA_	 Alignment	not modelled	60.1	44	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of putative hydrolase (yp_751971.1) from shewanella2 frigidimarina ncimb 400 at 1.80 a resolution
22	c5djsA_	 Alignment	not modelled	58.2	19	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcna2 transferase mutant - k341m
23	c2kg7B_	 Alignment	not modelled	57.5	19	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
24	c3ahrA_	 Alignment	not modelled	56.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: ero1-like protein alpha; PDBTitle: inactive human ero1
25	c4rqoB_	 Alignment	not modelled	54.7	18	PDB header: lyase Chain: B: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure of l-serine dehydratase from legionella pneumophila
26	d3cx5d1	 Alignment	not modelled	54.4	40	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
27	d1ppjd1	 Alignment	not modelled	53.1	35	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
28	c5azaA_	 Alignment	not modelled	52.8	19	PDB header: sugar binding protein, transferase Chain: A: PDB Molecule: maltose-binding periplasmic protein, oligosaccharyl PDBTitle: crystal structure of mbp-saglb fusion protein with a 20-residue spacer2 in the connector helix PDB header: oxidoreductase Chain: A: PDB Molecule: proline dehydrogenase/delta-1-pyrroline-

29	c4f9iA_	Alignment	not modelled	52.7	15	5-carboxylate PDBTitle: crystal structure of proline utilization a (puta) from geobacter2 sulfurreducens pca PDB header: hydrolase
30	c4jzaB_	Alignment	not modelled	51.4	41	Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a legionella phosphoinositide phosphatase:2 insights into lipid metabolism in pathogen host interaction
31	c1zrtD_	Alignment	not modelled	46.3	50	PDB header: oxidoreductase/metal transport Chain: D: PDB Molecule: cytochrome c1; PDBTitle: rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
32	c6ghrF_	Alignment	not modelled	46.2	59	PDB header: photosynthesis Chain: F: PDB Molecule: cp12 polypeptide; PDBTitle: cyanobacterial gapdh with full-length cp12
33	d1exta3	Alignment	not modelled	45.2	57	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
34	d1ncfb3	Alignment	not modelled	45.1	57	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
35	c6fhjA_	Alignment	not modelled	44.7	18	PDB header: hydrolase Chain: A: PDB Molecule: protein,protein; PDBTitle: structural dynamics and catalytic properties of a multi-modular2 xanthanase, native.
36	c3fpjA_	Alignment	not modelled	44.3	17	PDB header: biosynthetic protein, transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of e81q mutant of mtas in complex with s-2 adenosylmethionine
37	c3cwbQ_	Alignment	not modelled	44.1	35	PDB header: oxidoreductase Chain: Q: PDB Molecule: mitochondrial cytochrome c1, heme protein; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
38	c1qcrD_	Alignment	not modelled	43.2	35	PDB header: oxidoreductase Chain: D: PDB Molecule: ubiquinol cytochrome c oxidoreductase; PDBTitle: crystal structure of bovine mitochondrial cytochrome bc12 complex, alpha carbon atoms only
39	c3b5oA_	Alignment	not modelled	42.9	50	PDB header: oxidoreductase Chain: A: PDB Molecule: cadd-like protein of unknown function; PDBTitle: crystal structure of a cadd-like protein of unknown function2 (npun_f6505) from nostoc punctiforme pcc 73102 at 1.35 a resolution
40	d2a15a1	Alignment	not modelled	42.7	21	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
41	c3qx3B_	Alignment	not modelled	42.4	35	PDB header: isomerase/dna/isomerase inhibitor Chain: B: PDB Molecule: dna topoisomerase 2-beta; PDBTitle: human topoisomerase iibeta in complex with dna and etoposide
42	c4nl6C_	Alignment	not modelled	42.4	71	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
43	c4yfbD_	Alignment	not modelled	42.3	24	PDB header: hydrolase Chain: D: PDB Molecule: protein related to penicillin acylase; PDBTitle: structure of n-acylhomoserine lactone acylase macq in complex with2 phenylacetic acid
44	c6fhnA_	Alignment	not modelled	42.2	18	PDB header: hydrolase Chain: A: PDB Molecule: protein; PDBTitle: structural dynamics and catalytic properties of a multi-modular2 xanthanase (pt derivative)
45	c4fm9A_	Alignment	not modelled	42.0	30	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 2-alpha; PDBTitle: human topoisomerase ii alpha bound to dna
46	d1xkna_	Alignment	not modelled	41.7	14	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
47	d2fr1a1	Alignment	not modelled	40.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
48	c4lrV_	Alignment	not modelled	40.5	40	PDB header: dna binding protein Chain: L: PDB Molecule: dna sulfur modification protein dnde; PDBTitle: crystal structure of dnde from escherichia coli b7a involved in dna2 phosphorothioation modification
49	d1byra_	Alignment	not modelled	38.5	28	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Nuclease
50	c2yiuE_	Alignment	not modelled	38.2	50	PDB header: oxidoreductase Chain: E: PDB Molecule: cytochrome c1, heme protein; PDBTitle: x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
51	d1de4c2	Alignment	not modelled	37.7	3	Fold: The "swivelling" beta/beta/alpha domain Superfamily: PA domain Family: PA domain
52	c4urjA_	Alignment	not modelled	37.3	13	PDB header: unknown function Chain: A: PDB Molecule: protein fam83a; PDBTitle: crystal structure of human bj-tsa-9
53	c4q7oA_	Alignment	not modelled	37.1	38	PDB header: immune system Chain: A: PDB Molecule: immunity protein; PDBTitle: the crystal structure of an immunity protein nmb0503 from neisseria2 meningitidis mc58
54	d2gxfa1	Alignment	not modelled	36.9	12	Fold: Cystatin-like Superfamily: NTF2-like

						Family:YybH-like
55	c1p84D	Alignment	not modelled	36.7	40	PDB header: oxidoreductase Chain: D: PDB Molecule: cytochrome c1, heme protein; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
56	d1luaa2	Alignment	not modelled	36.4	18	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Methylene-tetrahydromethanopterin dehydrogenase
57	c5lzkB	Alignment	not modelled	36.3	4	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
58	c5aizA	Alignment	not modelled	35.2	15	PDB header: zinc-binding protein Chain: A: PDB Molecule: zinc finger miz domain-containing protein 1; PDBTitle: the pias-like coactivator zmiz1 is a direct and selective cofactor2 of notch1 in t-cell development and leukemia
59	c3vohA	Alignment	not modelled	34.9	13	PDB header: hydrolase Chain: A: PDB Molecule: cellobiohydrolase; PDBTitle: ccel6a catalytic domain complexed with cellobiose
60	c2vakF	Alignment	not modelled	34.9	27	PDB header: viral protein Chain: F: PDB Molecule: sigma a; PDBTitle: crystal structure of the avian reovirus inner capsid protein sigmaa
61	c2pheC	Alignment	not modelled	34.7	31	PDB header: transcription Chain: C: PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to pc4
62	c2fynH	Alignment	not modelled	34.6	35	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c1; PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
63	c2jg7G	Alignment	not modelled	34.0	16	PDB header: oxidoreductase Chain: G: PDB Molecule: antiquitin; PDBTitle: crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
64	c2wybA	Alignment	not modelled	33.5	15	PDB header: hydrolase Chain: A: PDB Molecule: acyl-homoserine lactone acylase pvdq subunit PDBTitle: the quorum quenching n-acyl homoserine lactone acylase pvdq2 with a covalently bound dodecanoic acid
65	c3pefA	Alignment	not modelled	32.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, nad-binding; PDBTitle: crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter metallireducens in complex with nadp+
66	c2k2uB	Alignment	not modelled	32.7	31	PDB header: transcription Chain: B: PDB Molecule: alpha trans-inducing protein; PDBTitle: nmr structure of the complex between tfb1 subunit of tfiih2 and the activation domain of vp16
67	c2wk1A	Alignment	not modelled	32.3	28	PDB header: transferase Chain: A: PDB Molecule: novp; PDBTitle: structure of the o-methyltransferase novp
68	d3cu3a1	Alignment	not modelled	32.3	16	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
69	c3rf7A	Alignment	not modelled	31.8	13	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
70	c5kf6B	Alignment	not modelled	31.8	21	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein puta; PDBTitle: structure of proline utilization a from sinorhizobium meliloti2 complexed with l-tetrahydrofuroic acid and nad+ in space group p21
71	d1bjta	Alignment	not modelled	31.6	22	Fold: Type II DNA topoisomerase Superfamily: Type II DNA topoisomerase Family: Type II DNA topoisomerase
72	c1bjtA	Alignment	not modelled	31.6	22	PDB header: topoisomerase Chain: A: PDB Molecule: topoisomerase ii; PDBTitle: topoisomerase ii residues 409-1201
73	c3hx8A	Alignment	not modelled	30.9	23	PDB header: isomerase Chain: A: PDB Molecule: putative ketosteroid isomerase; PDBTitle: crystal structure of putative ketosteroid isomerase (np_103587.1) from2 mesorhizobium loti at 1.45 a resolution
74	c3s8mA	Alignment	not modelled	30.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-acyl reductase; PDBTitle: the crystal structure of fabv
75	d1joga	Alignment	not modelled	30.0	17	Fold: Four-helical up-and-down bundle Superfamily: Nucleotidyltransferase substrate binding subunit/domain Family: Family 1 bi-partite nucleotidyltransferase subunit
76	c6iz9B	Alignment	not modelled	29.9	15	PDB header: transferase Chain: B: PDB Molecule: beta-transaminase; PDBTitle: crystal structure of the apo form of a beta-transaminase from2 mesorhizobium sp. strain luk
77	c4gfhA	Alignment	not modelled	29.9	23	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 2; PDBTitle: topoisomerase ii-dna-amppnp complex
78	d1jpdx2	Alignment	not modelled	29.9	21	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
79	c2ve5H	Alignment	not modelled	29.6	15	PDB header: oxidoreductase Chain: H: PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: crystallographic structure of betaine aldehyde2

						dehydrogenase from pseudomonas aeruginosa PDB header: transferase
80	c3q3hA_	Alignment	not modelled	29.0	13	Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
81	d1vkpa_	Alignment	not modelled	28.7	28	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
82	d1bvsa1	Alignment	not modelled	28.0	39	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
83	d1oy0a_	Alignment	not modelled	27.8	23	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
84	c3r8rj_	Alignment	not modelled	27.0	16	PDB header: transferase Chain: J: PDB Molecule: transaldolase; PDBTitle: transaldolase from bacillus subtilis
85	c6ajrA_	Alignment	not modelled	27.0	27	PDB header: dna binding protein Chain: A: PDB Molecule: uracil dna glycosylase superfamily protein; PDBTitle: complex form of uracil dna glycosylase x and uracil
86	c2v7iA_	Alignment	not modelled	27.0	29	PDB header: biosynthetic protein Chain: A: PDB Molecule: prnb; PDBTitle: prnb native
87	c3hazA_	Alignment	not modelled	26.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: proline dehydrogenase; PDBTitle: crystal structure of bifunctional proline utilization a2 (puta) protein
88	c3ly8A_	Alignment	not modelled	26.4	14	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: crystal structure of mutant d471e of the periplasmic domain of cadc
89	d2rh3a1	Alignment	not modelled	26.1	24	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: VirC2-like
90	c2phgB_	Alignment	not modelled	26.0	31	PDB header: transcription Chain: B: PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to tfiib
91	d1vefa1	Alignment	not modelled	25.9	18	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
92	c4xvzB_	Alignment	not modelled	25.7	28	PDB header: transferase Chain: B: PDB Molecule: mycinamicin iii 3''-o-methyltransferase; PDBTitle: mycf mycinamicin iii 3'-o-methyltransferase in complex with mg
93	c3sdoB_	Alignment	not modelled	25.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: nitritotriacetate monooxygenase; PDBTitle: structure of a nitritotriacetate monooxygenase from burkholderia2 pseudomallei
94	c2ordA_	Alignment	not modelled	25.6	16	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution
95	c4h7nA_	Alignment	not modelled	25.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: the structure of putative aldehyde dehydrogenase puta from anaebaena2 variabilis.
96	c6ca8A_	Alignment	not modelled	25.4	23	PDB header: isomerase Chain: A: PDB Molecule: dna topoisomerase 2; PDBTitle: crystal structure of plasmodium falciparum topoisomerase ii dna-2 binding, cleavage and re-ligation domain
97	d1c9ka_	Alignment	not modelled	25.3	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
98	c4i3wC_	Alignment	not modelled	25.2	26	PDB header: oxidoreductase Chain: C: PDB Molecule: aldehyde dehydrogenase (nad+); PDBTitle: structure of phosphonoacetaldehyde dehydrogenase in complex with2 glyceraldehyde-3-phosphate and cofactor nad+
99	c3r5zB_	Alignment	not modelled	25.2	22	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
100	c3u4jB_	Alignment	not modelled	24.9	21	PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent aldehyde dehydrogenase; PDBTitle: crystal structure of nad-dependent aldehyde dehydrogenase from2 sinorhizobium meliloti
101	c2axtc_	Alignment	not modelled	24.8	35	PDB header: electron transport Chain: C: PDB Molecule: photosystem ii cp43 protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
102	d2axtc1	Alignment	not modelled	24.8	35	Fold: Photosystem II antenna protein-like Superfamily: Photosystem II antenna protein-like Family: Photosystem II antenna protein-like
103	d1tpla_	Alignment	not modelled	24.8	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
104	c6cboB_	Alignment	not modelled	24.5	23	PDB header: transferase Chain: B: PDB Molecule: c-6' aminotransferase; PDBTitle: x-ray structure of genb1 from micromonospora echinospora in complex2 with neamine and plp (as the external aldimine)
105	d1vpxa_	Alignment	not modelled	24.5	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase

106	d2ewoa1	Alignment	not modelled	24.4	28	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
107	c3kb4D	Alignment	not modelled	24.3	19	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr8543 protein; PDBTitle: crystal structure of the alr8543 protein in complex with 2 geranylgeranyl monophosphate and magnesium ion from nostoc sp. pcc3 7120, northeast structural genomics consortium target nsr141
108	c5frgA	Alignment	not modelled	24.3	63	PDB header: protein binding Chain: A: PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
109	d1wx0a1	Alignment	not modelled	24.0	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
110	c2h7fx	Alignment	not modelled	24.0	18	PDB header: isomerase/dna Chain: X: PDB Molecule: dna topoisomerase 1; PDBTitle: structure of variola topoisomerase covalently bound to dna
111	c3k66A	Alignment	not modelled	23.7	26	PDB header: cell adhesion Chain: A: PDB Molecule: beta-amyloid-like protein; PDBTitle: x-ray crystal structure of the e2 domain of c. elegans apl-1
112	c5mqrA	Alignment	not modelled	23.6	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-l-arabinobiosidase; PDBTitle: sialidase bt_1020
113	c3fyqA	Alignment	not modelled	23.3	17	PDB header: cell adhesion Chain: A: PDB Molecule: cg6831-pa (talin); PDBTitle: structure of drosophila melanogaster talin ibs2 domain (residues 1981-2 2168)
114	c5cgaC	Alignment	not modelled	23.3	19	PDB header: transferase Chain: C: PDB Molecule: hydroxyethylthiazole kinase; PDBTitle: structure of hydroxyethylthiazole kinase thim from staphylococcus2 aureus in complex with substrate analog 2-(1,3,5-trimethyl-1h-3 pyrazole-4-yl)ethanol
115	c4evxA	Alignment	not modelled	23.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative phage endolysin; PDBTitle: crystal structure of putative phage endolysin from s. enterica
116	d2f7fa1	Alignment	not modelled	23.1	19	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
117	c2vikA	Alignment	not modelled	23.0	10	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: catalytic domain of clostridium thermocellum celt
118	c2nwqA	Alignment	not modelled	23.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: probable short-chain dehydrogenase; PDBTitle: short chain dehydrogenase from pseudomonas aeruginosa
119	c5jn6A	Alignment	not modelled	22.9	89	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the nmr solution structure of rpa3313
120	d1yymg1	Alignment	not modelled	22.9	33	Fold: gp120 core Superfamily: gp120 core Family: gp120 core