














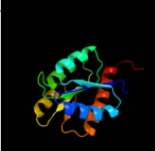

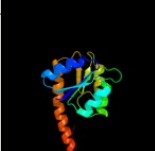



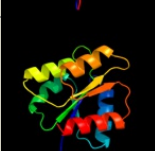



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1ny5A_</a>	 Alignment		100.0	42	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
2	<a href="#">c3dzdA_</a>	 Alignment		100.0	42	<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
3	<a href="#">c2c99A_</a>	 Alignment		100.0	43	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> psp operon transcriptional activator; <b>PDBTitle:</b> structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
4	<a href="#">d1ny5a2</a>	 Alignment		100.0	47	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
5	<a href="#">c1ojlF_</a>	 Alignment		100.0	48	<b>PDB header:</b> response regulator <b>Chain:</b> F: <b>PDB Molecule:</b> transcriptional regulatory protein zrar; <b>PDBTitle:</b> crystal structure of a sigma54-activator suggests the2 mechanism for the conformational switch necessary for3 sigma54 binding
6	<a href="#">c3co5B_</a>	 Alignment		100.0	25	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative two-component system transcriptional response <b>PDBTitle:</b> crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae
7	<a href="#">c2ayxA_</a>	 Alignment		99.9	28	<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
8	<a href="#">c2rjnA_</a>	 Alignment		99.9	26	<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
9	<a href="#">c1w25B_</a>	 Alignment		99.9	28	<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
10	<a href="#">d1krwa_</a>	 Alignment		99.9	98	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
11	<a href="#">d1dbwa_</a>	 Alignment		99.9	32	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related

12	<a href="#">c3eq2A_</a>	Alignment		99.9	31	<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
13	<a href="#">c3breA_</a>	Alignment		99.9	24	<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
14	<a href="#">d1mvoa_</a>	Alignment		99.9	31	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
15	<a href="#">c3cfyA_</a>	Alignment		99.9	26	<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
16	<a href="#">d1qkka_</a>	Alignment		99.9	37	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
17	<a href="#">d1w25a1</a>	Alignment		99.9	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
18	<a href="#">d1ny5a1</a>	Alignment		99.9	32	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
19	<a href="#">d2ayxa1</a>	Alignment		99.9	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
20	<a href="#">d1yioa2</a>	Alignment		99.9	35	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
21	<a href="#">c3i5aA_</a>	Alignment	not modelled	99.9	24	<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
22	<a href="#">d1ys7a2</a>	Alignment	not modelled	99.9	36	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
23	<a href="#">c3hv2B_</a>	Alignment	not modelled	99.9	29	<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
24	<a href="#">c2jrlA_</a>	Alignment	not modelled	99.9	33	<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
25	<a href="#">d1peya_</a>	Alignment	not modelled	99.9	34	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
26	<a href="#">d2a9pa1</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
27	<a href="#">c3nhzA_</a>	Alignment	not modelled	99.9	32	<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
28	<a href="#">c1a2oB_</a>	Alignment	not modelled	99.9	23	<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
						<b>Fold:</b> Flavodoxin-like

29	<a href="#">d2pl1a1</a>	Alignment	not modelled	99.9	29	<b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
30	<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
31	<a href="#">c3gt7A</a>	Alignment	not modelled	99.9	29	<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
32	<a href="#">d1kgsa2</a>	Alignment	not modelled	99.9	33	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
33	<a href="#">c3r0jA</a>	Alignment	not modelled	99.9	26	<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
34	<a href="#">c2qr3A</a>	Alignment	not modelled	99.9	28	<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
35	<a href="#">d1jbea</a>	Alignment	not modelled	99.9	30	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
36	<a href="#">c3jteA</a>	Alignment	not modelled	99.9	32	<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
37	<a href="#">c2qzjC</a>	Alignment	not modelled	99.9	22	<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
38	<a href="#">c3crnA</a>	Alignment	not modelled	99.9	20	<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
39	<a href="#">c3t6kB</a>	Alignment	not modelled	99.9	34	<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
40	<a href="#">d1zh2a1</a>	Alignment	not modelled	99.9	31	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
41	<a href="#">c3kcnA</a>	Alignment	not modelled	99.9	27	<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
42	<a href="#">d1zesa1</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
43	<a href="#">d1u0sy</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
44	<a href="#">c3cu5B</a>	Alignment	not modelled	99.8	28	<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
45	<a href="#">c3lteH</a>	Alignment	not modelled	99.8	28	<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
46	<a href="#">d1xhfa1</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
47	<a href="#">c1ys7B</a>	Alignment	not modelled	99.8	31	<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+
48	<a href="#">c3rqia</a>	Alignment	not modelled	99.8	22	<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
49	<a href="#">c3b2nA</a>	Alignment	not modelled	99.8	24	<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
50	<a href="#">d1zgza1</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
51	<a href="#">c2zayA</a>	Alignment	not modelled	99.8	19	<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
52	<a href="#">d1p6qa</a>	Alignment	not modelled	99.8	30	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
53	<a href="#">d1a04a2</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
						<b>PDB header:</b> transcription regulator

54	<a href="#">c3hdvB</a>	Alignment	not modelled	99.8	27	<b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of response regulator receiver protein from2 pseudomonas putida
55	<a href="#">c2jk1A</a>	Alignment	not modelled	99.8	21	<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
56	<a href="#">d1r6bx3</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
57	<a href="#">c3hdgE</a>	Alignment	not modelled	99.8	25	<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 wolinella3 succinogenes
58	<a href="#">c3pfiB</a>	Alignment		99.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruvb; <b>PDBTitle:</b> 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
59	<a href="#">c3cz5B</a>	Alignment	not modelled	99.8	24	<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 aurantiomonas sp. si85-9a1
60	<a href="#">d1heya</a>	Alignment	not modelled	99.8	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
61	<a href="#">d1s8na</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
62	<a href="#">c3eulB</a>	Alignment	not modelled	99.8	31	<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
63	<a href="#">c2gwrA</a>	Alignment	not modelled	99.8	29	<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
64	<a href="#">c2qxyB</a>	Alignment	not modelled	99.8	28	<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
65	<a href="#">c3c3mA</a>	Alignment	not modelled	99.8	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
66	<a href="#">c3cg4A</a>	Alignment	not modelled	99.8	27	<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
67	<a href="#">d1dz3a</a>	Alignment	not modelled	99.8	32	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
68	<a href="#">c3cnbC</a>	Alignment	not modelled	99.8	22	<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
69	<a href="#">d1k66a</a>	Alignment	not modelled	99.8	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
70	<a href="#">c3h1gA</a>	Alignment	not modelled	99.8	30	<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
71	<a href="#">c3q9sA</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> crystal structure of rra(1-215) from deinococcus radiodurans
72	<a href="#">d1p2fa2</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
73	<a href="#">d2r25b1</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
74	<a href="#">c3grcD</a>	Alignment	not modelled	99.8	22	<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
75	<a href="#">c3a0rB</a>	Alignment	not modelled	99.8	31	<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)
76	<a href="#">c3cg0A</a>	Alignment	not modelled	99.8	27	<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
77	<a href="#">c2qv0A</a>	Alignment	not modelled	99.8	25	<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
78	<a href="#">c1kgsA_</a>	Alignment	not modelled	99.8	32 <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
79	<a href="#">c3gl9B_</a>	Alignment	not modelled	99.8	31 <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
80	<a href="#">c3khtA_</a>	Alignment	not modelled	99.8	20 <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
81	<a href="#">c3eodA_</a>	Alignment	not modelled	99.8	28 <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
82	<a href="#">d1a2oa1</a>	Alignment	not modelled	99.8	24 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
83	<a href="#">c1zn2A_</a>	Alignment	not modelled	99.8	28 <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
84	<a href="#">d1w25a2</a>	Alignment	not modelled	99.8	23 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
85	<a href="#">c1p2fA_</a>	Alignment	not modelled	99.8	26 <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 ompr/phob homolog
86	<a href="#">c3hebB_</a>	Alignment	not modelled	99.8	23 <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
87	<a href="#">d1mb3a_</a>	Alignment	not modelled	99.8	24 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
88	<a href="#">c3hzhA_</a>	Alignment	not modelled	99.8	23 <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
89	<a href="#">c2rdmB_</a>	Alignment	not modelled	99.8	23 <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
90	<a href="#">c2oqrA_</a>	Alignment	not modelled	99.8	27 <b>PDB header:</b> transcription, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sensory transduction protein regx3; <b>PDBTitle:</b> the structure of the response regulator regx3 from mycobacterium2 tuberculosis
91	<a href="#">d1i3ca_</a>	Alignment	not modelled	99.8	21 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
92	<a href="#">c2j48A_</a>	Alignment	not modelled	99.8	20 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> two-component sensor kinase; <b>PDBTitle:</b> nmr structure of the pseudo-receiver domain of the cika2 protein.
93	<a href="#">c3snkA_</a>	Alignment	not modelled	99.8	16 <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
94	<a href="#">c3t8yA_</a>	Alignment	not modelled	99.8	24 <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
95	<a href="#">c2qvga_</a>	Alignment	not modelled	99.8	23 <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
96	<a href="#">c3ktoA_</a>	Alignment	not modelled	99.8	24 <b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver protein; <b>PDBTitle:</b> crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
97	<a href="#">c3nhmA_</a>	Alignment	not modelled	99.8	29 <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
98	<a href="#">c1r6bX_</a>	Alignment	not modelled	99.8	19 <b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein; <b>PDBTitle:</b> high resolution crystal structure of clpa
99	<a href="#">c1qvrB_</a>	Alignment	not modelled	99.8	22 <b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
100	<a href="#">c2hqaA_</a>	Alignment	not modelled	99.8	22 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
101	<a href="#">c3luaA_</a>	Alignment	not modelled	99.8	22 <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
102	<a href="#">c3eqzB_</a>	Alignment	not modelled	99.8	17 <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



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103	<a href="#">c3mmnA_</a>	Alignment	not modelled	99.8	24	<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+
104	<a href="#">c3f6cB_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> positive transcription regulator evga; <b>PDBTitle:</b> crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
105	<a href="#">d1dcfa_</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> Receiver domain of the ethylene receptor
106	<a href="#">d2b4aa1</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
107	<a href="#">c1in8A_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction dna helicase ruvb; <b>PDBTitle:</b> thermotoga maritima ruvb t158v
108	<a href="#">c3m6mF_</a>	Alignment	not modelled	99.8	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 rpfc complexed with rec domain of rpfc
109	<a href="#">c3ilhA_</a>	Alignment	not modelled	99.8	19	<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
110	<a href="#">c3lufB_</a>	Alignment	not modelled	99.8	15	<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
111	<a href="#">c3h5iA_</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> transcription protein/ggdef <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator/sensory box <b>PDBTitle:</b> crystal structure of the n-terminal domain of a response2 regulator/sensory box/ggdef 3-domain protein from3 carboxydotherrmus hydrogenoformans
112	<a href="#">c3pxiB_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/meccb; <b>PDBTitle:</b> structure of meca108:clpc
113	<a href="#">c3n0rA_</a>	Alignment	not modelled	99.8	26	<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
114	<a href="#">d1um8a_</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
115	<a href="#">c2hqrA_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
116	<a href="#">c3i42A_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver domain protein (chey-like)2 from methylobacillus flagellatus
117	<a href="#">d1qvra3</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
118	<a href="#">c3c97A_</a>	Alignment	not modelled	99.7	27	<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
119	<a href="#">d1k68a_</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
120	<a href="#">c3nbxX_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> atpase rava; <b>PDBTitle:</b> crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp