Phyre2

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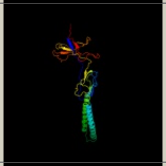
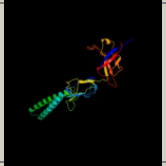
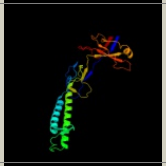
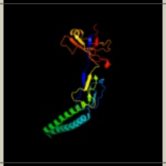
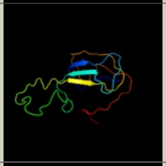
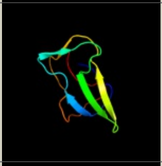
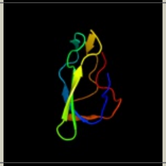
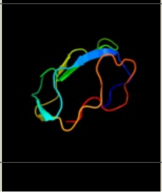
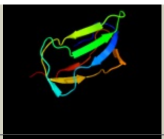
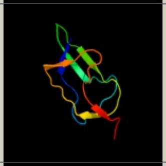
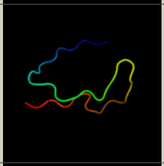
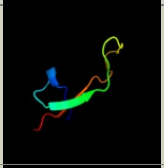
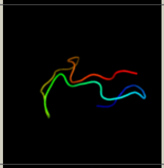
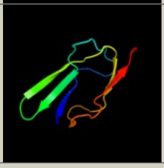
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2f1mA_	Alignment		100.0	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein a; **PDBTitle:** conformational flexibility in the multidrug efflux system protein acra
2	c3fppB_	Alignment		100.0	22	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**macrolide-specific efflux protein maca; **PDBTitle:** crystal structure of e.coli maca
3	c3lnnB_	Alignment		100.0	21	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**membrane fusion protein (mfp) heavy metal cation efflux **PDBTitle:** crystal structure of zneb from cupriavidus metallidurans
4	c1t5eB_	Alignment		99.9	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multidrug resistance protein mexa; **PDBTitle:** the structure of mexa
5	d1vf7a_	Alignment		99.9	21	**Fold:**HlyD-like secretion proteins **Superfamily:**HlyD-like secretion proteins **Family:**HlyD-like secretion proteins
6	c3h9iB_	Alignment		99.9	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cation efflux system protein cusb; **PDBTitle:** crystal structure of the membrane fusion protein cusb from escherichia2 coli
7	c2k33A_	Alignment		99.5	32	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**acra; **PDBTitle:** solution structure of an n-glycosylated protein using in2 vitro glycosylation
8	c2b8gA_	Alignment		98.3	27	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**biotin/lipoyl attachment protein; **PDBTitle:** solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
9	d1dcza_	Alignment		98.2	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
10	c2ejgD_	Alignment		98.1	24	**PDB header:**ligase **Chain:** D: **PDB Molecule:**149aa long hypothetical methylmalonyl-coa decarboxylase **PDBTitle:** crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
11	d1o78a_	Alignment		98.1	33	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains

12	c2ejmA_	Alignment		97.8	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methylcrotonoyl-coa carboxylase subunit alpha; **PDBTitle:** solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase
13	d1qjoa_	Alignment		97.4	29	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
14	c3n6rK_	Alignment		97.4	38	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
15	c2dn8A_	Alignment		97.4	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
16	c2l5tA_	Alignment		97.4	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase; **PDBTitle:** solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
17	d1iyua_	Alignment		97.4	14	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
18	c2kccA_	Alignment		97.3	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
19	d1bdoa_	Alignment		97.3	27	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
20	d1y8ob1	Alignment		97.2	32	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
21	d1k8ma_	Alignment	not modelled	97.1	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
22	d1ghja_	Alignment	not modelled	97.1	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
23	d1gjxa_	Alignment	not modelled	96.7	14	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
24	d1laba_	Alignment	not modelled	96.7	35	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
25	d1pmra_	Alignment	not modelled	96.6	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
26	d2pnrc1	Alignment	not modelled	96.4	15	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
27	c2q8iB_	Alignment	not modelled	96.3	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase component of **PDBTitle:** pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
28	d1glaf_	Alignment	not modelled	96.2	29	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
29	d2gpra_	Alignment	not modelled	96.1	39	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like

30	d1gpra_	Alignment	not modelled	96.1	29	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
31	d1uoua3	Alignment	not modelled	96.1	8	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
32	c2qf7A_	Alignment	not modelled	96.1	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
33	c2dncA_	Alignment	not modelled	96.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase protein x component; **PDBTitle:** solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
34	d2f3ga_	Alignment	not modelled	95.9	29	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
35	c2dneA_	Alignment	not modelled	95.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase
36	c2jkuA_	Alignment	not modelled	95.5	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**propionyl-coa carboxylase alpha chain, **PDBTitle:** crystal structure of the n-terminal region of the biotin2 acceptor domain of human propionyl-coa carboxylase
37	d2tpta3	Alignment	not modelled	95.3	20	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
38	c2dsjA_	Alignment	not modelled	94.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
39	d1brwa3	Alignment	not modelled	94.9	25	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
40	c3h5qA_	Alignment	not modelled	94.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
41	c2j0fC_	Alignment	not modelled	93.9	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
42	c1otpA_	Alignment	not modelled	93.8	20	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
43	c2hsiB_	Alignment	not modelled	92.1	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative peptidase m23; **PDBTitle:** crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
44	c2gu1A_	Alignment	not modelled	91.9	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
45	c1brwB_	Alignment	not modelled	90.2	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
46	d1qwya_	Alignment	not modelled	89.9	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Peptidoglycan hydrolase LytM
47	c2aukA_	Alignment	not modelled	89.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of e. coli rna polymerase beta' g/g' insert
48	c2qj8B_	Alignment	not modelled	88.5	9	**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
49	c3fmcC_	Alignment	not modelled	87.4	8	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative succinylglutamate desuccinylase / aspartoacylase; **PDBTitle:** crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
50	c3na6A_	Alignment	not modelled	86.5	15	**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
51	d1e2wa2	Alignment	not modelled	86.0	31	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
52	d1ci3m2	Alignment	not modelled	85.8	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
53	c2b44A_	Alignment	not modelled	84.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycyl-glycine endopeptidase lytm;

						PDBTitle: truncated s. aureus lytm, p 32 2 1 crystal form
54	d1qpoa2	Alignment	not modelled	84.8	29	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
55	c3cdxB_	Alignment	not modelled	82.2	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase; **PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
56	c2xhaB_	Alignment	not modelled	80.9	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of domain 2 of thermotoga maritima n-utilization2 substance g (nusg)
57	d1o4ua2	Alignment	not modelled	80.7	17	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
58	c3it5B_	Alignment	not modelled	80.5	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protease lasa; **PDBTitle:** crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
59	c3d4rE_	Alignment	not modelled	79.6	21	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**domain of unknown function from the pfam-b_34464 family; **PDBTitle:** crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution
60	d1qapa2	Alignment	not modelled	78.3	19	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
61	c2aujD_	Alignment	not modelled	74.5	28	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of thermus aquaticus rna polymerase beta'-subunit2 insert
62	c3nyyA_	Alignment	not modelled	74.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycyl-glycine endopeptidase lytm; **PDBTitle:** crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
63	c2xhcA_	Alignment	not modelled	74.3	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
64	c1e2vB_	Alignment	not modelled	72.4	31	**PDB header:**electron transport proteins **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** n153q mutant of cytochrome f from chlamydomonas reinhardtii
65	c1ctmA_	Alignment	not modelled	72.3	25	**PDB header:**electron transport(cytochrome) **Chain:** A: **PDB Molecule:**cytochrome f; **PDBTitle:** crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
66	c2jxmB_	Alignment	not modelled	72.2	31	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
67	c3gnnA_	Alignment	not modelled	69.9	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
68	c1tu2B_	Alignment	not modelled	69.7	31	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**apocytochrome f; **PDBTitle:** the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
69	c1q90A_	Alignment	not modelled	68.8	31	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**apocytochrome f; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
70	c2e75C_	Alignment	not modelled	65.8	38	**PDB header:**photosynthesis **Chain:** C: **PDB Molecule:**apocytochrome f; **PDBTitle:** crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
71	c3csqC_	Alignment	not modelled	64.8	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
72	d1tu2b2	Alignment	not modelled	64.0	31	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
73	c1o4uA_	Alignment	not modelled	63.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type ii quinolic acid phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
74	c3pajA_	Alignment	not modelled	60.5	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase, carboxylating; **PDBTitle:** 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
75	c1qapA_	Alignment	not modelled	59.4	22	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**quinolinic acid phosphoribosyltransferase; **PDBTitle:** quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid

76	c3tqvA_	Alignment	not modelled	57.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
77	c3l0gD_	Alignment	not modelled	57.2	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
78	c1qpoA_	Alignment	not modelled	55.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**quinolinate acid phosphoribosyl transferase; **PDBTitle:** quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
79	c2b7pA_	Alignment	not modelled	54.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
80	d1hcza2	Alignment	not modelled	52.6	25	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
81	c1x1oC_	Alignment	not modelled	48.8	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of project id tt0268 from thermus thermophilus hb8
82	c3iftA_	Alignment	not modelled	47.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
83	d1onla_	Alignment	not modelled	46.2	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
84	c2edgA_	Alignment	not modelled	45.3	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** solution structure of the gcv_h domain from mouse glycine
85	c3mxuA_	Alignment	not modelled	36.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from bartonella2 henselae
86	d1hpca_	Alignment	not modelled	35.7	19	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
87	c2jbmA_	Alignment	not modelled	34.3	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** qprtase structure from human
88	d1vf5c2	Alignment	not modelled	34.0	38	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
89	c3a8jF_	Alignment	not modelled	29.9	16	**PDB header:**transferase/transport protein **Chain:** F: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of et-ehred complex
90	d2je6i2	Alignment	not modelled	26.5	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
91	d1whla_	Alignment	not modelled	26.2	10	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
92	c3hd7A_	Alignment	not modelled	25.6	17	**PDB header:**exocytosis **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 2; **PDBTitle:** helical extension of the neuronal snare complex into the membrane,2 spacegroup c 1 2 1
93	d1h9ra2	Alignment	not modelled	25.4	10	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
94	c3tbiB_	Alignment	not modelled	22.2	36	**PDB header:**transcription **Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of t4 gp33 bound to e. coli rnap beta-flap domain
95	d1h9ra1	Alignment	not modelled	21.2	15	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**BiMOP, duplicated molybdate-binding domain
96	c2ka7A_	Alignment	not modelled	21.0	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** nmr solution structure of tm0212 at 40 c
97	d1udxa3	Alignment	not modelled	20.9	26	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
98	d1uwfa1	Alignment	not modelled	19.6	17	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Pilus subunits
99	d1krha1	Alignment	not modelled	19.3	29	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like