

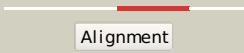



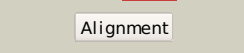



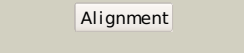

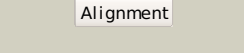

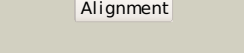



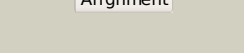

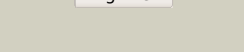



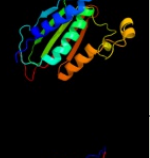
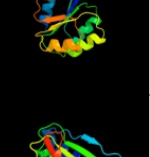

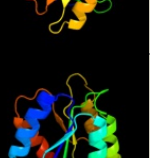

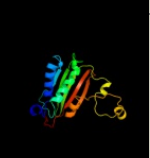
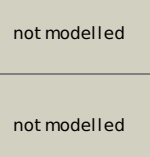


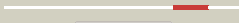



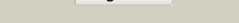
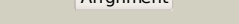
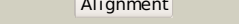

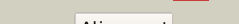
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2c2aA_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor histidine kinase; <b>PDBTitle:</b> structure of the entire cytoplasmic portion of a sensor2 histidine kinase protein
2	<a href="#">c3d2rB_</a>	 Alignment		100.0	16	<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
3	<a href="#">c2ayxA_</a>	 Alignment		100.0	100	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor kinase protein rcsc; <b>PDBTitle:</b> solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
4	<a href="#">c3d36B_</a>	 Alignment		100.0	25	<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
5	<a href="#">c2q8fA_</a>	 Alignment		100.0	18	<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
6	<a href="#">c1y8oA_</a>	 Alignment		100.0	15	<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
7	<a href="#">c2bu8A_</a>	 Alignment		100.0	16	<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 22 containing physiological and synthetic ligands
8	<a href="#">c3a0rA_</a>	 Alignment		100.0	25	<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)
9	<a href="#">c1g1vA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> [3-methyl-2-oxobutanoate dehydrogenase <b>PDBTitle:</b> branched-chain alpha-ketoacid dehydrogenase kinase (bck)2 complexed with atp-gamma-s
10	<a href="#">d2c2aa2</a>	 Alignment		100.0	30	<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
11	<a href="#">c1b3qA_</a>	 Alignment		100.0	20	<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

12	<a href="#">c3a0tA_</a>	Alignment		100.0	27	<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) in2 complex with adp and mg ion (trigonal)
13	<a href="#">c3lufB_</a>	Alignment		100.0	16	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> two-component system response regulator/ggdef <b>PDBTitle:</b> structure of probable two-component system response2 regulator/ggdef domain protein
14	<a href="#">d1gkza2</a>	Alignment		100.0	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
15	<a href="#">d2ayxa1</a>	Alignment		100.0	100	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
16	<a href="#">d1ld0a_</a>	Alignment		100.0	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
17	<a href="#">c1w25B_</a>	Alignment		100.0	31	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> stalked-cell differentiation controlling protein; <b>PDBTitle:</b> response regulator pled in complex with c-digmp
18	<a href="#">c3eq2A_</a>	Alignment		100.0	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable two-component response regulator; <b>PDBTitle:</b> structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
19	<a href="#">d1jm6a2</a>	Alignment		100.0	21	<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
20	<a href="#">d1bxda_</a>	Alignment		100.0	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
21	<a href="#">c3breA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable two-component response regulator; <b>PDBTitle:</b> crystal structure of p.aeruginosa pa3702
22	<a href="#">c3i5aA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator/ggdef domain protein; <b>PDBTitle:</b> crystal structure of full-length wpsr from pseudomonas syringae
23	<a href="#">c3jz3B_</a>	Alignment	not modelled	99.9	20	<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
24	<a href="#">d1ny5a1</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
25	<a href="#">c3cfyA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative luxo repressor protein; <b>PDBTitle:</b> crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus
26	<a href="#">c3gt7A_</a>	Alignment	not modelled	99.9	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
27	<a href="#">d1qkka_</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
28	<a href="#">c1ny5A_</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state

29	<a href="#">dljbea_</a>	Alignment	not modelled	99.9	37	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
30	<a href="#">c2ch4A_</a>	Alignment	not modelled	99.9	24	<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
31	<a href="#">d2pl1a1</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
32	<a href="#">d1w25a1</a>	Alignment	not modelled	99.9	32	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
33	<a href="#">c2rjnA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver:metal-dependent <b>PDBTitle:</b> crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
34	<a href="#">d1ysra1</a>	Alignment	not modelled	99.9	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> Histidine kinase
35	<a href="#">d1yioa2</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
36	<a href="#">d1k66a_</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
37	<a href="#">d1peya_</a>	Alignment	not modelled	99.9	31	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
38	<a href="#">c2zayA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator from desulfuromonas2 acetoxidans
39	<a href="#">d1s8na_</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
40	<a href="#">c3t6kB_</a>	Alignment	not modelled	99.9	31	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator receiver; <b>PDBTitle:</b> crystal structure of a hypothetical response regulator (caur_3799)2 from chloroflexus aurantiacus j-10-fl at 1.86 a resolution
41	<a href="#">d1mvoa_</a>	Alignment	not modelled	99.9	31	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
42	<a href="#">d1u0sy_</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
43	<a href="#">c3r0jA_</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> possible two component system response transcriptional <b>PDBTitle:</b> structure of phop from mycobacterium tuberculosis
44	<a href="#">d1ys7a2</a>	Alignment	not modelled	99.9	30	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
45	<a href="#">d1heya_</a>	Alignment	not modelled	99.9	36	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
46	<a href="#">c3cnbC_</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dna-binding response regulator, merr family; <b>PDBTitle:</b> crystal structure of signal receiver domain of dna binding response2 regulator protein (merr) from colwellia psychrerythraea 34h
47	<a href="#">d1i58a_</a>	Alignment	not modelled	99.9	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
48	<a href="#">c2zwmA_</a>	Alignment	not modelled	99.9	30	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein yycf; <b>PDBTitle:</b> crystal structure of yycf receiver domain from bacillus2 subtilis
49	<a href="#">c3jteA_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
50	<a href="#">c3hv2B_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator/hd domain protein; <b>PDBTitle:</b> crystal structure of signal receiver domain of hd domain-2 containing protein from pseudomonas fluorescens pf-5
51	<a href="#">c2qzjC_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> two-component response regulator; <b>PDBTitle:</b> crystal structure of a two-component response regulator from2 clostridium difficile
52	<a href="#">d1dbwa_</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
53	<a href="#">d1zh2a1</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
						<b>Fold:</b> Flavodoxin-like

54	<a href="#">d1krwa_</a>	Alignment	not modelled	99.9	29	<b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
55	<a href="#">d2a9pa1</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
56	<a href="#">d2r25b1</a>	Alignment	not modelled	99.9	34	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
57	<a href="#">c3cu5B_</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> two component transcriptional regulator, arac family; <b>PDBTitle:</b> crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
58	<a href="#">c3lteH_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
59	<a href="#">c3hdgE_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinnella3 succinogenes
60	<a href="#">c3mmnA_</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine kinase homolog; <b>PDBTitle:</b> crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+
61	<a href="#">d1zgza1</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
62	<a href="#">c2qr3A_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> two-component system response regulator; <b>PDBTitle:</b> crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
63	<a href="#">c3cg4A_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver domain protein (cheY-like); <b>PDBTitle:</b> crystal structure of response regulator receiver domain protein (cheY-2 like) from methanospirillum hungatei jf-1
64	<a href="#">d1kgsa2</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
65	<a href="#">c3gl9B_</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism
66	<a href="#">c3crnA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver domain protein, cheY-like; <b>PDBTitle:</b> crystal structure of response regulator receiver domain protein (cheY-2 like) from methanospirillum hungatei jf-1
67	<a href="#">d1zesa1</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
68	<a href="#">c3h1gA_</a>	Alignment	not modelled	99.9	32	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis protein cheY homolog; <b>PDBTitle:</b> crystal structure of cheY mutant t84a of helicobacter pylori
69	<a href="#">d1p6qa_</a>	Alignment	not modelled	99.9	31	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
70	<a href="#">c3nhzA_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> two component system transcriptional regulator mtra; <b>PDBTitle:</b> structure of n-terminal domain of mtra
71	<a href="#">c3n0rA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the phyr stress response regulator at 1.25 angstrom2 resolution
72	<a href="#">c3dzdA_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4 in the inactive2 state
73	<a href="#">c2jrlA_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> solution structure of the beryll fluoride-activated ntrc4 receiver2 domain dimer
74	<a href="#">d1xhfa1</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
75	<a href="#">c3b2nA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein q99uf4; <b>PDBTitle:</b> crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
76	<a href="#">d1mb3a_</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
77	<a href="#">c3khtA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of response regulator from hahella chejuensis
78	<a href="#">c3rqia_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein; <b>PDBTitle:</b> crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate

79	<a href="#">d1a04a2</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
80	<a href="#">c3c3mA</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1
81	<a href="#">c3cg0A</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver modulated diguanylate cyclase <b>PDBTitle:</b> crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding
82	<a href="#">c1ys7B</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein prra; <b>PDBTitle:</b> crystal structure of the response regulator protein prra complexed with2 mg2+
83	<a href="#">c2jk1A</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> dna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase transcriptional regulatory protein hupr1; <b>PDBTitle:</b> crystal structure of the wild-type hupr receiver domain
84	<a href="#">d1i3ca</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
85	<a href="#">c3m6mF</a>	Alignment	not modelled	99.9	31	<b>PDB header:</b> lyase/transferase <b>Chain:</b> F: <b>PDB Molecule:</b> sensory/regulatory protein rpfc; <b>PDBTitle:</b> crystal structure of rpff complexed with rec domain of rpfc
86	<a href="#">c2qvga</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> two component response regulator; <b>PDBTitle:</b> the crystal structure of a two-component response regulator2 from legionella pneumophila
87	<a href="#">c3ilhA</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> two component response regulator; <b>PDBTitle:</b> crystal structure of two component response regulator from cytophaga2 hutchinsonii
88	<a href="#">c2qxyB</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of a response regulator from thermotoga2 maritima
89	<a href="#">c3hebB</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator receiver domain protein (chey); <b>PDBTitle:</b> crystal structure of response regulator receiver domain from2 rhodospirillum rubrum
90	<a href="#">c2gwrA</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator mtra; <b>PDBTitle:</b> crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
91	<a href="#">c1a2oB</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> bacterial chemotaxis <b>Chain:</b> B: <b>PDB Molecule:</b> cheb methyltransferase; <b>PDBTitle:</b> structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
92	<a href="#">d1dz3a</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
93	<a href="#">d1dcfa</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> Receiver domain of the ethylene receptor
94	<a href="#">c3eulB</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> possible nitrate/nitrite response transcriptional <b>PDBTitle:</b> structure of the signal receiver domain of the putative2 response regulator narl from mycobacterium tuberculosis
95	<a href="#">c3hdvB</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of response regulator receiver protein from2 pseudomonas putida
96	<a href="#">c2qv0A</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein mrke; <b>PDBTitle:</b> crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
97	<a href="#">c3i42A</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver domain protein (chey- <b>PDBTitle:</b> structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
98	<a href="#">c3c97A</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> signaling protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> signal transduction histidine kinase; <b>PDBTitle:</b> crystal structure of the response regulator receiver domain2 of a signal transduction histidine kinase from aspergillus3 oryzae
99	<a href="#">c3cz5B</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> two-component response regulator, luxr family; <b>PDBTitle:</b> crystal structure of two-component response regulator, luxr family,2 from aurantimonas sp. si85-9a1
100	<a href="#">c1p2fA</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure analysis of response regulator drrb, a2 thermotoga maritima omprr/phob homolog
101	<a href="#">c3kcnA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylate cyclase homolog; <b>PDBTitle:</b> the crystal structure of adenylate cyclase from2 rhodopirellula baltica
102	<a href="#">c3h5iA</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator/sensory box protein/ggdef <b>PDBTitle:</b> crystal structure of the n-terminal domain of a response2 regulator/sensory box/ggdef 3-domain protein from3 carboxydotherrus hydrogenoformans

103	<a href="#">c3luaA_</a>	 Alignment	not modelled	99.9	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum
104	<a href="#">d1k68a_</a>	 Alignment	not modelled	99.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
105	<a href="#">d1p2fa2</a>	 Alignment	not modelled	99.9	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
106	<a href="#">c3nhmA_</a>	 Alignment	not modelled	99.9	31	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of a response regulator from myxococcus xanthus
107	<a href="#">c1kgsA_</a>	 Alignment	not modelled	99.9	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna binding response regulator d; <b>PDBTitle:</b> crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
108	<a href="#">c3hzhA_</a>	 Alignment	not modelled	99.9	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis response regulator (cheY-3); <b>PDBTitle:</b> crystal structure of the cheX-cheY-bef3-mg+2 complex from2 borrelia burgdorferi
109	<a href="#">c3grcD_</a>	 Alignment	not modelled	99.9	23	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> sensor protein, kinase; <b>PDBTitle:</b> crystal structure of a sensor protein from polaromonas sp.2 js666
110	<a href="#">c3eodA_</a>	 Alignment	not modelled	99.9	30	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein hnr; <b>PDBTitle:</b> crystal structure of n-terminal domain of e. coli rssb
111	<a href="#">d1w25a2</a>	 Alignment	not modelled	99.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
112	<a href="#">c3gieA_</a>	 Alignment	not modelled	99.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor histidine kinase desk; <b>PDBTitle:</b> crystal structure of deskc_h188e in complex with amp-pcp
113	<a href="#">c2rdmB_</a>	 Alignment	not modelled	99.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419
114	<a href="#">d1qo0d_</a>	 Alignment	not modelled	99.9	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> Positive regulator of the amidase operon AmiR
115	<a href="#">c3snkA_</a>	 Alignment	not modelled	99.9	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator cheY-like protein; <b>PDBTitle:</b> crystal structure of a response regulator cheY-like protein (ml16475)2 from mesorhizobium loti at 2.02 a resolution
116	<a href="#">c3t8yA_</a>	 Alignment	not modelled	99.9	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis response regulator protein-glutamate <b>PDBTitle:</b> crystal structure of the response regulator domain of thermotoga2 maritima cheb
117	<a href="#">c3a0rB_</a>	 Alignment	not modelled	99.9	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
118	<a href="#">d2b4aa1</a>	 Alignment	not modelled	99.9	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
119	<a href="#">c3eqzB_</a>	 Alignment	not modelled	99.9	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of a response regulator from colwellia2 psychrerythraea
120	<a href="#">c1zn2A_</a>	 Alignment	not modelled	99.9	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulatory protein; <b>PDBTitle:</b> low resolution structure of response regulator styr