


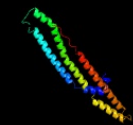



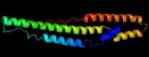

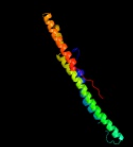

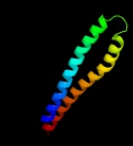





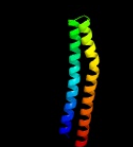

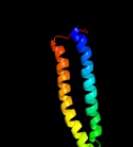



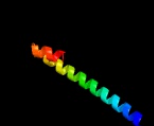
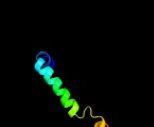

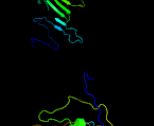
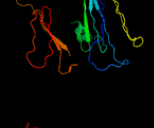

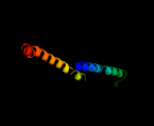



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3347c_(PPE55)_3743882_3753355
 Date Thu Aug 8 16:20:56 BST 2019
 Unique Job ID e86e9629ba82bcbf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	52	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	c2g38B_	 Alignment		100.0	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38b1	 Alignment		100.0	33	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	19	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
5	c4wj2A_	 Alignment		97.0	19	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		96.6	10	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	 Alignment		96.4	14	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
8	c3gvmA_	 Alignment		96.0	11	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		95.5	15	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		94.0	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c3jywF_	 Alignment		82.2	54	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

12	c5kf6B	Alignment		80.7	18	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
13	c4i0xA	Alignment		80.2	26	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		78.9	16	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	c5nxhB	Alignment		77.1	15	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
16	c2qqpG	Alignment		75.2	16	PDB header: virus Chain: G: PDB Molecule: large capsid protein; PDBTitle: crystal structure of authentic providence virus
17	d1wa8b1	Alignment		74.2	20	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
18	c4lwsA	Alignment		73.6	21	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
19	c4f9iA	Alignment		72.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: proline dehydrogenase/delta-1-pyrroline-5-carboxylate PDBTitle: crystal structure of proline utilization a (puta) from geobacter2 sulfurreducens pca
20	d1rp4a	Alignment		70.6	23	Fold: ERO1-like Superfamily: ERO1-like Family: ERO1-like
21	c3pe3D	Alignment	not modelled	64.8	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
22	c3ahrA	Alignment	not modelled	63.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ero1-like protein alpha; PDBTitle: inactive human ero1
23	c2vakF	Alignment	not modelled	59.6	19	PDB header: viral protein Chain: F: PDB Molecule: sigma a; PDBTitle: crystal structure of the avian reovirus inner capsid protein sigmaa
24	c3at7B	Alignment	not modelled	57.1	17	PDB header: structural protein Chain: B: PDB Molecule: alginate-binding flagellin; PDBTitle: crystal structure of bacterial cell-surface alginate-binding protein2 algp7
25	c4lwsB	Alignment	not modelled	55.3	15	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
26	c3hazA	Alignment	not modelled	53.3	28	PDB header: oxidoreductase Chain: A: PDB Molecule: proline dehydrogenase; PDBTitle: crystal structure of bifunctional proline utilization a2 (puta) protein
27	d1ncfb3	Alignment	not modelled	52.8	38	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
28	d1exta3	Alignment	not modelled	52.5	38	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
29	d2fr1a1	Alignment	not modelled	51.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

						Family:Tyrosine-dependent oxidoreductases
30	d1ui5a2	Alignment	not modelled	51.3	16	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
31	c2wybA	Alignment	not modelled	50.8	12	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
32	c5djsA	Alignment	not modelled	49.6	23	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcnae transferase mutant - k341m
33	c3lhoA	Alignment	not modelled	49.3	50	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
34	c4e4gF	Alignment	not modelled	49.2	14	PDB header: oxidoreductase Chain: F: PDB Molecule: methylmalonate-semialdehyde dehydrogenase; PDBTitle: crystal structure of putative methylmalonate-semialdehyde2 dehydrogenase from sinorhizobium meliloti 1021
35	c2vroB	Alignment	not modelled	48.6	22	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
36	c2kg7B	Alignment	not modelled	48.0	20	PDB header: unknown function Chain: B: PDB Molecule: resat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
37	d3cx5d1	Alignment	not modelled	47.3	25	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
38	c2ve5H	Alignment	not modelled	46.6	18	PDB header: oxidoreductase Chain: H: PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
39	d1ppid1	Alignment	not modelled	45.9	20	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
40	c4bgoA	Alignment	not modelled	45.6	12	PDB header: hydrolase Chain: A: PDB Molecule: efem m75 peptidase; PDBTitle: structural and functional role of the imelysin-like protein2 efem from pseudomonas syringae pv. syringae and3 implications in bacterial iron transport
41	d1xkna	Alignment	not modelled	44.9	18	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
42	c3ed6B	Alignment	not modelled	44.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus
43	d1oy0a	Alignment	not modelled	43.7	22	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
44	c4h7nA	Alignment	not modelled	43.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: the structure of putative aldehyde dehydrogenase puta from anabaena2 variabilis.
45	c4o5hD	Alignment	not modelled	42.7	21	PDB header: oxidoreductase Chain: D: PDB Molecule: phenylacetaldehyde dehydrogenase; PDBTitle: x-ray crystal structure of a putative phenylacetaldehyde dehydrogenase2 from burkholderia cenocepacia
46	c2jg7G	Alignment	not modelled	40.7	17	PDB header: oxidoreductase Chain: G: PDB Molecule: antiquitin; PDBTitle: crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
47	c3qx3B	Alignment	not modelled	40.2	31	PDB header: isomerase/dna/isomerase inhibitor Chain: B: PDB Molecule: dna topoisomerase 2-beta; PDBTitle: human topoisomerase ii beta in complex with dna and etoposide
48	c2mu3A	Alignment	not modelled	38.0	17	PDB header: structural protein Chain: A: PDB Molecule: aciniform spidroin 1; PDBTitle: spider wrapping silk fibre architecture arising from its modular2 soluble protein precursor
49	c1qcrD	Alignment	not modelled	37.3	20	PDB header: oxidoreductase Chain: D: PDB Molecule: ubiquinol cytochrome c oxidoreductase; PDBTitle: crystal structure of bovine mitochondrial cytochrome bc12 complex, alpha carbon atoms only
50	c4nl6C	Alignment	not modelled	37.3	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
51	c4fm9A	Alignment	not modelled	36.7	27	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 2-alpha; PDBTitle: human topoisomerase ii alpha bound to dna
52	c5fhzF	Alignment	not modelled	36.3	14	PDB header: oxidoreductase Chain: F: PDB Molecule: aldehyde dehydrogenase family 1 member a3; PDBTitle: human aldehyde dehydrogenase 1a3 complexed with nad(+) and retinoic2 acid
53	c4lrV	Alignment	not modelled	35.5	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
54	c1zrtD	Alignment	not modelled	35.1	30	PDB header: oxidoreductase/metal transport Chain: D: PDB Molecule: cytochrome c1; PDBTitle: rhodobacter capsulatus cytochrome bc1 complex with2

						stigmatellin bound
55	d1tpla_	Alignment	not modelled	35.1	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
56	c4q7oA_	Alignment	not modelled	32.7	32	PDB header: immune system Chain: A: PDB Molecule: immunity protein; PDBTitle: the crystal structure of an immunity protein nmb0503 from neisseria2 meningitidis mc58
57	c3cwbQ_	Alignment	not modelled	32.6	20	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
58	c4rqoB_	Alignment	not modelled	31.9	32	PDB header: lyase Chain: B: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure of l-serine dehydratase from legionella pneumophila
59	c2hg2A_	Alignment	not modelled	31.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase a; PDBTitle: structure of lactaldehyde dehydrogenase
60	c5ujuA_	Alignment	not modelled	31.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nad-dependent aldehyde dehydrogenase; PDBTitle: crystal structure of nad-dependent aldehyde dehydrogenase from2 burkholderia multivorans
61	c3u4jB_	Alignment	not modelled	31.5	20	PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent aldehyde dehydrogenase; PDBTitle: crystal structure of nad-dependent aldehyde dehydrogenase from2 sinorhizobium meliloti
62	c6ghrF_	Alignment	not modelled	30.7	59	PDB header: photosynthesis Chain: F: PDB Molecule: cp12 polypeptide; PDBTitle: cyanobacterial gapdh with full-length cp12
63	d1bi9a_	Alignment	not modelled	30.5	15	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
64	c3fpjA_	Alignment	not modelled	30.3	11	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
65	c5lzkB_	Alignment	not modelled	30.2	9	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
66	c1bjtA_	Alignment	not modelled	30.1	23	PDB header: topoisomerase Chain: A: PDB Molecule: topoisomerase ii; PDBTitle: topoisomerase ii residues 409-1201
67	d1bjta_	Alignment	not modelled	30.1	23	Fold: Type II DNA topoisomerase Superfamily: Type II DNA topoisomerase Family: Type II DNA topoisomerase
68	c3rf7A_	Alignment	not modelled	29.4	12	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
69	c4urjA_	Alignment	not modelled	29.3	19	PDB header: unknown function Chain: A: PDB Molecule: protein fam83a; PDBTitle: crystal structure of human bj-tsa-9
70	d1byra_	Alignment	not modelled	29.2	17	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Nuclease
71	d2a15a1	Alignment	not modelled	29.1	16	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
72	c2yiuE_	Alignment	not modelled	28.7	35	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
73	d2gxfa1	Alignment	not modelled	28.4	16	Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like
74	c4i3wC_	Alignment	not modelled	28.3	21	PDB header: oxidoreductase Chain: C: PDB Molecule: aldehyde dehydrogenase (nad+); PDBTitle: structure of phosphonoacetaldehyde dehydrogenase in complex with2 glycerlaldehyde-3-phosphate and cofactor nad+
75	c6fhjA_	Alignment	not modelled	27.6	20	PDB header: hydrolase Chain: A: PDB Molecule: protein,protein; PDBTitle: structural dynamics and catalytic properties of a multi-modular2 xanthanase, native.
76	c3vohA_	Alignment	not modelled	27.5	16	PDB header: hydrolase Chain: A: PDB Molecule: cellobiohydrolase; PDBTitle: cccel6a catalytic domain complexed with cellobiose
77	c2ordA_	Alignment	not modelled	27.5	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
78	c3q3hA_	Alignment	not modelled	27.0	10	PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
79	d1vkpa_	Alignment	not modelled	27.0	31	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
						Fold: Aminoacid dehydrogenase-like, N-terminal domain

80	d1luaa2	Alignment	not modelled	27.0	27	Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Methylene-tetrahydromethanopterin dehydrogenase
81	c4gfhA	Alignment	not modelled	26.4	23	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 2; PDBTitle: topoisomerase ii-dna-amppnp complex
82	c3kb4D	Alignment	not modelled	26.3	19	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr8543 protein; PDBTitle: crystal structure of the alr8543 protein in complex with2 geranylgeranyl monophosphate and magnesium ion from nostoc sp. pcc3 7120, northeast structural genomics consortium target nsr141
83	d2ewoa1	Alignment	not modelled	26.2	17	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
84	c1p84D	Alignment	not modelled	26.0	25	PDB header: oxidoreductase Chain: D: PDB Molecule: cytochrome c1, heme protein; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
85	c2fynH	Alignment	not modelled	25.3	30	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c1; PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
86	c5aizA	Alignment	not modelled	25.1	17	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
87	d1o66a	Alignment	not modelled	24.9	22	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
88	c4jzaB	Alignment	not modelled	24.9	27	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a legionella phosphoinositide phosphatase:2 insights into lipid metabolism in pathogen host interaction
89	c6dbbA	Alignment	not modelled	24.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative aldehyde dehydrogenase family protein; PDBTitle: crystal structure of a putative aldehyde dehydrogenase family protein2 burkholderia cenocepacia j2315 in complex with partially reduced nadh
90	d3cu3a1	Alignment	not modelled	24.8	24	Fold: Cystatin-like Superfamily: NTF2-like Family: BaiE/LinA-like
91	c5azaA	Alignment	not modelled	24.6	17	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
92	c6fhnA	Alignment	not modelled	24.6	20	PDB header: hydrolase Chain: A: PDB Molecule: protein; PDBTitle: structural dynamics and catalytic properties of a multi-modular2 xanthanase (pt derivative)
93	d1bvsa1	Alignment	not modelled	24.5	36	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
94	c3b5oA	Alignment	not modelled	24.1	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
95	d1vefa1	Alignment	not modelled	24.1	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
96	c2pheC	Alignment	not modelled	24.1	31	PDB header: transcription Chain: C: PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to pc4
97	c2wk1A	Alignment	not modelled	24.0	33	PDB header: transferase Chain: A: PDB Molecule: novp; PDBTitle: structure of the o-methyltransferase novp
98	c6ca8A	Alignment	not modelled	23.9	19	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
99	c6ajrA	Alignment	not modelled	23.7	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
100	c4ovmE	Alignment	not modelled	23.4	28	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein sgcj; PDBTitle: crystal structure of sgcj protein from streptomyces carzinostaticus
101	d1kzqa1	Alignment	not modelled	23.3	25	Fold: Cupredoxin-like Superfamily: Major surface antigen p30, SAG1 Family: Major surface antigen p30, SAG1
102	c6iz9B	Alignment	not modelled	23.3	14	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
103	c3ifzA	Alignment	not modelled	23.0	30	PDB header: isomerase Chain: A: PDB Molecule: dna gyrase subunit a; PDBTitle: crystal structure of the first part of the mycobacterium tuberculosis2 dna gyrase reaction core: the breakage and reunion domain at 2.7 a3 resolution
104	c2k2uB	Alignment	not modelled	23.0	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

105	c3hx8A_	Alignment	not modelled	23.0	27	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
106	c3r8rJ_	Alignment	not modelled	22.7	18	PDB header: transferase Chain: J: PDB Molecule: transaldolase; PDBTitle: transaldolase from bacillus subtilis
107	d1nfpA_	Alignment	not modelled	22.2	17	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
108	c5ur2C_	Alignment	not modelled	22.1	19	PDB header: oxidoreductase Chain: C: PDB Molecule: bifunctional protein puta; PDBTitle: crystal structure of proline utilization a (puta) from bdellovibrio2 bacteriovorus inactivated by n-propargylglycine
109	d1jpdX2	Alignment	not modelled	21.8	21	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
110	d2jera1	Alignment	not modelled	21.8	20	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
111	c4yfbD_	Alignment	not modelled	21.5	22	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
112	c3pefA_	Alignment	not modelled	21.4	13	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+
113	c6cboB_	Alignment	not modelled	21.0	19	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)
114	c4xvzB_	Alignment	not modelled	20.6	33	PDB header: transferase Chain: B: PDB Molecule: mycinamicin iii 3''-o-methyltransferase; PDBTitle: mycf mycinamicin iii 3'-o-methyltransferase in complex with mg
115	d1vpxa_	Alignment	not modelled	20.4	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
116	d1joga_	Alignment	not modelled	20.3	26	Fold: Four-helical up-and-down bundle Superfamily: Nucleotidyltransferase substrate binding subunit/domain Family: Family 1 bi-partite nucleotidyltransferase subunit
117	c3r5zB_	Alignment	not modelled	20.3	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
118	c3omeE_	Alignment	not modelled	20.3	15	PDB header: lyase Chain: E: PDB Molecule: enoyl-coa hydratase; PDBTitle: crystal structure of a probable enoyl-coa hydratase from mycobacterium2 smegmatis
119	c5ddwD_	Alignment	not modelled	20.2	14	PDB header: transferase Chain: D: PDB Molecule: crmg; PDBTitle: crystal structure of aminotransferase crmg from actinoalloteichus sp.2 wh1-2216-6 in complex with the pmp external aldimine adduct with3 caerulomycin m
120	c2jerG_	Alignment	not modelled	20.2	20	PDB header: hydrolase Chain: G: PDB Molecule: agmatine deiminase; PDBTitle: agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.