Phyre^2

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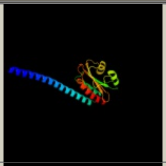
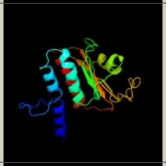
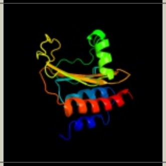
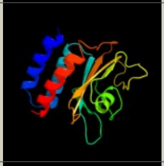
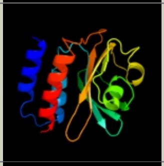
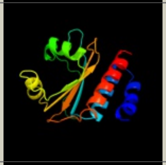
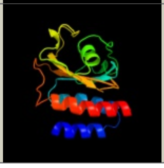
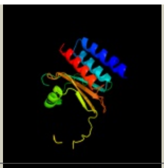
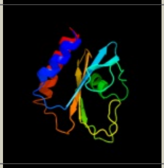
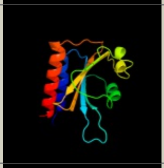
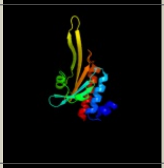
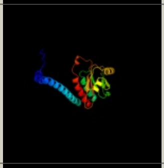
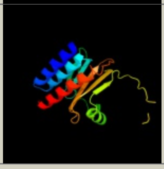
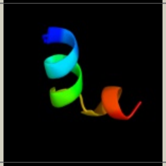
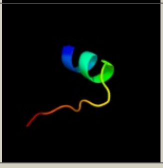
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3e98B_	Alignment		100.0	27	**PDB header:**unknown function **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
2	c3p01C_	Alignment		99.0	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
3	d2veaa1	Alignment		99.0	10	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
4	c3p01A_	Alignment		99.0	13	**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
5	c3mmhA_	Alignment		98.9	11	**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
6	c3ci6B_	Alignment		98.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase
7	c1vhmB_	Alignment		98.9	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein yebr; **PDBTitle:** crystal structure of an hypothetical protein
8	d1vhma_	Alignment		98.9	13	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
9	d2o9ca1	Alignment		98.9	14	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
10	c3ksiA_	Alignment		98.8	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of frmsr of staphylococcus aureus (complex with 2-propanol)
11	c3trcA_	Alignment		98.8	13	**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

12	d2oola1	Alignment		98.8	15	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
13	c3k2nB_	Alignment		98.7	12	**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
14	c3o5yA_	Alignment		98.6	14	**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
15	c3hcyB_	Alignment		98.6	10	**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
16	c1mc0A_	Alignment		98.5	9	**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
17	c3oovA_	Alignment		98.4	12	**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
18	c3e0yA_	Alignment		98.4	10	**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
19	c1ykdB_	Alignment		98.3	13	**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
20	c2oolA_	Alignment		98.3	11	**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
21	d2k2na1	Alignment	not modelled	98.3	18	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
22	d1f5ma_	Alignment	not modelled	98.3	11	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
23	d3c2wa1	Alignment	not modelled	98.3	11	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
24	c3eeaB_	Alignment	not modelled	98.2	12	**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
25	c3mf0A_	Alignment	not modelled	98.2	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of pde5a gaf domain (89-518)
26	c2lb5A_	Alignment	not modelled	98.1	14	**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
27	c2zmfA_	Alignment	not modelled	98.1	12	**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
28	c2o9bA_	Alignment	not modelled	98.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of bacteriophytochrome chromophore binding domain

29	c2qybA_	Alignment	not modelled	98.1	14	**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
30	c2vjwA_	Alignment	not modelled	98.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gaf family protein; **PDBTitle:** crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
31	c3ibjB_	Alignment	not modelled	97.9	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** x-ray structure of pde2a
32	c3dbaB_	Alignment	not modelled	97.9	8	**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
33	c2w3gA_	Alignment	not modelled	97.8	7	**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
34	d1mc0a1	Alignment	not modelled	97.8	8	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
35	c3c2wB_	Alignment	not modelled	97.7	8	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of the photosensory core domain of p.2 aeruginosa bacteriophytochrome pabphp in the pfr state
36	c2veaA_	Alignment	not modelled	97.3	10	**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.
37	d1mc0a2	Alignment	not modelled	97.2	8	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
38	c2k31A_	Alignment	not modelled	96.9	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphodiesterase 5a, cgmp-specific; **PDBTitle:** solution structure of cgmp-binding gaf domain of2 phosphodiesterase 5
39	c2xssB_	Alignment	not modelled	95.9	7	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-specific 3', 5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of gafb from the human phosphodiesterase 5
40	c2w1tB_	Alignment	not modelled	81.4	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt
41	c2w1rA_	Alignment	not modelled	80.1	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of the c-terminal domain of b. subtilis2 spovt
42	c2gx5B_	Alignment	not modelled	65.7	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**gtp-sensing transcriptional pleiotropic repressor cody; **PDBTitle:** n-terminal gaf domain of transcriptional pleiotropic repressor cody
43	d1ubea2	Alignment		55.0	13	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
44	d1mo6a2	Alignment		54.2	13	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
45	d1u94a2	Alignment		52.1	25	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
46	d2v0ea1	Alignment		50.1	17	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
47	d1xp8a2	Alignment	not modelled	49.8	19	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
48	c2ckaA_	Alignment	not modelled	48.3	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 8; **PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
49	d2ckaa1	Alignment	not modelled	48.3	31	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like

						Family:BRK domain-like
50	d2pnwa1	Alignment	not modelled	47.2	11	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**MLTA-like
51	c1pk1B_	Alignment	not modelled	46.4	9	**PDB header:**transcription repression **Chain:** B: **PDB Molecule:**sex comb on midleg cg9495-pa; **PDBTitle:** hetero sam domain structure of ph and scm.
52	c2avxA_	Alignment	not modelled	45.9	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein sdia; **PDBTitle:** solution structure of e coli sdia1-171
53	d1l3la2	Alignment	not modelled	45.5	12	**Fold:**Profilin-like **Superfamily:**Pheromone-binding domain of LuxR-like quorum-sensing transcription factors **Family:**Pheromone-binding domain of LuxR-like quorum-sensing transcription factors
54	c2ckcA_	Alignment	not modelled	45.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 7; **PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
55	d2ckca1	Alignment	not modelled	45.0	17	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
56	d1pk3a1	Alignment	not modelled	42.4	12	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
57	d2g5da1	Alignment	not modelled	42.1	21	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**MLTA-like
58	d1i27a_	Alignment	not modelled	40.9	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of the rap74 subunit of TFIIF
59	d2dl6a1	Alignment	not modelled	37.8	31	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
60	c2j5uB_	Alignment	not modelled	36.6	13	**PDB header:**cell shape regulation **Chain:** B: **PDB Molecule:**mrec protein; **PDBTitle:** mrec lysteria monocytogenes
61	c2wpyA_	Alignment	not modelled	35.3	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with one vxxnxxx motif2 coordinating chloride
62	c3c0rC_	Alignment	not modelled	35.2	19	**PDB header:**cell cycle, hydrolase **Chain:** C: **PDB Molecule:**ubiquitin thioesterase otu1; **PDBTitle:** structure of ovarian tumor (otu) domain in complex with ubiquitin
63	c1dipA_	Alignment	not modelled	34.3	22	**PDB header:**acetylation **Chain:** A: **PDB Molecule:**delta-sleep-inducing peptide immunoreactive **PDBTitle:** the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
64	d2ia7a1	Alignment	not modelled	33.1	22	**Fold:**gpW/gp25-like **Superfamily:**gpW/gp25-like **Family:**gpW/gp25-like
65	c3hefB_	Alignment	not modelled	32.8	31	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
66	c3pfyA_	Alignment	not modelled	32.8	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**otu domain-containing protein 5; **PDBTitle:** the catalytic domain of human otud5
67	c2k7rA_	Alignment	not modelled	32.6	33	**PDB header:**replication **Chain:** A: **PDB Molecule:**primosomal protein dnai; **PDBTitle:** n-terminal domain of the bacillus subtilis helicase-loading2 protein dnai
68	c3fkhB_	Alignment	not modelled	31.9	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative pyridoxamine 5'-phosphate oxidase; **PDBTitle:** crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_601736.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.51 a resolution
69	d2ff4a1	Alignment	not modelled	31.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
70	d2v0fa1	Alignment	not modelled	29.9	38	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
71	c3eoiB_	Alignment	not modelled	24.7	46	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**pilm; **PDBTitle:** crystal structure of putative protein pilm from escherichia coli b7a
72	c1ci6B_	Alignment	not modelled	24.0	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor c/ebp beta; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
73	c3iwfA_	Alignment	not modelled	22.6	3	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
74	d1gxqa_	Alignment	not modelled	22.0	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like

75	c1swiB_	Alignment	not modelled	21.9	27	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**gcn4p1; **PDBTitle:** gcn4-leucine zipper core mutant as n16a complexed with2 benzene
76	c1rb4A_	Alignment	not modelled	21.9	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal automatic solution
77	d2o3fa1	Alignment	not modelled	21.6	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**RpiR-like
78	c2o3fC_	Alignment	not modelled	21.6	25	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative hth-type transcriptional regulator ybbh; **PDBTitle:** structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
79	c2yxlA_	Alignment	not modelled	21.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**450aa long hypothetical fmu protein; **PDBTitle:** crystal structure of ph0851
80	c1rb6B_	Alignment	not modelled	21.0	27	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form
81	c1rb4B_	Alignment	not modelled	21.0	27	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal automatic solution
82	c1rb5C_	Alignment	not modelled	21.0	27	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a trigonal form
83	c2eanA_	Alignment	not modelled	20.7	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**connector enhancer of kinase suppressor of ras 2; **PDBTitle:** solution structure of the n-terminal sam-domain of human2 kiaa0902 protein (connector enhancer of kinase suppressor3 of ras 2)
84	c2uv0G_	Alignment	not modelled	20.4	15	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcriptional activator protein lasr; **PDBTitle:** structure of the p. aeruginosa lasr ligand-binding domain2 bound to its autoinducer
85	c1rb5B_	Alignment	not modelled	20.0	27	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a trigonal form
86	c1rb6A_	Alignment	not modelled	20.0	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form
87	c1rb5A_	Alignment	not modelled	20.0	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a trigonal form
88	c2oqqB_	Alignment	not modelled	19.9	33	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor hy5; **PDBTitle:** crystal structure of hy5 leucine zipper homodimer from2 arabidopsis thaliana
89	c3m6wA_	Alignment	not modelled	18.9	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** multi-site-specific 16s rrna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
90	d2o34a1	Alignment	not modelled	18.2	14	**Fold:**T-fold **Superfamily:**ApbE-like **Family:**DVU1097-like
91	c2wpzA_	Alignment	not modelled	18.1	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
92	c2nytB_	Alignment	not modelled	17.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable c->u-editing enzyme apobec-2; **PDBTitle:** the apobec2 crystal structure and functional implications2 for aid
93	c3cp3A_	Alignment	not modelled	17.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of conserved protein of unknown function dip18742 from corynebacterium diphtheriae
94	c2pywA_	Alignment	not modelled	17.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of a. thaliana 5-methylthioribose kinase in complex with adp2 and mtr
95	c2wpzB_	Alignment	not modelled	16.9	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
96	d1pvea_	Alignment	not modelled	16.8	25	**Fold:**XPC-binding domain **Superfamily:**XPC-binding domain **Family:**XPC-binding domain
97	d2vkva2	Alignment	not modelled	16.7	9	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
98	c2xh3B_	Alignment	not modelled	16.6	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**spd1 nuclease; **PDBTitle:** extracellular nuclease
99	c2nt8A_	Alignment	not modelled	16.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cobalamin adenosyltransferase; **PDBTitle:** atp bound at the active site of a pduo type atp:co(i)rrinoid2 adenosyltransferase from lactobacillus reuteri