Phyre2

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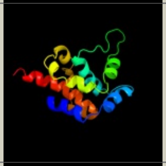
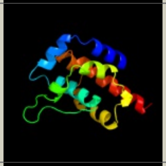
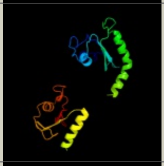
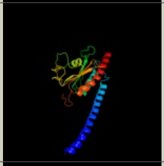
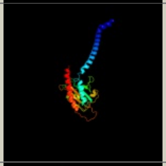
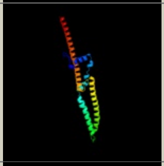
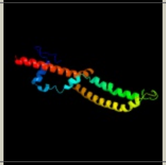
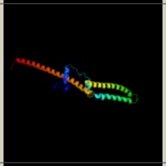
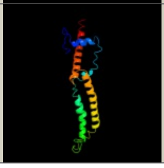
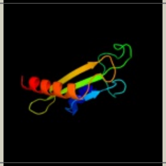
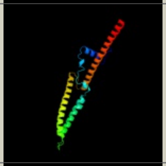
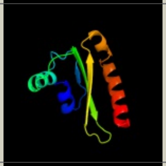
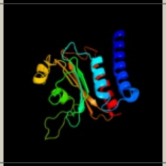
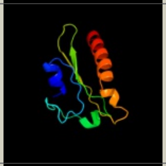
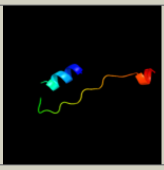
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3j1uA_	Alignment		98.7	14	**PDB header:**motor protein/structural protein **Chain:** A: **PDB Molecule:**cytoplasmic dynein 1 heavy chain 1, seryl t-rna synthetase **PDBTitle:** low affinity dynein microtubule binding domain - tubulin complex
2	c2rr7A_	Alignment		98.5	14	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**dynein heavy chain 9; **PDBTitle:** microtubule binding domain of dynein-c
3	c3errB_	Alignment		98.3	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**fusion protein of microtubule binding domain from **PDBTitle:** microtubule binding domain from mouse cytoplasmic dynein as2 a fusion with seryl-trna synthetase
4	c3ibjB_	Alignment		98.0	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** x-ray structure of pde2a
5	c3mf0A_	Alignment		97.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of pde5a gaf domain (89-518)
6	c3vkhA_	Alignment		97.7	16	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**dynein heavy chain, cytoplasmic; **PDBTitle:** x-ray structure of a functional full-length dynein motor domain
7	c1mc0A_	Alignment		97.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3',5'-cyclic nucleotide phosphodiesterase 2a; **PDBTitle:** regulatory segment of mouse 3',5'-cyclic nucleotide phosphodiesterase2 2a, containing the gaf a and gaf b domains
8	c3o4xE_	Alignment		97.3	15	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**protein diaphanous homolog 1; **PDBTitle:** crystal structure of complex between amino and carboxy terminal2 fragments of mdia1
9	d1ux5a_	Alignment		97.2	13	**Fold:**Formin homology 2 domain (FH2 domain) **Superfamily:**Formin homology 2 domain (FH2 domain) **Family:**Formin homology 2 domain (FH2 domain)
10	c3o4xF_	Alignment		97.2	14	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**protein diaphanous homolog 1; **PDBTitle:** crystal structure of complex between amino and carboxy terminal2 fragments of mdia1
11	c1y64B_	Alignment		96.9	13	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**bni1 protein; **PDBTitle:** bni1p formin homology 2 domain complexed with atp-actin

12	c2lb5A_	Alignment		96.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** refined structural basis for the photoconversion of a phytochrome to2 the activated far-red light-absorbing form
13	d1f5ma_	Alignment		96.8	20	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
14	d1v9da_	Alignment		96.7	16	**Fold:**Formin homology 2 domain (FH2 domain) **Superfamily:**Formin homology 2 domain (FH2 domain) **Family:**Formin homology 2 domain (FH2 domain)
15	c1vhmB_	Alignment		96.7	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein yebr; **PDBTitle:** crystal structure of an hypothetical protein
16	c3oovA_	Alignment		96.7	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein, putative; **PDBTitle:** crystal structure of a methyl-accepting chemotaxis protein, residues2 122 to 287
17	c3p01C_	Alignment		96.7	13	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
18	c4fofA_	Alignment		96.6	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of the blue-light absorbing form of the2 thermosynechococcus elongatus pixj gaf-domain
19	d1vhma_	Alignment		96.4	19	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
20	c2vjwA_	Alignment		96.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gaf family protein; **PDBTitle:** crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
21	c3rfbB_	Alignment	not modelled	96.3	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of frmsr
22	c1ykdB_	Alignment	not modelled	96.3	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of the tandem gaf domains from a cyanobacterial2 adenylyl cyclase: novel modes of ligand-binding and dimerization
23	c3ksiA_	Alignment	not modelled	96.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of frmsr of staphylococcus aureus (complex with 2-propanol)
24	c3p01A_	Alignment	not modelled	96.3	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
25	c4g3kB_	Alignment	not modelled	96.2	25	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator nlh1; **PDBTitle:** crystal structure of a. aeolicus nlh1 gaf domain in an inactive state
26	c3mmhA_	Alignment	not modelled	96.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase; **PDBTitle:** x-ray structure of free methionine-r-sulfoxide reductase from2 neisseria meningitidis in complex with its substrate
27	c4g3vB_	Alignment	not modelled	96.2	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator nlh2; **PDBTitle:** crystal structure of a. aeolicus nlh2 gaf domain in an inactive state
28	c3eeaB_	Alignment	not modelled	96.0	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**gaf domain/hd domain protein; **PDBTitle:** the crystal structure of the gaf domain/hd domain protein2 from geobacter sulfurreducens

29	c2k31A_	Alignment	not modelled	95.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphodiesterase 5a, cgmp-specific; **PDBTitle:** solution structure of cgmp-binding gaf domain of2 phosphodiesterase 5
30	c4eahE_	Alignment	not modelled	95.9	7	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**formin-like protein 3; **PDBTitle:** crystal structure of the formin homology 2 domain of fmnl3 bound to2 actin
31	d2o9ca1	Alignment	not modelled	95.9	11	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
32	c2qybA_	Alignment	not modelled	95.8	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**membrane protein, putative; **PDBTitle:** crystal structure of the gaf domain region of putative membrane2 protein from geobacter sulfurreducens pca
33	c3k2nB_	Alignment	not modelled	95.7	10	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**sigma-54-dependent transcriptional regulator; **PDBTitle:** the crystal structure of sigma-54-dependent transcriptional2 regulator domain from chlorobium tepidum tls
34	c2j1dG_	Alignment	not modelled	95.5	9	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**disheveled-associated activator of morphogenesis 1; **PDBTitle:** crystallization of hdaam1 c-terminal fragment
35	c3dbaB_	Alignment	not modelled	95.4	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cone cgmp-specific 3',5'-cyclic phosphodiesterase subunit **PDBTitle:** crystal structure of the cgmp-bound gaf a domain from the2 photoreceptor phosphodiesterase 6c
36	c2z6eC_	Alignment	not modelled	95.4	11	**PDB header:**protein fibril regulator **Chain:** C: **PDB Molecule:**disheveled-associated activator of morphogenesis **PDBTitle:** crystal structure of human daam1 fh2
37	d2k2na1	Alignment	not modelled	95.4	16	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
38	c3trcA_	Alignment	not modelled	95.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of the gaf domain from a phosphoenolpyruvate-protein2 phosphotransferase (ptsp) from coxiella burnetii
39	c2w3gA_	Alignment	not modelled	95.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component sensor histidine kinase devs (gaf **PDBTitle:** air-oxidized structure of the first gaf domain of2 mycobacterium tuberculosis doss
40	c3ci6B_	Alignment	not modelled	95.1	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase
41	c3hcyB_	Alignment	not modelled	94.5	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative two-component sensor histidine kinase protein; **PDBTitle:** the crystal structure of the domain of putative two-component sensor2 histidine kinase protein from sinorhizobium meliloti 1021
42	d2veaa1	Alignment	not modelled	94.4	16	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
43	c3o5yA_	Alignment	not modelled	94.3	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of the gaf domain of a two-component sensor2 histidine kinase from bacillus halodurans to 2.45a
44	c3w2zA_	Alignment	not modelled	94.1	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein; **PDBTitle:** crystal structure of the cyanobacterial protein
45	d1p0za_	Alignment	not modelled	93.2	18	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
46	c2zmfA_	Alignment	not modelled	93.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**camp and camp-inhibited cgmp 3',5'-cyclic phosphodiesterase **PDBTitle:** crystal structure of the c-terminal gaf domain of human2 phosphodiesterase 10a
47	c2oolA_	Alignment	not modelled	90.9	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the chromophore-binding domain of an unusual2 bacteriophytochrome rpbphp3 from r. palustris
48	c3e0yA_	Alignment	not modelled	88.9	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a conserved domain from a protein of2 geobacter sulfurreducens pca
49	d1mc0a1	Alignment	not modelled	88.6	10	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
50	d1mc0a2	Alignment	not modelled	88.0	14	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
51	d2oola1	Alignment	not modelled	87.4	8	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
52	d3c2wa1	Alignment	not modelled	86.6	8	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
						PDB header:unknown function

53	c3e98B_	Alignment	not modelled	86.0	12	**Chain:** B: **PDB Molecule:**gaf domain of unknown function; **PDBTitle:** crystal structure of a gaf domain containing protein that belongs to2 pfam duf484 family (pa5279) from pseudomonas aeruginosa at 2.43 a3 resolution
54	c3g36D_	Alignment	not modelled	85.0	29	**PDB header:**nuclear protein **Chain:** D: **PDB Molecule:**protein dpy-30 homolog; **PDBTitle:** crystal structure of the human dpy-30-like c-terminal domain
55	c4e04B_	Alignment	not modelled	84.1	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**bacteriophytochrome (light-regulated signal transduction **PDBTitle:** rpbphp2 chromophore-binding domain crystallized by homologue-directed2 mutagenesis.
56	c2au3A_	Alignment	not modelled	83.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
57	c2o9bA_	Alignment	not modelled	81.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of bacteriophytochrome chromophore binding domain
58	c2xssB_	Alignment	not modelled	78.8	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-specific 3', 5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of gafb from the human phosphodiesterase 5
59	c3su8X_	Alignment	not modelled	76.3	29	**PDB header:**apoptosis/signaling protein **Chain:** X: **PDB Molecule:**plexin-b1; **PDBTitle:** crystal structure of a truncated intracellular domain of plexin-b1 in2 complex with rac1
60	c2rbgB_	Alignment	not modelled	75.3	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein st0493; **PDBTitle:** crystal structure of hypothetical protein(st0493) from2 sulfolobus tokodaii
61	c2w1tB_	Alignment	not modelled	74.8	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt
62	c3hm6X_	Alignment	not modelled	74.1	29	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**plexin-b1; **PDBTitle:** crystal structure of the cytoplasmic domain of human plexin b1
63	c2g7uB_	Alignment	not modelled	73.9	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
64	d2o9aa1	Alignment	not modelled	72.5	15	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**IclR ligand-binding domain-like
65	c2o0yB_	Alignment	not modelled	72.5	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
66	c3ig3A_	Alignment	not modelled	66.4	16	**PDB header:**signaling protein, membrane protein **Chain:** A: **PDB Molecule:**plxna3 protein; **PDBTitle:** crystal strucure of mouse plexin a3 intracellular domain
67	d3by8a1	Alignment	not modelled	65.8	13	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
68	c2veaA_	Alignment	not modelled	63.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phytochrome-like protein cph1; **PDBTitle:** the complete sensory module of the cyanobacterial2 phytochrome cph1 in the pr-state.
69	c2ia2D_	Alignment	not modelled	63.8	12	**PDB header:**transcription **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
70	c2w1rA_	Alignment	not modelled	60.8	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of the c-terminal domain of b. subtilis2 spovt
71	c1mkmA_	Alignment	not modelled	60.7	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**iclr transcriptional regulator; **PDBTitle:** crystal structure of the thermotoga maritima iclr
72	c1yspA_	Alignment	not modelled	57.3	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator kdgr; **PDBTitle:** crystal structure of the c-terminal domain of e. coli transcriptional2 regulator kdgr.
73	d1tf1a_	Alignment	not modelled	56.3	14	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**IclR ligand-binding domain-like
74	c3hpbA_	Alignment		54.8	29	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**snx5 protein; **PDBTitle:** crystal structure of snx5-px domain in p212121 space group
75	d1guqa2	Alignment	not modelled	54.7	9	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
76	d1z2wa1	Alignment	not modelled	53.5	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
77	c3zxuC_	Alignment	not modelled	52.1	21	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**mcm21; **PDBTitle:** crystal structure of the ctf19-mcm21 kinetochore heterodimer from2 yeast

78	c3fldA_	Alignment	not modelled	51.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein trai; **PDBTitle:** crystal structure of the trai c-terminal domain
79	c3r4kD_	Alignment	not modelled	49.6	15	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**transcriptional regulator, iclr family; **PDBTitle:** crystal structure of a putative iclr transcriptional regulator2 (tm1040_3717) from silicibacter sp. tm1040 at 2.46 a resolution
80	c3obfA_	Alignment	not modelled	49.0	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator, iclr family; **PDBTitle:** crystal structure of putative transcriptional regulator, iclr family;2 targeted domain 129...302
81	c3nybA_	Alignment	not modelled	46.6	17	**PDB header:**transferase/rna binding protein **Chain:** A: **PDB Molecule:**poly(a) rna polymerase protein 2; **PDBTitle:** structure and function of the polymerase core of tramp, a rna2 surveillance complex
82	c3uksB_	Alignment	not modelled	43.1	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sedoheptulose-1,7 bisphosphatase, putative; **PDBTitle:** 1.85 angstrom crystal structure of putative sedoheptulose-1,72 bisphosphatase from toxoplasma gondii
83	d1rzya_	Alignment	not modelled	43.0	12	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
84	d1mkma2	Alignment	not modelled	42.2	12	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**IclR ligand-binding domain-like
85	c3c2wB_	Alignment	not modelled	40.4	9	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of the photosensory core domain of p. aeruginosa2 bacteriophytochrome pabphp in the pfr state
86	c3fosA_	Alignment	not modelled	40.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of two-component sensor histidine kinase domain from2 bacillus subtilis subsp. subtilis str. 168
87	c2rajA_	Alignment	not modelled	38.9	37	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**sorting nexin-9; **PDBTitle:** so4 bound px-bar membrane remodeling unit of sorting nexin 9
88	d1q46a1	Alignment	not modelled	36.5	14	**Fold:**SAM domain-like **Superfamily:**eIF2alpha middle domain-like **Family:**eIF2alpha middle domain-like
89	c2hq8B_	Alignment	not modelled	36.4	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**coelenterazine-binding protein ca-bound apo form; **PDBTitle:** crystal structure of coelenterazine-binding protein from2 renilla muelleri in the ca loaded apo form
90	c4f11A_	Alignment	not modelled	35.2	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**gamma-aminobutyric acid type b receptor subunit 2; **PDBTitle:** crystal structure of the extracellular domain of human gaba(b)2 receptor gbr2
91	d1riqa1	Alignment	not modelled	34.9	38	**Fold:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) **Superfamily:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) **Family:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)
92	c4gs4A_	Alignment	not modelled	34.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-tubulin n-acetyltransferase; **PDBTitle:** structure of the alpha-tubulin acetyltransferase, alpha-tat1
93	c3fzgA_	Alignment	not modelled	34.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**16s rrna methylase; **PDBTitle:** structure of the 16s rrna methylase arma
94	c3mq0A_	Alignment	not modelled	32.0	21	**PDB header:**transcription repressor **Chain:** A: **PDB Molecule:**transcriptional repressor of the blcabc operon; **PDBTitle:** crystal structure of agobacterium tumefaciens repressor blcr
95	c2pdtD_	Alignment	not modelled	29.8	25	**PDB header:**circadian clock protein **Chain:** D: **PDB Molecule:**vivid pas protein vvd; **PDBTitle:** 2.3 angstrom structure of phosphodiesterase treated vivid
96	c3cqrB_	Alignment	not modelled	29.6	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**violaxanthin de-epoxidase, chloroplast; **PDBTitle:** crystal structure of the lipocalin domain of violaxanthin de-epoxidase2 (vde) at ph5
97	c3jpyA_	Alignment	not modelled	29.5	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glutamate [nmda] receptor subunit epsilon-2; **PDBTitle:** crystal structure of the zinc-bound amino terminal domain of the nmda2 receptor subunit nr2b
98	d1j75a_	Alignment	not modelled	29.4	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
99	c2gl7C_	Alignment	not modelled	29.2	29	**PDB header:**transcription **Chain:** C: **PDB Molecule:**b-cell lymphoma 9 protein; **PDBTitle:** crystal structure of a beta-catenin/bcl9/tcf4 complex
100	c3sl9D_	Alignment	not modelled	29.2	29	**PDB header:**signaling protein, protein binding **Chain:** D: **PDB Molecule:**b-cell cll/lymphoma 9 protein; **PDBTitle:** x-ray structure of beta catenin in complex with bcl9
101	c1ydmC_	Alignment	not modelled	28.9	14	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein yqgn; **PDBTitle:** x-ray structure of northeast structural genomics target sr44

102	d1y23a_	Alignment	not modelled	28.8	16	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
103	c3u0kA_	Alignment	not modelled	28.6	14	**PDB header:**fluorescent protein **Chain:** A: **PDB Molecule:**rcamp; **PDBTitle:** crystal structure of the genetically encoded calcium indicator rcamp
104	d2ahua2	Alignment	not modelled	28.6	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
105	c1ysqA_	Alignment	not modelled	28.4	19	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator yiaj; **PDBTitle:** the crystal structure of transcriptional regulator yaij
106	c2lnbA_	Alignment	not modelled	28.2	33	**PDB header:**immune system **Chain:** A: **PDB Molecule:**z-dna-binding protein 1; **PDBTitle:** solution nmr structure of n-terminal domain (6-74) of human zbp12 protein, northeast structural genomics consortium target hr8174a.
107	d1r5la2	Alignment	not modelled	27.8	11	**Fold:**SpoIIaa-like **Superfamily:**CRAL/TRIO domain **Family:**CRAL/TRIO domain
108	d1v65a_	Alignment	not modelled	27.4	23	**Fold:**KRAB domain (Kruppel-associated box) **Superfamily:**KRAB domain (Kruppel-associated box) **Family:**KRAB domain (Kruppel-associated box)
109	d1ewqa3	Alignment	not modelled	27.3	14	**Fold:**Ribonuclease H-like motif **Superfamily:**DNA repair protein MutS, domain II **Family:**DNA repair protein MutS, domain II
110	c2qkpD_	Alignment	not modelled	27.1	14	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of c-terminal domain of smu_1151c from streptococcus2 mutans
111	c3li6G_	Alignment	not modelled	27.1	19	**PDB header:**metal binding protein **Chain:** G: **PDB Molecule:**calcium-binding protein; **PDBTitle:** crystal structure and trimer-monomer transition of n-terminal domain2 of ehcabp1 from entamoeba histolytica
112	c3li6A_	Alignment	not modelled	27.1	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calcium-binding protein; **PDBTitle:** crystal structure and trimer-monomer transition of n-terminal domain2 of ehcabp1 from entamoeba histolytica
113	c3rkxA_	Alignment	not modelled	26.2	40	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin-[acetyl-coa-carboxylase] ligase; **PDBTitle:** structural characterisation of staphylococcus aureus biotin protein2 ligase
114	c2c37L_	Alignment	not modelled	26.1	7	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**probable exosome complex exonuclease 1; **PDBTitle:** rnase ph core of the archaeal exosome in complex with u82 rna
115	d1g33a_	Alignment	not modelled	25.6	24	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Parvalbumin
116	c1ih0A_	Alignment	not modelled	25.2	24	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** structure of the c-domain of human cardiac troponin c in2 complex with ca2+ sensitizer emd 57033
117	d1ih0a_	Alignment	not modelled	25.2	24	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
118	c2aexA_	Alignment	not modelled	25.1	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coproporphyrinogen iii oxidase, mitochondrial; **PDBTitle:** the 1.58a crystal structure of human coproporphyrinogen oxidase2 reveals the structural basis of hereditary coproporphyria
119	c4ienB_	Alignment	not modelled	25.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative acyl-coa hydrolase; **PDBTitle:** crystal structure of acyl-coa hydrolase from neisseria meningitidis2 fam18
120	d1txna_	Alignment	not modelled	24.9	25	**Fold:**Coproporphyrinogen III oxidase **Superfamily:**Coproporphyrinogen III oxidase **Family:**Coproporphyrinogen III oxidase