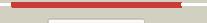
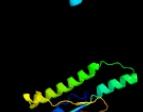


Phyre²

Email	mdejesus@rockefeller.edu
Description	RVBD3134c_(-)_3499940_3500746
Date	Thu Aug 8 16:20:32 BST 2019
Unique Job ID	e1df89fdb1346799

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jaxA_			100.0	26	PDB header: protein binding Chain: A: PDB Molecule: hypothetical protein tb31.7; PDBTitle: universal stress protein rv2623 from mycobacterium2 tuberculosis
2	c3lqgA_			100.0	15	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: the crystal structure of a universal stress protein from archaeoglobus2 fulgidus dsm 4304
3	c3mt0A_			100.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pa1789; PDBTitle: the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
4	c3olqA_			100.0	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein e; PDBTitle: the crystal structure of a universal stress protein e from proteus2 mirabilis hi4320
5	c3ab8B_			100.0	21	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein ttha0350; PDBTitle: crystal structure of the hypothetical tandem-type universal stress2 protein ttha0350 complexed with atps.
6	c4r2jA_			100.0	12	PDB header: metal binding protein, unknown function Chain: A: PDB Molecule: universal stress protein e; PDBTitle: crystal structure of ydaa (universal stress protein e) from salmonella2 typhimurium
7	c3s3tD_			99.8	34	PDB header: chaperone Chain: D: PDB Molecule: nucleotide-binding protein, universal stress protein uspa PDBTitle: universal stress protein uspa from lactobacillus plantarum
8	d2z3va1			99.7	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
9	c3hgmD_			99.7	27	PDB header: signaling protein Chain: D: PDB Molecule: universal stress protein tead; PDBTitle: universal stress protein tead from the trap transporter teabc of2 halomonas elongata
10	d1q77a_			99.7	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
11	d1tq8a_			99.7	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like

12	c5ahwC			99.6	25	PDB header: signaling protein Chain: C: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein msmeg_3811 in2 complex with camp
13	c3fg9B			99.6	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein of universal stress protein uspa family; PDBTitle: the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcf1
14	c3dloC			99.6	21	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: universal stress protein; PDBTitle: structure of universal stress protein from archaeoglobus fulgidus
15	d1mjha			99.6	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
16	c3fh0A			99.5	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative universal stress protein kpn_01444; PDBTitle: crystal structure of putative universal stress protein kpn_01444 -2 atpase
17	c4wnyA			99.5	26	PDB header: signaling protein Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of a protein from the universal stress protein2 family from burkholderia pseudomallei
18	c2pfSA			99.5	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: universal stress protein; PDBTitle: crystal structure of universal stress protein from nitrosomonas2 europaea
19	c4r2IB			99.5	21	PDB header: unknown function Chain: B: PDB Molecule: universal stress protein f; PDBTitle: crystal structure of ynf (universal stress protein f) from salmonella2 typhimurium
20	d2gm3a1			99.5	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
21	d1jmva		not modelled	99.5	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
22	c2dumD		not modelled	99.4	17	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ph0823; PDBTitle: crystal structure of hypothetical protein, ph0823
23	c3idfA		not modelled	99.4	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: usp-like protein; PDBTitle: the crystal structure of a usp-like protein from wolinella2 succinogenes to 2.0a
24	c3a2kB		not modelled	89.2	15	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysidine synthase; PDBTitle: crystal structure of tils complexed with trna
25	c5ol2E		not modelled	86.8	9	PDB header: flavoprotein Chain: E: PDB Molecule: electron transfer flavoprotein small subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
26	c2e21A		not modelled	85.0	10	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysidine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
27	c4kpuB		not modelled	83.1	11	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein alpha/beta-subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
28	c1ni5A		not modelled	81.5	23	PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj;

						PDBTitle: structure of the mesj pp-atpase from escherichia coli
29	c6fahB_		Alignment	not modelled	77.8	10 PDB header: flavoprotein Chain: B: PDB Molecule: cafeyle-coa reductase-etc complex subunit card; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
30	d1o94c_		Alignment	not modelled	74.9	12 Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
31	d3clsc1		Alignment	not modelled	74.4	12 Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
32	c3vrhA_		Alignment	not modelled	72.4	9 PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein ph0300; PDBTitle: crystal structure of ph0300
33	d1ni5a1		Alignment	not modelled	67.8	23 Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
34	c5ghaC_		Alignment	not modelled	67.0	14 PDB header: transferase/transport protein Chain: C: PDB Molecule: sulfur transferase ttua; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
35	c3zquA_		Alignment	not modelled	66.4	14 PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: structure of a probable aromatic acid decarboxylase
36	d1p5dx1		Alignment	not modelled	59.2	19 Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
37	c5h75B_		Alignment	not modelled	58.8	17 PDB header: lyase Chain: B: PDB Molecule: mersacidin decarboxylase,immunoglobulin g-binding protein PDBTitle: crystal structure of the mrsd-protein a fusion protein
38	d1wy5a1		Alignment	not modelled	57.0	8 Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
39	c6qlgD_		Alignment	not modelled	56.3	20 PDB header: transferase Chain: D: PDB Molecule: flavin prenyltransferase pad1, mitochondrial; PDBTitle: crystal structure of anubix (pada1) in complex with fmn and2 dimethylallyl pyrophosphate
40	c6eoA_		Alignment	not modelled	54.9	23 PDB header: flavoprotein Chain: A: PDB Molecule: phosphopantothenoylcysteine decarboxylase; PDBTitle: crystal structure of hal3 from cryptococcus neoformans
41	c3uw2A_		Alignment	not modelled	51.7	19 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
42	c5ow0B_		Alignment	not modelled	50.8	11 PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein, beta subunit; PDBTitle: crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
43	c5bmpA_		Alignment	not modelled	49.9	12 PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from xanthomonas citri2 complexed with glucose-1-phosphate
44	c3c04A_		Alignment	not modelled	49.0	19 PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase/phosphoglucomutase; PDBTitle: structure of the p368g mutant of pmm/pgm from p. aeruginosa
45	c2ejbA_		Alignment	not modelled	48.2	15 PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
46	d1zuna1		Alignment	not modelled	47.2	10 Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
47	c3mcuF_		Alignment	not modelled	46.6	13 PDB header: oxidoreductase Chain: F: PDB Molecule: dipicolinate synthase, b chain; PDBTitle: crystal structure of the dipicolinate synthase chain b from bacillus2 cereus. northeast structural genomics consortium target bcr215.
48	c3r8wC_		Alignment	not modelled	45.3	24 PDB header: oxidoreductase Chain: C: PDB Molecule: 3-isopropylmalate dehydrogenase 2, chloroplastic; PDBTitle: structure of 3-isopropylmalate dehydrogenase isoform 2 from2 arabidopsis thaliana at 2.2 angstrom resolution
49	c4rheB_		Alignment	not modelled	45.3	15 PDB header: lyase Chain: B: PDB Molecule: 3-octaprenyl-4-hydroxybenzoate carboxylyase; PDBTitle: crystal structure of ubix, an aromatic acid decarboxylase from the2 colwellia psychrerythraea 34h
50	c2c5sA_		Alignment	not modelled	44.6	17 PDB header: rna-binding protein Chain: A: PDB Molecule: probable thiamine biosynthesis protein thiI; PDBTitle: crystal structure of bacillus anthracis thiI, a trna-2 modifying enzyme containing the predicted rna-binding3 thumb domain
51	c1zunA_		Alignment	not modelled	44.5	10 PDB header: transferase Chain: A: PDB Molecule: sulfate adenyltransferase subunit 2; PDBTitle: crystal structure of a gtp-regulated atm sulfurylase2 heterodimer from pseudomonas syringae

52	c3qjgD	Alignment	not modelled	44.0	9	PDB header: oxidoreductase Chain: D: PDB Molecule: epidermin biosynthesis protein epid; PDBTitle: epidermin biosynthesis protein epid from staphylococcus aureus
53	c5hn6A	Alignment	not modelled	43.9	28	PDB header: oxidoreductase Chain: A: PDB Molecule: homoisocitrate dehydrogenase; PDBTitle: crystal structure of beta-decarboxylating dehydrogenase (tk280) from2 thermococcus kodakarensis complexed with mn and 3-isopropylmalate
54	d1sbza	Alignment	not modelled	41.2	18	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
55	d1v53a1	Alignment	not modelled	41.1	20	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
56	c4nzpA	Alignment	not modelled	40.8	12	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: the crystal structure of argininosuccinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
57	d2c5sa1	Alignment	not modelled	40.5	17	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ThiI-like
58	c3g8rA	Alignment	not modelled	40.2	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable spore coat polysaccharide biosynthesis protein e; PDBTitle: crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
59	d1p3y1	Alignment	not modelled	39.5	18	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
60	d1cnza	Alignment	not modelled	39.1	16	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
61	d1ecfa1	Alignment	not modelled	39.0	12	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
62	c2e0iD	Alignment	not modelled	38.6	9	PDB header: lyase Chain: D: PDB Molecule: 432aa long hypothetical deoxyribodipyrimidine photolyase; PDBTitle: crystal structure of archaeal photolyase from sulfolobus tokodaii with2 two fad molecules: implication of a novel light-harvesting cofactor
63	c6jlsA	Alignment	not modelled	38.4	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative flavoprotein decarboxylase; PDBTitle: crystal structure of fmn-dependent cysteine decarboxylases tva from2 thioviridamide biosynthesis
64	c1vl2C	Alignment	not modelled	38.2	12	PDB header: ligase Chain: C: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
65	c1mvIA	Alignment	not modelled	38.2	22	PDB header: lyase Chain: A: PDB Molecule: ppc decarboxylase athal3a; PDBTitle: ppc decarboxylase mutant c175s
66	d1mvla	Alignment	not modelled	38.2	22	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
67	c1tuoA	Alignment	not modelled	38.1	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative phosphomannomutase; PDBTitle: crystal structure of putative phosphomannomutase from2 thermus thermophilus hb8
68	c6jddA	Alignment	not modelled	37.6	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: cypemycin cysteine dehydrogenase (decarboxylating); PDBTitle: crystal structure of the cypemycin decarboxylase cypd.
69	c2derA	Alignment	not modelled	37.3	8	PDB header: transferase/rna Chain: A: PDB Molecule: tRNA-specific 2-thiouridylase mnma; PDBTitle: cocrystal structure of an rna sulfatase enzyme mnma and2 tRNA-glu in the initial tRNA binding state
70	d1g5qa	Alignment	not modelled	37.0	9	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
71	c4hjhA	Alignment	not modelled	36.9	15	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
72	c3u1hA	Alignment	not modelled	36.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-isopropylmalate dehydrogenase; PDBTitle: crystal structure of ipmdh from the last common ancestor of bacillus
73	c4kr7A	Alignment	not modelled	36.2	16	PDB header: transferase/rna Chain: A: PDB Molecule: probable tRNA sulfurtransferase; PDBTitle: crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp
74	d1t0la	Alignment	not modelled	35.1	15	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
75	c3i3wb	Alignment	not modelled	35.0	17	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: structure of a phosphoglucosamine mutase from

						francisella tularensis
76	d1cm7a	Alignment	not modelled	34.8	16	Fold: isocitrate/isopropylmalate dehydrogenase-like Superfamily: Isocitrate/isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
77	c3us8A	Alignment	not modelled	34.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: isocitrate dehydrogenase [nadp]; PDBTitle: crystal structure of an isocitrate dehydrogenase from sinorhizobium meliloti 1021
78	d1vbka1	Alignment	not modelled	33.6	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ThiI-like
79	d1efpb	Alignment	not modelled	33.0	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
80	c3lqkA	Alignment	not modelled	32.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit b; PDBTitle: crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
81	d1gph11	Alignment	not modelled	32.3	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
82	c3uduG	Alignment	not modelled	32.2	20	PDB header: oxidoreductase Chain: G: PDB Molecule: 3-isopropylmalate dehydrogenase; PDBTitle: crystal structure of putative 3-isopropylmalate dehydrogenase from2 campylobacter jejuni
83	d1g2ua	Alignment	not modelled	32.0	20	Fold: isocitrate/isopropylmalate dehydrogenase-like Superfamily: Isocitrate/isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
84	c4iwhA	Alignment	not modelled	31.2	24	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-isopropylmalate dehydrogenase; PDBTitle: crystal structure of a 3-isopropylmalate dehydrogenase from2 burkholderia pseudomallei
85	c1xuzA	Alignment	not modelled	30.5	7	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysialic acid capsule biosynthesis protein sia;
						PDBTitle: crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
86	c4aoyD	Alignment	not modelled	30.0	12	PDB header: oxidoreductase Chain: D: PDB Molecule: isocitrate dehydrogenase [nadp]; PDBTitle: open ctidh. the complex structures of isocitrate dehydrogenase from2 clostridium thermocellum and desulfotalea psychrophila, support a new3 active site locking mechanism
87	d1lwda	Alignment	not modelled	29.4	12	Fold: isocitrate/isopropylmalate dehydrogenase-like Superfamily: Isocitrate/isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
88	c4l2iA	Alignment	not modelled	28.7	13	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
89	d2g0ta1	Alignment	not modelled	28.6	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
90	d1efvb	Alignment	not modelled	28.5	16	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
91	d1w0da	Alignment	not modelled	28.0	24	Fold: isocitrate/isopropylmalate dehydrogenase-like Superfamily: Isocitrate/isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
92	c2uxqb	Alignment	not modelled	27.7	12	PDB header: oxidoreductase Chain: B: PDB Molecule: isocitrate dehydrogenase native; PDBTitle: isocitrate dehydrogenase from the psychrophilic bacterium2 desulfotalea psychrophila: biochemical properties and3 crystal structure analysis
93	c1wqaB	Alignment	not modelled	27.0	14	PDB header: isomerase Chain: B: PDB Molecule: phospho-sugar mutase; PDBTitle: crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
94	c2fzvC	Alignment	not modelled	26.5	10	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: putative arsenical resistance protein; PDBTitle: crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
95	c3pdkB	Alignment	not modelled	26.4	14	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucomamine mutase; PDBTitle: crystal structure of phosphoglucomamine mutase from b. anthracis
96	c2f7IA	Alignment	not modelled	26.3	7	PDB header: isomerase Chain: A: PDB Molecule: 455aa long hypothetical phospho-sugar mutase; PDBTitle: crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
97	d1vlca	Alignment	not modelled	26.2	24	Fold: isocitrate/isopropylmalate dehydrogenase-like Superfamily: Isocitrate/isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
98	c4u7jB	Alignment	not modelled	25.4	15	PDB header: ligase Chain: B: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase from mycobacterium2 thermoresistible
99	c6gyzB	Alignment	not modelled	25.4	12	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucomamine mutase; PDBTitle: crystal structure of glmm from staphylococcus aureus
100	c2dy0A	Alignment	not modelled	25.3	18	PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase;

				PDBTitle: crystal structure of project jw0458 from escherichia coli		
101	d2zdra2	Alignment	not modelled	23.8	7	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
102	d1vl2a1	Alignment	not modelled	23.8	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
103	c6ncsB_	Alignment	not modelled	23.2	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: n-acetylneuraminc acid (sialic acid) synthetase; PDBTitle: crystal structure of n-acetylneuraminc acid (sialic acid) synthetase2 from leptospira borgpetersenii serovar hardjo-bovis in complex with 3 citrate
104	d1lowla2	Alignment	not modelled	23.1	10	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
105	c1kh2D_	Alignment	not modelled	23.0	9	PDB header: ligase Chain: D: PDB Molecule: argininosuccinate synthetase; PDBTitle: crystal structure of thermus thermophilus hb8 argininosuccinate2 synthetase in complex with atp
106	c2qfyE_	Alignment	not modelled	22.8	12	PDB header: oxidoreductase Chain: E: PDB Molecule: isocitrate dehydrogenase [nadp]; PDBTitle: crystal structure of saccharomyces cerevesiae mitochondrial nadp(+)-2 dependent isocitrate dehydrogenase in complex with a-ketoglutarate
107	c3vl3A_	Alignment	not modelled	22.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-isopropylmalate dehydrogenase; PDBTitle: 3-isopropylmalate dehydrogenase from shewanella oneidensis mr-1 at 3402 mpa
108	d1wpwa_	Alignment	not modelled	22.6	20	Fold: Isocitrate/isopropylmalate dehydrogenase-like Superfamily: Isocitrate/isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
109	d3pmga1	Alignment	not modelled	22.4	21	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
110	c4qg5D_	Alignment	not modelled	22.2	18	PDB header: isomerase Chain: D: PDB Molecule: putative phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from leishmania major at 3.52 angstrom resolution
111	d1np7a2	Alignment	not modelled	22.2	10	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
112	c4hqnb_	Alignment	not modelled	21.7	19	PDB header: cell adhesion Chain: B: PDB Molecule: sporozoite surface protein 2; PDBTitle: crystal structure of manganese-loaded plasmodium vivax trap protein
113	d1a05a_	Alignment	not modelled	21.6	24	Fold: Isocitrate/isopropylmalate dehydrogenase-like Superfamily: Isocitrate/isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
114	c2nz2A_	Alignment	not modelled	21.2	13	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
115	d1j20a1	Alignment	not modelled	20.9	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
116	c5zgoB_	Alignment	not modelled	20.8	8	PDB header: transferase Chain: B: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of apt2 from thermus thermophilus hb8
117	c2rpia_	Alignment	not modelled	20.5	21	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h; PDBTitle: the nmr structure of the submillisecond folding2 intermediate of the thermus thermophilus ribonuclease h
118	c4m0kD_	Alignment	not modelled	20.4	13	PDB header: transferase Chain: D: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of adenine phosphoribosyltransferase from2 rhodothermus marinus dsm 4252, nysrc target 029775.
119	d1xaca_	Alignment	not modelled	20.4	13	Fold: Isocitrate/isopropylmalate dehydrogenase-like Superfamily: Isocitrate/isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
120	d1qzua_	Alignment	not modelled	20.1	31	Fold: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Superfamily: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD Family: Homo-oligomeric flavin-containing Cys decarboxylases, HFCD