Phyre²

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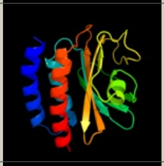
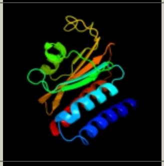
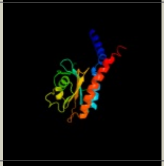
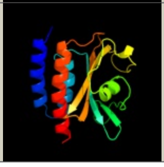
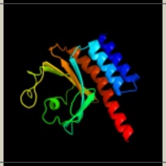
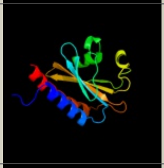
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vhmB_	Alignment		100.0	100	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein yebr; **PDBTitle:** crystal structure of an hypothetical protein
2	d1vhma_	Alignment		100.0	100	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
3	c3ksiA_	Alignment		100.0	51	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of frmsr of staphylococcus aureus (complex with 2-propanol)
4	c3mmhA_	Alignment		99.9	43	**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
5	d1f5ma_	Alignment		99.9	40	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
6	c3p01C_	Alignment		99.9	16	**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
7	d2o9ca1	Alignment		99.8	12	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
8	c3p01A_	Alignment		99.8	15	**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
9	c1mc0A_	Alignment		99.8	18	**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
10	c3o5yA_	Alignment		99.8	22	**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
11	c3trcA_	Alignment		99.8	16	**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	d2veaa1	Alignment		99.8	8	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
13	c3ci6B_	Alignment		99.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase
14	c2zmfA_	Alignment		99.8	13	**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
15	c3k2nB_	Alignment		99.8	9	**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
16	c3mf0A_	Alignment		99.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of pde5a gaf domain (89-518)
17	c3eeaB_	Alignment		99.8	18	**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
18	c3dbaB_	Alignment		99.8	14	**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
19	d2oola1	Alignment		99.8	10	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
20	c3e0yA_	Alignment		99.8	18	**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
21	c3ibjB_	Alignment	not modelled	99.8	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** x-ray structure of pde2a
22	c3oovA_	Alignment	not modelled	99.8	19	**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
23	c2vjwA_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gaf family protein; **PDBTitle:** crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
24	c1ykdB_	Alignment	not modelled	99.8	18	**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
25	c2lb5A_	Alignment	not modelled	99.7	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
26	c3hcyB_	Alignment	not modelled	99.7	14	**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
27	c2qybA_	Alignment	not modelled	99.7	17	**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

28	c2w3gA_	Alignment	not modelled	99.7	21	**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
29	c2k31A_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphodiesterase 5a, cgmp-specific; **PDBTitle:** solution structure of cgmp-binding gaf domain of2 phosphodiesterase 5
30	d2k2na1	Alignment	not modelled	99.7	17	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
31	c2oolA_	Alignment	not modelled	99.6	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
32	d1mc0a1	Alignment	not modelled	99.6	16	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
33	d3c2wa1	Alignment	not modelled	99.6	11	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
34	d1mc0a2	Alignment	not modelled	99.6	18	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
35	c3e98B_	Alignment	not modelled	99.5	17	**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
36	c2o9bA_	Alignment	not modelled	99.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of bacteriophytochrome chromophore binding domain
37	c3c2wB_	Alignment	not modelled	99.4	10	**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
38	c2xssB_	Alignment	not modelled	99.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-specific 3', 5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of gafb from the human phosphodiesterase 5
39	c2veaA_	Alignment	not modelled	99.3	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.
40	c2w1rA_	Alignment	not modelled	98.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of the c-terminal domain of b. subtilis2 spovt
41	c2w1tB_	Alignment	not modelled	98.3	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt
42	c2gx5B_	Alignment	not modelled	96.7	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**gtp-sensing transcriptional pleiotropic repressor cody; **PDBTitle:** n-terminal gaf domain of transcriptional pleiotropic repressor cody
43	c3qp1A_	Alignment	not modelled	93.1	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir ligand-binding domain bound to the native2 ligand c6-hsl
44	d1l3la2	Alignment	not modelled	92.2	10	**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
45	c2avxA_	Alignment	not modelled	78.8	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein sdia; **PDBTitle:** solution structure of e coli sdia1-171
46	c3qp5C_	Alignment	not modelled	77.7	11	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
47	c3citB_	Alignment	not modelled	75.4	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of the gaf domain of a putative sensor histidine2 kinase from pseudomonas syringae pv. tomato
48	d1tf1a_	Alignment	not modelled	75.3	15	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**IclR ligand-binding domain-like
49	c1yspA_	Alignment	not modelled	70.1	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator kdgr; **PDBTitle:** crystal structure of the c-terminal domain of e. coli transcriptional2 regulator kdgr.
50	c2o0yB_	Alignment	not modelled	64.1	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator rha1_ro069532 (iclr-family) from rhodococcus sp.
51	c1ysqA_	Alignment	not modelled	59.8	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator yiaj; **PDBTitle:** the crystal structure of transcriptional regulator yaij
52	c2g7uB_	Alignment	not modelled	58.7	15	**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

53	c3mq0A_	Alignment	not modelled	58.3	11	**PDB header:**transcription repressor **Chain:** A: **PDB Molecule:**transcriptional repressor of the blcabc operon; **PDBTitle:** crystal structure of agobacterium tumefaciens repressor blcr
54	c1stzB_	Alignment	not modelled	47.5	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat-inducible transcription repressor hrca homolog; **PDBTitle:** crystal structure of a hypothetical protein at 2.2 a resolution
55	c3d3oA_	Alignment	not modelled	47.5	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator, iclr family; **PDBTitle:** crystal structure of the effector domain of the putative2 transcriptional regulator iclr from acinetobacter sp. adp1
56	c3fpvC_	Alignment	not modelled	45.8	12	**PDB header:**heme binding protein **Chain:** C: **PDB Molecule:**extracellular haem-binding protein; **PDBTitle:** crystal structure of hbps
57	d1stza2	Alignment	not modelled	41.0	10	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**HrcA C-terminal domain-like
58	d2a2la1	Alignment	not modelled	34.8	17	**Fold:**Profilin-like **Superfamily:**GlcG-like **Family:**GlcG-like
59	c3bjnA_	Alignment	not modelled	30.9	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, putative; **PDBTitle:** crystal structure of c-terminal domain of putative transcriptional2 regulator from vibrio cholerae, targeted domain 79-240
60	c3obfA_	Alignment	not modelled	29.2	13	**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
61	d2o9aa1	Alignment	not modelled	25.4	15	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**IclR ligand-binding domain-like
62	c1mkmA_	Alignment	not modelled	24.9	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**iclr transcriptional regulator; **PDBTitle:** crystal structure of the thermotoga maritima iclr
63	c3e4pB_	Alignment	not modelled	24.6	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**c4-dicarboxylate transport sensor protein dctb; **PDBTitle:** crystal structure of malonate occupied dctb
64	c2uv0G_	Alignment	not modelled	23.0	16	**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
65	c2ia2D_	Alignment	not modelled	21.3	14	**PDB header:**transcription **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** the crystal structure of a putative transcriptional regulator rha061952 from rhodococcus sp. rha1
66	c1h0mD_	Alignment	not modelled	18.7	13	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcriptional activator protein trar; **PDBTitle:** three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
67	c3hlyA_	Alignment	not modelled	15.4	22	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
68	c3r4kD_	Alignment	not modelled	13.6	13	**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
69	d1p0za_	Alignment	not modelled	13.5	8	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
70	d1mkma2	Alignment	not modelled	13.0	13	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**IclR ligand-binding domain-like
71	d3by8a1	Alignment	not modelled	12.0	11	**Fold:**Profilin-like **Superfamily:**Sensory domain-like **Family:**Sensory domain of two-component sensor kinase
72	c2pfiA_	Alignment	not modelled	9.9	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**chloride channel protein clc-ka; **PDBTitle:** crystal structure of the cytoplasmic domain of the human2 chloride channel clc-ka
73	c3btpB_	Alignment	not modelled	9.5	19	**PDB header:**dna binding protein, chaperone **Chain:** B: **PDB Molecule:**protein vire1; **PDBTitle:** crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
74	c2q0oA_	Alignment	not modelled	8.3	5	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
75	c3fioB_	Alignment	not modelled	8.0	20	**PDB header:**nucleotide binding protein, metal bindin **Chain:** B: **PDB Molecule:**a cystathionine beta-synthase domain protein **PDBTitle:** crystal structure of a fragment of a cystathionine beta-2 synthase domain protein fused to a zn-ribbon-like domain
76	d2o16a3	Alignment	not modelled	7.9	33	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair

77	c3fosA_	Alignment	not modelled	7.4	11	**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
78	c2ev2B_	Alignment	not modelled	7.3	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** structure of rv1264n, the regulatory domain of the mycobacterial2 adenylyl cylcase rv1264, at ph 8.5
79	d1y5ha3	Alignment	not modelled	7.0	13	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
80	c2wukD_	Alignment	not modelled	7.0	16	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**septum site-determining protein diviva; **PDBTitle:** diviva n-terminal domain, f17a mutant
81	c3cagF_	Alignment	not modelled	7.0	14	**PDB header:**dna binding protein **Chain:** F: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines.
82	d2p5ma1	Alignment	not modelled	6.8	9	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
83	d2rc3a1	Alignment	not modelled	6.7	33	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
84	c2w0nA_	Alignment	not modelled	6.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein dcus; **PDBTitle:** plasticity of pas domain and potential role for signal2 transduction in the histidine-kinase dcus
85	c3libA_	Alignment	not modelled	6.6	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**hypothetical sensory transduction histidine kinase; **PDBTitle:** crystal structure of the extracellular domain of the putative2 histidine kinase mmhk1s-z3
86	d1k8ib2	Alignment	not modelled	6.5	13	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
87	d1b4ba_	Alignment	not modelled	6.4	14	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
88	d2yzia1	Alignment	not modelled	6.0	13	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
89	d1pbja3	Alignment	not modelled	5.6	33	**Fold:**CBS-domain pair **Superfamily:**CBS-domain pair **Family:**CBS-domain pair
90	d2pyqa1	Alignment	not modelled	5.4	15	**Fold:**Jann4075-like **Superfamily:**Jann4075-like **Family:**Jann4075-like