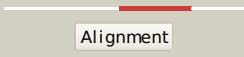
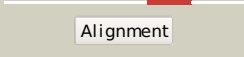
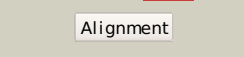
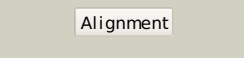
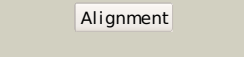
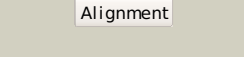
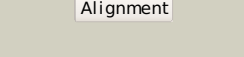
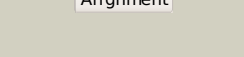
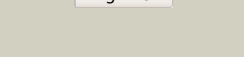


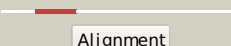
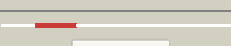
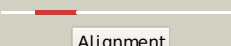
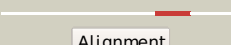
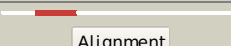
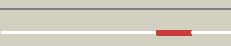
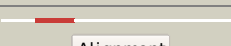
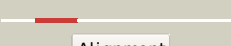
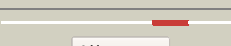
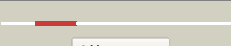
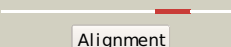
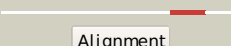
Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P30855
Date	Thu Jan 5 11:46:34 GMT 2012
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Detailed template information

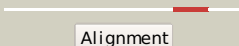
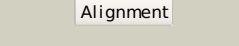
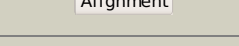
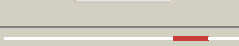
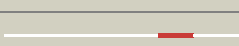
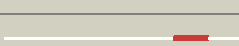
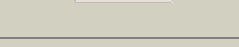
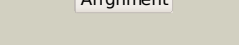
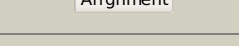
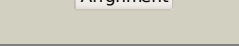
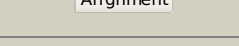
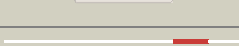
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2	c3a0rA_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of histidine kinase thka (tm1359) in complex with2 response regulator protein trra (tm1360)
3	c3d36B_	 Alignment		100.0	23	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: sporulation kinase b; PDBTitle: how to switch off a histidine kinase: crystal structure of2 geobacillus stearothermophilus kinb with the inhibitor sda
4	c3d2rB_	 Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 4; PDBTitle: crystal structure of pyruvate dehydrogenase kinase isoform 4 in2 complex with adp
5	c2q8fA_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 1; PDBTitle: structure of pyruvate dehydrogenase kinase isoform 1
6	c2bu8A_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase kinase isoenzyme 2; PDBTitle: crystal structures of human pyruvate dehydrogenase kinase 22 containing physiological and synthetic ligands
7	c1y8oA_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; PDBTitle: crystal structure of the pdk3-l2 complex
8	c1gqvA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: [3-methyl-2-oxobutanoate dehydrogenase PDBTitle: branched-chain alpha-ketoacid dehydrogenase kinase (bck)2 complexed with atp-gamma-s
9	c3mplA_	 Alignment		100.0	20	PDB header: signaling protein Chain: A: PDB Molecule: virulence sensor protein bvgs; PDBTitle: crystal structure of bordetella pertussis bvgs vft2 domain (double2 mutant f375e/q461e)
10	c3hv1A_	 Alignment		100.0	13	PDB header: transport protein Chain: A: PDB Molecule: polar amino acid abc uptake transporter substrate PDBTitle: crystal structure of a polar amino acid abc uptake2 transporter substrate binding protein from streptococcus3 thermophilus
11	c3kzgB_	 Alignment		100.0	12	PDB header: transport protein Chain: B: PDB Molecule: arginine 3rd transport system periplasmic binding PDBTitle: crystal structure of an arginine 3rd transport system2 periplasmic binding protein from legionella pneumophila

12	c2ayxA	Alignment		100.0	33	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
13	c3k4uA	Alignment		100.0	15	PDB header: transport protein Chain: A: PDB Molecule: binding component of abc transporter; PDBTitle: crystal structure of putative binding component of abc transporter2 from wolinnella succinogenes dsm 1740 complexed with lysine
14	c2ylnA	Alignment		100.0	12	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter, periplasmic binding protein, PDBTitle: crystal structure of the l-cystine solute receptor of2 neisseria gonorrhoeae in the closed conformation
15	d2a5sa1	Alignment		100.0	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
16	c3g41A	Alignment		100.0	14	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
17	c3r39A	Alignment		100.0	15	PDB header: transport protein Chain: A: PDB Molecule: putative periplasmic binding protein; PDBTitle: crystal structure of periplasmic d-alanine abc transporter from2 salmonella enterica
18	c2vhaB	Alignment		100.0	15	PDB header: transport protein Chain: B: PDB Molecule: periplasmic binding transport protein; PDBTitle: debp
19	c3i6vA	Alignment		100.0	11	PDB header: transport protein Chain: A: PDB Molecule: periplasmic his/glu/gln/arg/opine family-binding protein; PDBTitle: crystal structure of a periplasmic his/glu/gln/arg/opine family-2 binding protein from silicibacter pomeroyi in complex with lysine
20	d2c2aa2	Alignment		100.0	26	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
21	c1b3qA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: protein (chemotaxis protein chea); PDBTitle: crystal structure of chea-289, a signal transducing histidine kinase
22	c3h7mA	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of a histidine kinase sensor domain with2 similarity to periplasmic binding proteins
23	c2o1mB	Alignment	not modelled	100.0	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: probable amino-acid abc transporter PDBTitle: crystal structure of the probable amino-acid abc2 transporter extracellular-binding protein ytmk from3 bacillus subtilis. northeast structural genomics4 consortium target sr572
24	c2y7iB	Alignment	not modelled	100.0	11	PDB header: arginine-binding protein Chain: B: PDB Molecule: stm4351; PDBTitle: structural basis for high arginine specificity in salmonella2 typhimurium periplasmic binding protein stm4351.
25	d1hsla	Alignment	not modelled	100.0	17	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
26	c2q2aD	Alignment	not modelled	100.0	14	PDB header: transport protein Chain: D: PDB Molecule: artj; PDBTitle: crystal structures of the arginine-, lysine-, histidine-2 binding protein artj from the thermophilic bacterium3 geobacillus stearothermophilus
27	c3a0tA	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: catalytic domain of histidine kinase thka (tm1359) in2 complex with adp and mg ion (trigonal)
28	c2q89A	Alignment	not modelled	100.0	13	PDB header: transport protein Chain: A: PDB Molecule: putative abc transporter amino acid-binding protein; PDBTitle: crystal structure of ehuh in complex with hydroxyectoine

29	c2v25B		Alignment	not modelled	100.0	18	PDB header: receptor Chain: B: PDB Molecule: major cell-binding factor; PDBTitle: structure of the campylobacter jejuni antigen peb1a, an2 aspartate and glutamate receptor with bound aspartate
30	c3kbrA		Alignment	not modelled	100.0	12	PDB header: lyase Chain: A: PDB Molecule: cyclohexadienyl dehydratase; PDBTitle: the crystal structure of cyclohexadienyl dehydratase precursor from2 pseudomonas aeruginosa pa01
31	c2ieeB		Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: probable abc transporter extracellular-binding PDBTitle: crystal structure of yckb_bacsu from bacillus subtilis.2 northeast structural genomics consortium target sr574.
32	d1lsta		Alignment	not modelled	100.0	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
33	c3delC		Alignment	not modelled	100.0	15	PDB header: protein binding, transport protein Chain: C: PDB Molecule: arginine binding protein; PDBTitle: the structure of ct381, the arginine binding protein from the2 periplasm chlamydia trachomatis
34	d1gkza2		Alignment	not modelled	100.0	20	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain
35	d1wdna		Alignment	not modelled	99.9	14	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
36	d1bxda		Alignment	not modelled	99.9	20	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
37	d1id0a		Alignment	not modelled	99.9	20	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
38	d1jm6a2		Alignment	not modelled	99.9	22	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: alpha-ketoacid dehydrogenase kinase, C-terminal domain
39	d1pb7a		Alignment	not modelled	99.9	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
40	c2rc9A		Alignment	not modelled	99.9	13	PDB header: membrane protein Chain: A: PDB Molecule: glutamate [nmda] receptor subunit 3a; PDBTitle: crystal structure of the nr3a ligand binding core complex with acpc at2 1.96 angstrom resolution
41	c1xt8B		Alignment	not modelled	99.9	11	PDB header: transport protein Chain: B: PDB Molecule: putative amino-acid transporter periplasmic solute-binding PDBTitle: crystal structure of cysteine-binding protein from campylobacter2 jejuni at 2.0 a resolution
42	c3jz3B		Alignment	not modelled	99.9	18	PDB header: transferase Chain: B: PDB Molecule: sensor protein qsec; PDBTitle: structure of the cytoplasmic segment of histidine kinase qsec
43	c2yjpB		Alignment	not modelled	99.9	13	PDB header: transport protein Chain: B: PDB Molecule: putative abc transporter, periplasmic binding protein, PDBTitle: crystal structure of the solute receptors for l-cysteine of2 neisseria gonorrhoeae
44	d1xt8a1		Alignment	not modelled	99.9	11	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
45	c2ch4A		Alignment	not modelled	99.9	22	PDB header: transferase/chemotaxis Chain: A: PDB Molecule: chemotaxis protein chea; PDBTitle: complex between bacterial chemotaxis histidine kinase chea2 domains p4 and p5 and receptor-adaptor protein chew
46	d1ysra1		Alignment	not modelled	99.9	24	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
47	d1mqia		Alignment	not modelled	99.9	15	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
48	d1i58a		Alignment	not modelled	99.9	22	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
49	c1w25B		Alignment	not modelled	99.9	33	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
50	c3eq2A		Alignment	not modelled	99.9	30	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: structure of hexagonal crystal form of pseudomonas2 aeruginosa rssb
51	c3breA		Alignment	not modelled	99.9	21	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
52	d1ii5a		Alignment	not modelled	99.9	16	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II

						Family: Phosphate binding protein-like
53	c2ppyB_	Alignment	not modelled	99.9	11	PDB header: transport protein Chain: B: PDB Molecule: ionotropic glutamate receptor bacterial homologue; PDBTitle: crystal structure of the glur0 ligand-binding core from nostoc2 punctiforme in complex with (l)-glutamate
54	c2xx7B_	Alignment	not modelled	99.9	15	PDB header: transport protein Chain: B: PDB Molecule: glutamate receptor 2; PDBTitle: crystal structure of 1-(4-(1-pyrrolidinylcarbonyl)phenyl)-3-2 (trifluoromethyl)-4,5,6,7-tetrahydro-1h-indazole in complex with3 the ligand binding domain of the rat glua2 receptor and glutamate4 at 2.2a resolution.
55	d2ayxa1	Alignment	not modelled	99.9	47	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
56	c3i5aA_	Alignment	not modelled	99.9	21	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
57	c3n0rA_	Alignment	not modelled	99.9	18	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr stress response regulator at 1.25 angstrom2 resolution
58	d1peya_	Alignment	not modelled	99.9	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
59	d2pl1a1	Alignment	not modelled	99.9	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
60	d1jbea_	Alignment	not modelled	99.9	35	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
61	c1ny5A_	Alignment	not modelled	99.9	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
62	d1u0sy_	Alignment	not modelled	99.9	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
63	c3gt7A_	Alignment	not modelled	99.9	31	PDB header: hydrolase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
64	d1mvoa_	Alignment	not modelled	99.9	32	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
65	d1ny5a1	Alignment	not modelled	99.9	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
66	d1k66a_	Alignment	not modelled	99.9	20	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
67	c2zwmA_	Alignment	not modelled	99.9	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	99.9	25	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
69	c3t6kB_	Alignment	not modelled	99.9	31	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
70	d1w25a1	Alignment	not modelled	99.9	33	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
71	d1s8na_	Alignment		99.9	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
72	c3cfyA_	Alignment	not modelled	99.9	21	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
73	c2zayA_	Alignment	not modelled	99.9	23	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans
74	d1ys7a2	Alignment	not modelled	99.9	30	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
75	d2a9pa1	Alignment	not modelled	99.9	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
76	c3lteH_	Alignment	not modelled	99.9	24	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri

77	d1dbwa_	Alignment	not modelled	99.9	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
78	c3r0jA_	Alignment	not modelled	99.9	29	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
79	c2rjnA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
80	c3gl9B_	Alignment	not modelled	99.9	31	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
81	d2r25b1	Alignment	not modelled	99.9	35	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
82	d1mb3a_	Alignment	not modelled	99.9	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
83	d1zh2a1	Alignment	not modelled	99.9	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
84	d1s50a1	Alignment	not modelled	99.9	12	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
85	c3jteA_	Alignment	not modelled	99.9	23	PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
86	dlyioa2	Alignment	not modelled	99.9	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
87	d1heya_	Alignment	not modelled	99.9	33	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
88	c3hv2B_	Alignment	not modelled	99.9	27	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
89	d1kgsa2	Alignment	not modelled	99.9	26	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
90	c3nhza_	Alignment	not modelled	99.9	30	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
91	d2hkja3	Alignment	not modelled	99.9	20	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: DNA gyrase/MutL, N-terminal domain
92	c2qzjC_	Alignment	not modelled	99.9	26	PDB header: transcription Chain: C: PDB Molecule: two-component response regulator; PDBTitle: crystal structure of a two-component response regulator from2 clostridium difficile
93	c3h1gA_	Alignment	not modelled	99.9	38	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis protein chey homolog; PDBTitle: crystal structure of chey mutant t84a of helicobacter pylori
94	d1zgza1	Alignment	not modelled	99.9	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
95	c3cnbC_	Alignment	not modelled	99.9	22	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
96	d1p6qa_	Alignment	not modelled	99.9	33	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
97	c2qr3A_	Alignment	not modelled	99.9	19	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
98	c3b2nA_	Alignment	not modelled	99.9	19	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
99	d1zesa1	Alignment	not modelled	99.9	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
100	c3mmnA_	Alignment	not modelled	99.9	28	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+
101	d1krwa_	Alignment	not modelled	99.9	23	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related

102	c3lufB_		Alignment	not modelled	99.9	27	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
103	c3hdgE_		Alignment	not modelled	99.9	23	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 wolinella3 succinogenes
104	c3dzdA_		Alignment	not modelled	99.9	18	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
105	c3c3mA_		Alignment	not modelled	99.9	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
106	c2jrlA_		Alignment	not modelled	99.9	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
107	d1xhfa1		Alignment	not modelled	99.9	31	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
108	c3khtA_		Alignment	not modelled	99.9	24	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
109	d1dcfa_		Alignment	not modelled	99.9	24	Fold: Flavodoxin-like Superfamily: CheY-like Family: Receiver domain of the ethylene receptor
110	d1r62a_		Alignment	not modelled	99.9	23	Fold: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Superfamily: ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase Family: Histidine kinase
111	c1ys7B_		Alignment	not modelled	99.9	28	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed with2 mg2+
112	c3crnA_		Alignment	not modelled	99.9	22	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
113	c3cg4A_		Alignment	not modelled	99.9	21	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
114	c3eulB_		Alignment	not modelled	99.9	27	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
115	d1a04a2		Alignment	not modelled	99.9	29	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
116	c3cu5B_		Alignment	not modelled	99.9	25	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
117	c2qvgA_		Alignment	not modelled	99.9	24	PDB header: transferase Chain: A: PDB Molecule: two component response regulator; PDBTitle: the crystal structure of a two-component response regulator2 from legionella pneumophila
118	c3hdbV_		Alignment	not modelled	99.9	23	PDB header: transcription regulator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein from2 pseudomonas putida
119	c2gwrA_		Alignment	not modelled	99.9	28	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
120	c2qxyB_		Alignment	not modelled	99.9	21	PDB header: transcription Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from thermotoga2 maritima