



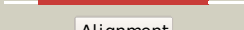






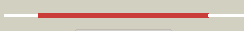





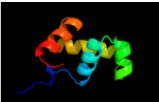



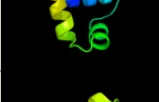




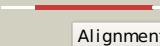

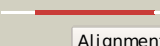



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1zn2A_</a>	 Alignment		100.0	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> response regulatory protein; <b>PDBTitle:</b> low resolution structure of response regulator styr
2	<a href="#">c1rnlA_</a>	 Alignment		100.0	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
3	<a href="#">c3c3wB_</a>	 Alignment		100.0	9	<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
4	<a href="#">c3klnC_</a>	 Alignment		99.9	12	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, luxr family; <b>PDBTitle:</b> vibrio cholerae vpst
5	<a href="#">c1kgsA_</a>	 Alignment		99.9	14	<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
6	<a href="#">c2oqrA_</a>	 Alignment		99.8	15	<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
7	<a href="#">c2qwrA_</a>	 Alignment		99.8	14	<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
8	<a href="#">c1ys7B_</a>	 Alignment		99.8	12	<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 +
9	<a href="#">c1p2fA_</a>	 Alignment		99.8	14	<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
10	<a href="#">c3sztB_</a>	 Alignment		99.8	28	<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
11	<a href="#">c3r0jA_</a>	 Alignment		99.8	14	<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

12	<a href="#">c2q0oA_</a>	Alignment		99.8	17	<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
13	<a href="#">c1h0mD_</a>	Alignment		99.8	17	<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
14	<a href="#">c2hqrA_</a>	Alignment		99.8	13	<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
15	<a href="#">c3cloC_</a>	Alignment		99.7	27	<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
16	<a href="#">d1p4wa_</a>	Alignment		99.7	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)
17	<a href="#">c3qp5C_</a>	Alignment		99.7	20	<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)
18	<a href="#">c2krfB_</a>	Alignment		99.7	19	<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
19	<a href="#">d1s8na_</a>	Alignment		99.7	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
20	<a href="#">c1zljE_</a>	Alignment		99.7	12	<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
21	<a href="#">d1l3la1</a>	Alignment	not modelled	99.7	16	<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)
22	<a href="#">d1fsea_</a>	Alignment	not modelled	99.7	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)
23	<a href="#">d1a04a1</a>	Alignment	not modelled	99.7	20	<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)
24	<a href="#">c2rnjA_</a>	Alignment	not modelled	99.7	22	<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
25	<a href="#">c1x3uA_</a>	Alignment	not modelled	99.7	30	<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
26	<a href="#">d1yioa1</a>	Alignment	not modelled	99.6	31	<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)
27	<a href="#">c2jpcA_</a>	Alignment	not modelled	99.6	34	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ssrb; <b>PDBTitle:</b> ssrb dna binding protein
28	<a href="#">c3rqia_</a>	Alignment	not modelled	99.5	16	<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
						<b>PDB header:</b> transferase

29	<a href="#">c2ayxA</a>	Alignment	not modelled	99.4	15	<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
30	<a href="#">c3cz5B</a>	Alignment	not modelled	99.4	8	<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
31	<a href="#">d1a04a2</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
32	<a href="#">c3b2nA</a>	Alignment	not modelled	99.4	16	<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
33	<a href="#">d2a9pa1</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
34	<a href="#">c3eq2A</a>	Alignment	not modelled	99.4	14	<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
35	<a href="#">c3eulB</a>	Alignment	not modelled	99.4	11	<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
36	<a href="#">c3f6cB</a>	Alignment	not modelled	99.4	20	<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
37	<a href="#">c1ny5A</a>	Alignment	not modelled	99.4	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="#">d1qkka</a>	Alignment	not modelled	99.4	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
39	<a href="#">c2zwmA</a>	Alignment	not modelled	99.4	13	<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
40	<a href="#">d1ys7a2</a>	Alignment	not modelled	99.4	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
41	<a href="#">d1peya</a>	Alignment	not modelled	99.4	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
42	<a href="#">c3breA</a>	Alignment	not modelled	99.4	14	<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
43	<a href="#">c3nhzA</a>	Alignment	not modelled	99.4	10	<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
44	<a href="#">d1p2fa2</a>	Alignment	not modelled	99.4	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
45	<a href="#">d1mvoa</a>	Alignment	not modelled	99.4	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
46	<a href="#">d1dbwa</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
47	<a href="#">d1mb3a</a>	Alignment	not modelled	99.4	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
48	<a href="#">d1ny5a1</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
49	<a href="#">d1jbea</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
50	<a href="#">c2rjnA</a>	Alignment	not modelled	99.4	12	<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
51	<a href="#">c2qr3A</a>	Alignment	not modelled	99.4	13	<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
52	<a href="#">d1kgsa2</a>	Alignment	not modelled	99.3	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
53	<a href="#">d2pl1a1</a>	Alignment	not modelled	99.3	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
						<b>PDB header:</b> protein binding

54	<a href="#">c3jteA_</a>	Alignment	not modelled	99.3	18	<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
55	<a href="#">d1yioa2</a>	Alignment	not modelled	99.3	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
56	<a href="#">d1u0sy_</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
57	<a href="#">d2ayxa1</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
58	<a href="#">c2qv0A_</a>	Alignment	not modelled	99.3	8	<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
59	<a href="#">c3i5aA_</a>	Alignment	not modelled	99.3	12	<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
60	<a href="#">c1a2oB_</a>	Alignment	not modelled	99.3	18	<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
61	<a href="#">d1zh2a1</a>	Alignment	not modelled	99.3	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
62	<a href="#">c1w25B_</a>	Alignment	not modelled	99.3	12	<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
63	<a href="#">d1krwa_</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
64	<a href="#">d1dz3a_</a>	Alignment	not modelled	99.3	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
65	<a href="#">c3hdgE_</a>	Alignment	not modelled	99.3	17	<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 wolinetlla succinogenes
66	<a href="#">d1zgza1</a>	Alignment	not modelled	99.3	8	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
67	<a href="#">c3cfyA_</a>	Alignment	not modelled	99.3	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative luxa repressor protein; <b>PDBTitle:</b> crystal structure of signal receiver domain of putative luxa2 repressor protein from vibrio parahaemolyticus
68	<a href="#">d1xhfa1</a>	Alignment	not modelled	99.3	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
69	<a href="#">c2jrlA_</a>	Alignment	not modelled	99.3	15	<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
70	<a href="#">c3dzdA_</a>	Alignment	not modelled	99.3	15	<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
71	<a href="#">c3t8yA_</a>	Alignment	not modelled	99.3	18	<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
72	<a href="#">c2qzjC_</a>	Alignment	not modelled	99.3	13	<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
73	<a href="#">c3cu5B_</a>	Alignment	not modelled	99.3	13	<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
74	<a href="#">d1a2oa1</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
75	<a href="#">c3gt7A_</a>	Alignment	not modelled	99.3	19	<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
76	<a href="#">d1w25a1</a>	Alignment	not modelled	99.3	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
77	<a href="#">c3hv2B_</a>	Alignment	not modelled	99.3	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
78	<a href="#">d1k66a_</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
79	<a href="#">c3eqzB_</a>	Alignment	not modelled	99.3	15	<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

80	<a href="#">c3t6kB</a>	 Alignment	not modelled	99.2	11	<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
81	<a href="#">c3snkA</a>	 Alignment	not modelled	99.2	10	<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="#">d1zesal</a>	 Alignment	not modelled	99.2	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
83	<a href="#">c2jk1A</a>	 Alignment	not modelled	99.2	18	<b>PDB header:</b> dna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase transcriptional regulatory protein hupr1; <b>PDBTitle:</b> crystal structure of the wild-type hupr receiver domain
84	<a href="#">c3kcnA</a>	 Alignment	not modelled	99.2	15	<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
85	<a href="#">c3lteH</a>	 Alignment	not modelled	99.2	14	<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
86	<a href="#">c3h1gA</a>	 Alignment	not modelled	99.2	15	<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
87	<a href="#">c3a0rB</a>	 Alignment	not modelled	99.2	13	<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)
88	<a href="#">d1p6qa</a>	 Alignment	not modelled	99.2	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
89	<a href="#">c3crnA</a>	 Alignment	not modelled	99.2	16	<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
90	<a href="#">c3hebB</a>	 Alignment	not modelled	99.2	12	<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
91	<a href="#">c3i42A</a>	 Alignment	not modelled	99.2	13	<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
92	<a href="#">d2b4aa1</a>	 Alignment	not modelled	99.2	8	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
93	<a href="#">d1i3ca</a>	 Alignment	not modelled	99.2	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
94	<a href="#">c2zayA</a>	 Alignment	not modelled	99.2	14	<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
95	<a href="#">c2qvga</a>	 Alignment	not modelled	99.2	8	<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="#">c3hdvB</a>	 Alignment	not modelled	99.2	16	<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
97	<a href="#">c3m6mF</a>	 Alignment	not modelled	99.2	13	<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
98	<a href="#">d1w25a2</a>	 Alignment	not modelled	99.2	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
99	<a href="#">c3grcD</a>	 Alignment	not modelled	99.2	12	<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
100	<a href="#">c3ilhA</a>	 Alignment	not modelled	99.2	15	<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
101	<a href="#">c3cnbC</a>	 Alignment	not modelled	99.2	17	<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
102	<a href="#">d1heya</a>	 Alignment	not modelled	99.2	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
103	<a href="#">c2qxyB</a>	 Alignment	not modelled	99.1	19	<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
104	<a href="#">c3nhmA</a>	 Alignment	not modelled	99.1	12	<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
105	<a href="#">c3cg0A_</a>	Alignment	not modelled	99.1	11 <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
106	<a href="#">c3mmnA_</a>	Alignment	not modelled	99.1	13 <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+
107	<a href="#">c3c3mA_</a>	Alignment	not modelled	99.1	11 <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
108	<a href="#">d2r25b1</a>	Alignment	not modelled	99.1	15 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
109	<a href="#">c3khtA_</a>	Alignment	not modelled	99.1	12 <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="#">c3cg4A_</a>	Alignment	not modelled	99.1	16 <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
111	<a href="#">c2rdmB_</a>	Alignment	not modelled	99.1	9 <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="#">c3gl9B_</a>	Alignment	not modelled	99.1	15 <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
113	<a href="#">c3c97A_</a>	Alignment	not modelled	99.1	14 <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
114	<a href="#">c3ktoA_</a>	Alignment	not modelled	99.1	10 <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
115	<a href="#">c2j48A_</a>	Alignment	not modelled	99.1	10 <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.
116	<a href="#">c3h5iA_</a>	Alignment	not modelled	99.1	13 <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 hydrogenofomans
117	<a href="#">c3hzhA_</a>	Alignment	not modelled	99.0	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
118	<a href="#">d1dcfa_</a>	Alignment	not modelled	99.0	13 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> Receiver domain of the ethylene receptor
119	<a href="#">c3luaA_</a>	Alignment	not modelled	99.0	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 a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum
120	<a href="#">d1k68a_</a>	Alignment	not modelled	99.0	13 <b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related