Phyre^2

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Description	RVBD2226_(-)_2498840_2500381
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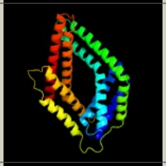
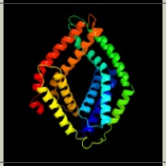
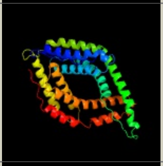
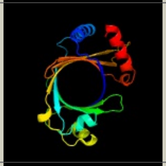
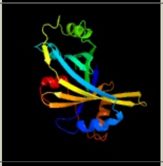
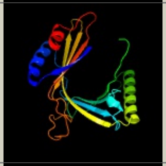
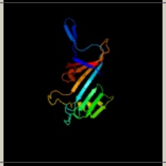
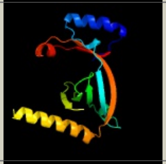
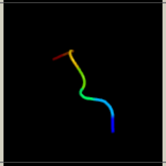
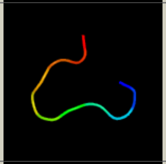
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5a61A_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic triphosphatase; **PDBTitle:** crystal structure of full-length e. coli ygif in complex2 with tripolyphosphate and two manganese ions.
2	c6rn5A_	Alignment		100.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**chad domain protein; **PDBTitle:** ppta from streptomyces chartreusis
3	c3e0sA_	Alignment		100.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from chlorobium2 tepidum
4	c6qv5A_	Alignment		100.0	22	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**chad domain; **PDBTitle:** crystal structure of the chad domain from the plant ricinus communis
5	c2gfgB_	Alignment		99.9	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**bh2851; **PDBTitle:** crystal structure of a putative adenylate cyclase (bh2851) from2 bacillus halodurans at 2.12 a resolution
6	c3sy3D_	Alignment		99.9	21	**PDB header:**lyase **Chain:** D: **PDB Molecule:**gbaa_1210 protein; **PDBTitle:** gbaa_1210 protein, a putative adenylate cyclase, from bacillus2 anthracis
7	d2jmua1	Alignment		99.8	21	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**CYTH domain
8	c3v85A_	Alignment		99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyth-like phosphatase; **PDBTitle:** 1.9 angstrom resolution crystal structure of the protein q9siy3 from2 arabidopsis thaliana
9	c2fjtA_	Alignment		99.7	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylyl cyclase class iv; **PDBTitle:** adenylyl cyclase class iv from yersinia pestis
10	d2acaa1	Alignment		99.7	15	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**CYTH domain
11	c2dc4A_	Alignment		99.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**165aa long hypothetical protein; **PDBTitle:** structure of ph1012 protein from pyrococcus horikoshii ot3

12	d1yema_	Alignment		99.5	18	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**CYTH domain
13	c2eenA_	Alignment		99.4	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1819; **PDBTitle:** structure of ph1819 protein from pyrococcus horikoshii ot3
14	c3g3rA_	Alignment		97.2	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**vacuolar transporter chaperone 4; **PDBTitle:** crystal structure of a eukaryotic polyphosphate polymerase2 in complex with appnhp-mn2+
15	d2fbla1	Alignment		97.1	25	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**CYTH domain
16	c3g3oA_	Alignment		96.6	22	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**vacuolar transporter chaperone 2; **PDBTitle:** crystal structure of the cytoplasmic tunnel domain in yeast2 vtc2p
17	c5iiqA_	Alignment		96.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**vacuolar transporter chaperone 4; **PDBTitle:** structure of the spx-ttm domain fragment of the yeast inorganic2 polyphophate polymerase vtc4 (form b).
18	c3oq0D_	Alignment		26.3	43	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**dbf4; **PDBTitle:** crystal structure of motif n of saccharomyces cerevisiae dbf4
19	c5utvA_	Alignment		18.9	55	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**papain-like proteinase; **PDBTitle:** sars-unique fold in the rousettus bat coronavirus hku9
20	d2es7a1	Alignment		14.9	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**HyaE-like
21	c6g2jY_	Alignment	not modelled	14.3	33	**PDB header:**oxidoreductase **Chain:** Y: **PDB Molecule:**mcg5603; **PDBTitle:** mouse mitochondrial complex i in the active state
22	c3dboA_	Alignment	not modelled	13.6	18	**PDB header:**toxin/antitoxin **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a member of the vapbc family of toxin-antitoxin2 systems, vapbc-5, from mycobacterium tuberculosis
23	d1jh6a_	Alignment	not modelled	13.5	16	**Fold:**LigT-like **Superfamily:**LigT-like **Family:**tRNA splicing product Appr>p cyclic nucleotide phosphodiesterase
24	c5d55A_	Alignment	not modelled	13.4	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**hdab,hdaa (adhesin), hus-associated diffuse adherence; **PDBTitle:** crystal structure of the e. coli hda pilus minor tip subunit, hdab
25	c4q88B_	Alignment	not modelled	12.7	30	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** glycosyl hydrolase family 88 from bacteroides vulgatus
26	c3f3bA_	Alignment	not modelled	12.7	67	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phage-like element pbsx protein xkdh; **PDBTitle:** structure of the phage-like element pbsx protein xkdh from bacillus2 subtilus. northeast structural genomics consortium target sr352.
27	c5tv7A_	Alignment	not modelled	12.5	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative peptidoglycan-binding/hydrolysing protein; **PDBTitle:** 2.05 angstrom resolution crystal structure of peptidoglycan-binding2 protein from clostridioides difficile in complex with glutamine3 hydroxamate.
						PDB header:transferase/transferase inhibitor

28	c6ntwA_	Alignment	not modelled	12.3	15	**Chain:** A: **PDB Molecule:**probable l,d-transpeptidase ycbb; **PDBTitle:** crystal structure of e. coli ycbb
29	c5y2vA_	Alignment	not modelled	12.2	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rubisco operon transcriptional regulator; **PDBTitle:** strcutrue of the full-length ccmr complexed with 2-og from2 synechocystis pcc6803
30	d1lk3a_	Alignment	not modelled	11.9	9	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
31	d1vlka_	Alignment	not modelled	11.3	8	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Interferons/interleukin-10 (IL-10)
32	c3f1iH_	Alignment	not modelled	11.1	17	**PDB header:**protein binding **Chain:** H: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** human escrt-0 core complex
33	c2ymbB_	Alignment	not modelled	11.0	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**mit domain-containing protein 1; **PDBTitle:** structures of mitd1
34	c5noaA_	Alignment	not modelled	10.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**family 88 glycosyl hydrolase; **PDBTitle:** polysaccharide lyase baccell_00875
35	c3fbiC_	Alignment	not modelled	10.6	0	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mediator of rna polymerase ii transcription **PDBTitle:** structure of the mediator submodule med7n/31
36	c5wfbB_	Alignment	not modelled	10.6	9	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**ap-4 complex accessory subunit tepsin; **PDBTitle:** tepsin tenth domain 1-136.
37	d1ka5a_	Alignment	not modelled	10.4	15	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
38	c2zw2B_	Alignment	not modelled	10.1	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
39	c6q2zB_	Alignment	not modelled	9.4	22	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0339 family protein; **PDBTitle:** nmr solution structure of the hvo_2922 protein from haloferax volcanii
40	c5lopC_	Alignment	not modelled	9.4	30	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**klla0a11308p; **PDBTitle:** structure of the active form of /k. lactis/ dcp1-dcp2-edc3 decapping2 complex bound to m7gdp
41	d2jeka1	Alignment	not modelled	9.4	8	**Fold:**Rv1873-like **Superfamily:**Rv1873-like **Family:**Rv1873-like
42	c1fftG_	Alignment	not modelled	9.2	18	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli
43	d1qr5a_	Alignment	not modelled	9.1	13	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
44	c3k11A_	Alignment	not modelled	9.1	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative glycosyl hydrolase; **PDBTitle:** crystal structure of putative glycosyl hydrolase (np_813087.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.80 a resolution
45	d1zsqa2	Alignment	not modelled	9.0	26	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Myotubularin-like phosphatases
46	d2nzul1	Alignment	not modelled	8.9	15	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
47	c5ldwY_	Alignment	not modelled	8.9	50	**PDB header:**oxidoreductase **Chain:** Y: **PDB Molecule:**nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit **PDBTitle:** structure of mammalian respiratory complex i, class1
48	c3r1fO_	Alignment	not modelled	8.7	18	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
49	c2y9xG_	Alignment	not modelled	8.5	33	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**lectin-like fold protein; **PDBTitle:** crystal structure of ppo3, a tyrosinase from agaricus bisporus, in2 deoxy-form that contains additional unknown lectin-like subunit,3 with inhibitor tropolone
50	c1rijA_	Alignment	not modelled	8.4	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**e6apn1 peptide; **PDBTitle:** e6-bind trp-cage (e6apn1)
51	c2dcpA_	Alignment	not modelled	8.4	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein (rafl09-17-b18); **PDBTitle:** fully automated nmr structure determination of the enth-vhs2 domain at3g16270 from arabidopsis thaliana
52	c2eqeA_	Alignment	not modelled	8.4	71	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tumor necrosis factor, alpha-induced protein 3; **PDBTitle:** solution structure of the fourth a20-type zinc finger2 domain from human tumor necrosis factor, alpha-induced3 protein3
53	c6eyvB_	Alignment	not modelled	8.3	39	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pvdp; **PDBTitle:** crystal structure of the pyoverdine maturation protein pvdp in complex2 with the mock substrates l-tyrosine and zinc.
						PDB header:metal binding protein

54	c5losA_	Alignment	not modelled	8.2	39	**Chain:** A: **PDB Molecule:**piin_05872; **PDBTitle:** piriformospora indica piin_05872
55	c2yomA_	Alignment	not modelled	8.2	40	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sensory box protein; **PDBTitle:** solution nmr structure of the c-terminal extension of two bacterial2 light, oxygen, voltage (lov) photoreceptor proteins from3 pseudomonas putida
56	c2hw2A_	Alignment	not modelled	8.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rifampin adp-ribosyl transferase; **PDBTitle:** crystal structure of rifampin adp-ribosyl transferase in complex with2 rifampin
57	d1ptfa_	Alignment	not modelled	8.0	23	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
58	c4njcE_	Alignment	not modelled	8.0	6	**PDB header:**transcription **Chain:** E: **PDB Molecule:**geobacillus stearothermophilus ykzg; **PDBTitle:** rna polymerase interacting protein ykzg from geobacillus2 stearothermophilus
59	c4g4mB_	Alignment	not modelled	7.9	33	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**alpha4f3(6-13); **PDBTitle:** crystal structure of the de novo designed fluorinated peptide2 alpha4f3(6-13)
60	c4g4mA_	Alignment	not modelled	7.9	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**alpha4f3(6-13); **PDBTitle:** crystal structure of the de novo designed fluorinated peptide2 alpha4f3(6-13)
61	c4hitD_	Alignment	not modelled	7.7	17	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**matrix protein; **PDBTitle:** crystal structure of h112w mutant of borna disease virus matrix2 protein
62	c6aafB_	Alignment	not modelled	7.7	50	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**transmembrane protein 184 homolog c30d11.06c; **PDBTitle:** crystal structure of fission yeast atg8 complexed with the helical aim2 of hfl1.
63	c4xaiP_	Alignment	not modelled	7.7	50	**PDB header:**transcription **Chain:** P: **PDB Molecule:**grunge, isoform j; **PDBTitle:** crystal structure of red flour beetle nr2e1/tlx
64	c2w0cC_	Alignment	not modelled	7.7	23	**PDB header:**virus **Chain:** C: **PDB Molecule:**major capsid protein p2; **PDBTitle:** x-ray structure of the entire lipid-containing bacteriophage pm2
65	c2kfsA_	Alignment	not modelled	7.7	11	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical regulatory protein; **PDBTitle:** nmr structure of rv2175c
66	c2ymbC_	Alignment	not modelled	7.7	19	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**mit domain-containing protein 1; **PDBTitle:** structures of mitd1
67	c4y7iB_	Alignment	not modelled	7.7	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**myotubularin-related protein 8; **PDBTitle:** crystal structure of mtmr8
68	c4kxrC_	Alignment	not modelled	7.6	10	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**espg5; **PDBTitle:** structure of the mycobacterium tuberculosis type vii secretion system2 chaperone espg5 in complex with pe25-ppe41 dimer
69	c5zjiH_	Alignment	not modelled	7.6	44	**PDB header:**membrane protein **Chain:** H: **PDB Molecule:**photosystem i reaction center subunit vi, chloroplastic; **PDBTitle:** structure of photosystem i supercomplex with light-harvesting2 complexes i and ii
70	d1hvxa1	Alignment	not modelled	7.5	33	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
71	d1pp0a_	Alignment	not modelled	7.5	19	**Fold:**CytB endotoxin-like **Superfamily:**CytB endotoxin-like **Family:**CytB endotoxin-like
72	c3mhvA_	Alignment	not modelled	7.5	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein vta1; **PDBTitle:** crystal structure of vps4 and vta1
73	d1y0ya2	Alignment	not modelled	7.5	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
74	d1v4aa1	Alignment	not modelled	7.5	11	**Fold:**Four-helical up-and-down bundle **Superfamily:**Nucleotidyltransferase substrate binding subunit/domain **Family:**Glutamine synthase adenylyltransferase GlnE, domain 2
75	c3pmmA_	Alignment	not modelled	7.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** the crystal structure of a possible member of gh105 family from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578
76	c3f7jB_	Alignment	not modelled	7.4	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**yvgn protein; **PDBTitle:** b.subtilis yvgn
77	c3u5eP_	Alignment	not modelled	7.4	24	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**60s ribosomal protein l17-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome a
78	c3ihsB_	Alignment	not modelled	7.4	23	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**phosphocarrier protein hpr; **PDBTitle:** crystal structure of a phosphocarrier protein hpr from2 bacillus anthracis str. ames
						PDB header:cell adhesion **Chain:** B: **PDB Molecule:**putative cell adhesion protein;

79	c4dguB_	Alignment	not modelled	7.3	25	**PDBTitle:** crystal structure of a putative cell adhesion protein (bt0320) from2 bacteroides thetaiotaomicron vpi-5482 at 2.37 a resolution
80	c3jywN_	Alignment	not modelled	7.3	24	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**60s ribosomal protein l17(a); **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
81	c3ln3A_	Alignment	not modelled	7.3	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of putative reductase (np_038806.2) from mus2 musculus at 1.18 a resolution
82	c2kdrX_	Alignment	not modelled	7.3	24	**PDB header:**viral protein, membrane protein **Chain:** X: **PDB Molecule:**non-structural protein 4b; **PDBTitle:** solution structure of hcv ns4b(227-254)
83	c5t58D_	Alignment	not modelled	7.2	12	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**klla0d15741p; **PDBTitle:** structure of the mind complex shows a regulatory focus of yeast2 kinetochore assembly
84	c4phxE_	Alignment	not modelled	7.2	17	**PDB header:**cell adhesion **Chain:** E: **PDB Molecule:**protein aggb; **PDBTitle:** crystal structure of aggb, the minor subunit of aggregative adherence2 fimbriae type i from the escherichia coli o4h104
85	c1xu2R_	Alignment	not modelled	7.2	43	**PDB header:**cytokine, hormone/growth factor receptor **Chain:** R: **PDB Molecule:**tumor necrosis factor receptor superfamily member 17; **PDBTitle:** the crystal structure of april bound to bcma
86	d1xu2r_	Alignment	not modelled	7.2	43	**Fold:**TNF receptor-like **Superfamily:**TNF receptor-like **Family:**BAFF receptor-like
87	d2oyza1	Alignment	not modelled	7.2	33	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**VPA0057-like
88	c3fbnC_	Alignment	not modelled	7.2	0	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 7; **PDBTitle:** structure of the mediator submodule med7n/31
89	c4a17Q_	Alignment	not modelled	7.2	12	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**rpl17; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
90	c2jxpA_	Alignment	not modelled	7.1	16	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**putative lipoprotein b; **PDBTitle:** solution nmr structure of uncharacterized lipoprotein b2 from nitrosomonas europaea. northeast structural genomics3 target ner45a
91	c3f7xA_	Alignment	not modelled	7.1	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of a putative polyketide cyclase (pp0894) from2 pseudomonas putida kt2440 at 1.24 a resolution
92	c4lt5A_	Alignment	not modelled	7.0	18	**PDB header:**oxidoreductase/dna **Chain:** A: **PDB Molecule:**naegleria tet-like dioxygenase; **PDBTitle:** structure of a naegleria tet-like dioxygenase in complex with 5-2 methylcytosine dna
93	d1d8ia_	Alignment	not modelled	7.0	31	**Fold:**CYTH-like phosphatases **Superfamily:**CYTH-like phosphatases **Family:**mRNA triphosphatase CET1
94	c6bk4A_	Alignment	not modelled	7.0	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**caprin homolog; **PDBTitle:** crystal structure of the hr-1 domain of drosophila caprin in the2 p212121 space group
95	c3krbB_	Alignment	not modelled	6.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldose reductase; **PDBTitle:** structure of aldose reductase from giardia lamblia at 1.75a resolution
96	d1pcha_	Alignment	not modelled	6.9	17	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
97	c6g2dB_	Alignment	not modelled	6.8	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coa carboxylase 1; **PDBTitle:** citrate-induced acetyl-coa carboxylase (acc-cit) filament at 5.4 a2 resolution
98	c3pu2G_	Alignment	not modelled	6.8	18	**PDB header:**structure genomics, unknown function **Chain:** G: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q3j4m4_rhos4 protein from rhodobacter2 sphaeroides. northeast structural genomics consortium target rhr263.
99	d1mtyg_	Alignment	not modelled	6.8	45	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Methane monooxygenase hydrolase, gamma subunit **Family:**Methane monooxygenase hydrolase, gamma subunit