Phyre^2

Email	l.a.kelley@imperial.ac.uk
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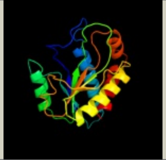
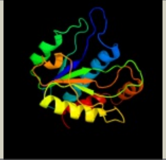
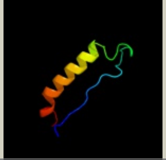
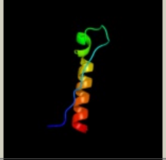
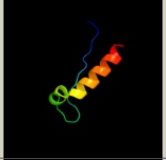
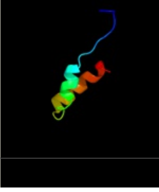
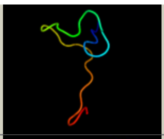
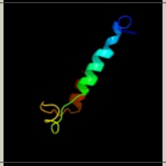
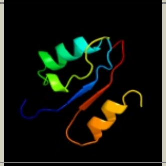
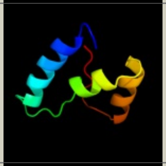
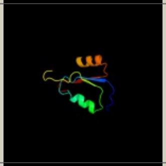
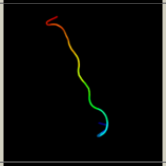
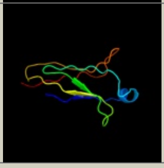
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ne8A_	Alignment		100.0	33	**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
2	d1jwqa_	Alignment		100.0	36	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**N-acetylmuramoyl-L-alanine amidase-like
3	c1xovA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ply protein; **PDBTitle:** the crystal structure of the listeria monocytogenes bacteriophage psa2 endolysin plypsa
4	c3czxA_	Alignment		100.0	20	**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
5	d1xova2	Alignment		100.0	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**N-acetylmuramoyl-L-alanine amidase-like
6	c3qayC_	Alignment		100.0	22	**PDB header:**lyase **Chain:** C: **PDB Molecule:**endolysin; **PDBTitle:** catalytic domain of cd27l endolysin targeting clostridia difficile
7	d2gfqa1	Alignment		89.2	32	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
8	c2gfqC_	Alignment		88.5	36	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**upf0204 protein ph0006; **PDBTitle:** structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
9	d1yqea1	Alignment		86.4	29	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
10	c2qvpC_	Alignment		77.2	19	**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
11	c1wwpA_	Alignment		54.9	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha0636; **PDBTitle:** crystal structure of ttk003001694 from thermus thermophilus2 hb8

12	c3fs2A_	Alignment		53.6	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate2 aldolase from bruciella melitensis at 1.85a resolution
13	d1fx0b1	Alignment		49.4	19	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
14	c1c4gB_	Alignment		49.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (alpha-d-glucose 1-phosphate **PDBTitle:** phosphoglucomutase vanadate based transition state analog2 complex
15	c2fuvB_	Alignment		44.9	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucomutase; **PDBTitle:** phosphoglucomutase from salmonella typhimurium.
16	d1nyra1	Alignment		41.3	14	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
17	c3i3wB_	Alignment		41.2	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** structure of a phosphoglucosamine mutase from francisella tularensis
18	c3k2kA_	Alignment		40.5	14	**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
19	d1kfia2	Alignment		38.7	21	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
20	d1txka1	Alignment		35.4	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
21	d2b3ya2	Alignment	not modelled	34.3	16	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
22	c3l2nA_	Alignment	not modelled	32.8	16	**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
23	c3t4cD_	Alignment	not modelled	32.6	39	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 1; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
24	c1nj2A_	Alignment	not modelled	31.5	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from methanothermobacter2 thermautotrophicus
25	c1z65A_	Alignment	not modelled	29.8	41	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**prion-like protein doppel; **PDBTitle:** mouse doppel 1-30 peptide
26	d1nj8a1	Alignment	not modelled	29.6	10	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
27	d1acoa2	Alignment	not modelled	28.7	22	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
28	d1skye1	Alignment	not modelled	28.0	13	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase

29	d1ad1a_	Alignment	not modelled	25.8	50	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
30	c2f7lA_	Alignment	not modelled	25.7	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**455aa long hypothetical phospho-sugar mutase; **PDBTitle:** crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
31	c5acnA_	Alignment	not modelled	25.1	22	**PDB header:**lyase(carbon-oxygen) **Chain:** A: **PDB Molecule:**aconitase; **PDBTitle:** structure of activated aconitase. formation of the (4fe-4s)2 cluster in the crystal
32	c2ronA_	Alignment	not modelled	24.6	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**surfactin synthetase thioesterase subunit; **PDBTitle:** the external thioesterase of the surfactin-synthetase
33	d1nj1a1	Alignment	not modelled	24.4	19	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
34	d1qm4a1	Alignment	not modelled	24.1	10	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
35	c2vf7B_	Alignment	not modelled	23.4	30	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans
36	c3l80A_	Alignment	not modelled	22.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1393c; **PDBTitle:** crystal structure of smu.1393c from streptococcus mutans ua159
37	c1k8wA_	Alignment	not modelled	22.8	64	**PDB header:**lyase/rna **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna
38	c2ae3A_	Alignment	not modelled	22.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaryl 7-aminocephalosporanic acid acylase; **PDBTitle:** glutaryl 7-aminocephalosporanic acid acylase: mutational study of2 activation mechanism
39	c3nh8A_	Alignment	not modelled	22.2	16	**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
40	d1b74a1	Alignment	not modelled	22.1	27	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
41	d1yw6a1	Alignment	not modelled	21.8	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**AstE/AspA-like
42	c3bghB_	Alignment	not modelled	21.6	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative neuraminyllactose-binding hemagglutinin homolog; **PDBTitle:** crystal structure of putative neuraminyllactose-binding hemagglutinin2 homolog from helicobacter pylori
43	d1mxaa1	Alignment	not modelled	21.3	13	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
44	c1kfiA_	Alignment	not modelled	20.9	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoglucomutase 1; **PDBTitle:** crystal structure of the exocytosis-sensitive2 phosphoprotein, pp63/parafusin (phosphoglucomutase) from3 paramecium
45	c2b3yB_	Alignment	not modelled	20.8	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**iron-responsive element binding protein 1; **PDBTitle:** structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
46	c2y5sA_	Alignment	not modelled	20.6	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
47	c3pdkB_	Alignment	not modelled	20.3	24	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** crystal structure of phosphoglucosamine mutase from b. anthracis
48	d2p02a1	Alignment	not modelled	19.9	8	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
49	d2ey4a2	Alignment	not modelled	19.6	67	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
50	d1p5dx2	Alignment	not modelled	19.2	17	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
51	c1ze2B_	Alignment	not modelled	18.6	67	**PDB header:**lyase/rna **Chain:** B: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** conformational change of pseudouridine 55 synthase upon its2 association with rna substrate
52	c2e85B_	Alignment	not modelled	18.5	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hydrogenase 3 maturation protease; **PDBTitle:** crystal structure of the hydrogenase 3 maturation protease
53	c2dzaA_	Alignment	not modelled	18.4	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate

54	d2fsja1	Alignment	not modelled	18.3	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ta0583-like
55	d2g4ca1	Alignment	not modelled	18.0	11	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
56	d1joga_	Alignment	not modelled	17.8	25	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Family 1 bi-partite nucleotidyltransferase subunit
57	c2ygrD_	Alignment	not modelled	17.4	26	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** mycobacterium tuberculosis uvra
58	d1qf6a1	Alignment	not modelled	17.3	4	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
59	d1g5ha1	Alignment	not modelled	16.9	11	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
60	c1u83A_	Alignment	not modelled	16.8	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
61	d1u83a_	Alignment	not modelled	16.8	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
62	c3ibtA_	Alignment	not modelled	16.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase; **PDBTitle:** structure of 1h-3-hydroxy-4-oxoquinoline 2,4-dioxygenase (qdo)
63	d2bodx1	Alignment	not modelled	16.7	36	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycosyl hydrolases family 6, cellulases **Family:**Glycosyl hydrolases family 6, cellulases
64	d1sgva2	Alignment	not modelled	16.5	58	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
65	c1b74A_	Alignment	not modelled	16.4	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** glutamate racemase from aquifex pyrophilus
66	c2vefB_	Alignment	not modelled	16.0	43	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** dihydropteroate synthase from streptococcus pneumoniae
67	c2vp8A_	Alignment	not modelled	15.9	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
68	d1cr5a2	Alignment	not modelled	15.9	20	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
69	d1ccwa_	Alignment	not modelled	15.8	17	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
70	d1r3ea2	Alignment	not modelled	15.8	67	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
71	d2apoa2	Alignment	not modelled	15.6	67	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
72	c1zcoA_	Alignment	not modelled	15.4	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphoheptonate aldolase; **PDBTitle:** crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
73	d1k8wa5	Alignment	not modelled	15.3	64	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
74	d1eyea_	Alignment	not modelled	15.2	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
75	d1c4xa_	Alignment	not modelled	15.2	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
76	c2jfoB_	Alignment	not modelled	14.9	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
77	c3a64A_	Alignment	not modelled	14.8	54	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** crystal structure of cccel6c, a glycoside hydrolase family 62 enzyme, from coprinopsis cinerea
78	c1tx2A_	Alignment	not modelled	14.6	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
79	d1tx2a_	Alignment	not modelled	14.6	50	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
80	c1y80A_	Alignment	not modelled	14.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted cobalamin binding protein; **PDBTitle:** structure of a corrinoid (factor iiim)-binding protein

						from2 moorella thermoacetica
81	d1wu7a1	Alignment	not modelled	14.4	13	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
82	c3uaiA_	Alignment	not modelled	14.4	50	**PDB header:**isomerase/chaperone **Chain:** A: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4; **PDBTitle:** structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
83	c2dakA_	Alignment	not modelled	14.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
84	d1dysa_	Alignment	not modelled	13.7	31	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycosyl hydrolases family 6, cellulases **Family:**Glycosyl hydrolases family 6, cellulases
85	c3na6A_	Alignment	not modelled	13.7	10	**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
86	c2gx8B_	Alignment	not modelled	13.6	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**nif3-related protein; **PDBTitle:** the crystal stucture of bacillus cereus protein related to nif3
87	d3bofa1	Alignment	not modelled	13.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
88	c2ey4A_	Alignment	not modelled	13.6	64	**PDB header:**isomerase/biosynthetic protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of a cbf5-nop10-gar1 complex
89	d1qjwa_	Alignment	not modelled	13.4	38	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycosyl hydrolases family 6, cellulases **Family:**Glycosyl hydrolases family 6, cellulases
90	c2daiA_	Alignment	not modelled	12.7	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquitin associated domain containing 1; **PDBTitle:** solution structure of the first uba domain in the human2 ubiquitin associated domain containing 1 (ubadc1)
91	c3r1jB_	Alignment	not modelled	12.5	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase; **PDBTitle:** crystal structure of alpha-ketoglutarate-dependent taurine dioxygenase2 from mycobacterium avium, native form
92	d3pmga2	Alignment	not modelled	12.5	15	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
93	c2apoA_	Alignment	not modelled	12.4	67	**PDB header:**isomerase/rna binding protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of the methanococcus jannaschii cbf52 nop10 complex
94	d1uoza_	Alignment	not modelled	12.4	25	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycosyl hydrolases family 6, cellulases **Family:**Glycosyl hydrolases family 6, cellulases
95	d1ifya_	Alignment	not modelled	12.0	18	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
96	c2jfqA_	Alignment	not modelled	11.9	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase; **PDBTitle:** crystal structure of staphylococcus aureus glutamate2 racemase in complex with d-glutamate
97	d1icxa_	Alignment	not modelled	11.9	30	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
98	d1fmfa_	Alignment	not modelled	11.8	21	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
99	d1oc7a_	Alignment	not modelled	11.8	36	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycosyl hydrolases family 6, cellulases **Family:**Glycosyl hydrolases family 6, cellulases