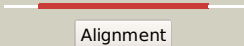

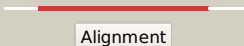

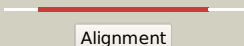







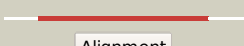




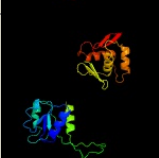



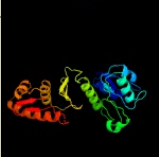











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0818_(-)_910975_911742
Date	Fri Jul 26 01:50:40 BST 2019
Unique Job ID	d8816777f5c5cad6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1ys7B_</a>			100.0	31	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulatory protein prra; <b>PDBTitle:</b> crystal structure of the response regulator protein prra complexed2 with mg2+
2	<a href="#">c2oqrA_</a>			100.0	31	<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
3	<a href="#">c4kfcB_</a>			100.0	24	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> B: <b>PDB Molecule:</b> kdp operon transcriptional regulatory protein kdpe; <b>PDBTitle:</b> crystal structure of a hyperactive mutant of response regulator kdpe2 complexed to its promoter dna
4	<a href="#">c4s05B_</a>			100.0	25	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding transcriptional regulator basr; <b>PDBTitle:</b> crystal structure of klebsiella pneumoniae pmra in complex with pmra2 box dna
5	<a href="#">c3r0jA_</a>			100.0	28	<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
6	<a href="#">c5u8mA_</a>			100.0	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> a novel family of redox sensors in the streptococci evolved from two-2 component response regulators
7	<a href="#">c2hqrA_</a>			100.0	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
8	<a href="#">c2gwrA_</a>			100.0	31	<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
9	<a href="#">c4b09F_</a>			100.0	27	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> transcriptional regulatory protein baer; <b>PDBTitle:</b> structure of unphosphorylated baer dimer
10	<a href="#">c1p2fA_</a>			100.0	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure analysis of response regulator drrb, a thermotoga2 maritima ompr/phob homolog
11	<a href="#">c1kgsA_</a>			100.0	25	<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

12	<a href="#">c3q9sA_</a>	Alignment		100.0	25	<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
13	<a href="#">c2rv8A_</a>	Alignment		99.9	30	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> solution structure of the phop dna-binding domain from mycobacterium2 tuberculosis
14	<a href="#">c2hqnA_</a>	Alignment		99.9	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative orphan response regulator protein <b>PDBTitle:</b> structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
15	<a href="#">c4uhtA_</a>	Alignment		99.9	35	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein cpxr; <b>PDBTitle:</b> crystal structure of the dna binding domain of cpxr from e. coli
16	<a href="#">c2m1bA_</a>	Alignment		99.9	28	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein, c terminal family <b>PDBTitle:</b> solution structure of the chxr dna-binding domain
17	<a href="#">c3zq7A_</a>	Alignment		99.9	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> kdp operon transcriptional regulatory protein kdpE; <b>PDBTitle:</b> the structure of dna-binding domain of response regulator from2 escherichia coli k-12
18	<a href="#">c2jzyA_</a>	Alignment		99.9	32	<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
19	<a href="#">c2hvwA_</a>	Alignment		99.9	48	<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.
20	<a href="#">d1gxqa_</a>	Alignment		99.9	35	<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
21	<a href="#">d1opca_</a>	Alignment	not modelled	99.9	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
22	<a href="#">c2pmuD_</a>	Alignment	not modelled	99.9	34	<b>PDB header:</b> transcription regulation <b>Chain:</b> D: <b>PDB Molecule:</b> response regulator phop; <b>PDBTitle:</b> crystal structure of the dna-binding domain of phop
23	<a href="#">c4ixaA_</a>	Alignment	not modelled	99.9	37	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator saer; <b>PDBTitle:</b> structure of dna-binding domain of the response regulator saer from2 staphylococcus epidermidis
24	<a href="#">c2zxB_</a>	Alignment	not modelled	99.9	46	<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
25	<a href="#">c5xt2C_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> response regulator fixj; <b>PDBTitle:</b> crystal structures of full-length fixj from b. japonicum crystallized2 in space group p212121
26	<a href="#">c5dcmB_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> phob family transcriptional regulator; <b>PDBTitle:</b> structure of a lantibiotic response regulator: c-terminal domain of2 the nisin resistance regulator nsrr
27	<a href="#">c2m87A_</a>	Alignment	not modelled	99.9	32	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein basr/pmra; <b>PDBTitle:</b> structural basis of dna recognition by the effector domain of2 klebsiella pneumoniae pmra
28	<a href="#">c3q9vB_</a>	Alignment	not modelled	99.9	36	<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

29	<a href="#">c3rjpA_</a>	Alignment	not modelled	99.9	36	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> covr; <b>PDBTitle:</b> crystal structure of the dna binding domain of covr from streptococcus2 pyogenes
30	<a href="#">c5ju7A_</a>	Alignment	not modelled	99.9	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional activator cadc; <b>PDBTitle:</b> dna binding domain of e.coli cadc
31	<a href="#">c2k4jA_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> arsr dna binding domain
32	<a href="#">c2nazA_</a>	Alignment	not modelled	99.9	35	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein rsta; <b>PDBTitle:</b> the solution nmr structure of the c-terminal effector domain of bfmr2 from acinetobacter baumannii
33	<a href="#">d1p2fa1</a>	Alignment	not modelled	99.9	36	<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
34	<a href="#">d1ys7a1</a>	Alignment	not modelled	99.9	41	<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
35	<a href="#">c1zn2A_</a>	Alignment	not modelled	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
36	<a href="#">d1kgsa1</a>	Alignment	not modelled	99.9	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
37	<a href="#">c5x5lM_</a>	Alignment	not modelled	99.9	31	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> M: <b>PDB Molecule:</b> ader; <b>PDBTitle:</b> crystal structure of a response regulator ader dna binding domain in2 complex with an intercistronic region
38	<a href="#">c5f64C_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> positive transcription regulator evga; <b>PDBTitle:</b> putative positive transcription regulator (sensor evgs) from shigella2 flexneri
39	<a href="#">c4hyeB_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transcription activator <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> crystal structure of a response regulator spr1814 from streptococcus2 pneumoniae reveals unique interdomain contacts among narl family3 proteins
40	<a href="#">c4if4A_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> crystal structure of the magnesium and beryll fluoride-activated vvar2 from staphylococcus aureus
41	<a href="#">c3c3wB_</a>	Alignment	not modelled	99.8	23	<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
42	<a href="#">c2ayxA_</a>	Alignment	not modelled	99.8	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
43	<a href="#">c1rnlA_</a>	Alignment	not modelled	99.8	22	<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
44	<a href="#">c3eq2A_</a>	Alignment	not modelled	99.8	17	<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 pseudomonas aeruginosa rssb
45	<a href="#">c5hevC_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> response regulator protein vvar; <b>PDBTitle:</b> crystal structure of the beryll fluoride-activated liar from2 enterococcus faecium
46	<a href="#">c4o1iA_</a>	Alignment	not modelled	99.8	99	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> crystal structure of the regulatory domain of mtbglnr
47	<a href="#">c1w25B_</a>	Alignment	not modelled	99.8	18	<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
48	<a href="#">c1ny5A_</a>	Alignment	not modelled	99.7	16	<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
49	<a href="#">c5ep0A_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative repressor protein luxo; <b>PDBTitle:</b> quorum-sensing signal integrator luxo - receiver+catalytic domains
50	<a href="#">c3rqIA_</a>	Alignment	not modelled	99.7	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
51	<a href="#">c3breA_</a>	Alignment	not modelled	99.7	16	<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
52	<a href="#">d1ys7a2</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
53	<a href="#">c3w9sB_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> signaling protein/antimicrobial protein <b>Chain:</b> B: <b>PDB Molecule:</b> ompr family response regulator in two-component regulatory

						<b>PDBTitle:</b> crystal structure analysis of the n-terminal receiver domain of f2 response regulator pmra
54	<a href="#">c6od1A_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of rpos; <b>PDBTitle:</b> irad-bound to rssb d58p variant
55	<a href="#">c5x5jA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ader; <b>PDBTitle:</b> crystal structure of response regulator ader receiver domain
56	<a href="#">c3i5aA_</a>	Alignment	not modelled	99.7	17	<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
57	<a href="#">c3dzdA_</a>	Alignment	not modelled	99.7	10	<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
58	<a href="#">d1mvoa_</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
59	<a href="#">d1ny5a1</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
60	<a href="#">c6ifhA_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sporulation initiation phosphotransferase f; <b>PDBTitle:</b> unphosphorylated spo0f from paenisporosarcina sp. tg-14
61	<a href="#">d1kgsa2</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
62	<a href="#">d2ff4a1</a>	Alignment	not modelled	99.7	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> PhoB-like
63	<a href="#">d2ayxa1</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
64	<a href="#">c5uicA_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> two-component response regulator; <b>PDBTitle:</b> structure of the francisella response regulator receiver domain, qseb
65	<a href="#">c4qpiC_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> signaling protein/dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> cell cycle response regulator ctra; <b>PDBTitle:</b> 2.7 angstrom structure of a phosphotransferase in complex with a2 receiver domain
66	<a href="#">d2pl1a1</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
67	<a href="#">d2a9pa1</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
68	<a href="#">c2zwmA_</a>	Alignment	not modelled	99.7	18	<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
69	<a href="#">c5m7nA_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen assimilation regulatory protein; <b>PDBTitle:</b> crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
70	<a href="#">c3cfyA_</a>	Alignment	not modelled	99.7	12	<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 luxo repressor2 protein from vibrio parahaemolyticus
71	<a href="#">d1qkka_</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
72	<a href="#">c2jrlA_</a>	Alignment	not modelled	99.7	12	<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
73	<a href="#">c3a0rB_</a>	Alignment	not modelled	99.7	16	<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)
74	<a href="#">d1dbwa_</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
75	<a href="#">c4lzlA_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the inactive form of the regulatory domain from the2 repressor of iron transport regulator (ritr)
76	<a href="#">c2qv0A_</a>	Alignment	not modelled	99.7	11	<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 of protein mrke2 from klebsiella pneumoniae
77	<a href="#">c6m8oA_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding response regulator; <b>PDBTitle:</b> crystal structure of the receiver domain of lytr from staphylococcus2 aureus
78	<a href="#">c4q7eA_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator of a two component regulatory system; <b>PDBTitle:</b> non-phosphorylated hemr receiver domain from leptospira biflexa
						<b>Fold:</b> Flavodoxin-like

79	<a href="#">d1yioa2</a>	Alignment	not modelled	99.7	14	<b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
80	<a href="#">c3klnC</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, luxr family; <b>PDBTitle:</b> vibrio cholerae vpst
81	<a href="#">d1peya</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
82	<a href="#">c5e3jB</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator rsta; <b>PDBTitle:</b> the response regulator rsta is a potential drug target for2 acinetobacter baumannii
83	<a href="#">c2rjnA</a>	Alignment	not modelled	99.7	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
84	<a href="#">d1krwa</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
85	<a href="#">d1w25a1</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
86	<a href="#">d1jbea</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
87	<a href="#">c5t3yA</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> two-component system response regulator; <b>PDBTitle:</b> solution structure of response regulator protein from burkholderia2 multivorans
88	<a href="#">c4h60A</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> chemotaxis protein chey; <b>PDBTitle:</b> high resolution structure of vibrio cholerae chemotaxis protein chey42 crystallized in low ph (4.0) condition
89	<a href="#">d1zh2a1</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
90	<a href="#">c2qr3A</a>	Alignment	not modelled	99.7	15	<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
91	<a href="#">c5o8yG</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> transcriptional regulatory protein rcsb; <b>PDBTitle:</b> conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
92	<a href="#">c3t6kB</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> response regulator receiver; <b>PDBTitle:</b> crystal structure of a putative response regulator (caur_3799) from2 chloroflexus aurantiacus j-10-fl at 1.86 a resolution
93	<a href="#">d1zgza1</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
94	<a href="#">d1p2fa2</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
95	<a href="#">c5jyuA</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> sigaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> two-component sensor histidine kinase; <b>PDBTitle:</b> nmr structure of pseudo receiver domain of cika from2 thermosynechococcus elongatus
96	<a href="#">d1s8na</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
97	<a href="#">d1mb3a</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
98	<a href="#">c3gt7A</a>	Alignment	not modelled	99.6	17	<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 signal transduction2 histidine kinase from syntrophus aciditrophicus
99	<a href="#">c3hv2B</a>	Alignment	not modelled	99.6	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-containing2 protein from pseudomonas fluorescens pf-5
100	<a href="#">d1zesa1</a>	Alignment	not modelled	99.6	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
101	<a href="#">c3nhzA</a>	Alignment	not modelled	99.6	19	<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
102	<a href="#">c3jteA</a>	Alignment	not modelled	99.6	17	<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 domain protein from2 clostridium thermocellum
103	<a href="#">c2qzjC</a>	Alignment	not modelled	99.6	12	<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
104	<a href="#">d2b4aa1</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like

						<b>Family:</b> CheY-related
105	<a href="#">c4uhsA</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein cpxr; <b>PDBTitle:</b> crystal structure of the receiver domain of cpxr from e. coli2 (tetragonal form)
106	<a href="#">c3cu5B</a>	Alignment	not modelled	99.6	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
107	<a href="#">c4eukA</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> histidine kinase 5; <b>PDBTitle:</b> crystal structure
108	<a href="#">c3crnA</a>	Alignment	not modelled	99.6	13	<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
109	<a href="#">c3n0rA</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator; <b>PDBTitle:</b> structure of the phyr stress response regulator at 1.25 angstrom2 resolution
110	<a href="#">c2zayA</a>	Alignment	not modelled	99.6	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
111	<a href="#">c2rdmB</a>	Alignment	not modelled	99.6	17	<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="#">c3i42A</a>	Alignment	not modelled	99.6	18	<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> structure of response regulator receiver domain (chey-like) from2 methylobacillus flagellatus
113	<a href="#">c5kxbB</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> osmolarity two-component system protein ssk1; <b>PDBTitle:</b> co-crystal structure of the saccharomyces cerevisiae histidine2 phosphotransfer signaling protein ypd1 and the receiver domain of its3 downstream response regulator ssk1
114	<a href="#">c6ekhY</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> Y: <b>PDB Molecule:</b> chemotaxis protein chey; <b>PDBTitle:</b> crystal structure of activated chey from methanococcus maripaludis
115	<a href="#">d1xhfa1</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
116	<a href="#">c3hdgE</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinella3 succinogenes
117	<a href="#">c4g97A</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> response regulator receiver; <b>PDBTitle:</b> crystal structure of the response regulator phyr from brucella abortus
118	<a href="#">c3b2nA</a>	Alignment	not modelled	99.6	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
119	<a href="#">d1dz3a</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> CheY-like <b>Family:</b> CheY-related
120	<a href="#">c4d6yA</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> bacterial regulatory, fis family protein; <b>PDBTitle:</b> crystal structure of the receiver domain of ntrx from2 brucella abortus in complex with beryll fluoride and3 magnesium