Phyre²

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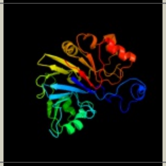
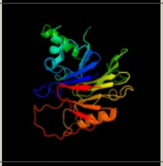
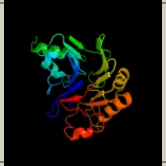
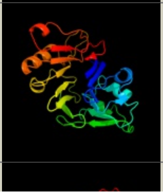
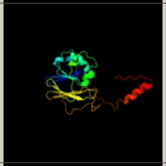
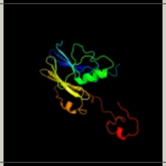
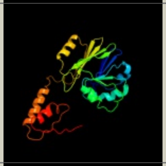
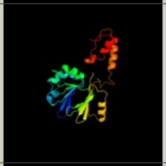
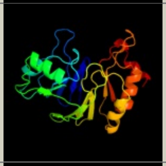
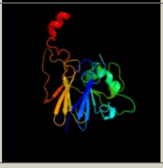
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3g1pA_	Alignment		100.0	100	**PDB header:**lyase **Chain:** A: **PDB Molecule:**protein phnp; **PDBTitle:** crystals structure of phnp from e.coli k-12
2	c3md7A_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase-like; **PDBTitle:** crystal structure of a beta-lactamase-like protein bound to gmp from2 brucella melitensis
3	d1xtoa_	Alignment		100.0	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Coenzyme PQQ synthesis protein B, PqqB
4	c3zwfA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc phosphodiesterase elac protein 1; **PDBTitle:** crystal structure of human trnase z, short form (elac1).
5	d2cbna1	Alignment		100.0	25	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**RNase Z-like
6	d1y44a1	Alignment		100.0	25	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**RNase Z-like
7	c1zkpD_	Alignment		100.0	18	**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
8	d1zkpa1	Alignment		100.0	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**YhfI-like
9	c2p4zA_	Alignment		100.0	13	**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
10	c3rpcD_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**possible metal-dependent hydrolase; **PDBTitle:** the crystal structure of a possible metal-dependent hydrolase from2 veillonella parvula dsm 2008
11	d2e7ya1	Alignment		100.0	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**RNase Z-like

12	c3kl7A_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metal-dependent hydrolase; **PDBTitle:** crystal structure of putative metal-dependent hydrolase2 (yp_001302908.1) from parabacteroides distasonis atcc 8503 at 2.30 a3 resolution
13	c2wylF_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**l-ascorbate-6-phosphate lactonase ulag; **PDBTitle:** apo structure of a metallo-b-lactamase
14	d2i7ta1	Alignment		99.9	15	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
15	c2az4A_	Alignment		99.9	15	**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
16	c3zq4C_	Alignment		99.9	19	**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
17	c3bk2A_	Alignment		99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal dependent hydrolase; **PDBTitle:** crystal structure analysis of the rnase j/ump complex
18	d2dkfa1	Alignment		99.9	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
19	c3bv6D_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**metal-dependent hydrolase; **PDBTitle:** crystal structure of uncharacterized metallo protein from vibrio2 cholerae with beta-lactamase like fold
20	c2xr1A_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cleavage and polyadenylation specificity factor 100 kd **PDBTitle:** dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
21	c2xr1B_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cleavage and polyadenylation specificity factor 100 kd **PDBTitle:** dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
22	c2ycbA_	Alignment	not modelled	99.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cleavage and polyadenylation specificity factor; **PDBTitle:** structure of the archaeal beta-casp protein with n-terminal2 kh domains from methanothermobacter thermautotrophicus
23	c3af5A_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1404; **PDBTitle:** the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
24	c3h3eA_	Alignment	not modelled	99.9	12	**PDB header:**structural genomics, metal binding prote **Chain:** A: **PDB Molecule:**uncharacterized protein tm1679; **PDBTitle:** crystal structure of tm1679, a metal-dependent hydrolase of2 the beta-lactamase superfamily
25	d1vjna_	Alignment	not modelled	99.9	15	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Hypothetical protein TM0207
26	d2i7xa1	Alignment	not modelled	99.9	13	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
27	c2i7xA_	Alignment	not modelled	99.9	13	**PDB header:**rna binding protein, protein binding **Chain:** A: **PDB Molecule:**protein cft2; **PDBTitle:** structure of yeast cpsf-100 (ydh1p)
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**teichoic acid phosphorylcholine

28	c2bibA_	Alignment	not modelled	99.8	14	esterase/ choline binding **PDBTitle:** crystal structure of the complete modular teichioic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus3 pneumoniae
29	c2r2dC_	Alignment	not modelled	99.7	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**zn-dependent hydrolases; **PDBTitle:** structure of a quorum-quenching lactonase (aiib) from agrobacterium2 tumefaciens
30	d1k07a_	Alignment	not modelled	99.7	12	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
31	d2az4a1	Alignment	not modelled	99.7	13	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**beta-CASP RNA-metabolising hydrolases
32	d2aioa1	Alignment	not modelled	99.7	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
33	c3adrA_	Alignment	not modelled	99.7	18	**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 sulfolobus tokodaii
34	d1p9ea_	Alignment	not modelled	99.7	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Methyl parathion hydrolase
35	c1p9eA_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methyl parathion hydrolase; **PDBTitle:** crystal structure analysis of methyl parathion hydrolase from2 pseudomonas sp wbc-3
36	c1vmeB_	Alignment	not modelled	99.7	14	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
37	c3lvzA_	Alignment	not modelled	99.7	13	**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
38	c2ohiB_	Alignment	not modelled	99.7	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
39	c1e5dA_	Alignment	not modelled	99.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
40	c2q9uB_	Alignment	not modelled	99.6	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
41	d2gmna1	Alignment	not modelled	99.6	15	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
42	c3eshB_	Alignment	not modelled	99.6	18	**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
43	c2zo4A_	Alignment	not modelled	99.6	17	**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
44	d1vmea2	Alignment	not modelled	99.6	12	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
45	c2br6A_	Alignment	not modelled	99.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aiia-like protein; **PDBTitle:** crystal structure of quorum-quenching n-acyl homoserine2 lactone lactonase
46	c3hnnD_	Alignment	not modelled	99.6	11	**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
47	c3aj3A_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**4-pyridoxolactonase; **PDBTitle:** crystal structure of selenomethionine substituted 4-pyridoxolactonase2 from mesorhizobium loti
48	d1ztca1	Alignment	not modelled	99.6	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**TM0894-like
49	c3l6nA_	Alignment	not modelled	99.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase; **PDBTitle:** crystal structure of metallo-beta-lactamase ind-7
50	d1ko3a_	Alignment	not modelled	99.6	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
51	c2fhxB_	Alignment	not modelled	99.6	14	**PDB header:**hydrolase, metal binding protein **Chain:** B: **PDB Molecule:**spm-1; **PDBTitle:** pseudomonas aeruginosa spm-1 metallo-beta-lactamase
52	d1znba_	Alignment	not modelled	99.6	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
53	c1ychD_	Alignment	not modelled	99.6	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a

						scavenging nitric oxide reductase
54	d1ycga2	Alignment	not modelled	99.5	11	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
55	d1wraa1	Alignment	not modelled	99.5	13	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Pce catalytic domain-like
56	d2q0ia1	Alignment	not modelled	99.5	13	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**PqsE-like
57	d1m2xa_	Alignment	not modelled	99.5	13	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
58	c2yz3B_	Alignment	not modelled	99.5	15	**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
59	d1mqoa_	Alignment	not modelled	99.5	13	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
60	d1jjta_	Alignment	not modelled	99.5	15	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
61	c2zwrA_	Alignment	not modelled	99.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallo-beta-lactamase superfamily protein; **PDBTitle:** crystal structure of ttha1623 from thermus thermophilus hb8
62	d1qh5a_	Alignment	not modelled	99.5	20	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
63	c3sd9B_	Alignment	not modelled	99.5	18	**PDB header:**hydrolase **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
64	c2gcuD_	Alignment	not modelled	99.5	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative hydroxyacylglutathione hydrolase 3; **PDBTitle:** x-ray structure of gene product from arabidopsis thaliana2 at1g53580
65	d1x8ha_	Alignment	not modelled	99.5	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
66	d1e5da2	Alignment	not modelled	99.5	17	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**ROO N-terminal domain-like
67	c3rkjA_	Alignment	not modelled	99.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-lactamase ndm-1; **PDBTitle:** crystal structure of new delhi metallo-beta-lactamase-1 from2 klebsiella pnueumoniae
68	c3spuB_	Alignment	not modelled	99.4	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactamase ndm-1; **PDBTitle:** apo ndm-1 crystal structure
69	c3tp9B_	Alignment	not modelled	99.4	15	**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
70	d1xm8a_	Alignment	not modelled	99.4	16	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
71	c3r2uC_	Alignment	not modelled	99.4	15	**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
72	c2p18A_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glyoxalase ii; **PDBTitle:** crystal structure of the leishmania infantum glyoxalase ii
73	c2xf4A_	Alignment	not modelled	99.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydroxyacylglutathione hydrolase; **PDBTitle:** crystal structure of salmonella enterica serovar2 typhimurium ycbl
74	d2qeda1	Alignment	not modelled	99.3	19	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Glyoxalase II (hydroxyacylglutathione hydrolase)
75	c2cfuA_	Alignment	not modelled	99.2	13	**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.
76	d2cfua2	Alignment	not modelled	99.2	13	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Alkylsulfatase-like
77	d2p97a1	Alignment	not modelled	98.8	18	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Ava3068-like
78	c3lnbA_	Alignment	not modelled	67.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase family protein; **PDBTitle:** crystal structure analysis of arylamine n-acetyltransferase c from2 bacillus anthracis

79	c2pfrB_	Alignment	not modelled	63.8	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arylamine n-acetyltransferase 2; **PDBTitle:** human n-acetyltransferase 2
80	d2bsza1	Alignment	not modelled	62.8	14	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
81	d1e2ta_	Alignment	not modelled	45.7	16	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
82	c3l6dB_	Alignment	not modelled	42.1	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
83	d1w4ta1	Alignment	not modelled	39.0	17	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
84	d1obba1	Alignment	not modelled	38.2	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
85	c3rhgA_	Alignment	not modelled	35.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phophotriesterase; **PDBTitle:** crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
86	c2p10D_	Alignment	not modelled	33.9	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
87	c3c7cB_	Alignment	not modelled	27.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**octopine dehydrogenase; **PDBTitle:** a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
88	d1s6ya1	Alignment	not modelled	24.3	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
89	d1hvca_	Alignment	not modelled	22.3	22	**Fold:**Acid proteases **Superfamily:**Acid proteases **Family:**Retroviral protease (retropepsin)
90	d1ag9a_	Alignment	not modelled	21.7	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
91	c3fefB_	Alignment	not modelled	21.3	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glucosidase lpld; **PDBTitle:** crystal structure of putative glucosidase lpld from2 bacillus subtilis
92	c1s6yA_	Alignment	not modelled	19.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phospho-beta-glucosidase; **PDBTitle:** 2.3a crystal structure of phospho-beta-glucosidase
93	c3k2gA_	Alignment	not modelled	19.5	20	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
94	c3d9wA_	Alignment	not modelled	18.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure analysis of nocardia farcinica arylamine2 n-acetyltransferase
95	d1ks9a2	Alignment	not modelled	18.6	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
96	c2ofpB_	Alignment	not modelled	18.2	40	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketopantoate reductase; **PDBTitle:** crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
97	d1o98a1	Alignment	not modelled	18.2	28	**Fold:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Superfamily:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain **Family:**2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
98	c1n1uA_	Alignment	not modelled	18.1	33	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**kalata b1; **PDBTitle:** nmr structure of [ala1,15]kalata b1
99	d1n1ua_	Alignment	not modelled	18.1	33	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Kalata B1