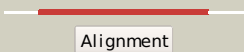

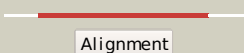

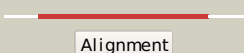

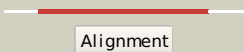
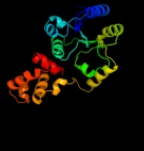
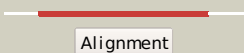

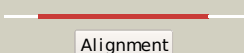
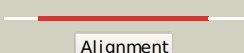
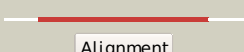
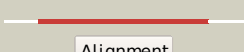

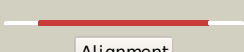

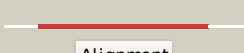




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1rnIA_	 Alignment		100.0	98	PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl; PDBTitle: the nitrate/nitrite response regulator protein narl from narl
2	c3c3wB_	 Alignment		100.0	29	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
3	c1zn2A_	 Alignment		100.0	30	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
4	c3klnC_	 Alignment		100.0	18	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
5	c1kgsA_	 Alignment		99.9	19	PDB header: dna binding protein Chain: A: PDB Molecule: dna binding response regulator d; PDBTitle: crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
6	c3q9sA_	 Alignment		99.9	27	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra(1-215) from deinococcus radiodurans
7	c3r0jA_	 Alignment		99.9	19	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
8	c1ys7B_	 Alignment		99.9	24	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed with2 mg2 +
9	c2gwrA_	 Alignment		99.9	24	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator mtra; PDBTitle: crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
10	c2oqrA_	 Alignment		99.9	23	PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis
11	c2hqrA_	 Alignment		99.9	18	PDB header: signaling protein Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism

12	c1p2fA_	Alignment		99.8	18	PDB header: transcription Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure analysis of response regulator drrb, a2 thermotoga maritima ompr/phob homolog
13	d1s8na_	Alignment		99.8	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
14	c3szbB_	Alignment		99.7	27	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
15	d1a04a2	Alignment		99.7	100	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
16	c1h0mD_	Alignment		99.7	21	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
17	c2q0oA_	Alignment		99.7	19	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
18	c1a2oB_	Alignment		99.7	28	PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
19	c3cz5B_	Alignment		99.7	32	PDB header: transcription regulator Chain: B: PDB Molecule: two-component response regulator, luxr family; PDBTitle: crystal structure of two-component response regulator, luxr family,2 from aurantiimonas sp. si85-9a1
20	c3eq2A_	Alignment		99.7	36	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
21	c3eulB_	Alignment	not modelled	99.7	37	PDB header: transcription Chain: B: PDB Molecule: possible nitrate/nitrite response transcriptional PDBTitle: structure of the signal receiver domain of the putative2 response regulator narl from mycobacterium tuberculosis
22	c2ayxA_	Alignment	not modelled	99.7	23	PDB header: transferase Chain: A: PDB Molecule: sensor kinase protein rcsc; PDBTitle: solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
23	c3qp5C_	Alignment	not modelled	99.7	37	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
24	c3b2nA_	Alignment	not modelled	99.7	28	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
25	d2ayxa1	Alignment	not modelled	99.6	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
26	d1dz3a_	Alignment	not modelled	99.6	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
27	d1a2oa1	Alignment	not modelled	99.6	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
28	c1w25B_	Alignment	not modelled	99.6	28	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein;

						PDBTitle: response regulator pled in complex with c-digmp PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of the response regulator domain of thermotoga2 maritima cheb
29	c3t8yA_	Alignment	not modelled	99.6	31	
30	d1a04a1	Alignment	not modelled	99.6	100	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
31	c3i5aA_	Alignment	not modelled	99.6	30	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
32	c3breA_	Alignment	not modelled	99.6	27	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
33	d1jbea_	Alignment	not modelled	99.6	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
34	c3cu5B_	Alignment	not modelled	99.6	24	PDB header: transcription regulator Chain: B: PDB Molecule: two component transcriptional regulator, arac family; PDBTitle: crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
35	c3dzdA_	Alignment	not modelled	99.6	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
36	c3cloC_	Alignment	not modelled	99.6	31	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: 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
37	d1p4wa_	Alignment	not modelled	99.6	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
38	c1zljE_	Alignment	not modelled	99.6	37	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
39	c1ny5A_	Alignment	not modelled	99.6	28	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
40	d1ys7a2	Alignment	not modelled	99.6	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
41	d1p6qa_	Alignment	not modelled	99.6	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
42	d1ny5a1	Alignment	not modelled	99.6	28	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
43	c2krfB_	Alignment	not modelled	99.6	25	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
44	d1u0sy_	Alignment	not modelled	99.6	30	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
45	d1l3la1	Alignment	not modelled	99.6	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
46	c2qv0A_	Alignment	not modelled	99.6	21	PDB header: transcription Chain: A: PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
47	c2rjnA_	Alignment	not modelled	99.5	25	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
48	d1fsea_	Alignment	not modelled	99.5	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
49	d1dbwa_	Alignment	not modelled	99.5	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
50	d1kgsa2	Alignment	not modelled	99.5	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
51	c3rqiA_	Alignment	not modelled	99.5	25	PDB header: transcription Chain: A: PDB Molecule: response regulator protein; PDBTitle: crystal structure of a response regulator protein from burkholderia2 pseudomallei with a phosphorylated aspartic acid, calcium ion and3 citrate
52	d1mvoa_	Alignment	not modelled	99.5	30	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
53	d1peya_	Alignment	not modelled	99.5	22	Fold: Flavodoxin-like Superfamily: CheY-like

					Family: CheY-related
54	d1krwa_	Alignment	not modelled	99.5	23 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
55	d2a9pa1	Alignment	not modelled	99.5	30 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
56	c3cfyA_	Alignment	not modelled	99.5	24 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative luxO repressor protein; PDBTitle: crystal structure of signal receiver domain of putative luxO2 repressor protein from vibrio parahaemolyticus
57	c3f6cB_	Alignment	not modelled	99.5	27 PDB header: dna binding protein Chain: B: PDB Molecule: positive transcription regulator evga; PDBTitle: crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
58	c2rniA_	Alignment	not modelled	99.5	38 PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
59	c1x3uA_	Alignment	not modelled	99.5	40 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
60	c3hv2B_	Alignment	not modelled	99.5	25 PDB header: signaling protein Chain: B: PDB Molecule: response regulator/hd domain protein; PDBTitle: crystal structure of signal receiver domain of hd domain-2 containing protein from pseudomonas fluorescens pf-5
61	d2pl1a1	Alignment	not modelled	99.5	25 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
62	c3t6kB_	Alignment	not modelled	99.5	23 PDB header: signaling protein Chain: B: PDB Molecule: response regulator receiver; PDBTitle: crystal structure of a hypothetical response regulator (caur_3799)2 from chloroflexus aurantiacus j-10-fl at 1.86 a resolution
63	d1k66a_	Alignment	not modelled	99.5	21 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
64	c2qr3A_	Alignment	not modelled	99.5	24 PDB header: transcription Chain: A: PDB Molecule: two-component system response regulator; PDBTitle: crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
65	c3khtA_	Alignment	not modelled	99.5	19 PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
66	c3hdgE_	Alignment	not modelled	99.5	28 PDB header: structural genomics, unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinetella3 succinogenes
67	c2zwmA_	Alignment	not modelled	99.5	29 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
68	d1qkka_	Alignment	not modelled	99.5	21 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
69	d1zgza1	Alignment	not modelled	99.5	26 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
70	d1yioa2	Alignment	not modelled	99.5	28 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
71	c3nhzA_	Alignment	not modelled	99.5	32 PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
72	d1heya_	Alignment	not modelled	99.5	20 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
73	d1i3ca_	Alignment	not modelled	99.5	26 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
74	d1xhfa1	Alignment	not modelled	99.5	26 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
75	d1w25a1	Alignment	not modelled	99.5	27 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
76	c2jrlA_	Alignment	not modelled	99.5	22 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryll fluoride-activated ntrc4 receiver2 domain dimer
77	c2jpcA_	Alignment	not modelled	99.5	33 PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
78	c3cnbC_	Alignment	not modelled	99.5	20 PDB header: dna binding protein Chain: C: PDB Molecule: dna-binding response regulator, merr family; PDBTitle: crystal structure of signal receiver domain of dna binding response2 regulator protein (merr) from colwellia psychrerythraea 34h
					PDB header: transcription

79	c2qzjC_	Alignment	not modelled	99.5	25	Chain: C: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of a two-component response regulator from2 clostridium difficile
80	dlyioa1	Alignment	not modelled	99.5	39	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
81	c3a0rB_	Alignment	not modelled	99.5	26	PDB header: transferase Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
82	c3lteH_	Alignment	not modelled	99.5	23	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
83	d1zh2a1	Alignment	not modelled	99.5	30	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
84	c3c97A_	Alignment	not modelled	99.5	19	PDB header: signaling protein, transferase Chain: A: PDB Molecule: signal transduction histidine kinase; PDBTitle: crystal structure of the response regulator receiver domain2 of a signal transduction histidine kinase from aspergillus3 oryzae
85	c3gt7A_	Alignment	not modelled	99.4	21	PDB header: hydrolase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
86	c3i42A_	Alignment	not modelled	99.4	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey- PDBTitle: structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
87	c2qvqA_	Alignment	not modelled	99.4	25	PDB header: transferase Chain: A: PDB Molecule: two component response regulator; PDBTitle: the crystal structure of a two-component response regulator2 from legionella pneumophila
88	c3kyiB_	Alignment	not modelled	99.4	27	PDB header: transferase Chain: B: PDB Molecule: chey6 protein; PDBTitle: crystal structure of the phosphorylated p1 domain of chea3 in complex2 with chey6 from r. sphaeroides
89	c3cg4A_	Alignment	not modelled	99.4	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey-like); PDBTitle: crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
90	c3ilhA_	Alignment	not modelled	99.4	20	PDB header: transcription regulator Chain: A: PDB Molecule: two component response regulator; PDBTitle: crystal structure of two component response regulator from cytophaga2 hutchinsonii
91	c3hebB_	Alignment	not modelled	99.4	21	PDB header: transcription regulator Chain: B: PDB Molecule: response regulator receiver domain protein (chey); PDBTitle: crystal structure of response regulator receiver domain from2 rhodospirillum rubrum
92	c3crnA_	Alignment	not modelled	99.4	27	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver domain protein, chey-like; PDBTitle: crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
93	c3jteA_	Alignment	not modelled	99.4	24	PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
94	d1zesa1	Alignment	not modelled	99.4	27	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
95	c3h1gA_	Alignment	not modelled	99.4	28	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis protein chey homolog; PDBTitle: crystal structure of chey mutant t84a of helicobacter pylori
96	c3hzhA_	Alignment	not modelled	99.4	21	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis response regulator (chey-3); PDBTitle: crystal structure of the chex-chey-bef3-mg+2 complex from2 borrelia burgdorferi
97	d2b4aa1	Alignment	not modelled	99.4	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
98	c3c3mA_	Alignment	not modelled	99.4	22	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1
99	c3snkA_	Alignment	not modelled	99.4	16	PDB header: signaling protein Chain: A: PDB Molecule: response regulator chey-like protein; PDBTitle: crystal structure of a response regulator chey-like protein (ml16475)2 from mesorhizobium loti at 2.02 a resolution
100	d1mb3a_	Alignment	not modelled	99.4	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
101	c3hdvB_	Alignment	not modelled	99.4	20	PDB header: transcription regulator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein from2 pseudomonas putida
102	c2zayA_	Alignment	not modelled	99.4	17	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans
103	d2r25b1	Alignment	not modelled	99.4	20	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related

104	c3m6mF_	 Alignment	not modelled	99.4	32	PDB header: lyase/transferase Chain: F: PDB Molecule: sensory/regulatory protein rpfc; PDBTitle: crystal structure of rpfc complexed with rec domain of rpfc
105	c3kcnA_	 Alignment	not modelled	99.4	25	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase homolog; PDBTitle: the crystal structure of adenylate cyclase from2 rhodopirellula baltica
106	c2qxyB_	 Alignment	not modelled	99.4	21	PDB header: transcription Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from thermotoga2 maritima
107	c2jk1A_	 Alignment	not modelled	99.4	27	PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain
108	c2rdmB_	 Alignment	not modelled	99.4	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419
109	c3mmnA_	 Alignment	not modelled	99.4	24	PDB header: transferase Chain: A: PDB Molecule: histidine kinase homolog; PDBTitle: crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+
110	c3grcD_	 Alignment	not modelled	99.4	18	PDB header: transferase Chain: D: PDB Molecule: sensor protein, kinase; PDBTitle: crystal structure of a sensor protein from polaromonas sp.2 js666
111	d1p2fa2	 Alignment	not modelled	99.4	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
112	c3cg0A_	 Alignment	not modelled	99.4	20	PDB header: lyase Chain: A: PDB Molecule: response regulator receiver modulated diguanylate cyclase PDBTitle: crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding
113	c3n0rA_	 Alignment	not modelled	99.3	18	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr stress response regulator at 1.25 angstrom2 resolution
114	c3nhmA_	 Alignment	not modelled	99.3	25	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from myxococcus xanthus
115	c2j48A_	 Alignment	not modelled	99.3	24	PDB header: transferase Chain: A: PDB Molecule: two-component sensor kinase; PDBTitle: nmr structure of the pseudo-receiver domain of the cika2 protein.
116	c3gl9B_	 Alignment	not modelled	99.3	32	PDB header: signaling protein Chain: B: PDB Molecule: response regulator; PDBTitle: the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism
117	d1dcfa_	 Alignment	not modelled	99.3	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: Receiver domain of the ethylene receptor
118	c3cwoX_	 Alignment	not modelled	99.3	23	PDB header: de novo protein Chain: X: PDB Molecule: beta/alpha-barrel protein based on 1thf and 1trny; PDBTitle: a beta/alpha-barrel built by the combination of fragments2 from different folds
119	c3lufB_	 Alignment	not modelled	99.3	22	PDB header: signaling protein Chain: B: PDB Molecule: two-component system response regulator/ggdef PDBTitle: structure of probable two-component system response2 regulator/ggdef domain protein
120	c3eodA_	 Alignment	not modelled	99.3	26	PDB header: signaling protein Chain: A: PDB Molecule: protein hnr; PDBTitle: crystal structure of n-terminal domain of e. coli rssb