


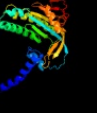
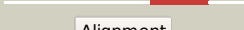

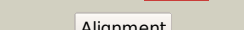

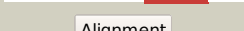

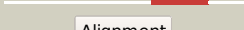

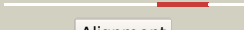






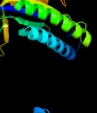
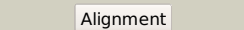



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2435c_(-) _2730567_2732759
Date	Wed Aug 7 12:50:05 BST 2019
Unique Job ID	1621a807d566e316

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6r4oA_</a>	 Alignment		100.0	22	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase 9; <b>PDBTitle:</b> structure of a truncated adenylyl cyclase bound to mant-gtp, forskolin2 and an activated stimulatory galphas protein
2	<a href="#">c6fhtB_</a>	 Alignment		100.0	24	<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 adenylyl/guanylyl cyclase in its dark adapted pr form
3	<a href="#">c6r4pA_</a>	 Alignment		100.0	25	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase 9; <b>PDBTitle:</b> structure of a soluble domain of adenylyl cyclase bound to an2 activated stimulatory g protein
4	<a href="#">c4yusA_</a>	 Alignment		99.9	18	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> family 3 adenylyl cyclase; <b>PDBTitle:</b> crystal structure of photoactivated adenylyl cyclase of a2 cyanobacteriaosillatoria acuminata in hexagonal form
5	<a href="#">c5nbyA_</a>	 Alignment		99.9	21	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> beta subunit of photoactivated adenylyl cyclase; <b>PDBTitle:</b> structure of a bacterial light-regulated adenylyl cyclase
6	<a href="#">c5o5kC_</a>	 Alignment		99.9	31	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> x-ray structure of a bacterial adenylyl cyclase soluble domain
7	<a href="#">c1cjkA_</a>	 Alignment		99.9	28	<b>PDB header:</b> lyase/lyase/signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase, type v; <b>PDBTitle:</b> complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
8	<a href="#">dlazsa_</a>	 Alignment		99.9	28	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
9	<a href="#">c4cIIA_</a>	 Alignment		99.9	17	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> adenylate cyclase type 10; <b>PDBTitle:</b> crystal structure of human soluble adenylyl cyclase in complex with2 bicarbonate
10	<a href="#">c1wc6B_</a>	 Alignment		99.9	19	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
11	<a href="#">c2w01C_</a>	 Alignment		99.9	27	<b>PDB header:</b> lyase <b>Chain:</b> C; <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> crystal structure of the guanylyl cyclase cya2

12	<a href="#">d1wc1a_</a>	Alignment		99.8	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
13	<a href="#">c3r5gB_</a>	Alignment		99.8	25	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> cyab; <b>PDBTitle:</b> crystal structure of the adenylyl cyclase cyab from p. aeruginosa
14	<a href="#">c3uvjC_</a>	Alignment		99.8	26	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> guanylate cyclase soluble subunit alpha-3; <b>PDBTitle:</b> crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
15	<a href="#">d1azsb_</a>	Alignment		99.8	31	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
16	<a href="#">c1y10C_</a>	Alignment		99.8	21	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein rv1264/mt1302; <b>PDBTitle:</b> mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
17	<a href="#">d1fx2a_</a>	Alignment		99.8	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
18	<a href="#">c2wz1B_</a>	Alignment		99.8	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> guanylate cyclase soluble subunit beta-1; <b>PDBTitle:</b> structure of the catalytic domain of human soluble guanylate cyclase 12 beta 3.
19	<a href="#">c6fu4D_</a>	Alignment		99.8	15	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> probable chemotaxis transducer; <b>PDBTitle:</b> ligand binding domain (lbd) of the p. aeruginosa histamine receptor2 tlpq
20	<a href="#">c5t65A_</a>	Alignment		99.8	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein pcta; <b>PDBTitle:</b> ligand binding domain of pseudomonas aeruginosa pao1 amino acid2 chemoreceptor pcta in complex with l-ile
21	<a href="#">d1fx4a_</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Nucleotide cyclase <b>Family:</b> Adenylyl and guanylyl cyclase catalytic domain
22	<a href="#">c4wy9A_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative mcp-type signal transduction protein; <b>PDBTitle:</b> crystal structure of the periplasmic sensory domain of the2 campylobacter jejuni chemoreceptor tlp1
23	<a href="#">c6dtmA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein tlpA; <b>PDBTitle:</b> crystal structure of helicobacter pylori tlpA chemoreceptor ligand2 binding domain
24	<a href="#">c1yk9A_</a>	Alignment	not modelled	99.8	34	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate cyclase; <b>PDBTitle:</b> crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
25	<a href="#">c4xmrB_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative methyl-accepting chemotaxis signal transduction <b>PDBTitle:</b> crystal structure of the sensory domain of the campylobacter jejuni2 chemoreceptor tlp3 (ccml) with isoleucine bound.
26	<a href="#">c6aqaA_</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> bacterio-rhodopsin/guanylyl cyclase 1 fusion protein; <b>PDBTitle:</b> monomeric crystal structure of the e497/c566d double mutant of the2 guanylyl cyclase domain of the rhogc fusion protein from the aquatic3 fungus blastocladiella emersonii
27	<a href="#">c6d8vA_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable chemoreceptor (methyl-accepting chemotaxis) <b>PDBTitle:</b> methyl-accepting chemotaxis protein x

28	<a href="#">c3c8cB</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of mcp_n and cache domains of methyl-accepting2 chemotaxis protein from vibrio cholerae
29	<a href="#">c2p7jA</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative sensory box/ggdef family protein; <b>PDBTitle:</b> crystal structure of the domain of putative sensory box/ggdef family2 protein from vibrio parahaemolyticus
30	<a href="#">c3libA</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical sensory transduction histidine kinase; <b>PDBTitle:</b> crystal structure of the extracellular domain of the putative2 histidine kinase mmhk1s-z3
31	<a href="#">c5ltoB</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein pctb; <b>PDBTitle:</b> ligand binding domain of pseudomonas aeruginosa pao1 amino acid2 chemoreceptors pctb in complex with l-gln
32	<a href="#">c6ioqA</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> the ligand binding domain of mlp24 with glycine
33	<a href="#">c6f9gE</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> signaling protein <b>Chain:</b> E: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein mcpu; <b>PDBTitle:</b> ligand binding domain of p. putida kt2440 polyamine chemoreceptors2 mcpu in complex putrescine.
34	<a href="#">c5wbfB</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> methyl-accepting chemotaxis transducer (tlpc); <b>PDBTitle:</b> double cache (dcache) sensing domain of tlpc chemoreceptor from2 helicobacter pylori
35	<a href="#">c3liaA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical sensory transduction histidine kinase; <b>PDBTitle:</b> crystal structure of the extracellular domain of the putative2 histidine kinase mmhk1s-z2
36	<a href="#">c3e4pB</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> c4-dicarboxylate transport sensor protein dctb; <b>PDBTitle:</b> crystal structure of malonate occupied dctb
37	<a href="#">c1ybuA</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipj; <b>PDBTitle:</b> mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
38	<a href="#">c5ltvA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemotactic transducer pctc; <b>PDBTitle:</b> ligand binding regions of pseudomonas aeruginosa pao1 amino acid2 chemoreceptors pctc in complex with gaba
39	<a href="#">c4wp3E</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> ma1120; <b>PDBTitle:</b> crystal structure of adenylyl cyclase from mycobacterium avium ma11202 wild type
40	<a href="#">c3et6A</a>	Alignment	not modelled	99.7	31	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> soluble guanylyl cyclase beta; <b>PDBTitle:</b> the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
41	<a href="#">c3mr7B</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate/guanylate cyclase/hydrolase, alpha/beta fold <b>PDBTitle:</b> crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi
42	<a href="#">c3lifA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative diguanylate cyclase (ggdef) with pas/pac domain; <b>PDBTitle:</b> crystal structure of the extracellular domain of the putative2 histidine kinase rphk1s-z16
43	<a href="#">c3by9A</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of the v. cholerae histidine kinase dctb sensor2 domain
44	<a href="#">c3licA</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of the extracellular domain of the putative2 histidine kinase sohk1s-z6
45	<a href="#">c4e40A</a>	Alignment	not modelled	99.5	7	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the haptoglobin-hemoglobin receptor of trypanosoma congolense
46	<a href="#">c3fosA</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of two-component sensor histidine kinase domain from2 bacillus subtilis subsp. subtilis str. 168
47	<a href="#">d2p7ja2</a>	Alignment	not modelled	99.4	11	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Sensory domain-like <b>Family:</b> Ykul C-terminal domain-like
48	<a href="#">c3ur1C</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> the structure of a ternary complex between chea domains p4 and p5 with2 chew and with a truncated fragment of tm14, a chemoreceptor analog3 from thermotoga maritima.
49	<a href="#">c3zx6A</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> signaling <b>Chain:</b> A: <b>PDB Molecule:</b> hamp, methyl-accepting chemotaxis protein i; <b>PDBTitle:</b> structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
50	<a href="#">c4yvwA</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein kinase walk; <b>PDBTitle:</b> crystal structure of the extracellular receptor domain of the2 essential sensor kinase walk from staphylococcus aureus
51	<a href="#">c5ereA</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular ligand-binding receptor; <b>PDBTitle:</b> extracellular ligand binding receptor from desulfohalobium retbaense2 dsm5692

52	<a href="#">c1qu7A</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein i; <b>PDBTitle:</b> four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
53	<a href="#">c5jefA</a>	Alignment	not modelled	98.3	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate/nitrite sensor protein narq; <b>PDBTitle:</b> fragment of nitrate/nitrite sensor histidine kinase narq (wt) in2 asymmetric holo state
54	<a href="#">c4gn0D</a>	Alignment	not modelled	98.3	24	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> hamp domain of af1503; <b>PDBTitle:</b> de novo phasing of a hamp-complex using an improved arcimboldo method
55	<a href="#">c5gjfF</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> voltage-dependent calcium channel subunit alpha-2/delta-1; <b>PDBTitle:</b> structure of the mammalian voltage-gated calcium channel cav1.12 complex at near atomic resolution
56	<a href="#">c3lnrA</a>	Alignment	not modelled	97.8	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> aerotaxis transducer aer2; <b>PDBTitle:</b> crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
57	<a href="#">d1p0za</a>	Alignment	not modelled	97.8	18	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Sensory domain-like <b>Family:</b> Sensory domain of two-component sensor kinase
58	<a href="#">d3by8a1</a>	Alignment	not modelled	97.7	11	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Sensory domain-like <b>Family:</b> Sensory domain of two-component sensor kinase
59	<a href="#">c2ch7A</a>	Alignment	not modelled	97.6	8	<b>PDB header:</b> chemotaxis <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
60	<a href="#">d2basa2</a>	Alignment	not modelled	97.3	12	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Sensory domain-like <b>Family:</b> Ykul C-terminal domain-like
61	<a href="#">c3jbrF</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> voltage-dependent calcium channel subunit alpha-2/delta-1; <b>PDBTitle:</b> cryo-em structure of the rabbit voltage-gated calcium channel cav1.12 complex at 4.2 angstrom
62	<a href="#">d2asxa1</a>	Alignment	not modelled	97.0	31	<b>Fold:</b> HAMP domain-like <b>Superfamily:</b> HAMP domain-like <b>Family:</b> HAMP domain
63	<a href="#">c3g67A</a>	Alignment	not modelled	96.8	9	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of a soluble chemoreceptor from thermotoga2 maritima
64	<a href="#">c2qhkA</a>	Alignment	not modelled	96.7	9	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of methyl-accepting chemotaxis protein from vibrio2 parahaemolyticus rimd 2210633
65	<a href="#">c4exoA</a>	Alignment	not modelled	96.6	9	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> revised, rerefined crystal structure of pdb entry 2qhk, methyl2 accepting chemotaxis protein
66	<a href="#">c3ub9B</a>	Alignment	not modelled	96.6	12	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> chemoreceptor tlpb; <b>PDBTitle:</b> periplasmic portion of the helicobacter pylori chemoreceptor tlpb with2 hydroxyurea bound
67	<a href="#">c5g4yA</a>	Alignment	not modelled	96.0	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis protein; <b>PDBTitle:</b> structural basis for carboxylic acid recognition by a cache2 chemosensory domain.
68	<a href="#">c4onxB</a>	Alignment	not modelled	95.9	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor histidine kinase; <b>PDBTitle:</b> 2.8 angstrom crystal structure of sensor domain of histidine kinase2 from clostridium perfringens.
69	<a href="#">c4k08A</a>	Alignment	not modelled	95.6	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis sensory transducer; <b>PDBTitle:</b> periplasmic sensor domain of chemotaxis protein, adeh 3718
70	<a href="#">c3zrwB</a>	Alignment	not modelled	94.8	23	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> af1503 protein, osmolarity sensor protein envz; <b>PDBTitle:</b> the structure of the dimeric hamp-dhp fusion a291v mutant
71	<a href="#">c2w27A</a>	Alignment	not modelled	94.8	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ykui protein; <b>PDBTitle:</b> crystal structure of the bacillus subtilis ykui protein, with an eal2 domain, in complex with substrate c-di-gmp and calcium
72	<a href="#">c4i5sA</a>	Alignment	not modelled	93.3	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
73	<a href="#">c2rm8A</a>	Alignment	not modelled	93.1	38	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sensory rhodopsin ii transducer; <b>PDBTitle:</b> the solution structure of phototactic transducer protein2 htrii linker region from natronomonas pharaonis
74	<a href="#">c4ctiA</a>	Alignment	not modelled	86.7	30	<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
75	<a href="#">c2qkpD</a>	Alignment	not modelled	86.5	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of c-terminal domain of smu_1151c from streptococcus2 mutans
76	<a href="#">c4biuB</a>	Alignment	not modelled	84.1	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein cpaxa; <b>PDBTitle:</b> crystal structure of cpaxadc (orthorhombic form 1)

77	<a href="#">c3caxA_</a>	Alignment	not modelled	80.3	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pf0695; <b>PDBTitle:</b> crystal structure of uncharacterized protein pf0695
78	<a href="#">c5fq1A_</a>	Alignment	not modelled	68.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine kinase; <b>PDBTitle:</b> structure of the cytoplasmic pas domain of the geobacillus2 thermodenitrificans histidine kinase cita
79	<a href="#">c3b42B_</a>	Alignment	not modelled	64.4	21	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein, putative; <b>PDBTitle:</b> periplasmic sensor domain of chemotaxis protein gsu0935
80	<a href="#">c3mxqC_</a>	Alignment	not modelled	62.1	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
81	<a href="#">d2hjea1</a>	Alignment	not modelled	61.0	14	<b>Fold:</b> Profilin-like <b>Superfamily:</b> Sensory domain-like <b>Family:</b> LuxQ-periplasmic domain-like
82	<a href="#">c5iu1A_</a>	Alignment	not modelled	54.4	21	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> ctr1-like protein; <b>PDBTitle:</b> n-terminal pas domain homodimer of ppnpr map3k from physcomitrella2 patens.
83	<a href="#">c3c38A_</a>	Alignment	not modelled	52.0	12	<b>PDB header:</b> signaling protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> autoinducer 2 sensor kinase/phosphatase luxq; <b>PDBTitle:</b> crystal structure of the periplasmic domain of vibrio2 cholerae luxq
84	<a href="#">c2kseA_</a>	Alignment	not modelled	51.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein qsec; <b>PDBTitle:</b> backbone structure of the membrane domain of e. coli histidine kinase2 receptor qsec, center for structures of membrane proteins (csmpr)3 target 4311c
85	<a href="#">c2gx5B_</a>	Alignment	not modelled	44.7	10	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> gtp-sensing transcriptional pleiotropic repressor cody; <b>PDBTitle:</b> n-terminal gaf domain of transcriptional pleiotropic repressor cody
86	<a href="#">c2w0nA_</a>	Alignment	not modelled	43.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein dcus; <b>PDBTitle:</b> plasticity of pas domain and potential role for signal2 transduction in the histidine-kinase dcus
87	<a href="#">c5ey0A_</a>	Alignment	not modelled	43.4	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-sensing transcriptional pleiotropic repressor cody; <b>PDBTitle:</b> crystal structure of cody from staphylococcus aureus with gtp and ile
88	<a href="#">c4fofA_</a>	Alignment	not modelled	38.4	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
89	<a href="#">c2qj3A_</a>	Alignment	not modelled	37.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen fixation regulatory protein; <b>PDBTitle:</b> crystal structure of the fad-containing pas domain of the protein nifl2 from azotobacter vinelandii.
90	<a href="#">c2kogA_</a>	Alignment	not modelled	36.8	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vesicle-associated membrane protein 2; <b>PDBTitle:</b> lipid-bound synaptobrevin solution nmr structure
91	<a href="#">c2ykfA_</a>	Alignment	not modelled	31.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable sensor histidine kinase pdtas; <b>PDBTitle:</b> sensor region of a sensor histidine kinase
92	<a href="#">c5ey2A_</a>	Alignment	not modelled	29.6	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-sensing transcriptional pleiotropic repressor cody; <b>PDBTitle:</b> crystal structure of cody from bacillus cereus
93	<a href="#">c5wdaL_</a>	Alignment	not modelled	29.0	15	<b>PDB header:</b> protein transport <b>Chain:</b> L: <b>PDB Molecule:</b> general secretion pathway protein g; <b>PDBTitle:</b> structure of the pulg pseudopilus
94	<a href="#">c3bjnA_</a>	Alignment	not modelled	26.9	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, putative; <b>PDBTitle:</b> crystal structure of c-terminal domain of putative transcriptional2 regulator from vibrio cholerae, targeted domain 79-240
95	<a href="#">c2qv6D_</a>	Alignment	not modelled	23.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> gtp cyclohydrolase iii; <b>PDBTitle:</b> gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
96	<a href="#">c3lyxA_</a>	Alignment	not modelled	22.6	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> sensory box/ggdef domain protein; <b>PDBTitle:</b> crystal structure of the pas domain of the protein cps_12912 from colwellia psychrerythraea. northeast structural3 genomics consortium target id csr222b
97	<a href="#">d1oqwa_</a>	Alignment	not modelled	19.9	15	<b>Fold:</b> Pili subunits <b>Superfamily:</b> Pili subunits <b>Family:</b> Pilin
98	<a href="#">c3mmhA_</a>	Alignment	not modelled	19.4	14	<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
99	<a href="#">c2w1rA_</a>	Alignment	not modelled	17.9	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> stage v sporulation protein t; <b>PDBTitle:</b> crystal structure of the c-terminal domain of b. subtilis spovt