







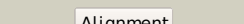

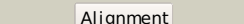

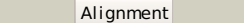

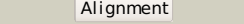

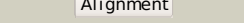

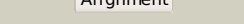

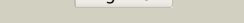












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2oqrA_</a>	 Alignment		100.0	33	<b>PDB header:</b> transcription,signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> sensory transduction protein regx3; <b>PDBTitle:</b> the structure of the response regulator regx3 from mycobacterium2 tuberculosis
2	<a href="#">c1ys7B_</a>	 Alignment		100.0	28	<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+
3	<a href="#">c2gwrA_</a>	 Alignment		100.0	37	<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
4	<a href="#">c3r0jA_</a>	 Alignment		100.0	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
5	<a href="#">c2hqrA_</a>	 Alignment		100.0	24	<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
6	<a href="#">c1p2fA_</a>	 Alignment		100.0	32	<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
7	<a href="#">c1kgsA_</a>	 Alignment		100.0	29	<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
8	<a href="#">c3q9sA_</a>	 Alignment		100.0	32	<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
9	<a href="#">c1zn2A_</a>	 Alignment		99.9	22	<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
10	<a href="#">c2ayxA_</a>	 Alignment		99.9	21	<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
11	<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

12	<a href="#">c3breA_</a>	Alignment		99.9	27	<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
13	<a href="#">c3eq2A_</a>	Alignment		99.9	28	<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
14	<a href="#">d2a9pa1</a>	Alignment		99.9	32	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
15	<a href="#">d1s8na_</a>	Alignment		99.9	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
16	<a href="#">c2jrlA_</a>	Alignment		99.9	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
17	<a href="#">c3cfyA_</a>	Alignment		99.9	22	<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
18	<a href="#">d1mvoa_</a>	Alignment		99.9	35	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
19	<a href="#">c2qziC_</a>	Alignment		99.9	25	<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
20	<a href="#">c2zwmA_</a>	Alignment		99.9	38	<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
21	<a href="#">c3i5aA_</a>	Alignment	not modelled	99.9	28	<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="#">d1zh2a1</a>	Alignment	not modelled	99.9	30	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
23	<a href="#">c3nhzA_</a>	Alignment	not modelled	99.9	41	<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
24	<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
25	<a href="#">c3crnA_</a>	Alignment	not modelled	99.9	24	<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
26	<a href="#">d2pl1a1</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
27	<a href="#">d1ys7a2</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
						<b>PDB header:</b> transcription

28	<a href="#">c3c3wB_</a>	Alignment	not modelled	99.9	21	<b>Chain:</b> B: <b>PDB Molecule:</b> two component transcriptional regulatory protein devr; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
29	<a href="#">c3jteA_</a>	Alignment	not modelled	99.9	20	<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
30	<a href="#">d1xhfa1</a>	Alignment	not modelled	99.9	31	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
31	<a href="#">d1w25a1</a>	Alignment	not modelled	99.9	33	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
32	<a href="#">d1zgza1</a>	Alignment	not modelled	99.9	31	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
33	<a href="#">c3dzdA_</a>	Alignment	not modelled	99.9	16	<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
34	<a href="#">c3rqia_</a>	Alignment	not modelled	99.9	18	<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
35	<a href="#">c3gt7A_</a>	Alignment	not modelled	99.9	27	<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
36	<a href="#">c3cg0A_</a>	Alignment	not modelled	99.9	22	<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
37	<a href="#">c1ny5A_</a>	Alignment	not modelled	99.9	20	<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
38	<a href="#">d1zesa1</a>	Alignment	not modelled	99.9	32	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
39	<a href="#">d1qkka_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
40	<a href="#">d1ny5a1</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
41	<a href="#">d1krwa_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
42	<a href="#">c3c3mA_</a>	Alignment	not modelled	99.9	24	<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
43	<a href="#">d2ayxa1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
44	<a href="#">c3b2nA_</a>	Alignment	not modelled	99.9	21	<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
45	<a href="#">c2zayA_</a>	Alignment	not modelled	99.9	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
46	<a href="#">c2rjnA_</a>	Alignment	not modelled	99.9	16	<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
47	<a href="#">d1kgsa2</a>	Alignment	not modelled	99.9	32	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
48	<a href="#">d1dbwa_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
49	<a href="#">d1yioa2</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
50	<a href="#">d1k66a_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
51	<a href="#">d1peya_</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
52	<a href="#">d1jbea_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
53	<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
54	<a href="#">c3hv2B_</a>	Alignment	not modelled	99.9	21	<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
55	<a href="#">c3cg4A_</a>	Alignment	not modelled	99.9	23	<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
56	<a href="#">d1p6qa_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
57	<a href="#">c3khtA_</a>	Alignment	not modelled	99.9	24	<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
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="#">c3cnbC_</a>	Alignment	not modelled	99.9	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
60	<a href="#">d1u0sy_</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
61	<a href="#">c1a2oB_</a>	Alignment	not modelled	99.9	26	<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
62	<a href="#">c3h1gA_</a>	Alignment	not modelled	99.9	24	<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
63	<a href="#">c3hdgE_</a>	Alignment	not modelled	99.9	20	<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 wolinetella succinogenes
64	<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
65	<a href="#">c3t8yA_</a>	Alignment	not modelled	99.9	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
66	<a href="#">d1heya_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
67	<a href="#">c3cu5B_</a>	Alignment	not modelled	99.9	17	<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
68	<a href="#">d1mb3a_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
69	<a href="#">c3h5iA_</a>	Alignment	not modelled	99.9	28	<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 carboxydotherrmus hydrogenoformans
70	<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
71	<a href="#">d2r25b1</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
72	<a href="#">c2jk1A_</a>	Alignment	not modelled	99.9	19	<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
73	<a href="#">c1rnlA_</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> signal transduction protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate/nitrite response regulator protein narl; <b>PDBTitle:</b> the nitrate/nitrite response regulator protein narl from narl
74	<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
75	<a href="#">c3grcD_</a>	Alignment	not modelled	99.9	20	<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
76	<a href="#">c3i42A_</a>	Alignment	not modelled	99.9	18	<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

77	<a href="#">d1a04a2</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
78	<a href="#">c2qv0A</a>	Alignment	not modelled	99.9	23	<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
79	<a href="#">c2qxyB</a>	Alignment	not modelled	99.9	24	<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
80	<a href="#">c3eulB</a>	Alignment	not modelled	99.9	22	<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
81	<a href="#">d1a2oa1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
82	<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
83	<a href="#">d1p2fa2</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
84	<a href="#">c3cz5B</a>	Alignment	not modelled	99.9	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 aurantimonas sp. si85-9a1
85	<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
86	<a href="#">c3hdvB</a>	Alignment	not modelled	99.9	17	<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
87	<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
88	<a href="#">c3a0rB</a>	Alignment	not modelled	99.8	25	<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)
89	<a href="#">c3nhmA</a>	Alignment	not modelled	99.8	21	<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
90	<a href="#">c2hgoA</a>	Alignment	not modelled	99.8	23	<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
91	<a href="#">c3eqzB</a>	Alignment	not modelled	99.8	21	<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
92	<a href="#">d1w25a2</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
93	<a href="#">c3n0rA</a>	Alignment	not modelled	99.8	22	<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
94	<a href="#">c3luaA</a>	Alignment	not modelled	99.8	19	<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
95	<a href="#">c2nt3A</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator homolog; <b>PDBTitle:</b> receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
96	<a href="#">c3hzhA</a>	Alignment	not modelled	99.8	16	<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
97	<a href="#">c3snkA</a>	Alignment	not modelled	99.8	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
98	<a href="#">c3ilhA</a>	Alignment	not modelled	99.8	17	<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
99	<a href="#">c2qvga</a>	Alignment	not modelled	99.8	21	<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
100	<a href="#">d1dcfa</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> Receiver domain of the ethylene receptor
101	<a href="#">d1k68a</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related



102	<a href="#">c3eodA_</a>	Alignment	not modelled	99.8	23	<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
103	<a href="#">c3c97A_</a>	Alignment	not modelled	99.8	19	<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
104	<a href="#">c3n53B_</a>	Alignment	not modelled	99.8	30	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator receiver modulated diguanylate cyclase; <b>PDBTitle:</b> crystal structure of a response regulator receiver modulated2 diguanylate cyclase from pelobacter carbinolicus
105	<a href="#">d1opca_</a>	Alignment	not modelled	99.8	32	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> PhoB-like
106	<a href="#">c2j48A_</a>	Alignment	not modelled	99.8	18	<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.
107	<a href="#">c3mmnA_</a>	Alignment	not modelled	99.8	20	<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+
108	<a href="#">c3m6mF_</a>	Alignment	not modelled	99.8	22	<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
109	<a href="#">c3ktoA_</a>	Alignment	not modelled	99.8	13	<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
110	<a href="#">c2zxB_</a>	Alignment	not modelled	99.8	35	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein walr; <b>PDBTitle:</b> crystal structure of yycf dna-binding domain from staphylococcus2 aureus
111	<a href="#">c2rdmB_</a>	Alignment	not modelled	99.8	22	<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
112	<a href="#">c3lufB_</a>	Alignment	not modelled	99.8	26	<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
113	<a href="#">d2b4aa1</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
114	<a href="#">c2hwwA_</a>	Alignment	not modelled	99.8	38	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator vicr; <b>PDBTitle:</b> crystal structure of an essential response regulator dna binding2 domain, vicrc in enterococcus faecalis, a member of the yycf3 subfamily.
115	<a href="#">d1gxqa_</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> PhoB-like
116	<a href="#">d1qo0d_</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> Positive regulator of the amidase operon AmiR
117	<a href="#">c2jzvA_</a>	Alignment	not modelled	99.8	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein pcor; <b>PDBTitle:</b> solution structure of c-terminal effector domain of2 putative two-component-system response regulator involved3 in copper resistance from klebsiella pneumoniae
118	<a href="#">c2hqnA_</a>	Alignment	not modelled	99.8	26	<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
119	<a href="#">c2k4jA_</a>	Alignment	not modelled	99.8	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> arsr dna binding domain
120	<a href="#">c3q9vB_</a>	Alignment	not modelled	99.8	31	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> crystal structure of rra c-terminal domain(123-221) from deinococcus2 radiodurans