

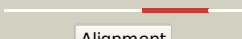






















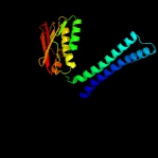


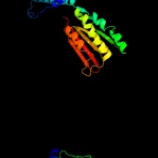
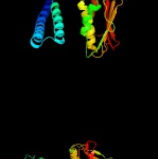



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2027c_(-)_2272795_2274516
Date	Mon Aug 5 13:25:13 BST 2019
Unique Job ID	8c22470b83c62c4e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ew8A_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein divl; <b>PDBTitle:</b> crystal structure of a c-terminal part of tyrosine kinase (divl) from2 caulobacter crescentus cb15 at 2.50 a resolution (psi community3 target, shapiro l.)
2	<a href="#">c4i5sA_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative histidine kinase covs; vick-like protein; <b>PDBTitle:</b> structure and function of sensor histidine kinase
3	<a href="#">c3d36B_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> sporulation kinase b; <b>PDBTitle:</b> how to switch off a histidine kinase: crystal structure of2 geobacillus stearothermophilus kinb with the inhibitor sda
4	<a href="#">c2c2aA_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor histidine kinase; <b>PDBTitle:</b> structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
5	<a href="#">c4kp4B_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase/signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> osmolarity sensor protein envz, histidine kinase; <b>PDBTitle:</b> deciphering cis-trans directionality and visualizing2 autophosphorylation in histidine kinases.
6	<a href="#">c4u7nA_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine protein kinase sensor protein; <b>PDBTitle:</b> inactive structure of histidine kinase
7	<a href="#">c5idjA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cell cycle histidine kinase ccka; <b>PDBTitle:</b> bifunctional histidine kinase ccka (domains dhp-ca) in complex with2 adp/mg2+
8	<a href="#">c3d2rB_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> [pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; <b>PDBTitle:</b> crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
9	<a href="#">c6dk8B_</a>	 Alignment		100.0	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> rets (regulator of exopolysaccharide and type iii <b>PDBTitle:</b> rets kinase region without cobalt
10	<a href="#">c2q8fA_</a>	 Alignment		100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; <b>PDBTitle:</b> structure of pyruvate dehydrogenase kinase isoform 1
11	<a href="#">c2bu8A_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase kinase isoenzyme 2; <b>PDBTitle:</b> crystal structures of human pyruvate dehydrogenase kinase 2 containing2 physiological and synthetic ligands

12	<a href="#">c3crlB</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate dehydrogenase [lipoamide] kinase isozyme 2, <b>PDBTitle:</b> crystal structure of the pdhk2-l2 complex.
13	<a href="#">c1qjvA</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase; <b>PDBTitle:</b> branched-chain alpha-ketoacid dehydrogenase kinase (bck) complexed with2 atp-gamma-s
14	<a href="#">c3tz5A</a>	Alignment		100.0	19	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, <b>PDBTitle:</b> crystal structure of branched-chain alpha-ketoacid dehydrogenase2 kinase/phenylbutyrate complex with adp
15	<a href="#">c4biyD</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> sensor protein cpxa; <b>PDBTitle:</b> crystal structure of cpxahdc (monoclinic form 2)
16	<a href="#">c1y8oA</a>	Alignment		100.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; <b>PDBTitle:</b> crystal structure of the pdk3-l2 complex
17	<a href="#">c4gczB</a>	Alignment		100.0	19	<b>PDB header:</b> signaling protein, de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> blue-light photoreceptor, sensor protein fixl; <b>PDBTitle:</b> structure of a blue-light photoreceptor
18	<a href="#">c1b3qA</a>	Alignment		99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (chemotaxis protein chea); <b>PDBTitle:</b> crystal structure of chea-289, a signal transducing histidine kinase
19	<a href="#">c4biuB</a>	Alignment		99.9	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein cpxa; <b>PDBTitle:</b> crystal structure of cpxahdc (orthorhombic form 1)
20	<a href="#">c3a0rA</a>	Alignment		99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
21	<a href="#">c4r39A</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> blue-light-activated histidine kinase 2; <b>PDBTitle:</b> histidine kinase domain from erythrobacter litoralis el346 blue-light2 activated histidine kinase
22	<a href="#">c5idmA</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cell cycle histidine kinase ccka; <b>PDBTitle:</b> bifunctional histidine kinase ccka (domain, ca) in complex with c-di-2 gmp and amppnp/mg2+
23	<a href="#">c6blkB</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> signal transduction histidine-protein kinase/phosphatase <b>PDBTitle:</b> mycobacterial sensor histidine kinase mprb
24	<a href="#">d2c2aa2</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
25	<a href="#">d1bxda</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
26	<a href="#">c3zxqA</a>	Alignment	not modelled	99.9	100	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypoxia sensor histidine kinase response regulator dost; <b>PDBTitle:</b> crystal structure of the atp-binding domain of mycobacterium2 tuberculosis dost
27	<a href="#">d1ysra1</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase

28	<a href="#">c2ch4A</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> transferase/chemotaxis <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis protein chea; <b>PDBTitle:</b> complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew
29	<a href="#">d1gkza2</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> alpha-ketoacid dehydrogenase kinase, C-terminal domain
30	<a href="#">c4pl9A</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ethylene receptor 1; <b>PDBTitle:</b> structure of the catalytic domain of etr1 from arabidopsis thaliana
31	<a href="#">c4gt8A</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein vras; <b>PDBTitle:</b> crystal structure of the catalytic and atp-binding domain from vras in2 complex with adp
32	<a href="#">c3sl2A</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor histidine kinase yycg; <b>PDBTitle:</b> atp forms a stable complex with the essential histidine kinase walk2 (yycg) domain
33	<a href="#">d1jm6a2</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> alpha-ketoacid dehydrogenase kinase, C-terminal domain
34	<a href="#">d1id0a</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
35	<a href="#">d1i58a</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
36	<a href="#">c3a0tA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> catalytic domain of histidine kinase thka (tm1359) in complex with adp2 and mg ion (trigonal)
37	<a href="#">c4r3aA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> blue-light-activated histidine kinase 2; <b>PDBTitle:</b> erythrobacter litoralis el346 blue-light activated histidine kinase
38	<a href="#">c3gieA</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor histidine kinase desk; <b>PDBTitle:</b> crystal structure of desk_h188e in complex with amp-pcp
39	<a href="#">c3jz3B</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein qsec; <b>PDBTitle:</b> structure of the cytoplasmic segment of histidine kinase qsec
40	<a href="#">c3zxoB</a>	Alignment	not modelled	99.9	60	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> redox sensor histidine kinase response regulator devs; <b>PDBTitle:</b> crystal structure of the mutant atp-binding domain of2 mycobacterium tuberculosis doss
41	<a href="#">c4fmtB</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> chpt protein; <b>PDBTitle:</b> crystal structure of a chpt protein (cc_3470) from caulobacter2 crescentus cb15 at 2.30 a resolution
42	<a href="#">c3ehgA</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor kinase (yocf protein); <b>PDBTitle:</b> crystal structure of the atp-binding domain of desk in complex with2 atp
43	<a href="#">c5epvB</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> blue-light-activated histidine kinase; <b>PDBTitle:</b> histidine kinase domain from the lov-hk blue-light receptor from2 brucella abortus
44	<a href="#">c6nb0A</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine kinase; <b>PDBTitle:</b> crystal structure of histidine kinase from burkholderia phymatum2 stm815
45	<a href="#">c6mzbA</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> rod cgmp-specific 3',5'-cyclic phosphodiesterase subunit <b>PDBTitle:</b> cryo-em structure of phosphodiesterase 6
46	<a href="#">c4qpkA</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphotransferase; <b>PDBTitle:</b> 1.7 angstrom structure of a bacterial phosphotransferase
47	<a href="#">c4ctiA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> osmolarity sensor protein envz, af1503; <b>PDBTitle:</b> escherichia coli envz histidine kinase catalytic part fused to2 archaeoglobus fulgidus af1503 hamp domain
48	<a href="#">c6e95A</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> staphylococcus aureus agrc histidine kinase module fused to <b>PDBTitle:</b> chimeric structure of saccharomyces cerevisiae gcn4 leucine zipper2 fused to staphylococcus aureus agrc cytoplasmic histidine kinase3 module (dataset isotropically truncated by hkl2000)
49	<a href="#">d1r62a</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
50	<a href="#">c3ibjB</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cgmp-dependent 3',5'-cyclic phosphodiesterase; <b>PDBTitle:</b> x-ray structure of pde2a
51	<a href="#">c4bwiA</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phytochrome-like protein cph2; <b>PDBTitle:</b> structure of the phytochrome cph2 from synechocystis

						sp. pcc6803
52	<a href="#">d2hkja3</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
53	<a href="#">c4bxiA</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> accessory gene regulator protein c; <b>PDBTitle:</b> crystal structure of atp binding domain of agrc from2 staphylococcus aureus
54	<a href="#">c3mf0A</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cgmp-specific 3',5'-cyclic phosphodiesterase; <b>PDBTitle:</b> crystal structure of pde5a gaf domain (89-518)
55	<a href="#">d1th8a</a>	Alignment	not modelled	99.6	26	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
56	<a href="#">c1mc0A</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 3',5'-cyclic nucleotide phosphodiesterase 2a; <b>PDBTitle:</b> regulatory segment of mouse 3',5'-cyclic nucleotide phosphodiesterase2 2a, containing the gaf a and gaf b domains
57	<a href="#">c3ci6B</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase; <b>PDBTitle:</b> crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase
58	<a href="#">c6oeiA</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> spindle pole body component spc42,sigma-54-dependent <b>PDBTitle:</b> yeast spc42 n-terminal coiled-coil fused to pdb: 3k2n
59	<a href="#">c3trcA</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase; <b>PDBTitle:</b> structure of the gaf domain from a phosphoenolpyruvate-protein2 phosphotransferase (ptsp) from coxiella burnetii
60	<a href="#">c2zkbB</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> type 2 dna topoisomerase 6 subunit b; <b>PDBTitle:</b> crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
61	<a href="#">c3p01C</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> two-component response regulator; <b>PDBTitle:</b> crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
62	<a href="#">c2w3gA</a>	Alignment	not modelled	99.5	72	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> two component sensor histidine kinase devs (gaf) <b>PDBTitle:</b> air-oxidized structure of the first gaf domain of2 mycobacterium tuberculosis doss
63	<a href="#">c3p01A</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> two-component response regulator; <b>PDBTitle:</b> crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
64	<a href="#">c5w10A</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cgmp-specific phosphodiesterase; <b>PDBTitle:</b> lcd1 gaf domain in complex with camp ligand
65	<a href="#">d2o9ca1</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GAF domain-like <b>Family:</b> GAF domain
66	<a href="#">c1mx0D</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> type ii dna topoisomerase vi subunit b; <b>PDBTitle:</b> structure of topoisomerase subunit
67	<a href="#">d2veaa1</a>	Alignment	not modelled	99.4	9	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GAF domain-like <b>Family:</b> GAF domain
68	<a href="#">c4g3vB</a>	Alignment	not modelled	99.4	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator nlh2; <b>PDBTitle:</b> crystal structure of a. aeolicus nlh2 gaf domain in an inactive state
69	<a href="#">d1h7sa2</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
70	<a href="#">c3eeaB</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> gaf domain/hd domain protein; <b>PDBTitle:</b> the crystal structure of the gaf domain/hd domain protein2 from geobacter sulfurreducens
71	<a href="#">c2qybA</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> membrane protein, putative; <b>PDBTitle:</b> crystal structure of the gaf domain region of putative membrane2 protein from geobacter sulfurreducens pca
72	<a href="#">c3w2zA</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of the cyanobacterial protein
73	<a href="#">c2zmfA</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> camp and camp-inhibited cgmp 3',5'-cyclic phosphodiesterase <b>PDBTitle:</b> crystal structure of the c-terminal gaf domain of human2 phosphodiesterase 10a
74	<a href="#">c2q2eB</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> type 2 dna topoisomerase 6 subunit b; <b>PDBTitle:</b> crystal structure of the topoisomerase vi holoenzyme from2 methanosarcina mazei
75	<a href="#">c4fofA</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of the blue-light absorbing form of the2

						thermosynechococcus elongatus pixj gaf-domain
76	<a href="#">c3dbaB_</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cone cgmp-specific 3',5'-cyclic phosphodiesterase subunit <b>PDBTitle:</b> crystal structure of the cgmp-bound gaf a domain from the2 photoreceptor phosphodiesterase 6c
77	<a href="#">c3mmhA_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-r-sulfoxide reductase; <b>PDBTitle:</b> x-ray structure of free methionine-r-sulfoxide reductase from2 neisseria meningitidis in complex with its substrate
78	<a href="#">c6g20A_</a>	Alignment	not modelled	99.4	11	<b>PDB header:</b> fluorescent protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriophytochrome protein; <b>PDBTitle:</b> crystal structure of a fluorescence optimized bathy phytochrome2 pairfp2 derived from wild-type agp2 in its functional meta-f3 intermediate state.
79	<a href="#">c4s21B_</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> bacteriophytochrome (light-regulated signal transduction <b>PDBTitle:</b> crystal structure of the photosensory core module of2 bacteriophytochrome rpa3015 from r. palustris
80	<a href="#">d2oola1</a>	Alignment	not modelled	99.4	10	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GAF domain-like <b>Family:</b> GAF domain
81	<a href="#">c3oovA_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein, putative; <b>PDBTitle:</b> crystal structure of a methyl-accepting chemotaxis protein, residues2 122 to 287
82	<a href="#">c2vjwA_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gaf family protein; <b>PDBTitle:</b> crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
83	<a href="#">c4mcwA_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> metal dependent phosphohydrolase; <b>PDBTitle:</b> metallo-enzyme from p. marina
84	<a href="#">c4wkkA_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacteriophytochrome protein; <b>PDBTitle:</b> the photosensory module (pas-gaf-phy) of the bacterial phytochrome2 agp1 (atbphp1) in the pr form, chromophore modelled with an exocyclic3 double bond at pyrrole ring a.
85	<a href="#">c3k2nB_</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> sigma-54-dependent transcriptional regulator; <b>PDBTitle:</b> the crystal structure of sigma-54-dependent transcriptional regulator2 domain from chlorobium tepidum t1s
86	<a href="#">c3rfbB_</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of frmsr
87	<a href="#">d1mc0a1</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GAF domain-like <b>Family:</b> GAF domain
88	<a href="#">c3c2wB_</a>	Alignment	not modelled	99.3	11	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> bacteriophytochrome; <b>PDBTitle:</b> crystal structure of the photosensory core domain of p. aeruginosa2 bacteriophytochrome pabphp in the pfr state
89	<a href="#">c1ykdB_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> crystal structure of the tandem gaf domains from a cyanobacterial2 adenyl cyclase: novel modes of ligand-binding and dimerization
90	<a href="#">c3e0yA_</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved domain protein; <b>PDBTitle:</b> the crystal structure of a conserved domain from a protein of2 geobacter sulfurreducens pca
91	<a href="#">c4iukB_</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> nitrate-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> nrea protein; <b>PDBTitle:</b> crystal structure of nrea of staphylococcus carnosus with bound2 nitrate
92	<a href="#">c3e98B_</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> gaf domain of unknown function; <b>PDBTitle:</b> crystal structure of a gaf domain containing protein that belongs to2 pfam duf484 family (pa5279) from pseudomonas aeruginosa at 2.43 a3 resolution
93	<a href="#">d3c2wa1</a>	Alignment	not modelled	99.2	12	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GAF domain-like <b>Family:</b> GAF domain
94	<a href="#">c1vhmB_</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein yebf; <b>PDBTitle:</b> crystal structure of an hypothetical protein
95	<a href="#">d1ixma_</a>	Alignment	not modelled	99.2	12	<b>Fold:</b> Sporulation response regulatory protein Spo0B <b>Superfamily:</b> Sporulation response regulatory protein Spo0B <b>Family:</b> Sporulation response regulatory protein Spo0B
96	<a href="#">d1vhma_</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GAF domain-like <b>Family:</b> GAF domain
97	<a href="#">c4g3kB_</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator nh1; <b>PDBTitle:</b> crystal structure of a. aeolicus nh1 gaf domain in an inactive state
98	<a href="#">c4geeA_</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> isomerase/isomerase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> dna gyrase subunit b; <b>PDBTitle:</b> pyrrolopyrimidine inhibitors of dna gyrase b and topoisomerase iv,2 part i: structure guided discovery and optimization of dual targeting3 agents with potent, broad-spectrum enzymatic activity.
						<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative two-component sensor histidine

99	<a href="#">c3hcyB_</a>	Alignment	not modelled	99.2	13	kinase protein; <b>PDBTitle:</b> the crystal structure of the domain of putative two-component sensor2 histidine kinase protein from sinorhizobium meliloti 1021
100	<a href="#">c3ksiA_</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> structure of frmsr of staphylococcus aureus (complex with 2-propanol)
101	<a href="#">c3o5yA_</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> the crystal structure of the gaf domain of a two-component sensor2 histidine kinase from bacillus halodurans to 2.45a
102	<a href="#">c2k31A_</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphodiesterase 5a, cgmp-specific; <b>PDBTitle:</b> solution structure of cgmp-binding gaf domain of 2 phosphodiesterase 5
103	<a href="#">c4rq9A_</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> photoreceptor-histidine kinase bphp; <b>PDBTitle:</b> crystal structure of the chromophore-binding domain of stigmatella2 aurantiaca bacteriophytochrome (thr289his mutant) in the pr state
104	<a href="#">d1bkna2</a>	Alignment	not modelled	99.1	22	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
105	<a href="#">c4ehoD_</a>	Alignment	not modelled	99.1	14	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> bacteriophytochrome, pas/pac sensor; <b>PDBTitle:</b> crystal structure of the bacteriophytochrome rpbphp1
106	<a href="#">d1b63a2</a>	Alignment	not modelled	99.1	24	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> DNA gyrase/MutL, N-terminal domain
107	<a href="#">c4pauA_</a>	Alignment	not modelled	99.1	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen regulatory protein a; <b>PDBTitle:</b> hypothetical protein sa1058 from s. aureus.
108	<a href="#">c5dfxA_</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine kinase; <b>PDBTitle:</b> structure of the parental state of gaf3 from slr1393 of synechocystis2 sp. pcc6803 (in vivo assembled protein/chromophore)
109	<a href="#">c6mghB_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> fluorescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> mirfp670nano; <b>PDBTitle:</b> x-ray structure of monomeric near-infrared fluorescent protein2 mirfp670nano
110	<a href="#">c5hl6B_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative gaf sensor protein; <b>PDBTitle:</b> crystal structure of a putative gaf sensor protein from burkholderia2 vietnamiensis
111	<a href="#">c4mmdD_</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein ta0848; <b>PDBTitle:</b> structural and biochemical analysis of type ii free methionine-r-2 sulfoxide reductase from thermoplasma acidophilum
112	<a href="#">d2k2na1</a>	Alignment	not modelled	99.0	22	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GAF domain-like <b>Family:</b> GAF domain
113	<a href="#">c2lb5A_</a>	Alignment	not modelled	99.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor histidine kinase; <b>PDBTitle:</b> refined structural basis for the photoconversion of a phytochrome to2 the activated far-red light-absorbing form
114	<a href="#">c2veaA_</a>	Alignment	not modelled	99.0	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phytochrome-like protein cph1; <b>PDBTitle:</b> the complete sensory module of the cyanobacterial2 phytochrome cph1 in the pr-state.
115	<a href="#">d1y8oa2</a>	Alignment	not modelled	98.9	13	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> alpha-ketoacid dehydrogenase kinase, C-terminal domain
116	<a href="#">c5llxB_</a>	Alignment	not modelled	98.9	8	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> diguanylate cyclase (ggdef) domain-containing protein; <b>PDBTitle:</b> bacteriophytochrome activated diguanylyl cyclase from idiomarina2 species a28l with gtp bound
117	<a href="#">c4b6cB_</a>	Alignment	not modelled	98.9	23	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> dna gyrase subunit b,dna gyrase subunit b,dna gyrase <b>PDBTitle:</b> structure of the m. smegmatis gyrb atpase domain in complex with an2 aminopyrazinamide
118	<a href="#">c6fhtB_</a>	Alignment	not modelled	98.9	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> bacteriophytochrome,adenylate cyclase; <b>PDBTitle:</b> crystal structure of an artificial phytochrome regulated2 adenylate/guanylate cyclase in its dark adapted pr form
119	<a href="#">c4qprA_</a>	Alignment	not modelled	98.8	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein kdpd; <b>PDBTitle:</b> crystal structure of gaf domain of potassium sensor histidine kinase2 kdpd from escherichia coli
120	<a href="#">d1mc0a2</a>	Alignment	not modelled	98.8	21	<b>Fold:</b> Profilin-like <b>Superfamily:</b> GAF domain-like <b>Family:</b> GAF domain