Phyre^2

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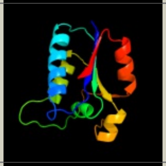
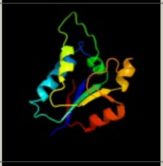
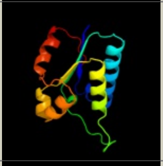
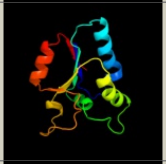
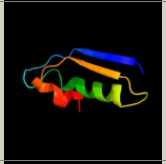
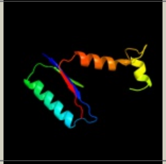
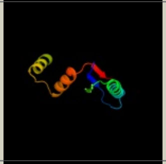
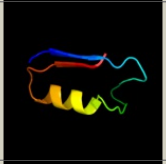
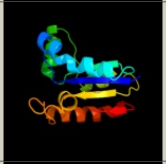
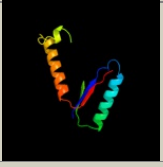
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jx7a_	Alignment		100.0	98	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
2	d2hy5a1	Alignment		100.0	22	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
3	d2d1pa1	Alignment		100.0	24	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
4	d2hy5b1	Alignment		100.0	23	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
5	d2d1pb1	Alignment		99.9	23	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
6	c3mc3A_	Alignment		99.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dsre/dsrf-like family protein; **PDBTitle:** crystal structure of dsre/dsrf-like family protein (np_342589.1) from2 sulfolobus solfataricus at 1.49 a resolution
7	c2qs7D_	Alignment		99.8	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative oxidoreductase of the dsre/dsrf-like2 family (sso1126) from sulfolobus solfataricus p2 at 2.09 a resolution
8	c3pnxF_	Alignment		99.7	21	**PDB header:**transferase **Chain:** F: **PDB Molecule:**putative sulfurtransferase dsre; **PDBTitle:** crystal structure of a putative sulfurtransferase dsre (swol_2425)2 from syntrophomonas wolfei str. goettingen at 1.92 a resolution
9	d2hy5c1	Alignment		99.4	24	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrH-like
10	c2fb6A_	Alignment		99.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** structure of conserved protein of unknown function bt1422 from2 bacteroides thetaiotaomicron
11	d1l1sa_	Alignment		99.1	13	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like

12	c2pd2A_	Alignment		99.1	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein st0148; **PDBTitle:** crystal structure of (st0148) conserved hypothetical from sulfolobus2 tokodaii strain7
13	d2d1pc1	Alignment		98.8	22	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrH-like
14	d1x9aa_	Alignment		98.3	21	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrH-like
15	c3ia7A_	Alignment		88.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
16	d1t5ba_	Alignment		88.0	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
17	d1qrda_	Alignment		84.5	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
18	c2r60A_	Alignment		82.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
19	d1qgoa_	Alignment		80.3	20	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Cobalt chelatase CbiK
20	d2z98a1	Alignment		74.3	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
21	d1rtta_	Alignment	not modelled	70.3	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
22	c2ejbA_	Alignment	not modelled	69.1	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
23	c1gshA_	Alignment	not modelled	59.0	16	**PDB header:**glutathione biosynthesis ligase **Chain:** A: **PDB Molecule:**glutathione biosynthetic ligase; **PDBTitle:** structure of escherichia coli glutathione synthetase at ph 7.5
24	c3lcmB_	Alignment	not modelled	58.6	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
25	d1f0ka_	Alignment	not modelled	54.6	22	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
26	d1u7za_	Alignment	not modelled	52.8	15	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
27	d1gsaa1	Alignment	not modelled	51.0	19	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Prokaryotic glutathione synthetase, N-terminal domain
28	d2afhe1	Alignment	not modelled	47.2	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
						PDB header:transferase

29	c3iaaB_	Alignment	not modelled	45.4	9	**Chain:** B: **PDB Molecule:**calg2; **PDBTitle:** crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form
30	c3c1oA_	Alignment	not modelled	43.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**eugenol synthase; **PDBTitle:** the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
31	c2iyfA_	Alignment	not modelled	43.2	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
32	d1xbta1	Alignment	not modelled	41.0	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Type II thymidine kinase
33	c2q3eH_	Alignment	not modelled	38.9	12	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
34	c2x0dA_	Alignment	not modelled	37.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wsaf; **PDBTitle:** apo structure of wsaf
35	d1pn3a_	Alignment	not modelled	34.9	27	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
36	d1p9oa_	Alignment	not modelled	34.8	24	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
37	c2iyaB_	Alignment	not modelled	34.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**oleandomycin glycosyltransferase; **PDBTitle:** the crystal structure of macrolide glycosyltransferases: a2 blueprint for antibiotic engineering
38	d1b93a_	Alignment	not modelled	34.0	16	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
39	c3dzcA_	Alignment	not modelled	32.3	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
40	c3okaA_	Alignment	not modelled	29.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gdp-mannose-dependent alpha-(1-6)-phosphatidylinositol **PDBTitle:** crystal structure of corynebacterium glutamicum pimb' in complex with2 gdp-man (triclinic crystal form)
41	c3prjB_	Alignment	not modelled	29.0	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
42	c3othB_	Alignment	not modelled	28.5	12	**PDB header:**transferase/antibiotic **Chain:** B: **PDB Molecule:**calg1; **PDBTitle:** crystal structure of calg1, calicheamicin glycostyltransferase, tdp2 and calicheamicin alpha3i bound form
43	d1vmda_	Alignment	not modelled	27.3	18	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
44	d1ihua1	Alignment	not modelled	27.3	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
45	d1g3qa_	Alignment	not modelled	26.0	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
46	c3l8hC_	Alignment	not modelled	26.0	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of d,d-heptose 1.7-bisphosphate phosphatase from b.2 bronchiseptica complexed with magnesium and phosphate
47	d2qwxa1	Alignment	not modelled	25.1	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
48	c2gk4A_	Alignment	not modelled	25.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** the crystal structure of the dna/pantothenate metabolism flavoprotein2 from streptococcus pneumoniae
49	d1wzca1	Alignment	not modelled	24.5	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
50	c3oy2A_	Alignment	not modelled	24.4	13	**PDB header:**viral protein,transferase **Chain:** A: **PDB Molecule:**glycosyltransferase b736l; **PDBTitle:** crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
51	c2bekB_	Alignment	not modelled	24.3	17	**PDB header:**chromosome segregation **Chain:** B: **PDB Molecule:**segregation protein; **PDBTitle:** structure of the bacterial chromosome segregation protein2 soj
52	c3mt0A_	Alignment	not modelled	24.2	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pa1789; **PDBTitle:** the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
53	c1hyqA_	Alignment	not modelled	24.1	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division inhibitor (mind-1); **PDBTitle:** mind bacterial cell division regulator from a. fulgidus
54	d1hyqa_	Alignment	not modelled	24.1	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases

						Family: Nitrogenase iron protein-like
55	d1p3y1_	Alignment	not modelled	23.7	14	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
56	c3qjgD_	Alignment	not modelled	23.4	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**epidermin biosynthesis protein epid; **PDBTitle:** epidermin biosynthesis protein epid from staphylococcus aureus
57	c1zcoA_	Alignment	not modelled	23.2	16	**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
58	c3rpeA_	Alignment	not modelled	22.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**modulator of drug activity b; **PDBTitle:** 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92.
59	d1l7da2	Alignment	not modelled	22.6	24	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**L-alanine dehydrogenase-like
60	c2xvzA_	Alignment	not modelled	21.9	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**chelatase, putative; **PDBTitle:** cobalt chelatase cbik (periplasmatic) from desulvobrio2 vulgaris hildenborough (co-crystallized with cobalt)
61	c2p6pB_	Alignment	not modelled	21.9	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase; **PDBTitle:** x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
62	d1pjca1	Alignment	not modelled	20.9	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
63	c2gejA_	Alignment	not modelled	20.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol mannosyltransferase (pima); **PDBTitle:** crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
64	c3fozB_	Alignment	not modelled	20.4	17	**PDB header:**transferase/rna **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate transferase; **PDBTitle:** structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
65	d1nrwa_	Alignment	not modelled	20.4	11	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
66	d2vgna3	Alignment	not modelled	19.9	10	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
67	c2o3jC_	Alignment	not modelled	19.7	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** structure of caenorhabditis elegans udp-glucose dehydrogenase
68	d1n1ea2	Alignment	not modelled	19.6	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
69	c2jugB_	Alignment	not modelled	19.5	10	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**tubc protein; **PDBTitle:** multienzyme docking in hybrid megasynthetases
70	c3l12A_	Alignment	not modelled	19.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycerophosphoryl diester phosphodiesterase; **PDBTitle:** crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (yp_165505.1) from silicibacter pomeroyi dss-3 at3 1.60 a resolution
71	c3niwA_	Alignment	not modelled	19.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron
72	c3fzqA_	Alignment	not modelled	18.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
73	d1x52a1	Alignment	not modelled	18.7	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**ERF1/Dom34 C-terminal domain-like
74	d1iira_	Alignment	not modelled	18.6	16	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
75	c3dhnA_	Alignment	not modelled	18.6	19	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
76	d1dxqa_	Alignment	not modelled	18.1	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
77	c2yvuA_	Alignment	not modelled	18.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable adenylyl-sulfate kinase; **PDBTitle:** crystal structure of ape1195
78	d2b8ea1	Alignment	not modelled	17.8	8	**Fold:**HAD-like **Superfamily:**HAD-like

						Family: Meta-cation ATPase, catalytic domain P
79	c2hx1D_	Alignment	not modelled	17.7	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted sugar phosphatases of the had **PDBTitle:** crystal structure of possible sugar phosphatase, had2 superfamily (zp_00311070.1) from cytophaga hutchinsonii3 atcc 33406 at 2.10 a resolution
80	d1nmpa_	Alignment	not modelled	16.8	12	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
81	d1rzua_	Alignment	not modelled	16.8	18	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Glycosyl transferases group 1
82	c2rirA_	Alignment	not modelled	16.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
83	c3dnpA_	Alignment	not modelled	16.6	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**stress response protein yhax; **PDBTitle:** crystal structure of stress response protein yhax from bacillus2 subtilis
84	d1xpja_	Alignment	not modelled	16.4	7	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
85	d1tjna_	Alignment	not modelled	16.2	5	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**CbiX-like
86	c1tjnA_	Alignment	not modelled	16.2	5	**PDB header:**lyase **Chain:** A: **PDB Molecule:**sirohydrochlorin cobaltochelatase; **PDBTitle:** crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
87	c3d0qB_	Alignment	not modelled	16.1	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein calg3; **PDBTitle:** crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
88	c3fvwA_	Alignment	not modelled	16.0	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nad(p)h-dependent fmn reductase; **PDBTitle:** crystal structure of the q8dwd8_strmu protein from2 streptococcus mutans. northeast structural genomics3 consortium target smr99.
89	c3crqA_	Alignment	not modelled	15.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** structure of trna dimethylallyltransferase: rna2 modification through a channel
90	d1g5ta_	Alignment	not modelled	15.2	7	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
91	c3c4vB_	Alignment	not modelled	15.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**predicted glycosyltransferases; **PDBTitle:** structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
92	c1gpjA_	Alignment	not modelled	14.5	19	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri
93	d1jfla1	Alignment	not modelled	14.5	14	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
94	c3no3A_	Alignment	not modelled	14.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerophosphodiester phosphodiesterase; **PDBTitle:** crystal structure of a glycerophosphodiester phosphodiesterase2 (bdi_0402) from parabacteroides distasonis atcc 8503 at 1.89 a3 resolution
95	c3d4oA_	Alignment	not modelled	14.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit a; **PDBTitle:** crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
96	d1q77a_	Alignment	not modelled	13.7	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**Universal stress protein-like
97	c2vedA_	Alignment	not modelled	13.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**membrane protein capa1, protein tyrosine kinase; **PDBTitle:** crystal structure of the chimerical mutant capabk55m2 protein
98	c3ouzA_	Alignment	not modelled	13.6	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
99	d1cp2a_	Alignment	not modelled	13.4	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like