







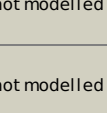
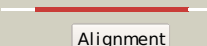
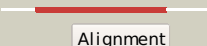
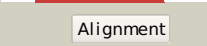
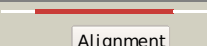
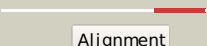
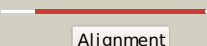

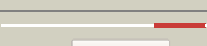
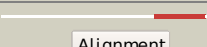
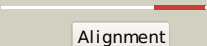

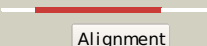
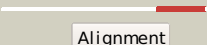
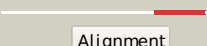

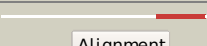


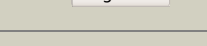
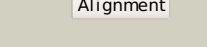

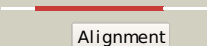
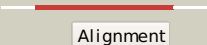
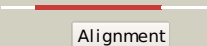



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1zn2A_</a>	 Alignment		99.9	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulatory protein; <b>PDBTitle:</b> low resolution structure of response regulator styr
2	<a href="#">c3c3wB_</a>	 Alignment		99.9	20	<b>PDB header:</b> transcription <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
3	<a href="#">c1rn1A_</a>	 Alignment		99.8	17	<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
4	<a href="#">c1h0mD_</a>	 Alignment		99.8	15	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional activator protein trar; <b>PDBTitle:</b> three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
5	<a href="#">c2q0oA_</a>	 Alignment		99.7	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional activator protein trar; <b>PDBTitle:</b> crystal structure of an anti-activation complex in bacterial quorum2 sensing
6	<a href="#">c3klnC_</a>	 Alignment		99.7	19	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, luxr family; <b>PDBTitle:</b> vibrio cholerae vpst
7	<a href="#">c3qp5C_</a>	 Alignment		99.7	15	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> cvir transcriptional regulator; <b>PDBTitle:</b> crystal structure of cvir bound to antagonist chlorolactone (cl)
8	<a href="#">c3sztB_</a>	 Alignment		99.6	29	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> quorum-sensing control repressor; <b>PDBTitle:</b> quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
9	<a href="#">c3q9sA_</a>	 Alignment		99.6	13	<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
10	<a href="#">c1kgsA_</a>	 Alignment		99.6	10	<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
11	<a href="#">c1zljE_</a>	 Alignment		99.5	24	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> dormancy survival regulator; <b>PDBTitle:</b> crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain

12	<a href="#">d1p4wa_</a>	Alignment		99.5	25	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
13	<a href="#">c2krfB_</a>	Alignment		99.5	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein coma; <b>PDBTitle:</b> nmr solution structure of the dna binding domain of competence protein2 a
14	<a href="#">c3cloC_</a>	Alignment		99.5	35	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
15	<a href="#">d1a04a1</a>	Alignment		99.4	26	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
16	<a href="#">c2oqrA_</a>	Alignment		99.4	14	<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
17	<a href="#">d1yioa1</a>	Alignment		99.4	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> GerE-like (LuxR/UhpA family of transcriptional regulators)
18	<a href="#">c1ys7B_</a>	Alignment		99.4	13	<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 +
19	<a href="#">d1l3la1</a>	Alignment		99.4	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
20	<a href="#">d1fsea_</a>	Alignment		99.4	37	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> GerE-like (LuxR/UhpA family of transcriptional regulators)
21	<a href="#">c2gwrA_</a>	Alignment	not modelled	99.4	13	<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
22	<a href="#">c3r0jA_</a>	Alignment	not modelled	99.4	12	<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
23	<a href="#">c2rnjA_</a>	Alignment	not modelled	99.4	36	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> nmr structure of the s. aureus vvar dna binding domain
24	<a href="#">c1x3uA_</a>	Alignment	not modelled	99.3	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein fixj; <b>PDBTitle:</b> solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
25	<a href="#">c1p2fA_</a>	Alignment	not modelled	99.3	13	<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 omppr/phob homolog
26	<a href="#">c2jpcA_</a>	Alignment	not modelled	99.2	33	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
27	<a href="#">c2hqrA_</a>	Alignment	not modelled	99.1	10	<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
28	<a href="#">d1s8na_</a>	Alignment	not modelled	98.8	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related

29	<a href="#">c3cz5B</a>	 Alignment	not modelled	98.4	12	<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
30	<a href="#">c3eulB</a>	 Alignment	not modelled	98.3	12	<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 narI from mycobacterium tuberculosis
31	<a href="#">c3b2nA</a>	 Alignment	not modelled	98.3	13	<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
32	<a href="#">d1a04a2</a>	 Alignment	not modelled	98.3	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
33	<a href="#">d1ttya</a>	 Alignment	not modelled	98.2	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
34	<a href="#">c3rqia</a>	 Alignment	not modelled	98.2	11	<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="#">c3cwoX</a>	 Alignment	not modelled	98.2	14	<b>PDB header:</b> de novo protein <b>Chain:</b> X: <b>PDB Molecule:</b> beta/alpha-barrel protein based on 1thf and 1trny; <b>PDBTitle:</b> a beta/alpha-barrel built by the combination of fragments2 from different folds
36	<a href="#">d2p7vb1</a>	 Alignment	not modelled	98.1	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
37	<a href="#">d1smyf2</a>	 Alignment	not modelled	98.1	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
38	<a href="#">d1rp3a2</a>	 Alignment	not modelled	98.1	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
39	<a href="#">d1ku3a</a>	 Alignment	not modelled	98.0	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
40	<a href="#">d1u0sy</a>	 Alignment	not modelled	98.0	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
41	<a href="#">d1or7a1</a>	 Alignment	not modelled	98.0	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
42	<a href="#">d1ku7a</a>	 Alignment	not modelled	98.0	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
43	<a href="#">c2o8xA</a>	 Alignment	not modelled	98.0	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-c factor; <b>PDBTitle:</b> crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
44	<a href="#">d1xsva</a>	 Alignment	not modelled	98.0	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
45	<a href="#">c3hugA</a>	 Alignment	not modelled	98.0	18	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigI
46	<a href="#">c3mzyA</a>	 Alignment	not modelled	98.0	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-h factor; <b>PDBTitle:</b> the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
47	<a href="#">c3cu5B</a>	 Alignment	not modelled	97.9	12	<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
48	<a href="#">c2ayxA</a>	 Alignment	not modelled	97.9	8	<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
49	<a href="#">d1jbea</a>	 Alignment	not modelled	97.9	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
50	<a href="#">c3f6cB</a>	 Alignment	not modelled	97.9	13	<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
51	<a href="#">d1mvoa</a>	 Alignment	not modelled	97.9	8	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
52	<a href="#">d1krwa</a>	 Alignment	not modelled	97.9	8	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
						<b>Fold:</b> Flavodoxin-like

53	<a href="#">d1peya_</a>	Alignment	not modelled	97.9	12	<b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
54	<a href="#">c3breA_</a>	Alignment	not modelled	97.9	6	<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
55	<a href="#">d2a9pa1</a>	Alignment	not modelled	97.9	8	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
56	<a href="#">c1ny5A_</a>	Alignment	not modelled	97.9	12	<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
57	<a href="#">d1ny5a1</a>	Alignment	not modelled	97.9	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
58	<a href="#">d1s7oa_</a>	Alignment	not modelled	97.9	28	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
59	<a href="#">d1ys7a2</a>	Alignment	not modelled	97.8	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
60	<a href="#">d1dbwa_</a>	Alignment	not modelled	97.8	7	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
61	<a href="#">c1w25B_</a>	Alignment	not modelled	97.8	7	<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
62	<a href="#">c1rp3G_</a>	Alignment	not modelled	97.8	27	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> rna polymerase sigma factor sigma-28 (fliA); <b>PDBTitle:</b> cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgm
63	<a href="#">d1qkka_</a>	Alignment	not modelled	97.8	7	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
64	<a href="#">c3dzdA_</a>	Alignment	not modelled	97.8	8	<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
65	<a href="#">c2rjnA_</a>	Alignment	not modelled	97.8	10	<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
66	<a href="#">c2zwmA_</a>	Alignment	not modelled	97.8	9	<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
67	<a href="#">c1or7A_</a>	Alignment	not modelled	97.7	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-e factor; <b>PDBTitle:</b> crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
68	<a href="#">d2pl1a1</a>	Alignment	not modelled	97.7	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
69	<a href="#">c3i5aA_</a>	Alignment	not modelled	97.7	9	<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
70	<a href="#">c3cfyA_</a>	Alignment	not modelled	97.7	8	<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
71	<a href="#">c2jrlA_</a>	Alignment	not modelled	97.7	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> solution structure of the berylliofluoride-activated ntrc4 receiver2 domain dimer
72	<a href="#">c3hdgE_</a>	Alignment	not modelled	97.7	10	<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 wolinetlla3 succinogenes
73	<a href="#">d1dz3a_</a>	Alignment	not modelled	97.7	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
74	<a href="#">d2ayxa1</a>	Alignment	not modelled	97.6	8	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
75	<a href="#">c2qr3A_</a>	Alignment	not modelled	97.6	16	<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
76	<a href="#">d1kgsa2</a>	Alignment	not modelled	97.6	6	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
77	<a href="#">c3nhzA_</a>	Alignment	not modelled	97.6	11	<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
78	<a href="#">d1k66a_</a>	Alignment	not modelled	97.6	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like

					<b>Family:</b> CheY-related
79	<a href="#">dlheya_</a>	Alignment	not modelled	97.6	10 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
80	<a href="#">dlw25a1</a>	Alignment	not modelled	97.6	7 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
81	<a href="#">c3snkA_</a>	Alignment	not modelled	97.6	8 <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
82	<a href="#">dlyioa2</a>	Alignment	not modelled	97.6	9 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
83	<a href="#">c3cg0A_</a>	Alignment	not modelled	97.5	7 <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
84	<a href="#">c3h1gA_</a>	Alignment	not modelled	97.5	8 <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
85	<a href="#">c3eq2A_</a>	Alignment	not modelled	97.5	12 <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
86	<a href="#">c3gt7A_</a>	Alignment	not modelled	97.5	9 <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
87	<a href="#">c3hv2B_</a>	Alignment	not modelled	97.5	10 <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
88	<a href="#">c2q1zA_</a>	Alignment	not modelled	97.4	14 <b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rpoe, ecf sig;e; <b>PDBTitle:</b> crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
89	<a href="#">c3jteA_</a>	Alignment	not modelled	97.4	11 <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
90	<a href="#">c3t6kB_</a>	Alignment	not modelled	97.4	6 <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
91	<a href="#">dlzh2a1</a>	Alignment	not modelled	97.4	11 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
92	<a href="#">c2qzjC_</a>	Alignment	not modelled	97.4	8 <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
93	<a href="#">c1a2oB_</a>	Alignment	not modelled	97.4	11 <b>PDB header:</b> bacterial chemotaxis <b>Chain:</b> B: <b>PDB Molecule:</b> cheb methylesterase; <b>PDBTitle:</b> structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
94	<a href="#">c2qv0A_</a>	Alignment	not modelled	97.3	16 <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
95	<a href="#">dlzesal</a>	Alignment	not modelled	97.3	9 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
96	<a href="#">c3lteH_</a>	Alignment	not modelled	97.3	9 <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
97	<a href="#">c3crnA_</a>	Alignment	not modelled	97.3	7 <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
98	<a href="#">d1a2oa1</a>	Alignment	not modelled	97.3	11 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
99	<a href="#">d1xhfa1</a>	Alignment	not modelled	97.3	6 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
100	<a href="#">d1zgza1</a>	Alignment	not modelled	97.3	6 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
101	<a href="#">c3hebB_</a>	Alignment	not modelled	97.2	10 <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
102	<a href="#">d1p6qa_</a>	Alignment	not modelled	97.2	7 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
103	<a href="#">c3t72a</a>	Alignment	not modelled	97.2	10 <b>PDB header:</b> transcription/dna <b>Chain:</b> O: <b>PDB Molecule:</b> pho box dna (strand 1);



103	<a href="#">c3vz0_</a>	Alignment	not modelled	97.2	19	<b>PDBTitle:</b> phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex <b>PDB header:</b> lyase/transferase
104	<a href="#">c3m6mF_</a>	Alignment	not modelled	97.2	9	<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
105	<a href="#">c2zayA_</a>	Alignment	not modelled	97.2	6	<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
106	<a href="#">c1l9uH_</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> sigma factor siga; <b>PDBTitle:</b> thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
107	<a href="#">d1p2fa2</a>	Alignment	not modelled	97.1	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
108	<a href="#">c2qxyB_</a>	Alignment	not modelled	97.1	10	<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
109	<a href="#">c3khtA_</a>	Alignment	not modelled	97.0	8	<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
110	<a href="#">d1i3ca_</a>	Alignment	not modelled	97.0	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
111	<a href="#">d1jhfa1</a>	Alignment	not modelled	97.0	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> LexA repressor, N-terminal DNA-binding domain
112	<a href="#">c3cnbC_</a>	Alignment	not modelled	97.0	12	<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
113	<a href="#">c3ilhA_</a>	Alignment	not modelled	97.0	10	<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
114	<a href="#">c3t8yA_</a>	Alignment	not modelled	96.9	11	<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
115	<a href="#">c2yxbA_</a>	Alignment	not modelled	96.9	4	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme b12-dependent mutase; <b>PDBTitle:</b> crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
116	<a href="#">d1w25a2</a>	Alignment	not modelled	96.9	7	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
117	<a href="#">c3hzhA_</a>	Alignment	not modelled	96.9	10	<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
118	<a href="#">c3c3mA_</a>	Alignment	not modelled	96.9	8	<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
119	<a href="#">c2a6eF_</a>	Alignment	not modelled	96.9	13	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor rpod; <b>PDBTitle:</b> crystal structure of the t. thermophilus rna polymerase2 holoenzyme
120	<a href="#">c3ktoA_</a>	Alignment	not modelled	96.8	12	<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