Phyre^2

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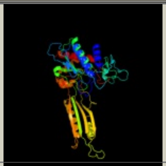
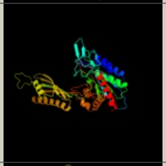
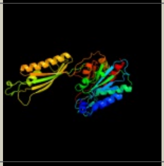
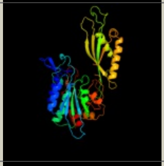
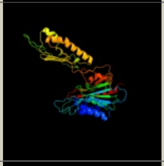
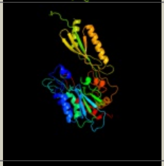
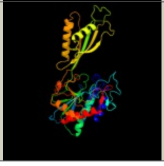
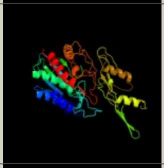
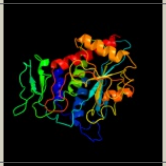
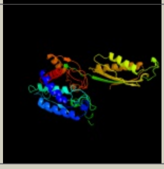
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vixA_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** crystal structure of a putative peptidase t
2	c3ifeA_	Alignment		100.0	53	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** 1.55 angstrom resolution crystal structure of peptidase t (pept-1)2 from bacillus anthracis str. 'ames ancestor'.
3	c3gb0A_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** crystal structure of aminopeptidase pept (np_980509.1) from bacillus2 cereus atcc 10987 at 2.04 a resolution
4	c3rzaA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tripeptidase; **PDBTitle:** crystal structure of a tripeptidase (sav1512) from staphylococcus2 aureus subsp. aureus mu50 at 2.10 a resolution
5	c3pfeA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of a m20a metallo peptidase (dape, lpg0809) from2 legionella pneumophila subsp. pneumophila str. philadelphia 1 at 1.503 a resolution
6	c3pfoB_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative acetylornithine deacetylase; **PDBTitle:** crystal structure of a putative acetylornithine deacetylase (rpa2325)2 from rhodopseudomonas palustris cga009 at 1.90 a resolution
7	c3mruB_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacyl-histidine dipeptidase; **PDBTitle:** crystal structure of aminoacylhistidine dipeptidase from vibrio2 alginolyticus
8	c2zogA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosolic non-specific dipeptidase; **PDBTitle:** crystal structure of mouse carnosinase cn2 complexed with zn and2 bestatin
9	c2qyvB_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xaa-his dipeptidase; **PDBTitle:** crystal structure of putative xaa-his dipeptidase (yp_718209.1) from2 haemophilus somnus 129pt at 2.11 a resolution
10	c3dljB_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-ala-his dipeptidase; **PDBTitle:** crystal structure of human carnosine dipeptidase 1
11	c2pokB_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase, m20/m25/m40 family; **PDBTitle:** crystal structure of a m20 family metallo peptidase from streptococcus2 pneumoniae

12	d1vixa1	Alignment		100.0	100	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
13	c1cg2D_	Alignment		100.0	20	**PDB header:**metallocarboxypeptidase **Chain:** D: **PDB Molecule:**carboxypeptidase g2; **PDBTitle:** carboxypeptidase g2
14	c1lfwA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pepv; **PDBTitle:** crystal structure of pepv
15	c1vgyB_	Alignment		100.0	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of succinyl diaminopimelate desuccinylase
16	c3n5fB_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**n-carbamoyl-l-amino acid hydrolase; **PDBTitle:** crystal structure of l-n-carbamoylase from geobacillus2 stearothermophilus cect43
17	c3ic1A_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of zinc-bound succinyl-diaminopimelate desuccinylase2 from haemophilus influenzae
18	c2rb7A_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase, m20/m25/m40 family; **PDBTitle:** crystal structure of co-catalytic metallopeptidase (yp_387682.1) from2 desulfovibrio desulfuricans g20 at 1.60 a resolution
19	d1fnoa4	Alignment		100.0	93	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
20	c2imoA_	Alignment		100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoate amidohydrolase; **PDBTitle:** crystal structure of allantoate amidohydrolase from escherichia coli2 at ph 4.6
21	c3tx8A_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of a succinyl-diaminopimelate desuccinylase (arge)2 from corynebacterium glutamicum atcc 13032 at 2.97 a resolution
22	c2f7vA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aectylcitrulline deacetylase; **PDBTitle:** structure of acetylcitrulline deacetylase complexed with2 one co
23	c3khzA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative dipeptidase sacol1801; **PDBTitle:** crystal structure of r350a mutant of staphylococcus aureus2 metallopeptidase (sapep/dape) in the apo-form
24	c2v8gD_	Alignment	not modelled	100.0	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-alanine synthase; **PDBTitle:** crystal structure of beta-alanine synthase from2 saccharomyces kluyveri in complex with the product beta-3 alanine
25	c1ysjB_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein yxep; **PDBTitle:** crystal structure of bacillus subtilis yxep protein (apc1829), a2 dinuclear metal binding peptidase from m20 family
26	c3ct9B_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acetylornithine deacetylase; **PDBTitle:** crystal structure of a putative zinc peptidase (np_812461.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.31 a resolution
27	c2q43A_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**iaa-amino acid hydrolase ilr1-like 2; **PDBTitle:** ensemble refinement of the protein crystal structure of iaa-aminoacid2 hydrolase from arabidopsis thaliana gene at5g56660
						PDB header:hydrolase

28	c3ramC_	Alignment	not modelled	100.0	17	**Chain:** C: **PDB Molecule:**hmra protein; **PDBTitle:** crystal structure of hmra
29	c1vheA_	Alignment	not modelled	100.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**aminopeptidase/glucanase homolog; **PDBTitle:** crystal structure of a aminopeptidase/glucanase homolog
30	d1lfwa1	Alignment	not modelled	100.0	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
31	c3kl9F_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**glutamyl aminopeptidase; **PDBTitle:** crystal structure of pepa from streptococcus pneumoniae
32	d1z2la1	Alignment	not modelled	100.0	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
33	c1yloA_	Alignment	not modelled	100.0	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein sf2450; **PDBTitle:** crystal structure of protein of unknown function (possible2 aminopeptidase) s2589 from shigella flexneri 2a str. 2457t
34	c1vhoA_	Alignment	not modelled	100.0	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of a putative peptidase/endoglucanase
35	c2cf4A_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein ph0519; **PDBTitle:** pyrococcus horikoshii tet1 peptidase can assemble into a2 tetrahedron or a large octahedral shell
36	c1y0yA_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**frv operon protein frvx; **PDBTitle:** crystal structure of tetrahedral aminopeptidase from p. horikoshii in2 complex with amastatin
37	c3io1B_	Alignment	not modelled	100.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminobenzoyl-glutamate utilization protein; **PDBTitle:** crystal structure of aminobenzoyl-glutamate utilization2 protein from klebsiella pneumoniae
38	c2pe3A_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**354aa long hypothetical operon protein frv; **PDBTitle:** crystal structure of frv operon protein frvx (ph1821)from pyrococcus2 horikoshii ot3
39	c3isxA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1050) from thermotoga2 maritima at 1.40 a resolution
40	c2fvgA_	Alignment	not modelled	100.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution
41	c3t6mA_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinyl-diaminopimelate desuccinylase; **PDBTitle:** crystal structure of the catalytic domain of dape protein from2 v.cholerea in the zn bound form
42	d1cg2a1	Alignment	not modelled	100.0	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
43	d1vhea2	Alignment	not modelled	100.0	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
44	d1yloa2	Alignment	not modelled	100.0	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
45	d1vhoa2	Alignment	not modelled	100.0	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
46	d1xfoa2	Alignment	not modelled	100.0	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
47	c3cpxC_	Alignment	not modelled	100.0	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**aminopeptidase, m42 family; **PDBTitle:** crystal structure of putative m42 glutamyl aminopeptidase2 (yp_676701.1) from cytophaga hutchinsonii atcc 33406 at 2.39 a3 resolution
48	c2greC_	Alignment	not modelled	99.9	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**deblocking aminopeptidase; **PDBTitle:** crystal structure of deblocking aminopeptidase from bacillus cereus
49	d1r3na1	Alignment	not modelled	99.9	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
50	c1q7lA_	Alignment	not modelled	99.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminoacylase-1; **PDBTitle:** zn-binding domain of the t347g mutant of human aminoacylase-2 i
51	d2fvga2	Alignment	not modelled	99.9	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
52	d1xmba1	Alignment	not modelled	99.9	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
53	d1vgya1	Alignment	not modelled	99.9	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases

54	d2grea2	Alignment	not modelled	99.9	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
55	d1ysja1	Alignment	not modelled	99.8	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
56	d1tkja1	Alignment	not modelled	99.7	25	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
57	c3l6sA_	Alignment	not modelled	99.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aspartyl aminopeptidase; **PDBTitle:** crystal structure of human aspartyl aminopeptidase (dnpep),2 in complex with aspartic acid hydroxamate
58	d1rtqa_	Alignment	not modelled	99.6	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
59	d1y0ya2	Alignment	not modelled	99.6	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
60	c2glfB_	Alignment	not modelled	99.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable m18-family aminopeptidase 1; **PDBTitle:** crystal structure of aminipeptidase (m18 family) from thermotoga2 maritima
61	c1y7eA_	Alignment	not modelled	99.5	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable m18-family aminopeptidase 1; **PDBTitle:** the crystal structure of aminopeptidase i from borrelia burgdorferi2 b31
62	c2ijzF_	Alignment	not modelled	99.5	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**probable m18-family aminopeptidase 2; **PDBTitle:** crystal structure of aminopeptidase
63	c1q7lB_	Alignment	not modelled	99.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminoacylase-1; **PDBTitle:** zn-binding domain of the t347g mutant of human aminoacylase-2 i
64	c3tc8A_	Alignment	not modelled	99.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine aminopeptidase; **PDBTitle:** crystal structure of a hypothetical zn-dependent exopeptidase2 (bdi_3547) from parabacteroides distasonis atcc 8503 at 1.06 a3 resolution
65	d1y7ea2	Alignment	not modelled	99.3	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
66	c3pb6X_	Alignment	not modelled	99.3	20	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glutaminyl-peptide cyclotransferase-like protein; **PDBTitle:** crystal structure of the catalytic domain of human golgi-resident2 glutaminyl cyclase at ph 6.5
67	d2afwa1	Alignment	not modelled	99.3	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Glutaminyl-peptide cyclotransferase-like
68	d1z2la2	Alignment	not modelled	99.2	11	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
69	d1cg2a2	Alignment	not modelled	99.2	19	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
70	d1r3na2	Alignment	not modelled	99.2	10	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
71	c3guxA_	Alignment	not modelled	99.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative zn-dependent exopeptidase; **PDBTitle:** crystal structure of a putative zn-dependent exopeptidase (bvu_1317)2 from bacteroides vulgatus atcc 8482 at 1.80 a resolution
72	d1vgya2	Alignment	not modelled	99.1	11	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
73	c2gljR_	Alignment	not modelled	98.9	11	**PDB header:**hydrolase **Chain:** R: **PDB Molecule:** **PDBTitle:** crystal structure of aminopeptidase i from clostridium2 acetobutylicum
74	c3iibA_	Alignment	not modelled	98.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase m28; **PDBTitle:** crystal structure of peptidase m28 precursor (yp_926796.1) from2 shewanella amazonensis sb2b at 1.70 a resolution
75	d1ysja2	Alignment	not modelled	98.8	14	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
76	c2ek8A_	Alignment	not modelled	98.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase; **PDBTitle:** aminopeptidase from aneurinibacillus sp. strain am-1
77	d3bi1a3	Alignment	not modelled	98.8	26	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FolH catalytic domain-like
78	d1fnoa3	Alignment	not modelled	98.6	92	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
79	d1xmba2	Alignment	not modelled	98.3	16	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain

80	d1lfwa2	Alignment	not modelled	98.2	13	**Fold:**Ferredoxin-like **Superfamily:**Bacterial exopeptidase dimerisation domain **Family:**Bacterial exopeptidase dimerisation domain
81	d1de4c3	Alignment	not modelled	98.1	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FolH catalytic domain-like
82	c2ootA_	Alignment	not modelled	96.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutamate carboxypeptidase 2; **PDBTitle:** a high resolution structure of ligand-free human glutamate2 carboxypeptidase ii
83	c3rbuA_	Alignment	not modelled	96.7	25	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**glutamate carboxypeptidase 2; **PDBTitle:** n-terminally avitev-tagged human glutamate carboxypeptidase ii in2 complex with 2-pmpa
84	c1cx8F_	Alignment	not modelled	96.5	16	**PDB header:**metal transport **Chain:** F: **PDB Molecule:**transferrin receptor protein; **PDBTitle:** crytal structure of the ectodomain of human transferrin receptor
85	c3k9tA_	Alignment	not modelled	93.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative peptidase; **PDBTitle:** crystal structure of putative peptidase (np_348812.1) from clostridium2 acetobutylicum at 2.37 a resolution
86	c2l2qA_	Alignment	not modelled	84.0	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, cellobiose-specific iib component (cela); **PDBTitle:** solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
87	d1iiba_	Alignment	not modelled	78.8	5	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
88	d1v4na_	Alignment	not modelled	46.1	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
89	c1wtaA_	Alignment	not modelled	43.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5'-methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-deoxy-5'-methylthioadenosine from aeropyrum2 pernix (r32 form)
90	d1weka_	Alignment	not modelled	35.6	20	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
91	d1gxha_	Alignment	not modelled	32.0	17	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
92	d1wj9a2	Alignment	not modelled	28.3	13	**Fold:**Ferredoxin-like **Superfamily:**CRISPR-associated protein **Family:**CRISPR-associated protein
93	d1ayia_	Alignment	not modelled	27.8	17	**Fold:**Acyl carrier protein-like **Superfamily:**Colicin E immunity proteins **Family:**Colicin E immunity proteins
94	c3ozbF_	Alignment	not modelled	26.5	16	**PDB header:**transferase **Chain:** F: **PDB Molecule:**methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
95	c2nv2U_	Alignment	not modelled	25.7	17	**PDB header:**lyase/transferase **Chain:** U: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
96	d1jhfa1	Alignment	not modelled	23.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
97	d1sqsa_	Alignment	not modelled	21.6	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
98	c2jmkA_	Alignment	not modelled	21.3	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**hypothetical protein ta0956; **PDBTitle:** solution structure of ta0956
99	d1dfup_	Alignment	not modelled	20.9	12	**Fold:**Ribosomal protein L25-like **Superfamily:**Ribosomal protein L25-like **Family:**Ribosomal protein L25-like
100	c3femB_	Alignment	not modelled	20.6	13	**PDB header:**biosynthetic protein, transferase **Chain:** B: **PDB Molecule:**pyridoxine biosynthesis protein snz1; **PDBTitle:** structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae