Phyre2

Email	l.a.kelley@imperial.ac.uk
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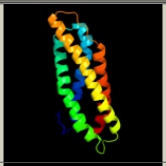
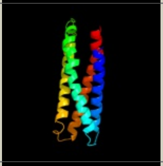
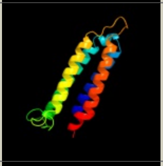
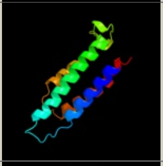
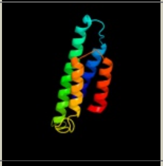
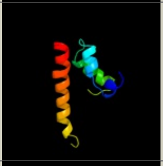
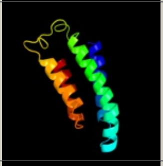
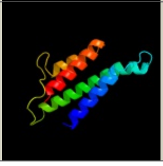
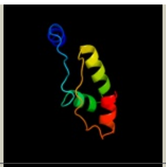
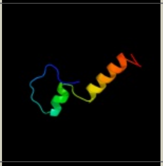
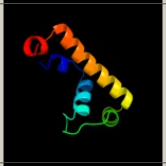
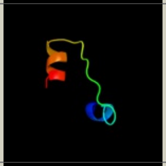
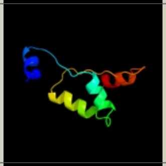
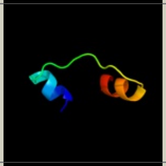
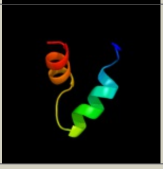
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2p0nA_	Alignment		99.7	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein nmb1532; **PDBTitle:** nmb1532 protein from neisseria meningitidis, unknown function
2	c2k5eA_	Alignment		99.6	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
3	c2k53A_	Alignment		99.5	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**a3dk08 protein; **PDBTitle:** nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
4	c3caxA_	Alignment		98.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pf0695; **PDBTitle:** crystal structure of uncharacterized protein pf0695
5	d2fi0a1	Alignment		97.3	14	**Fold:**SP0561-like **Superfamily:**SP0561-like **Family:**SP0561-like
6	c2awyB_	Alignment		93.9	14	**PDB header:**oxygen storage/transport **Chain:** B: **PDB Molecule:**hemerythrin-like domain protein dcrh; **PDBTitle:** met-dcrh-hr
7	d2mhra_	Alignment		72.7	17	**Fold:**Four-helical up-and-down bundle **Superfamily:**Hemerythrin-like **Family:**Hemerythrin-like
8	d2hmza_	Alignment		71.7	16	**Fold:**Four-helical up-and-down bundle **Superfamily:**Hemerythrin-like **Family:**Hemerythrin-like
9	d2pt0a1	Alignment		70.7	16	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Myo-inositol hexaphosphate phosphohydrolase (phytase) PhyA
10	d1i4ya_	Alignment		67.2	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**Hemerythrin-like **Family:**Hemerythrin-like
11	d1hrba_	Alignment		57.7	16	**Fold:**Four-helical up-and-down bundle **Superfamily:**Hemerythrin-like **Family:**Hemerythrin-like

12	d1qwga_	Alignment		50.4	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
13	d1r9ja3	Alignment		48.2	15	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
14	d1ku7a_	Alignment		47.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
15	c3o8nA_	Alignment		39.7	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase, muscle type; **PDBTitle:** structure of phosphofructokinase from rabbit skeletal muscle
16	d1d4ca3	Alignment		39.0	6	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
17	c1u83A_	Alignment		38.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
18	d1u83a_	Alignment		38.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
19	c2higA_	Alignment		38.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phospho-1-fructokinase; **PDBTitle:** crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
20	d1sm4a2	Alignment		36.9	34	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
21	c2lfcA_	Alignment	not modelled	35.3	15	**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
22	d2p5zx2	Alignment	not modelled	35.0	15	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
23	d1y0pa3	Alignment	not modelled	35.0	12	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
24	d4pfka_	Alignment	not modelled	31.6	15	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
25	c3o8oB_	Alignment	not modelled	30.5	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructokinase subunit beta; **PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae
26	c2p9jH_	Alignment	not modelled	29.8	13	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**hypothetical protein aq2171; **PDBTitle:** crystal structure of aq2171 from aquifex aeolicus
27	d2djia2	Alignment	not modelled	29.8	13	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
28	d2phcb1	Alignment	not modelled	29.4	15	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like

						Family:PH0987 C-terminal domain-like
29	c3k2qA_	Alignment	not modelled	29.3	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrophosphate-dependent phosphofructokinase; **PDBTitle:** crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
30	c3o8oC_	Alignment	not modelled	29.3	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**6-phosphofructokinase subunit alpha; **PDBTitle:** structure of phosphofructokinase from saccharomyces cerevisiae
31	d1pfka_	Alignment	not modelled	29.1	20	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
32	c1zxxA_	Alignment	not modelled	28.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phosphofructokinase; **PDBTitle:** the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
33	c2kebA_	Alignment	not modelled	28.6	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna polymerase subunit alpha b; **PDBTitle:** nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
34	c2l1lB_	Alignment	not modelled	27.8	16	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**exportin-1; **PDBTitle:** nmr solution structure of the phi0 pki nes peptide in complex with2 crm1-rangtp
35	c1fncA_	Alignment	not modelled	25.4	34	**PDB header:**oxidoreductase (nadp+(a),ferredoxin(a)) **Chain:** A: **PDB Molecule:**ferredoxin-nadp+ reductase; **PDBTitle:** refined crystal structure of spinach ferredoxin reductase2 at 1.7 angstroms resolution: oxidized, reduced, and 2'-3 phospho-5'-amp bound states
36	c2p5zX_	Alignment	not modelled	23.7	15	**PDB header:**structural genomics, unknown function **Chain:** X: **PDB Molecule:**type vi secretion system component; **PDBTitle:** the e. coli c3393 protein is a component of the type vi secretion2 system and exhibits structural similarity to t4 bacteriophage tail3 proteins gp27 and gp5
37	c3opyH_	Alignment	not modelled	23.0	29	**PDB header:**transferase **Chain:** H: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
38	c3n1uA_	Alignment	not modelled	22.6	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, had superfamily, subfamily iii a; **PDBTitle:** structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
39	c3opyB_	Alignment	not modelled	22.1	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**6-phosphofructo-1-kinase beta-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
40	d1ffva1	Alignment	not modelled	22.0	18	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
41	d1zxia1	Alignment	not modelled	21.4	21	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
42	d1v97a1	Alignment	not modelled	20.3	13	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
43	c3opyG_	Alignment	not modelled	20.2	29	**PDB header:**transferase **Chain:** G: **PDB Molecule:**6-phosphofructo-1-kinase alpha-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
44	d2f48a1	Alignment	not modelled	20.2	19	**Fold:**Phosphofructokinase **Superfamily:**Phosphofructokinase **Family:**Phosphofructokinase
45	d2al3a1	Alignment	not modelled	19.8	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
46	c3g7pA_	Alignment	not modelled	19.8	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**nitrogen fixation protein; **PDBTitle:** crystal structure of a nifx-associated protein of unknown function2 (afe_1514) from acidithiobacillus ferrooxidans atcc at 2.00 a3 resolution
47	c3fiwB_	Alignment	not modelled	19.7	20	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** structure of sco0253, a tetr-family transcriptional regulator from2 streptomyces coelicolor
48	d2piaa3	Alignment	not modelled	18.6	4	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
49	d1ozha2	Alignment	not modelled	18.1	7	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
50	d3e9va1	Alignment	not modelled	17.8	15	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
51	d2z15a1	Alignment	not modelled	17.6	18	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
52	c3hl4B_	Alignment	not modelled	17.3	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**choline-phosphate cytidylyltransferase a; **PDBTitle:** crystal structure of a mammalian ctp:phosphocholine2 cytidylyltransferase with cdp-choline
						PDB header:dna binding protein **Chain:** A: **PDB Molecule:**hrdc domain from bloom syndrome

53	c2rrdA_	Alignment	not modelled	17.1	14	protein; **PDBTitle:** structure of hrdc domain from human bloom syndrome protein, blm
54	c2pmzN_	Alignment	not modelled	16.7	14	**PDB header:**translation, transferase **Chain:** N: **PDB Molecule:**dna-directed rna polymerase subunit n; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
55	d1qo8a3	Alignment	not modelled	16.4	12	**Fold:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Superfamily:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
56	c3nj2B_	Alignment	not modelled	16.4	9	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**duf269-containing protein; **PDBTitle:** crystal structure of cce_0566 from the cyanobacterium cyanothece2 51142, a protein associated with nitrogen fixation from the duf2693 family
57	d1jt6a1	Alignment	not modelled	16.1	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
58	d1d8ba_	Alignment	not modelled	15.9	18	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
59	c2zp2B_	Alignment	not modelled	15.6	23	**PDB header:**transferase inhibitor **Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
60	d1n62a1	Alignment	not modelled	15.5	18	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
61	d1wrua2	Alignment	not modelled	14.9	26	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
62	d1f3ta2	Alignment	not modelled	14.9	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
63	d1nd9a_	Alignment	not modelled	14.7	20	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**N-terminal subdomain of bacterial translation initiation factor IF2
64	c3m8jA_	Alignment	not modelled	14.5	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**focb protein; **PDBTitle:** crystal structure of e.coli focb at 1.4 a resolution
65	c2xvcA_	Alignment	not modelled	14.4	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**escrt-iii; **PDBTitle:** molecular and structural basis of escrt-iii recruitment to2 membranes during archaeal cell division
66	d2p7vb1	Alignment	not modelled	14.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
67	c3opyE_	Alignment	not modelled	14.3	27	**PDB header:**transferase **Chain:** E: **PDB Molecule:**6-phosphofructo-1-kinase alpha-subunit; **PDBTitle:** crystal structure of pichia pastoris phosphofructokinase in the t-2 state
68	c3b81A_	Alignment	not modelled	14.0	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, acrr family; **PDBTitle:** crystal structure of predicted dna-binding transcriptional regulator2 of tetr/acrr family (np_350189.1) from clostridium acetobutylicum at3 2.10 a resolution
69	d1rm6c1	Alignment	not modelled	14.0	13	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
70	c3he0A_	Alignment	not modelled	13.6	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, tetr family; **PDBTitle:** the structure of a putative transcriptional regulator tetr family2 protein from vibrio parahaemolyticus.
71	c2wuiA_	Alignment	not modelled	13.6	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of mexz, a key repressor responsible for2 antibiotic resistance in pseudomonas aeruginosa.
72	c2nvaH_	Alignment	not modelled	13.6	6	**PDB header:**lyase **Chain:** H: **PDB Molecule:**arginine decarboxylase, a207r protein; **PDBTitle:** the x-ray crystal structure of the paramecium bursaria2 chlorella virus arginine decarboxylase bound to agmatine
73	c2qwwB_	Alignment	not modelled	13.5	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of multiple antibiotic-resistance repressor (marr)2 (yp_013417.1) from listeria monocytogenes 4b f2365 at 2.07 a3 resolution
74	d1gaqb_	Alignment	not modelled	13.4	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
75	d1pvda2	Alignment	not modelled	13.3	18	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
76	d2i10a1	Alignment	not modelled	13.1	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
77	c2b5oA_	Alignment	not modelled	12.9	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** ferredoxin-nadp reductase
78	c1pfuA_	Alignment	not modelled	12.9	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from escherichia coli

						complexed2 with methionine phosphinate
79	c3ccyA_	Alignment	not modelled	12.8	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative tetr-family transcriptional regulator; **PDBTitle:** crystal structure of a tetr-family transcriptional regulator from2 bordetella parapertussis 12822
80	d1gawa2	Alignment	not modelled	12.7	28	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
81	d1losc_	Alignment	not modelled	12.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
82	d2np5a1	Alignment	not modelled	12.6	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
83	c3f6wE_	Alignment	not modelled	12.5	13	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**xre-family like protein; **PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
84	c2qcoA_	Alignment	not modelled	12.5	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**cmer; **PDBTitle:** crystal structure of the transcriptional regulator cmer from2 campylobacter jejuni
85	d2cg4a1	Alignment	not modelled	12.4	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
86	d3cdda2	Alignment	not modelled	12.4	14	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
87	d1oe8a1	Alignment	not modelled	12.3	22	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
88	d1h3na3	Alignment	not modelled	12.3	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
89	d2fd5a1	Alignment	not modelled	12.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
90	c3bcgA_	Alignment	not modelled	12.2	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator acrr; **PDBTitle:** conformational changes of the acrr regulator reveal a2 mechanism of induction
91	c2k29A_	Alignment	not modelled	12.2	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
92	c2kwpA_	Alignment	not modelled	12.2	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** solution structure of the aminoterminal domain of e. coli nusa
93	d2g7la1	Alignment	not modelled	12.1	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
94	d1pb6a1	Alignment	not modelled	12.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
95	c3nbmA_	Alignment	not modelled	12.1	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iibc components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
96	c1wygA_	Alignment	not modelled	12.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
97	c2dg7A_	Alignment	not modelled	12.0	23	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
98	d4fxca_	Alignment	not modelled	11.9	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
99	d2id3a1	Alignment	not modelled	11.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain