Phyre²

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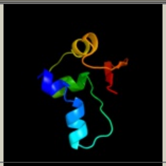
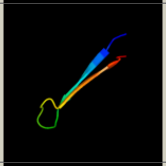
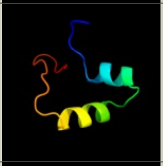
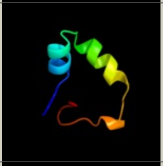
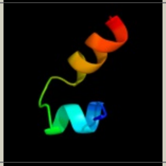
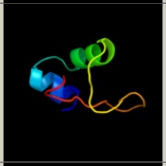
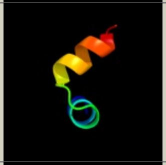
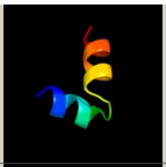
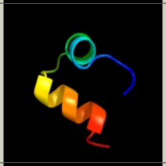
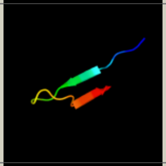
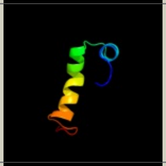
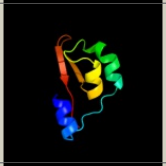
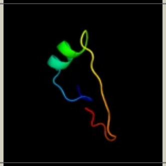
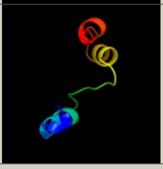
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wi9a_	Alignment		72.8	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
2	d1od5a1	Alignment		60.9	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
3	c2kxxA_	Alignment		52.7	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small protein a; **PDBTitle:** nmr structure of escherichia coli bame, a lipoprotein component of the2 beta-barrel assembly machinery complex
4	c3f2hA_	Alignment		52.7	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alkylmercury lyase; **PDBTitle:** crystal structure of the mercury-bound form of merb mutant2 c160s, the organomercurial lyase involved in a bacterial3 mercury resistance system
5	d1s6la1	Alignment		42.0	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MerB N-terminal domain-like
6	c1y6uA_	Alignment		35.7	16	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excisionase from transposon tn916; **PDBTitle:** the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
7	d1j9ia_	Alignment		32.3	11	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
8	d1l0oc_	Alignment		32.1	32	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
9	c1l0oC_	Alignment		32.1	32	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**sigma factor; **PDBTitle:** crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
10	c2kfsA_	Alignment		30.0	18	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical regulatory protein; **PDBTitle:** nmr structure of rv2175c
11	d1fxza1	Alignment		29.2	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein

12	d1rp3a1	Alignment		28.8	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
13	d1fxza2	Alignment		26.8	4	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
14	c3fljA_	Alignment		25.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein conserved in bacteria with a **PDBTitle:** crystal structure of uncharacterized protein conserved in bacteria2 with a cystatin-like fold (yp_168589.1) from silicibacter pomeroyi3 dss-3 at 2.00 a resolution
15	d1dgwa_	Alignment		24.6	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
16	d1t47a2	Alignment		24.1	8	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
17	c2cw1A_	Alignment		23.7	26	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sn4m; **PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein
18	d1od5a2	Alignment		23.7	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
19	d1wdva_	Alignment		22.8	17	**Fold:**YbaK/ProRS associated domain **Superfamily:**YbaK/ProRS associated domain **Family:**YbaK/ProRS associated domain
20	d1y0pa3	Alignment		22.4	10	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
21	d1ku2a1	Alignment	not modelled	21.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
22	d1hlva1	Alignment	not modelled	20.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
23	d3e11a1	Alignment	not modelled	20.8	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TTHA0227-like
24	d1bw6a_	Alignment	not modelled	20.6	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
25	d2phla1	Alignment	not modelled	19.5	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
26	d1qo8a3	Alignment	not modelled	19.5	11	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
27	c3t72o_	Alignment	not modelled	19.4	21	**PDB header:**transcription/dna **Chain:** O: **PDB Molecule:**pho box dna (strand 1); **PDBTitle:** phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex
28	d1uika1	Alignment	not modelled	18.2	11	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein

29	d1uika2	Alignment	not modelled	17.4	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
30	c3r1fO_	Alignment	not modelled	17.4	12	**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
31	d1rzhh2	Alignment	not modelled	17.2	17	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
32	d3orca_	Alignment	not modelled	16.7	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
33	c1hlvA_	Alignment	not modelled	16.5	19	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**major centromere autoantigen b; **PDBTitle:** crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
34	d1eysh2	Alignment	not modelled	16.1	13	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
35	d2oa4a1	Alignment	not modelled	15.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**SPO1678-like
36	c2jo1A_	Alignment	not modelled	15.6	17	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
37	d1l9bh2	Alignment	not modelled	15.3	17	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
38	d2rcrh2	Alignment	not modelled	15.0	20	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
39	c2e9qA_	Alignment	not modelled	14.9	19	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**11s globulin subunit beta; **PDBTitle:** recombinant pro-11s globulin of pumpkin
40	d2jn6a1	Alignment	not modelled	14.7	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
41	c2d5fB_	Alignment	not modelled	14.6	19	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**glycinin a3b4 subunit; **PDBTitle:** crystal structure of recombinant soybean proglycinin a3b4 subunit, its2 comparison with mature glycinin a3b4 subunit, responsible for hexamer3 assembly
42	c2jrtA_	Alignment	not modelled	14.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
43	c3f8xD_	Alignment	not modelled	14.4	24	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative delta-5-3-ketosteroid isomerase; **PDBTitle:** crystal structure of a putative delta-5-3-ketosteroid isomerase2 (eca2236) from pectobacterium atrosepticum scri1043 at 1.55 a3 resolution
44	d2et1a1	Alignment	not modelled	14.2	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
45	c1dgrW_	Alignment	not modelled	14.1	15	**PDB header:**plant protein **Chain:** W: **PDB Molecule:**canavalin; **PDBTitle:** refined crystal structure of canavalin from jack bean
46	d3dxoa1	Alignment	not modelled	13.6	28	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Atu0744-like
47	d2phcb1	Alignment	not modelled	13.5	10	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
48	d1bl0a1	Alignment	not modelled	13.4	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
49	d2p7vb1	Alignment	not modelled	12.5	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
50	c2rn7A_	Alignment	not modelled	12.5	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**is629 orfa; **PDBTitle:** nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
51	d1sqda2	Alignment	not modelled	12.4	13	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
52	c2elhA_	Alignment	not modelled	11.5	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cg11849-pa; **PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
						Fold:DNA/RNA-binding 3-helical bundle

53	d1ufma_	Alignment	not modelled	11.5	22	**Superfamily:**"Winged helix" DNA-binding domain **Family:**PCI domain (PINT motif)
54	d2hq2a1	Alignment	not modelled	11.2	19	**Fold:**Heme iron utilization protein-like **Superfamily:**Heme iron utilization protein-like **Family:**HemS/ChuS-like
55	c2k9lA_	Alignment	not modelled	11.0	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** structure of the core binding domain of sigma54
56	c2htfA_	Alignment	not modelled	11.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** the solution structure of the brct domain from human2 polymerase reveals homology with the tdt brct domain
57	d1t1da_	Alignment	not modelled	10.9	0	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
58	c2zp2B_	Alignment	not modelled	10.8	14	**PDB header:**transferase inhibitor **Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
59	d1b4ua_	Alignment	not modelled	10.1	14	**Fold:**LigA subunit of an aromatic-ring-opening dioxygenase LigAB **Superfamily:**LigA subunit of an aromatic-ring-opening dioxygenase LigAB **Family:**LigA subunit of an aromatic-ring-opening dioxygenase LigAB
60	c3lsgD_	Alignment	not modelled	10.1	18	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**two-component response regulator yesn; **PDBTitle:** the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
61	c2lfcA_	Alignment	not modelled	10.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fumarate reductase, flavoprotein subunit; **PDBTitle:** solution nmr structure of fumarate reductase flavoprotein subunit from2 lactobacillus plantarum, northeast structural genomics consortium3 target lpr145j
62	c1y66D_	Alignment	not modelled	9.8	30	**PDB header:**de novo protein **Chain:** D: **PDB Molecule:**engrailed homeodomain; **PDBTitle:** dioxane contributes to the altered conformation and2 oligomerization state of a designed engrailed homeodomain3 variant
63	d2ofya1	Alignment	not modelled	9.8	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
64	c3msoA_	Alignment	not modelled	9.8	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**steroid delta-isomerase; **PDBTitle:** crystal structure of a steroid delta-isomerase (np_250810.1) from2 pseudomonas aeruginosa at 2.57 a resolution
65	d2p6ra2	Alignment	not modelled	9.6	9	**Fold:**Sec63 N-terminal domain-like **Superfamily:**Sec63 N-terminal domain-like **Family:**Achaeal helicase C-terminal domain
66	c2v9vA_	Alignment	not modelled	9.5	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** crystal structure of moorella thermoacetica selb(377-511)
67	c2phcB_	Alignment	not modelled	9.3	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ph0987; **PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
68	c3bd1B_	Alignment	not modelled	9.2	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cro protein; **PDBTitle:** structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
69	c1tfzA_	Alignment	not modelled	9.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase; **PDBTitle:** structural basis for herbicidal inhibitor selectivity revealed by2 comparison of crystal structures of plant and mammalian 4-3 hydroxyphenylpyruvate dioxygenases
70	c2k9sA_	Alignment	not modelled	9.2	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**arabinose operon regulatory protein; **PDBTitle:** solution structure of dna binding domain of e. coli arac
71	d1ku3a_	Alignment	not modelled	9.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
72	d1sp9a_	Alignment	not modelled	8.7	11	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Extradiol dioxygenases
73	c1cauB_	Alignment	not modelled	8.7	15	**PDB header:**seed storage protein **Chain:** B: **PDB Molecule:**canavalin; **PDBTitle:** determination of three crystal structures of canavalin by molecular2 replacement
74	d1p7ia_	Alignment	not modelled	8.5	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
75	c1k6nH_	Alignment	not modelled	8.5	17	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**photosynthetic reaction center h subunit; **PDBTitle:** e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides
76	c2kpjA_	Alignment	not modelled	8.2	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sos-response transcriptional repressor, lexa; **PDBTitle:** solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
77	d1pbja3	Alignment	not modelled	8.1	20	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair

						Family:CBS-domain pair
78	d1xd7a_	Alignment	not modelled	8.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator Rrf2
79	c1sp8A_	Alignment	not modelled	8.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxyphenylpyruvate dioxygenase; **PDBTitle:** 4-hydroxyphenylpyruvate dioxygenase
80	c3t76A_	Alignment	not modelled	8.0	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
81	d1yava3	Alignment	not modelled	7.8	3	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
82	d2d30a1	Alignment	not modelled	7.7	13	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Cytidine deaminase
83	d1wj6a_	Alignment	not modelled	7.7	8	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
84	d1d5ya1	Alignment	not modelled	7.7	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
85	c3a03A_	Alignment	not modelled	7.7	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**t-cell leukemia homeobox protein 2; **PDBTitle:** crystal structure of hox11l1 homeodomain
86	c1fxzC_	Alignment	not modelled	7.6	3	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**glycinin g1; **PDBTitle:** crystal structure of soybean proglycinin a1ab1b homotrimer
87	d1j58a_	Alignment	not modelled	7.6	12	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
88	d1u5tb1	Alignment	not modelled	7.5	44	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
89	c3bdnB_	Alignment	not modelled	7.4	7	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**lambda repressor; **PDBTitle:** crystal structure of the lambda repressor
90	d1pn0a3	Alignment	not modelled	7.3	33	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**PHBH-like
91	d1ttya_	Alignment	not modelled	7.3	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
92	c2ph0A_	Alignment	not modelled	7.2	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the q6d2t7_erwct protein from erwinia2 carotovora. nesg target ewr41.
93	c2f9jP_	Alignment	not modelled	7.2	7	**PDB header:**rna binding protein **Chain:** P: **PDB Molecule:**splicing factor 3b subunit 1; **PDBTitle:** 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
94	d1mh3a1	Alignment	not modelled	7.2	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
95	c1eysH_	Alignment	not modelled	7.0	13	**PDB header:**electron transport **Chain:** H: **PDB Molecule:**photosynthetic reaction center; **PDBTitle:** crystal structure of photosynthetic reaction center from a2 thermophilic bacterium, thermochromatium tepidum
96	c2fjrB_	Alignment	not modelled	7.0	9	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of bacteriophage 186
97	d2yzia1	Alignment	not modelled	6.9	14	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
98	c2r5vA_	Alignment	not modelled	6.9	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pcza361.1; **PDBTitle:** hydroxymandelate synthase crystal structure
99	c2vqaC_	Alignment	not modelled	6.9	14	**PDB header:**metal-binding protein **Chain:** C: **PDB Molecule:**sll1358 protein; **PDBTitle:** protein-folding location can regulate mn versus cu- or zn-2 binding. crystal structure of mnca.