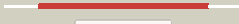



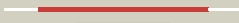

















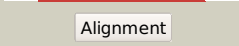



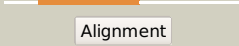

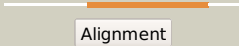

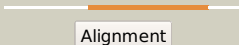

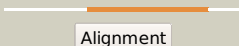

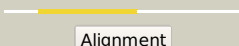

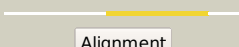

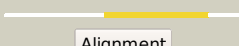

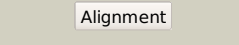
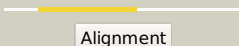
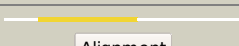
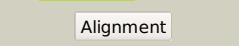
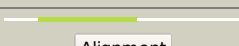


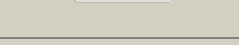


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3717 (-)_4161226_4161951
Date	Fri Aug 9 18:20:41 BST 2019
Unique Job ID	0eafc0f4931d43d0

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5j72B_	 Alignment		100.0	26	PDB header: hydrolase Chain: B; PDB Molecule: putative n-acetylmuramoyl-l-alanine amidase,autolysin cwp6; PDBTitle: cwp6 from clostridium difficile
2	c4binA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A; PDB Molecule: n-acetylmuramoyl-l-alanine amidase amic; PDBTitle: crystal structure of the e. coli n-acetylmuramoyl-l-alanine amidase2 amic
3	c4m6iA_	 Alignment		100.0	99	PDB header: hydrolase Chain: A; PDB Molecule: peptidoglycan amidase rv3717; PDBTitle: structure of the reduced, zn-bound form of mycobacterium tuberculosis2 peptidoglycan amidase rv3717
4	c3ne8A_	 Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: n-acetylmuramoyl-l-alanine amidase; PDBTitle: the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of bartonella henselae str. houston-1
5	c4rn7A_	 Alignment		100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: n-acetylmuramoyl-l-alanine amidase; PDBTitle: the crystal structure of n-acetylmuramoyl-l-alanine amidase from2 clostridium difficile 630
6	d1jwqa_	 Alignment		100.0	25	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: N-acetylmuramoyl-L-alanine amidase-like
7	c5emiA_	 Alignment		100.0	30	PDB header: hydrolase Chain: A; PDB Molecule: cell wall hydrolase/autolysin; PDBTitle: n-acetylmuramoyl-l-alanine amidase amic2 of nostoc punctiforme
8	c1xovA_	 Alignment		100.0	18	PDB header: hydrolase Chain: A; PDB Molecule: ply protein; PDBTitle: the crystal structure of the listeria monocytogenes bacteriophage psa2 endolysin plypsa
9	c3czxA_	 Alignment		100.0	12	PDB header: hydrolase Chain: A; PDB Molecule: putative n-acetylmuramoyl-l-alanine amidase; PDBTitle: the crystal structure of the putative n-acetylmuramoyl-l-2 alanine amidase from neisseria meningitidis
10	c3qayC_	 Alignment		100.0	18	PDB header: lyase Chain: C; PDB Molecule: endolysin; PDBTitle: catalytic domain of cd271 endolysin targeting clostridia difficile
11	d1xova2	 Alignment		100.0	16	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: N-acetylmuramoyl-L-alanine amidase-like

12	c4q6qA	 Alignment		95.5	21	PDB header: hydrolase Chain: A; PDB Molecule: conserved hypothetical secreted protein; PDBTitle: structural analysis of the zn-form ii of helicobacter pylori csd4, a2 d,l-carboxypeptidase
13	c4a37A	 Alignment		90.7	11	PDB header: hydrolase Chain: A; PDB Molecule: metallo-carboxypeptidase; PDBTitle: metallo-carboxypeptidase from pseudomonas aeruginosa
14	c3i3wB	 Alignment		88.1	24	PDB header: isomerase Chain: B; PDB Molecule: phosphoglucosamine mutase; PDBTitle: structure of a phosphoglucosamine mutase from francisella tularensis
15	c3i2nA	 Alignment		87.1	15	PDB header: hydrolase Chain: A; PDB Molecule: peptidase m14, carboxypeptidase a; PDBTitle: crystal structure of putative carboxypeptidase a (yp_562911.1) from2 shewanella denitrificans os-217 at 2.39 a resolution
16	c3k2kA	 Alignment		86.9	10	PDB header: hydrolase Chain: A; PDB Molecule: putative carboxypeptidase; PDBTitle: crystal structure of putative carboxypeptidase (yp_103406.1) from2 burkholderia mallei atcc 23344 at 2.49 a resolution
17	d1yqea1	 Alignment		84.6	14	Fold: Phosphorylase/hydrolase-like Superfamily: AF0625-like Family: AF0625-like
18	c3uw2A	 Alignment		79.2	23	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
19	c3a9iB	 Alignment		78.5	14	PDB header: hydrolase Chain: B; PDB Molecule: poly-gamma-glutamate hydrolase; PDBTitle: structure of bacteriophage poly-gamma-glutamate hydrolase
20	c3cdxB	 Alignment		76.4	15	PDB header: hydrolase Chain: B; PDB Molecule: succinylglutamatedesuccinylase/aspartoacylase; PDBTitle: crystal structure of succinylglutamatedesuccinylase/aspartoacylase2 from rhodobacter sphaeroides
21	c4hjhA	 Alignment	not modelled	75.8	25	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
22	d1p5dx2	 Alignment	not modelled	75.0	24	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
23	c1wqaB	 Alignment	not modelled	73.6	32	PDB header: isomerase Chain: B; PDB Molecule: phospho-sugar mutase; PDBTitle: crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
24	c4rapD	 Alignment	not modelled	69.6	25	PDB header: transferase Chain: D; PDB Molecule: glycosyltransferase tbc; PDBTitle: crystal structure of bacterial iron-containing dodecameric2 glycosyltransferase tbc from enterotoxigenic e.coli h10407
25	c6gyzB	 Alignment	not modelled	69.4	15	PDB header: isomerase Chain: B; PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of glmm from staphylococcus aureus
26	c3na6A	 Alignment	not modelled	69.0	9	PDB header: hydrolase Chain: A; PDB Molecule: succinylglutamate desuccinylase/aspartoacylase; PDBTitle: crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
27	c3bghB	 Alignment	not modelled	68.7	21	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative neuraminylactose-binding hemagglutinin homolog; PDBTitle: crystal structure of putative neuraminylactose-binding hemagglutinin2 homolog from helicobacter pylori
		 Alignment				PDB header: isomerase

28	c3pdkB	Alignment	not modelled	67.2	16	Chain: B: PDB Molecule: phosphoglucosamine mutase; PDBTitle: crystal structure of phosphoglucosamine mutase from b. anthracis
29	c2fuvB	Alignment	not modelled	65.5	18	PDB header: isomerase Chain: B: PDB Molecule: phosphoglucomutase; PDBTitle: phosphoglucomutase from salmonella typhimurium.
30	d2naca2	Alignment	not modelled	64.3	16	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
31	c6mn8A	Alignment	not modelled	64.0	14	PDB header: ligase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of prolyl-trna synthetase from onchocerca volvulus2 with bound halofuginone and nucleotide
32	c3c04A	Alignment	not modelled	61.7	24	PDB header: isomerase Chain: A: PDB Molecule: phosphomannomutase/phosphoglucomutase; PDBTitle: structure of the p368g mutant of pmm/pgm from p. aeruginosa
33	c1u83A	Alignment	not modelled	61.2	13	PDB header: lyase Chain: A: PDB Molecule: phosphosulfolactate synthase; PDBTitle: psl synthase from bacillus subtilis
34	d1u83a	Alignment	not modelled	61.2	13	Fold: TIM beta/alpha-barrel Superfamily: (2r)-phospho-3-sulfolactate synthase ComA Family: (2r)-phospho-3-sulfolactate synthase ComA
35	c1c4gB	Alignment	not modelled	60.9	16	PDB header: transferase Chain: B: PDB Molecule: protein (alpha-d-glucose 1-phosphate phosphoglucomutase); PDBTitle: phosphoglucomutase vanadate based transition state analog complex
36	c6cluC	Alignment	not modelled	59.6	34	PDB header: antimicrobial protein Chain: C: PDB Molecule: dihydropteroate synthase; PDBTitle: staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
37	c3nh8A	Alignment	not modelled	58.1	14	PDB header: hydrolase Chain: A: PDB Molecule: aspartoacylase-2; PDBTitle: crystal structure of murine aminoacylase 3 in complex with n-acetyl-s-2 1,2-dichlorovinyl-l-cysteine
38	c4hwtA	Alignment	not modelled	55.6	15	PDB header: ligase/ligase inhibitor Chain: A: PDB Molecule: threonine--trna ligase, cytoplasmic; PDBTitle: crystal structure of human threonyl-trna synthetase bound to a novel2 inhibitor
39	d1nyra1	Alignment	not modelled	51.9	14	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
40	c5bmpA	Alignment	not modelled	51.1	17	PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase; PDBTitle: crystal structure of phosphoglucomutase from xanthomonas citri2 complexed with glucose-1-phosphate
41	c1nj2A	Alignment	not modelled	50.4	16	PDB header: ligase Chain: A: PDB Molecule: proline-trna synthetase; PDBTitle: crystal structure of prolyl-trna synthetase from methanothermobacter2 thermotrophicus
42	c2gx8B	Alignment	not modelled	50.1	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: nif3-related protein; PDBTitle: the crystal structure of bacillus cereus protein related to nif3
43	c5ucmB	Alignment	not modelled	48.9	14	PDB header: ligase Chain: B: PDB Molecule: proline--trna ligase; PDBTitle: crystal structure of prolyl-trna synthetase from pseudomonas2 aeruginosa
44	c2qvpC	Alignment	not modelled	48.5	16	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative metallopeptidase (sama_0725) from2 shewanella amazonensis sb2b at 2.00 a resolution
45	c2f7IA	Alignment	not modelled	47.3	32	PDB header: isomerase Chain: A: PDB Molecule: 455aa long hypothetical phospho-sugar mutase; PDBTitle: crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
46	d2gx8a1	Alignment	not modelled	46.2	18	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
47	c2gfgC	Alignment	not modelled	46.0	11	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: upf0204 protein ph0006; PDBTitle: structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
48	c3l80A	Alignment	not modelled	45.8	19	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein smu.1393c; PDBTitle: crystal structure of smu.1393c from streptococcus mutans ua159
49	c3l1jB	Alignment	not modelled	44.5	44	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, short chain dehydrogenase/reductase family; PDBTitle: structure of a putative short chain dehydrogenase from pseudomonas2 syringae
50	d1wu7a1	Alignment	not modelled	43.1	11	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
51	d2fywa1	Alignment	not modelled	42.6	26	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
52	c3o38D	Alignment	not modelled	42.2	21	PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from

						mycobacterium2 smegmatis
53	d2odfa1	Alignment	not modelled	42.0	13	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Fase-like
54	d1ad1a	Alignment	not modelled	40.9	31	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
55	d1w6ua	Alignment	not modelled	39.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
56	c4hvcB	Alignment	not modelled	38.4	10	PDB header: ligase/ligase inhibitor Chain: B: PDB Molecule: bifunctional glutamate/proline--trna ligase; PDBTitle: crystal structure of human prolyl-trna synthetase in complex with2 halofuginone and atp analogue
57	c2o2sA	Alignment	not modelled	38.3	34	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-acyl carrier reductase; PDBTitle: the structure of t. gondii enoyl acyl carrier protein reductase in2 complex with nad and triclosan
58	d1g0oa	Alignment	not modelled	38.1	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
59	d1kfa2	Alignment	not modelled	35.9	14	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
60	c3gafF	Alignment	not modelled	35.5	30	PDB header: oxidoreductase Chain: F: PDB Molecule: 7-alpha-hydroxysteroid dehydrogenase; PDBTitle: 2.2a crystal structure of 7-alpha-hydroxysteroid dehydrogenase from2 brucella melitensis
61	c3i1iA	Alignment	not modelled	34.8	10	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
62	d1qe0a1	Alignment	not modelled	34.3	10	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
63	c4qloA	Alignment	not modelled	33.5	18	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of homoserine o-acetyltransferase from2 staphylococcus aureus
64	c4e51B	Alignment	not modelled	33.1	19	PDB header: ligase Chain: B: PDB Molecule: histidine--trna ligase; PDBTitle: crystal structure of a histidyl-trna synthetase hisrs from2 burkholderia thailandensis bound to histidine
65	c3netB	Alignment	not modelled	33.1	13	PDB header: ligase Chain: B: PDB Molecule: histidyl-trna synthetase; PDBTitle: crystal structure of histidyl-trna synthetase from nostoc sp. pcc 7120
66	d1xhfa1	Alignment	not modelled	32.7	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
67	c4zgwB	Alignment	not modelled	32.4	43	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase; PDBTitle: short-chain dehydrogenase/reductase from serratia marcescens bcrc2 10948
68	d2g4ca1	Alignment	not modelled	32.3	9	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
69	c3ctmH	Alignment	not modelled	31.9	22	PDB header: oxidoreductase Chain: H: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
70	c5esrA	Alignment	not modelled	31.8	16	PDB header: hydrolase Chain: A: PDB Molecule: haloalkane dehalogenase; PDBTitle: crystal structure of haloalkane dehalogenase (dcca) from caulobacter2 crescentus
71	c5zy9D	Alignment	not modelled	31.8	13	PDB header: ligase Chain: D: PDB Molecule: threonyl-trna synthase; PDBTitle: structural basis for a trna synthetase
72	d1zl0a2	Alignment	not modelled	31.4	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
73	c4fn4A	Alignment	not modelled	31.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: short-chain nad(h)-dependent dehydrogenase/reductase from sulfobolbus2 acidocaldarius
74	c4weoD	Alignment	not modelled	31.1	43	PDB header: oxidoreductase Chain: D: PDB Molecule: putative acetoin(diacetyl) reductase; PDBTitle: crystal structure of a putative acetoin(diacetyl) reductase2 burkholderia cenocepacia
75	c5f9yB	Alignment	not modelled	30.6	12	PDB header: ligase Chain: B: PDB Molecule: aminoacyl-trna synthetase; PDBTitle: crystal structure of prolyl-trna synthetase from cryptosporidium2 parvum complexed with l-proline and amp
76	c2ronA	Alignment	not modelled	30.4	21	PDB header: hydrolase Chain: A: PDB Molecule: surfactin synthetase thioesterase subunit; PDBTitle: the external thioesterase of the surfactin-synthetase
77	c3vvlA	Alignment	not modelled	30.0	13	PDB header: transferase Chain: A: PDB Molecule: homoserine o-acetyltransferase; PDBTitle: crystal structure of l-serine-o-acetyltransferase found in d-2 cycloserine biosynthetic pathway
78	d1qf6a1	Alignment	not modelled	29.6	15	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
						PDB header: oxidoreductase/oxidoreductase inhibitor Chain: D: PDB Molecule: enoyl-facvl-carrier-protein1 reductase

79	c4q9nD_	Alignment	not modelled	29.4	25	[nadh]; PDBTitle: crystal structure of chlamydia trachomatis enoyl-acyl reductase (fabI)2 in complex with nadh and afn-1252 PDB header: unknown function Chain: B: PDB Molecule: upf0135 protein sa1388; PDBTitle: crystal structure of staphylococcus aureus hypothetical protein sa1388
80	c2nydB_	Alignment	not modelled	29.1	18	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: dihydropteroate synthase from streptococcus pneumoniae
81	c2vefB_	Alignment	not modelled	29.1	37	PDB header: ligase Chain: A: PDB Molecule: proline--trna ligase; PDBTitle: crystal structure of prolyl-trna synthetase (prs) from plasmodium2 falciparum
82	c4twaA_	Alignment	not modelled	29.0	6	PDB header: isomerase Chain: A: PDB Molecule: phosphoacetylglucosamine mutase; PDBTitle: crystal structure of n-acetylglucosamine-phosphate mutase,2 a member of the alpha-d-phosphohexomutase superfamily, in3 the product complex
83	c2dkdA_	Alignment	not modelled	28.9	20	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
84	c3nhzA_	Alignment	not modelled	28.9	24	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: AstE/AspA-like
85	d2i3ca1	Alignment	not modelled	28.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a putative short chain dehydrogenase from2 burkholderia cenocepacia
86	c5jydA_	Alignment	not modelled	28.5	26	PDB header: isomerase Chain: A: PDB Molecule: rhcc; PDBTitle: crystal structure of native rhcc (yp_702633.1) from rhodococcus jostii2 rha1 at 1.78 angstrom
87	c4u5pA_	Alignment	not modelled	28.0	13	PDB header: aminoacyl-trna synthetase Chain: D: PDB Molecule: prolyl-trna synthetase; PDBTitle: prolyl-trna synthetase from thermus thermophilus complexed2 with l-proline
88	c1h4tD_	Alignment	not modelled	27.8	24	PDB header: transferase Chain: A: PDB Molecule: two-component sensor kinase; PDBTitle: nmr structure of the pseudo-receiver domain of the cika protein.
89	c2j48A_	Alignment	not modelled	27.8	23	Fold: Anticodon-binding domain-like Superfamily: XCC0632-like Family: NLBH-like
90	d2i9ia1	Alignment	not modelled	27.8	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of helicobacter pylori protein hp0492
91	c2i9iA_	Alignment	not modelled	27.8	6	PDB header: biosynthetic protein Chain: C: PDB Molecule: pterin-4-alpha-carbinolamine dehydratase moab2; PDBTitle: crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
92	c3rfqC_	Alignment	not modelled	27.6	15	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1
93	c3c3mA_	Alignment	not modelled	27.4	18	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of the apo form of d-alanine:d-alanine ligase (ddl)2 from streptococcus mutans
94	c3k3pA_	Alignment	not modelled	27.4	18	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
95	d1zgza1	Alignment	not modelled	27.3	15	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
96	c2an1D_	Alignment	not modelled	26.8	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
97	c1y80A_	Alignment	not modelled	26.7	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
98	d1zh2a1	Alignment	not modelled	26.5	25	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab2; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
99	c2is8A_	Alignment	not modelled	26.4	13	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator mtra; PDBTitle: crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
100	c2gwrA_	Alignment	not modelled	26.4	26	PDB header: ligase Chain: A: PDB Molecule: probable threonyl-trna synthetase 1; PDBTitle: crystal structure of putative threonyl-trna synthetase thrrs-1 from2 aeropyrum pernix
101	c3a32A_	Alignment	not modelled	26.3	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ta0583-like
102	d2fsja1	Alignment	not modelled	26.3	33	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
103	d1vmea1	Alignment	not modelled	26.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: renilla-luciferin 2-monooxygenase; PDBTitle: crystal structures of the luciferase and green fluorescent2
104	c2pseA_	Alignment	not modelled	26.1	14	

						protein from renilla reniformis
105	c2jahB_	Alignment	not modelled	26.1	46	PDB header: oxidoreductase Chain: B: PDB Molecule: clavulanic acid dehydrogenase; PDBTitle: biochemical and structural analysis of the clavulanic acid2 dehydrogenase (cad) from streptomyces clavuligerus
106	c1wvpA_	Alignment	not modelled	26.0	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ttha0636; PDBTitle: crystal structure of ttk003001694 from thermus thermophilus2 hb8
107	c5odhH_	Alignment	not modelled	25.9	8	PDB header: oxidoreductase Chain: H: PDB Molecule: heterodisulfide reductase, subunit b; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus soaked with heterodisulfide3 for 3.5 minutes
108	c3a0rB_	Alignment	not modelled	25.4	13	PDB header: transferase Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
109	c4axvA_	Alignment	not modelled	25.4	22	PDB header: hydrolase Chain: A: PDB Molecule: mpaa; PDBTitle: biochemical and structural characterization of the mpaa2 amidase as part of a conserved scavenging pathway for3 peptidoglycan derived peptides in gamma-proteobacteria
110	d1yxma1	Alignment	not modelled	25.3	37	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
111	c5xiiC_	Alignment	not modelled	25.1	12	PDB header: ligase Chain: C: PDB Molecule: prolyl-trna synthetase (prors); PDBTitle: crystal structure of toxoplasma gondii prolyl-trna synthetase (tgprs)2 in complex with inhibitor 6
112	c2aamA_	Alignment	not modelled	25.1	19	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein tm1410; PDBTitle: crystal structure of a putative glycosidase (tm1410) from thermotoga2 maritima at 2.20 a resolution
113	d2aama1	Alignment	not modelled	25.1	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: TM1410-like
114	d2h7ma1	Alignment	not modelled	25.1	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
115	d2bela_	Alignment	not modelled	24.6	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
116	d2o23a1	Alignment	not modelled	24.5	46	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
117	c2yxba_	Alignment	not modelled	24.4	18	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
118	d3c70a1	Alignment	not modelled	24.3	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Hydroxynitrile lyase-like
119	c5kxbB_	Alignment	not modelled	24.1	18	PDB header: signaling protein Chain: B: PDB Molecule: osmolarity two-component system protein ssk1; PDBTitle: co-crystal structure of the saccharomyces cerevisiae histidine2 phosphotransfer signaling protein ypd1 and the receiver domain of its3 downstream response regulator ssk1
120	c1kfiA_	Alignment	not modelled	24.0	14	PDB header: isomerase Chain: A: PDB Molecule: phosphoglucomutase 1; PDBTitle: crystal structure of the exocytosis-sensitive2 phosphoprotein, pp63/parafusin (phosphoglucomutase) from3 paramecium