























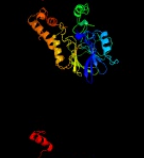
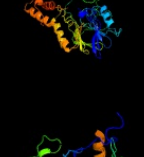




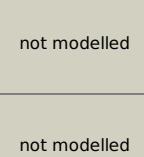


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0939 (-) _1048416_1050350
Date	Fri Jul 26 01:50:53 BST 2019
Unique Job ID	d718ca136a5ea631

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lzkC_	 Alignment		100.0	25	PDB header: hydrolase Chain: C: PDB Molecule: fumarylacetoacetate hydrolase family protein; PDBTitle: the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
2	c6iyxB_	 Alignment		100.0	34	PDB header: hydrolase Chain: B: PDB Molecule: 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase; PDBTitle: fumarylacetoacetate hydrolase (eafah) from psychrophilic2 exiguobacterium antarcticum
3	c3r6oA_	 Alignment		100.0	29	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1, 7-dioateisomerase; PDBTitle: crystal structure of a probable 2-hydroxyhepta-2,4-diene-1, 7-2 dioateisomerase from mycobacterium abscessus
4	c4dbhA_	 Alignment		100.0	25	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of cg1458 with inhibitor
5	c2q1dX_	 Alignment		100.0	22	PDB header: lyase Chain: X: PDB Molecule: 2-keto-3-deoxy-d-arabinonate dehydratase; PDBTitle: 2-keto-3-deoxy-d-arabinonate dehydratase complexed with magnesium and2 2,5-dioxopentanoate
6	c2dfuB_	 Alignment		100.0	27	PDB header: isomerase Chain: B: PDB Molecule: probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from thermus thermophilus hb8
7	c1wzoC_	 Alignment		100.0	29	PDB header: isomerase Chain: C: PDB Molecule: hpce; PDBTitle: crystal structure of the hpce from thermus thermophilus hb8
8	c6jvwA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: maleylpyruvate hydrolase; PDBTitle: crystal structure of maleylpyruvate hydrolase from sphingobium sp.2 syk-6 in complex with manganese (ii) ion and pyruvate
9	c3qdfA_	 Alignment		100.0	29	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from mycobacterium marinum
10	c4qkuC_	 Alignment		100.0	27	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase; PDBTitle: crystal structure of a putative hydrolase from burkholderia2 cenocepacia
11	c2yheD_	 Alignment		100.0	22	PDB header: hydrolase Chain: D: PDB Molecule: sec-alkyl sulfatase; PDBTitle: structure determination of the stereoselective inverting sec-2 alkylsulfatase pisa1 from pseudomonas sp.

12	c1hyoB_	Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: fumarylacetoacetate hydrolase; PDBTitle: crystal structure of fumarylacetoacetate hydrolase2 complexed with 4-(hydroxymethylphosphinoyl)-3-oxo-butanoic acid
13	c4nurB_	Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: psdsa; PDBTitle: crystal structure of thermostable alkylsulfatase sdsap from2 pseudomonas sp. s9
14	c2cfuA_	Alignment		100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: sdsa1; PDBTitle: crystal structure of sdsa1, an alkylsulfatase from2 pseudomonas aeruginosa, in complex with 1-decane-sulfonic-3 acid.
15	d2cfua2	Alignment		100.0	21	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Alkylsulfatase-like
16	cli7oC_	Alignment		100.0	25	PDB header: isomerase, lyase Chain: C: PDB Molecule: 4-hydroxyphenylacetate degradation bifunctional PDBTitle: crystal structure of hpce
17	c4pdxB_	Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: putative alkyl/aryl-sulfatase yjcs; PDBTitle: crystal structure of escherchia coli uncharacterized protein yjcs
18	c4maqB_	Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: putative fumarylpyruvate hydrolase; PDBTitle: crystal structure of a putative fumarylpyruvate hydrolase from2 burkholderia cenocepacia
19	d1hyoa2	Alignment		100.0	27	Fold: FAH Superfamily: FAH Family: FAH
20	d1gta2	Alignment		100.0	26	Fold: FAH Superfamily: FAH Family: FAH
21	c3s52A_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: putative fumarylacetoacetate hydrolase family protein; PDBTitle: crystal structure of a putative fumarylacetoacetate hydrolase family2 protein from yersinia pestis co92
22	c3l53F_	Alignment	not modelled	100.0	24	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative fumarylacetoacetate isomerase/hydrolase; PDBTitle: crystal structure of a putative fumarylacetoacetate2 isomerase/hydrolase from oleispira antarctica
23	d1nr9a_	Alignment	not modelled	100.0	24	Fold: FAH Superfamily: FAH Family: FAH
24	d1gta1	Alignment	not modelled	100.0	20	Fold: FAH Superfamily: FAH Family: FAH
25	d1nkqa_	Alignment	not modelled	100.0	22	Fold: FAH Superfamily: FAH Family: FAH
26	d1sawa_	Alignment	not modelled	100.0	21	Fold: FAH Superfamily: FAH Family: FAH
27	d1ko3a_	Alignment	not modelled	100.0	27	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
28	c3rkjA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase ndm-1; PDBTitle: crystal structure of new delhi metallo-beta-lactamase-1 from2 klebsiella pneumoniae

29	c5i0pB_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase domain protein; PDBTitle: crystal structure of a beta-lactamase domain protein from burkholderia2 ambifaria
30	d1jta_	Alignment	not modelled	100.0	19	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
31	d1m2xa_	Alignment	not modelled	100.0	16	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
32	c4wd6B_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystal structure of dim-1 metallo-beta-lactamase
33	c3spuB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase ndm-1; PDBTitle: apo ndm-1 crystal structure
34	d1znba_	Alignment	not modelled	100.0	24	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
35	c2ynuB_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: gim-1 protein; PDBTitle: apo gim-1 with 2mol. crystal structures of pseudomonas aeruginosa2 gim-1: active site plasticity in metallo-beta-lactamases
36	c3l6nA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystal structure of metallo-beta-lactamase ind-7
37	c2fhxB_	Alignment	not modelled	100.0	16	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: spm-1; PDBTitle: pseudomonas aeruginosa spm-1 metallo-beta-lactamase
38	c2yz3B_	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase; PDBTitle: crystallographic investigation of inhibition mode of the2 vim-2 metallo-beta-lactamase from pseudomonas aeruginosa3 with mercaptocarboxylate inhibitor
39	c5mmdF_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: F: PDB Molecule: metallo-beta-lactamase 1; PDBTitle: tmb-1. structural insights into tmb-1 and the role of residue 119 and2 228 in substrate and inhibitor binding
40	c4ad9E_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: E: PDB Molecule: beta-lactamase-like protein 2; PDBTitle: crystal structure of human lactb2.
41	c6cqsA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: sediminispirochaeta smaragdinae sps-1 metallo-beta-lactamase
42	d1mqoa_	Alignment	not modelled	100.0	22	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
43	d2q0ia1	Alignment	not modelled	100.0	17	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: PqsE-like
44	c2zo4A_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: crystal structure of metallo-beta-lactamase family protein ttha14292 from thermus thermophilus hb8
45	d1x8ha_	Alignment	not modelled	100.0	21	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
46	c6dn4A_	Alignment	not modelled	100.0	19	PDB header: metal binding protein Chain: A: PDB Molecule: beta-lactamase; PDBTitle: cronobacter sakazakii (enterobacter sakazakii) metallo-beta-lactamase2 harldq motif
47	c2ohiB_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: type a flavoprotein fpra; PDBTitle: crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
48	c6h0cA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: flv1 flavodiiron core from synechocystis sp. pcc6803
49	c3lvzA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: blr6230 protein; PDBTitle: new refinement of the crystal structure of bjp-1, a subclass b32 metallo-beta-lactamase of bradyrhizobium japonicum
50	c2q9uB_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: aa-type flavoprotein; PDBTitle: crystal structure of the flavodiiron protein from giardia2 intestinalis
51	c5aebA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: lra-12; PDBTitle: crystal structure of the class b3 di-zinc metallo-beta-lactamase lra-2 12 from an alaskan soil metagenome.
52	d2gmna1	Alignment	not modelled	100.0	18	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
53	c4awyB_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase aim-1; PDBTitle: crystal structure of the mobile metallo-beta-lactamase aim-1 from2 pseudomonas aeruginosa: insights into antibiotic binding and the role3 of gln157
54	d2aioa1	Alignment	not modelled	100.0	18	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
						PDB header: hydrolase

55	c3sd9B_	Alignment	not modelled	100.0	15	Chain: B: PDB Molecule: beta-lactamase; PDBTitle: crystal structure of serratia fonticola sfh-i: source of the2 nucleophile in the catalytic mechanism of mono-zinc metallo-beta-3 lactamases
56	c5k0wA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: class b carbapenemase gob-18; PDBTitle: crystal structure of the metallo-beta-lactamase gob-18 from2 elizabethkingia meningoseptica
57	c1ychD_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: D: PDB Molecule: nitric oxide reductase; PDBTitle: x-ray crystal structures of moorella thermoacetica fpa. novel diiron2 site structure and mechanistic insights into a scavenging nitric3 oxide reductase
58	c1vmeB_	Alignment	not modelled	100.0	24	PDB header: electron transport Chain: B: PDB Molecule: flavoprotein; PDBTitle: crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
59	d1sv6a_	Alignment	not modelled	100.0	19	Fold: FAH Superfamily: FAH Family: FAH
60	c6n36A_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: beta-lactamase; PDBTitle: beta-lactamase from chitinophaga pinensis
61	c6aufB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase-like protein; PDBTitle: crystal structure of metallo beta lactamases mim-1 from novosphingobium2 pentaromativorans
62	c6qrqB_	Alignment	not modelled	100.0	17	PDB header: signaling protein Chain: B: PDB Molecule: oxygen-binding diiron protein; PDBTitle: apo conformation of chemotaxis sensor odp
63	c4d02A_	Alignment	not modelled	100.0	19	PDB header: electron transport Chain: A: PDB Molecule: anaerobic nitric oxide reductase flavorubredoxin; PDBTitle: the crystallographic structure of flavorubredoxin from escherichia2 coli
64	c6e0sA_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: mem-a1; PDBTitle: crystal structure of mem-a1, a subclass b3 metallo-beta-lactamase2 isolated from a soil metagenome library
65	c3hnnD_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: putative diflavin flavoprotein a 5; PDBTitle: crystal structure of putative diflavin flavoprotein a 5 (fragment 1-2 254) from nostoc sp. pcc 7120, northeast structural genomics3 consortium target nsr435a
66	c1e5dA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin\oxygen oxidoreductase; PDBTitle: rubredoxin oxygen:oxidoreductase (roo) from anaerobe desulfovibrio2 gigas
67	c5iqkB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase rm3; PDBTitle: rm3 metallo-beta-lactamase
68	d1k07a_	Alignment	not modelled	100.0	17	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Zn metallo-beta-lactamase
69	c3vqzA_	Alignment	not modelled	100.0	18	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: metallobeta-lactamase; PDBTitle: crystal structure of metallo-beta-lactamase, smb-1, in a complex with2 mercaptoacetic acid
70	d1e5da2	Alignment	not modelled	100.0	19	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like
71	c3adrA_	Alignment	not modelled	100.0	17	PDB header: signaling protein Chain: A: PDB Molecule: putative uncharacterized protein st1585; PDBTitle: the first crystal structure of an archaeal metallo-beta-lactamase2 superfamily protein; st1585 from sulfobolus tokodaii
72	c6qnmB_	Alignment	not modelled	100.0	15	PDB header: signaling protein Chain: B: PDB Molecule: oxygen-binding di-iron protein; PDBTitle: apo state of chemotaxis sensor odp from t. denticola
73	c5d2hA_	Alignment	not modelled	100.0	18	PDB header: lyase Chain: A: PDB Molecule: 4-oxalocrotonate decarboxylase nahk; PDBTitle: 4-oxalocrotonate decarboxylase from pseudomonas putida g7 - complexed2 with magnesium and alpha-ketoglutarate
74	d1xm8a_	Alignment	not modelled	100.0	17	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
75	d1ycga2	Alignment	not modelled	99.9	18	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like
76	c2eb5D_	Alignment	not modelled	99.9	18	PDB header: lyase Chain: D: PDB Molecule: 2-oxo-hept-3-ene-1,7-dioate hydratase; PDBTitle: crystal structure of hpcg complexed with oxalate
77	c4yskA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase domain protein; PDBTitle: crystal structure of apo-form sdoa from pseudomonas putida
78	d2qeda1	Alignment	not modelled	99.9	19	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
79	c4efzB_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: B: PDB Molecule: metallobeta-lactamase family protein; PDBTitle: crystal structure of a hypothetical metallo-beta-lactamase from2 burkholderia pseudomallei
80	d1vmea2	Alignment	not modelled	99.9	24	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: ROO N-terminal domain-like

81	c4chlA	Alignment	not modelled	99.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: persulfide dioxygenase ethe1, mitochondrial; PDBTitle: human ethylmalonic encephalopathy protein 1 (hethe1)
82	c2xf4A	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: hydroxyacylglutathione hydrolase; PDBTitle: crystal structure of salmonella enterica serovar2 typhimurium ycb1
83	c3r2uC	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: C: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: 2.1 angstrom resolution crystal structure of metallo-beta-lactamase2 from staphylococcus aureus subsp. aureus col
84	c2gcuD	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: D: PDB Molecule: putative hydroxyacylglutathione hydrolase 3; PDBTitle: x-ray structure of gene product from arabidopsis thaliana at1g53580
85	d2p97a1	Alignment	not modelled	99.9	18	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Ava3068-like
86	c2zwrA	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: metallo-beta-lactamase superfamily protein; PDBTitle: crystal structure of ttha1623 from thermus thermophilus hb8
87	c3aj3A	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: 4-pyridoxolactonase; PDBTitle: crystal structure of selenomethionine substituted 4-pyridoxolactonase2 from mesorhizobium loti
88	c4ysbB	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: crystal structure of ethe1 from myxococcus xanthus
89	c3tp9B	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactamase and rhodanese domain protein; PDBTitle: crystal structure of alicyclobacillus acidocaldarius protein with2 beta-lactamase and rhodanese domains
90	d1qh5a	Alignment	not modelled	99.9	24	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Glyoxalase II (hydroxyacylglutathione hydrolase)
91	c2p18A	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: glyoxalase ii; PDBTitle: crystal structure of the leishmania infantum glyoxalase ii
92	c5ve5C	Alignment	not modelled	99.9	25	PDB header: oxidoreductase, transferase Chain: C: PDB Molecule: bpprf; PDBTitle: crystal structure of persulfide dioxygenase rhodanese fusion protein2 with rhodanese domain inactivating mutation (c314s) from burkholderia3 phytofirmans in complex with glutathione
93	c6ch0L	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: I: PDB Molecule: beta-lactamase; PDBTitle: structure of the quorum quenching lactonase from alicyclobacillus2 acidoterrestris bound to a glycerol molecule
94	c4v0hC	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: C: PDB Molecule: metallo-beta-lactamase domain-containing protein 1 1; PDBTitle: human metallo beta lactamase domain containing protein 1 (hmb1ac1)
95	c2r2dC	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: C: PDB Molecule: zn-dependent hydrolases; PDBTitle: structure of a quorum-quenching lactonase (aiib) from agrobacterium2 tumefaciens
96	c2br6A	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: A: PDB Molecule: aiia-like protein; PDBTitle: crystal structure of quorum-quenching n-acyl homoserine2 lactone lactonase
97	c4xukB	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: B: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of hydrolase aboph in beta lactamase superfamily
98	c3eshB	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: B: PDB Molecule: protein similar to metal-dependent hydrolase; PDBTitle: crystal structure of a probable metal-dependent hydrolase2 from staphylococcus aureus. northeast structural genomics3 target zr314
99	c4zo3A	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: acylhomoserine lactonase; PDBTitle: aidc, a dizinc quorum-quenching lactonase, in complex with a product2 n-hexnoyl-l-homoserine
100	c1p9eA	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: methyl parathion hydrolase; PDBTitle: crystal structure analysis of methyl parathion hydrolase from2 pseudomonas sp wbc-3
101	d1p9ea	Alignment	not modelled	99.8	17	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Methyl parathion hydrolase
102	d1ztca1	Alignment	not modelled	99.7	15	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: TM0894-like
103	c4le6B	Alignment	not modelled	99.7	22	PDB header: hydrolase Chain: B: PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of the phosphotriesterase ophc2 from pseudomonas2 pseudoalcaligenes
104	c2p4zA	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: A: PDB Molecule: metal-dependent hydrolases of the beta-lactamase PDBTitle: a ferredoxin-like metallo-beta-lactamase superfamily protein from2 thermoanaerobacter tengcongensis PDB header: structural genomics, metal binding prote

105	c3h3eA	Alignment	not modelled	99.6	18	Chain: A: PDB Molecule: uncharacterized protein tm1679; PDBTitle: crystal structure of tm1679, a metal-dependent hydrolase of2 the beta-lactamase superfamily
106	c3zq4C	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: C: PDB Molecule: ribonuclease j 1; PDBTitle: unusual, dual endo- and exo-nuclease activity in the degradosome2 explained by crystal structure analysis of rnase j1
107	c5a0tA	Alignment	not modelled	99.4	20	PDB header: hydrolase/rna Chain: A: PDB Molecule: ribonuclease j; PDBTitle: catalysis and 5' end sensing by ribonuclease rnase j of the2 metallo-beta-lactamase family
108	c5habB	Alignment	not modelled	99.4	17	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease j; PDBTitle: crystal structure of mpy-rnase j (mutant h84a), an archaeal rnase j2 from methanobus psychrophilus r15, complex with rna
109	c3x30A	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: A: PDB Molecule: upf0173 metal-dependent hydrolase tm_1162; PDBTitle: crystal structure of metallo-beta-lactamase from thermotoga maritima
110	c2az4A	Alignment	not modelled	99.3	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ef2904; PDBTitle: crystal structure of a protein of unknown function from enterococcus2 faecalis v583
111	c4xwwA	Alignment	not modelled	99.3	15	PDB header: rna binding protein/rna Chain: A: PDB Molecule: dr2417; PDBTitle: crystal structure of rnase j complexed with rna
112	c6i1dA	Alignment	not modelled	99.3	15	PDB header: gene regulation Chain: A: PDB Molecule: endoribonuclease ysh1; PDBTitle: structure of the ysh1-mpe1 nuclease complex from s.cerevisiae
113	c6b9vA	Alignment	not modelled	99.3	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase-like protein; PDBTitle: crystal structure of a new diphosphatase from the phnp family
114	c3bk2A	Alignment	not modelled	99.3	19	PDB header: hydrolase Chain: A: PDB Molecule: metal dependent hydrolase; PDBTitle: crystal structure analysis of the rnase j/ump complex
115	d2i7ta1	Alignment	not modelled	99.2	15	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
116	c3af5A	Alignment	not modelled	99.2	20	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ph1404; PDBTitle: the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
117	d2dkfa1	Alignment	not modelled	99.2	16	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases
118	c1zkpD	Alignment	not modelled	99.1	16	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein ba1088; PDBTitle: 1.5a resolution crystal structure of a metallo beta lactamase family2 protein, the elac homolgue of bacillus anthracis, a putative3 ribonuclease
119	c3g1pA	Alignment	not modelled	99.1	20	PDB header: lyase Chain: A: PDB Molecule: protein phnp; PDBTitle: crystals structure of phnp from e.coli k-12
120	d2az4a1	Alignment	not modelled	99.1	17	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: beta-CASP RNA-metabolising hydrolases