Phyre2

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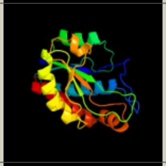
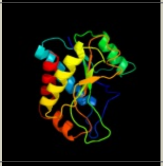
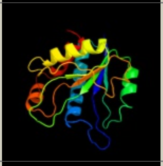
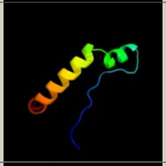
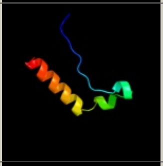
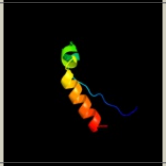
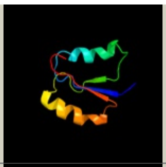
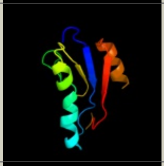
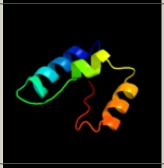
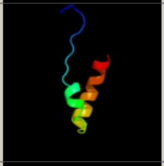
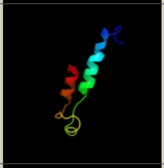
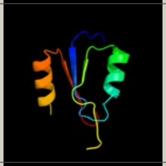
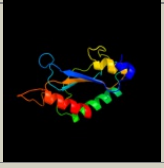
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ne8A_	Alignment		100.0	38	**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	35	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**N-acetylmuramoyl-L-alanine amidase-like
3	c1xovA_	Alignment		100.0	16	**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	21	**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	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**N-acetylmuramoyl-L-alanine amidase-like
6	c3qayC_	Alignment		100.0	25	**PDB header:**lyase **Chain:** C: **PDB Molecule:**endolysin; **PDBTitle:** catalytic domain of cd27l endolysin targeting clostridia difficile
7	d2gfqa1	Alignment		87.2	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
8	c2gfqC_	Alignment		85.0	25	**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	c2qvpC_	Alignment		84.2	15	**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
10	d1yqea1	Alignment		82.4	33	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
11	c1c4gB_	Alignment		61.5	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (alpha-d-glucose 1-phosphate **PDBTitle:** phosphoglucomutase vanadate based transition state analog2 complex

12	c2fuvB_	Alignment		58.8	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucomutase; **PDBTitle:** phosphoglucomutase from salmonella typhimurium.
13	c1wqaB_	Alignment		47.4	29	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phospho-sugar mutase; **PDBTitle:** crystal structure of pyrococcus horikoshii2 phosphomannomutase/phosphoglucomutase complexed with mg2+
14	d1nyra1	Alignment		46.0	18	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
15	c2f7lA_	Alignment		44.3	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**455aa long hypothetical phospho-sugar mutase; **PDBTitle:** crystal structure of sulfolobus tokodaii2 phosphomannomutase/phosphoglucomutase
16	c1wwpA_	Alignment		43.3	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha0636; **PDBTitle:** crystal structure of ttk003001694 from thermus thermophilus2 hb8
17	d1fx0b1	Alignment		40.8	15	**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
18	c3i3wB_	Alignment		40.6	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** structure of a phosphoglucosamine mutase from francisella tularensis
19	d1kfia2	Alignment		38.5	21	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
20	c3l2nA_	Alignment		35.9	18	**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
21	d1skye1	Alignment	not modelled	35.8	18	**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
22	d3pmga2	Alignment	not modelled	34.2	14	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
23	c3nh8A_	Alignment	not modelled	33.7	15	**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
24	c3r1jB_	Alignment	not modelled	31.3	16	**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
25	d1ad1a_	Alignment	not modelled	29.9	75	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
26	c1nj2A_	Alignment	not modelled	29.5	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from methanothermobacter2 thermautotrophicus
27	d2g4ca1	Alignment	not modelled	29.4	15	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
28	c3k2kA_	Alignment	not modelled	29.2	18	**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
29	c3bghB_	Alignment	not modelled	27.6	19	**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
30	d1wu7a1	Alignment	not modelled	24.5	18	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
31	d1nj8a1	Alignment	not modelled	24.3	16	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
32	d1nj1a1	Alignment	not modelled	23.8	22	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
33	c2y5sA_	Alignment	not modelled	23.8	63	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
34	d1qf6a1	Alignment	not modelled	23.0	7	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
35	d1g5ha1	Alignment	not modelled	22.4	17	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
36	c3l80A_	Alignment	not modelled	21.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.1393c; **PDBTitle:** crystal structure of smu.1393c from streptococcus mutans ua159
37	c2dzaA_	Alignment	not modelled	21.5	63	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
38	d1p5dx2	Alignment	not modelled	21.5	34	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
39	d1kija1	Alignment	not modelled	20.2	13	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
40	d1u83a_	Alignment	not modelled	18.9	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
41	c1u83A_	Alignment	not modelled	18.9	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
42	d1eyea_	Alignment	not modelled	18.7	44	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
43	c1kfiA_	Alignment	not modelled	18.4	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphoglucomutase 1; **PDBTitle:** crystal structure of the exocytosis-sensitive2 phosphoprotein, pp63/parafusin (phosphoglucomutase) from3 paramecium
44	c2vp8A_	Alignment	not modelled	18.1	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
45	c2ae3A_	Alignment	not modelled	17.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaryl 7-aminocephalosporanic acid acylase; **PDBTitle:** glutaryl 7-aminocephalosporanic acid acylase: mutational study of2 activation mechanism
46	c2ronA_	Alignment	not modelled	17.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**surfactin synthetase thioesterase subunit; **PDBTitle:** the external thioesterase of the surfactin-synthetase
47	c2gx8B_	Alignment	not modelled	17.8	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**nif3-related protein; **PDBTitle:** the crystal stucture of bacillus cereus protein related to nif3
48	d1tx2a_	Alignment	not modelled	17.8	47	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
49	c1tx2A_	Alignment	not modelled	17.8	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
50	d2b3ya2	Alignment	not modelled	17.5	20	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
51	c2e85B_	Alignment	not modelled	17.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hydrogenase 3 maturation protease; **PDBTitle:** crystal structure of the hydrogenase 3 maturation protease
52	c3ibtA_	Alignment	not modelled	16.4	18	**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)
53	d1ei1a1	Alignment	not modelled	15.7	19	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain

54	c1k8wA_	Alignment	not modelled	15.6	55	**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
55	d1ccwa_	Alignment	not modelled	15.4	17	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
56	c2vf7B_	Alignment	not modelled	15.4	28	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans
57	d2gx8a1	Alignment	not modelled	14.7	23	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
58	c1ze2B_	Alignment	not modelled	14.5	58	**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
59	c3netB_	Alignment	not modelled	14.2	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**histidyl-trna synthetase; **PDBTitle:** crystal structure of histidyl-trna synthetase from nostoc sp. pcc 7120
60	c3t4cD_	Alignment	not modelled	14.0	21	**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
61	d1qe0a1	Alignment	not modelled	13.7	13	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
62	c3cwvB_	Alignment	not modelled	13.7	3	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase, b subunit, truncated; **PDBTitle:** crystal structure of b-subunit of the dna gyrase from myxococcus2 xanthus
63	c2qj8B_	Alignment	not modelled	13.6	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mlr6093 protein; **PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
64	d3bula2	Alignment	not modelled	13.4	17	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
65	c2i4lC_	Alignment	not modelled	13.2	11	**PDB header:**ligase **Chain:** C: **PDB Molecule:**proline-trna ligase; **PDBTitle:** rhodopseudomonas palustris prolyl-trna synthetase
66	c5acnA_	Alignment	not modelled	13.2	20	**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
67	d1c4xa_	Alignment	not modelled	13.0	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
68	c2yxbA_	Alignment	not modelled	12.9	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
69	d1acoa2	Alignment	not modelled	12.8	20	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
70	d2bodx1	Alignment	not modelled	12.7	29	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycosyl hydrolases family 6, cellulases **Family:**Glycosyl hydrolases family 6, cellulases
71	d2fsja1	Alignment	not modelled	12.4	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ta0583-like
72	d1joga_	Alignment	not modelled	12.3	25	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Family 1 bi-partite nucleotidyltransferase subunit
73	d1cr5a2	Alignment	not modelled	12.2	21	**Fold:**Cdc48 domain 2-like **Superfamily:**Cdc48 domain 2-like **Family:**Cdc48 domain 2-like
74	c2wj4B_	Alignment	not modelled	11.9	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1h-3-hydroxy-4-oxoquinaldine 2,4-dioxygenase; **PDBTitle:** crystal structure of the cofactor-devoid 1-h-3-hydroxy-4-2 oxoquinaldine 2,4-dioxygenase (hod) from arthrobacter3 nitroguajacolicus ru61a anaerobically complexed with its4 natural substrate 1-h-3-hydroxy-4-oxoquinaldine
75	d2ey4a2	Alignment	not modelled	11.8	55	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
76	c1g5hA_	Alignment	not modelled	11.5	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mitochondrial dna polymerase accessory subunit; **PDBTitle:** crystal structure of the accessory subunit of murine mitochondrial2 polymerase gamma
77	d1kjna_	Alignment	not modelled	11.4	20	**Fold:**Hypothetical protein MTH777 (MT0777) **Superfamily:**Hypothetical protein MTH777 (MT0777) **Family:**Hypothetical protein MTH777 (MT0777)
78	d1ifya_	Alignment	not modelled	11.3	12	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
						PDB header:hydrolase

79	c3cdxB_	Alignment	not modelled	11.2	20	**Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase; **PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
80	c3lnuA_	Alignment	not modelled	11.1	6	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit b; **PDBTitle:** crystal structure of pare subunit
81	d2fywa1	Alignment	not modelled	10.9	28	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
82	c3dyvA_	Alignment	not modelled	10.9	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase d; **PDBTitle:** snapshots of esterase d from lactobacillus rhamnosus:2 insights into a rotation driven catalytic mechanism
83	c2b3yB_	Alignment	not modelled	10.9	20	**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)
84	d1sgva2	Alignment	not modelled	10.8	55	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
85	d1uoza_	Alignment	not modelled	10.4	31	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycosyl hydrolases family 6, cellulases **Family:**Glycosyl hydrolases family 6, cellulases
86	d1uuqa_	Alignment	not modelled	10.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
87	c1uz4A_	Alignment	not modelled	10.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**man5a; **PDBTitle:** common inhibition of beta-glucosidase and beta-mannosidase2 by isofagomine lactam reflects different conformational3 intineraries for glucoside and mannoside hydrolysis
88	d2apoa2	Alignment	not modelled	10.3	55	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
89	d1k8wa5	Alignment	not modelled	10.0	55	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
90	d1r3ea2	Alignment	not modelled	10.0	64	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
91	c3qvmA_	Alignment	not modelled	10.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**olei00960; **PDBTitle:** the structure of olei00960, a hydrolase from oleispira antarctica
92	c2dlnA_	Alignment	not modelled	9.9	18	**PDB header:**ligase(peptidoglycan synthesis) **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution
93	c3a64A_	Alignment	not modelled	9.8	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** crystal structure of cccel6c, a glycoside hydrolase family 62 enzyme, from coprinopsis cinerea
94	c2i9oA_	Alignment	not modelled	9.7	21	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**mhb8a peptide; **PDBTitle:** design of bivalent miniprotein consisting of two2 independent elements, a b-hairpin peptide and a-helix3 peptide, tethered by eight glycines
95	c2daiA_	Alignment	not modelled	9.5	16	**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)
96	c1y37A_	Alignment	not modelled	9.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fluoroacetate dehalogenase; **PDBTitle:** structure of fluoroacetate dehalogenase from burkholderia sp. fa1
97	c1y80A_	Alignment	not modelled	9.4	22	**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
98	d1s16a1	Alignment	not modelled	9.4	10	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**DNA gyrase/MutL, second domain
99	c3pdkB_	Alignment	not modelled	9.3	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**phosphoglucosamine mutase; **PDBTitle:** crystal structure of phosphoglucosamine mutase from b. anthracis