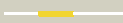
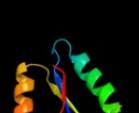
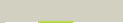
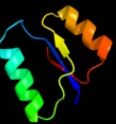
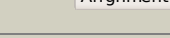
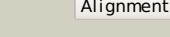
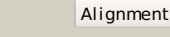
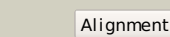


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cniA_	 Alignment		99.3	13	PDB header: transport protein Chain: A: PDB Molecule: putative abc type-2 transporter; PDBTitle: crystal structure of a domain of a putative abc type-2 transporter2 from thermotoga maritima msb8
2	d2p0sa1	 Alignment		94.6	10	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: PG0945 N-terminal domain-like
3	c3eulB_	 Alignment		79.8	11	PDB header: transcription Chain: B: PDB Molecule: possible nitrate/nitrite response transcriptional PDBTitle: structure of the signal receiver domain of the putative2 response regulator narI from mycobacterium tuberculosis
4	c2gwrA_	 Alignment		73.8	11	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
5	d1heya_	 Alignment		72.2	9	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
6	d1p6qa_	 Alignment		69.1	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
7	c3cg4A_	 Alignment		67.0	13	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
8	d2ayxa1	 Alignment		66.0	4	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
9	c3fkqA_	 Alignment		66.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntrc-like two-domain protein; PDBTitle: crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
10	c3r0jA_	 Alignment		65.9	6	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
11	d1ys7a2	 Alignment		63.6	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related

12	c2rjnA	 Alignment		63.0	4	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
13	dlzgza1	 Alignment		60.9	6	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
14	c1a2oB	 Alignment		60.7	11	PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
15	dls8na	 Alignment		60.7	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
16	d1dbwa	 Alignment		59.9	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
17	c3hv2B	 Alignment		59.0	6	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
18	c1rnlA	 Alignment		58.2	8	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
19	c3t6kB	 Alignment		57.9	10	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
20	c1kgsA	 Alignment		57.8	8	PDB header: dna binding protein Chain: A: PDB Molecule: dna binding response regulator d; PDBTitle: crystal structure at 1.50 a of an omp/phob homolog from thermotoga2 maritima
21	c3nhmA	 Alignment	not modelled	57.6	16	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from myxococcus xanthus
22	d1xhfa1	 Alignment	not modelled	56.5	8	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
23	c2oqrA	 Alignment	not modelled	55.5	14	PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis
24	c1ys7B	 Alignment	not modelled	54.8	12	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed with2 mg2+
25	c3nhzA	 Alignment	not modelled	54.3	10	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
26	d1kgsa2	 Alignment	not modelled	54.2	8	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
27	d1jbea	 Alignment	not modelled	52.9	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
28	c3lteH	 Alignment	not modelled	52.8	9	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
29	c3b2nA	 Alignment	not modelled	52.6	8	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr

					family, from2 staphylococcus aureus
30	c3a0rB_	Alignment	not modelled	52.5	10 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)
31	c2qxyB_	Alignment	not modelled	50.9	18 PDB header: transcription Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from thermotoga2 maritima
32	d1ny5a1	Alignment	not modelled	50.2	6 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
33	d1a04a2	Alignment	not modelled	48.8	8 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
34	c3hdgE_	Alignment	not modelled	48.6	10 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 wolinnella3 succinogenes
35	d1mvoa_	Alignment	not modelled	48.2	12 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
36	c3grcD_	Alignment	not modelled	47.8	8 PDB header: transferase Chain: D: PDB Molecule: sensor protein, kinase; PDBTitle: crystal structure of a sensor protein from polaromonas sp.2 js666
37	c2jrlA_	Alignment	not modelled	47.6	12 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryll fluoride-activated ntrc4 receiver2 domain dimer
38	c3cz5B_	Alignment	not modelled	47.4	9 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 aurantimonas sp. si85-9a1
39	c3k2dA_	Alignment	not modelled	47.1	11 PDB header: immune system Chain: A: PDB Molecule: abc-type metal ion transport system, periplasmic component; PDBTitle: crystal structure of immunogenic lipoprotein a from vibrio vulnificus
40	c3breA_	Alignment	not modelled	46.5	12 PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
41	c1zn2A_	Alignment	not modelled	46.1	12 PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
42	c3c3mA_	Alignment	not modelled	46.0	10 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
43	c2zayA_	Alignment	not modelled	45.7	14 PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans
44	c3c97A_	Alignment	not modelled	45.6	14 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
45	d1mb3a_	Alignment	not modelled	43.9	10 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
46	d1zh2a1	Alignment	not modelled	42.9	14 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
47	c2qzjC_	Alignment	not modelled	41.8	14 PDB header: transcription Chain: C: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of a two-component response regulator from2 clostridium difficile
48	c2zwmA_	Alignment	not modelled	40.1	4 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
49	d2pl1a1	Alignment	not modelled	40.0	8 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
50	d1dz3a_	Alignment	not modelled	40.0	13 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
51	c3cfyA_	Alignment	not modelled	39.4	12 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
52	c2qv0A_	Alignment	not modelled	38.4	14 PDB header: transcription Chain: A: PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
53	d2a9pa1	Alignment	not modelled	37.9	10 Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
54	c2qr3A_	Alignment	not modelled	36.8	6 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

55	c1ny5A	Alignment	not modelled	36.8	6	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
56	d1krwa	Alignment	not modelled	36.7	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
57	d1w25a1	Alignment	not modelled	36.5	8	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
58	c3i42A	Alignment	not modelled	36.0	10	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
59	d1a2oa1	Alignment	not modelled	35.0	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
60	d1yioa2	Alignment	not modelled	34.9	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
61	d1peya	Alignment	not modelled	34.6	6	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
62	c3cnbC	Alignment	not modelled	34.1	19	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
63	c2ayxA	Alignment	not modelled	33.3	7	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
64	d1zesa1	Alignment	not modelled	33.3	2	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
65	c3n53B	Alignment	not modelled	30.3	10	PDB header: transcription Chain: B: PDB Molecule: response regulator receiver modulated diguanylate cyclase; PDBTitle: crystal structure of a response regulator receiver modulated2 diguanylate cyclase from pelobacter carbinolicus
66	c2j48A	Alignment	not modelled	29.2	8	PDB header: transferase Chain: A: PDB Molecule: two-component sensor kinase; PDBTitle: nmr structure of the pseudo-receiver domain of the cika2 protein.
67	c3eq2A	Alignment	not modelled	29.0	6	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
68	c1w25B	Alignment	not modelled	28.8	8	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
69	c3ir1F	Alignment	not modelled	28.5	6	PDB header: protein binding Chain: F: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of lipoprotein gna1946 from neisseria2 meningitidis
70	c3gl9B	Alignment	not modelled	28.4	13	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
71	c3t8yA	Alignment	not modelled	28.4	11	PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of the response regulator domain of thermotoga2 maritima cheb
72	d1xs5a	Alignment	not modelled	27.9	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
73	c3c3wB	Alignment	not modelled	27.9	14	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
74	c3ktoA	Alignment	not modelled	26.6	6	PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
75	c3gt7A	Alignment	not modelled	26.6	8	PDB header: hydrolase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
76	d1v95a	Alignment	not modelled	23.9	11	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
77	c3i5aA	Alignment	not modelled	21.6	14	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
78	c3on1A	Alignment	not modelled	21.3	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh2414 protein; PDBTitle: the structure of a protein with unknown function from

						bacillus2 halodurans c PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain
79	c2jk1A_	Alignment	not modelled	20.0	8	
80	d1qkka_	Alignment	not modelled	19.8	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
81	c3rqia_	Alignment	not modelled	19.3	10	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
82	d2cvoa1	Alignment	not modelled	19.2	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
83	d2q49a1	Alignment	not modelled	18.6	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
84	c3f6cB_	Alignment	not modelled	18.4	8	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
85	c2ixaA_	Alignment	not modelled	17.9	10	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyyme, n-acetylgalactosaminidase
86	c3mwbA_	Alignment	not modelled	17.8	11	PDB header: lyase Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aureescens to 2.0a
87	c1p99A_	Alignment	not modelled	17.2	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg110; PDBTitle: 1.7a crystal structure of protein pg110 from staphylococcus2 aureus
88	d1p99a_	Alignment	not modelled	17.2	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
89	d1hsla_	Alignment	not modelled	17.1	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
90	c3kyiB_	Alignment	not modelled	16.9	19	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
91	c3snkA_	Alignment	not modelled	16.1	10	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
92	c3luaA_	Alignment	not modelled	15.9	8	PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of a signal receiver domain of two component signal2 transduction (histidine kinase) from clostridium thermocellum
93	c3h1gA_	Alignment	not modelled	15.7	13	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis protein chey homolog; PDBTitle: crystal structure of chey mutant t84a of helicobacter pylori
94	c3hdvB_	Alignment	not modelled	15.1	18	PDB header: transcription regulator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein from2 pseudomonas putida
95	d1u0sy_	Alignment	not modelled	14.4	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
96	c3gxaA_	Alignment	not modelled	14.0	6	PDB header: protein binding Chain: A: PDB Molecule: outer membrane lipoprotein gna1946; PDBTitle: crystal structure of gna1946
97	c2hqrA_	Alignment	not modelled	13.8	12	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
98	c3g41A_	Alignment	not modelled	13.8	26	PDB header: transport protein Chain: A: PDB Molecule: amino acid abc transporter, periplasmic amino acid-binding PDBTitle: the structure of cpn0482, the arginine binding protein from the2 periplasm of chlamydia pneumoniae
99	d1yl7a1	Alignment	not modelled	13.7	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain