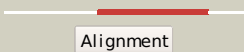

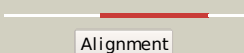
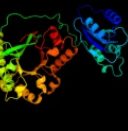






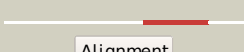











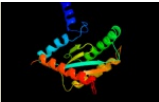











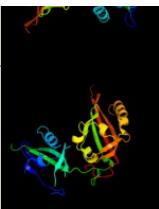

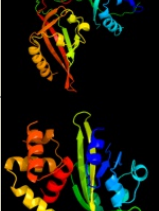
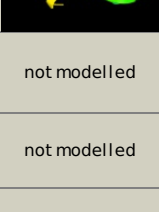



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pjwA_	 Alignment		100.0	25	PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
2	c3gfbB_	 Alignment		100.0	20	PDB header: hydrolase, signaling protein Chain: B: PDB Molecule: klebsiella pneumoniae blrp1; PDBTitle: klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
3	c3hvbB_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: protein fimx; PDBTitle: crystal structure of the dual-domain ggdef-eal module of2 fimx from pseudomonas aeruginosa
4	c3hv9A_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx eal domain from pseudomonas aeruginosa
5	c3s83A_	 Alignment		100.0	34	PDB header: signaling protein Chain: A: PDB Molecule: ggdef family protein; PDBTitle: crystal structure of eal domain from caulobacter crescentus cb15
6	c3pfmA_	 Alignment		100.0	27	PDB header: signaling protein Chain: A: PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of a eal domain of ggdef domain protein from2 pseudomonas fluorescens pf
7	c2w27A_	 Alignment		100.0	20	PDB header: signaling protein Chain: A: PDB Molecule: ykui protein; PDBTitle: crystal structure of the bacillus subtilis ykui protein,2 with an eal domain, in complex with substrate c-di-gmp and3 calcium
8	c2r6oB_	 Alignment		100.0	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative diguanylate cyclase/phosphodiesterase (ggdef & eal) PDBTitle: crystal structure of putative diguanylate cyclase/phosphodiesterase2 from thiobacillus denitrificans
9	d2basa1	 Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: EAL domain-like Family: EAL domain
10	c3kzpA_	 Alignment		100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative diguanylate cyclase/phosphodiesterase; PDBTitle: crystal structure of putative diguanylate cyclase/phosphodiesterase2 from listeria monocytigenes
11	c1w25B_	 Alignment		100.0	25	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp

12	c3ezuA	Alignment		100.0	19	PDB header: signaling protein Chain: A: PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
13	c3breA	Alignment		100.0	24	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
14	c3i5aA	Alignment		100.0	24	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
15	c3mtkA	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase/phosphodiesterase; PDBTitle: x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c
16	c3icIA	Alignment		100.0	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: eal/ggdef domain protein; PDBTitle: x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium3 target mcr174c
17	c3i5bA	Alignment		100.0	22	PDB header: signaling protein Chain: A: PDB Molecule: wpsr response regulator; PDBTitle: crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
18	c3i5cA	Alignment		100.0	20	PDB header: signaling protein Chain: A: PDB Molecule: fusion of general control protein gcn4 and wpsr response PDBTitle: crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wpsr from pseudomonas aeruginosa
19	c3qvyB	Alignment		100.0	20	PDB header: signaling protein/inhibitor Chain: B: PDB Molecule: response regulator; PDBTitle: a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5)-cyclic di-gmp
20	c3ignA	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of the ggdef domain from marinobacter2 aquaeolei diguanylate cyclase complexed with c-di-gmp -3 northeast structural genomics consortium target mqr89a
21	c3hvaA	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
22	dlw25a3	Alignment	not modelled	100.0	26	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: GGDEF domain
23	c3hvwA	Alignment	not modelled	99.9	21	PDB header: lyase Chain: A: PDB Molecule: diguanylate-cyclase (dgc); PDBTitle: crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c
24	c3rtyA	Alignment		99.9	11	PDB header: circadian clock protein Chain: A: PDB Molecule: period circadian protein; PDBTitle: structure of an enclosed dimer formed by the drosophila period protein
25	c3ewkA	Alignment		99.9	19	PDB header: flavoprotein Chain: A: PDB Molecule: sensor protein; PDBTitle: structure of the redox sensor domain of methylococcus capsulatus2 (bath) mmos
26	c3gecA	Alignment		99.9	13	PDB header: circadian clock protein Chain: A: PDB Molecule: period circadian protein; PDBTitle: crystal structure of a tandem pas domain fragment of2

						drosophila period
27	c3gdiB_	<div><div></div></div> Alignment		99.8	11	PDB header: transcription Chain: B: PDB Molecule: period circadian protein homolog 2; PDBTitle: mammalian clock protein mper2 - crystal struture of a pas2 domain fragment
28	d1ew0a_	<div><div></div></div> Alignment		99.8	27	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
29	c1wa9A_	<div><div></div></div> Alignment		99.8	10	PDB header: circadian rhythm Chain: A: PDB Molecule: period circadian protein; PDBTitle: crystal structure of the pas repeat region of the2 drosophila clock protein period
30	c3p7nB_	<div><div></div></div> Alignment		99.8	17	PDB header: dna binding protein Chain: B: PDB Molecule: sensor histidine kinase; PDBTitle: crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
31	c2pr6A_	<div><div></div></div> Alignment	not modelled	99.7	22	PDB header: flavoprotein, signaling protein Chain: A: PDB Molecule: blue-light photoreceptor; PDBTitle: structural basis for light-dependent signaling in the dimeric lov2 photosensor ytva (light structure)
32	d1y28a_	<div><div></div></div> Alignment	not modelled	99.7	22	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
33	c2r78D_	<div><div></div></div> Alignment	not modelled	99.7	18	PDB header: transferase Chain: D: PDB Molecule: sensor protein; PDBTitle: crystal structure of a domain of the sensory box sensor2 histidine kinase/response regulator from geobacter3 sulfurreducens
34	c3bwlA_	<div><div></div></div> Alignment	not modelled	99.7	18	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of pas domain of htr-like protein from haloarcula2 marismortui
35	c2wkqA_	<div><div></div></div> Alignment	not modelled	99.7	20	PDB header: transferase, cell adhesion Chain: A: PDB Molecule: nph1-1, ras-related c3 botulinum toxin substrate PDBTitle: structure of a photoactivatable rac1 containing the lov22 c450a mutant
36	c1v9yA_	<div><div></div></div> Alignment	not modelled	99.7	100	PDB header: signaling protein Chain: A: PDB Molecule: heme pas sensor protein; PDBTitle: crystal structure of the heme pas sensor domain of ec dos (ferric2 form)
37	d1v9ya_	<div><div></div></div> Alignment	not modelled	99.7	100	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
38	c3mfxA_	<div><div></div></div> Alignment	not modelled	99.7	10	PDB header: transcription Chain: A: PDB Molecule: sensory box/ggdef family protein; PDBTitle: crystal structure of the sensory box domain of the sensory-2 box/ggdef protein so_1695 from shewanella oneidensis,3 northeast structural genomics consortium target sor288b
39	c2v1bA_	<div><div></div></div> Alignment	not modelled	99.7	19	PDB header: transferase Chain: A: PDB Molecule: nph1-1; PDBTitle: n- and c-terminal helices of oat lov2 (404-546) are2 involved in light-induced signal transduction (room3 temperature (293k) light structure of lov2 (404-546))
40	c3mqoB_	<div><div></div></div> Alignment	not modelled	99.7	14	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: the crystal structure of the pas domain in complex with isopropanol of2 a transcriptional regulator in the luxr family from burkholderia3 thailandensis to 1.7a
41	c3mjgB_	<div><div></div></div> Alignment	not modelled	99.7	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the pas domain of q24qt8_deshy protein from2 desulfitobacterium hafniense. northeast structural genomics3 consortium target dhr85c.
42	c3oloB_	<div><div></div></div> Alignment	not modelled	99.7	12	PDB header: transferase Chain: B: PDB Molecule: two-component sensor histidine kinase; PDBTitle: crystal structure of a pas domain from two-component sensor histidine2 kinase
43	d1xi3a1	<div><div></div></div> Alignment	not modelled	99.6	26	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Heme-binding PAS domain
44	c2gj3A_	<div><div></div></div> Alignment	not modelled	99.6	23	PDB header: transferase Chain: A: PDB Molecule: nitrogen fixation regulatory protein; PDBTitle: crystal structure of the fad-containing pas domain of the2 protein nifl from azotobacter vinelandii.
45	c3b33A_	<div><div></div></div> Alignment	not modelled	99.6	14	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of the pas domain of nitrogen regulation protein2 nr(ii) from vibrio parahaemolyticus
46	c3luqC_	<div><div></div></div> Alignment	not modelled	99.6	13	PDB header: transferase Chain: C: PDB Molecule: sensor protein; PDBTitle: the crystal structure of a pas domain from a sensory box2 histidine kinase regulator from geobacter sulfurreducens to3

					2.5a
47	c3mxqC_	Alignment	not modelled	99.6	14 PDB header: transferase Chain: C: PDB Molecule: sensory protein; PDBTitle: crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
48	c3lyxA_	Alignment	not modelled	99.6	20 PDB header: transcription Chain: A: PDB Molecule: sensory box/ggdef domain protein; PDBTitle: crystal structure of the pas domain of the protein cps_12912 from colwellia psychrerythraea. northeast structural3 genomics consortium target id csr222b
49	c3caxA_	Alignment	not modelled	99.6	17 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pf0695; PDBTitle: crystal structure of uncharacterized protein pf0695
50	c3mr0B_	Alignment	not modelled	99.6	14 PDB header: transcription regulator Chain: B: PDB Molecule: sensory box histidine kinase/response regulator; PDBTitle: crystal structure of sensory box histidine kinase/response regulator2 from burkholderia thailandensis e264
51	d1p97a_	Alignment	not modelled	99.5	12 Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Hypoxia-inducible factor Hif2a, C-terminal domain
52	c2l4rA_	Alignment	not modelled	99.5	19 PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily h member 2; PDBTitle: nmr solution structure of the n-terminal pas domain of herg
53	d1n9la_	Alignment	not modelled	99.5	20 Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain
54	c3f1oB_	Alignment	not modelled	99.5	13 PDB header: transcription Chain: B: PDB Molecule: aryl hydrocarbon receptor nuclear translocator; PDBTitle: crystal structure of the high affinity heterodimer of hif22 alpha and arnt c-terminal pas domains, with an internally-3 bound artificial ligand
55	c2vlgD_	Alignment	not modelled	99.5	18 PDB header: transferase Chain: D: PDB Molecule: sporulation kinase a; PDBTitle: kina pas-a domain, homodimer
56	d1jnua_	Alignment	not modelled	99.5	22 Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain
57	d1bywa_	Alignment	not modelled	99.5	22 Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: Flavin-binding PAS domain
58	c3k3dA_	Alignment	not modelled	99.5	11 PDB header: signaling protein Chain: A: PDB Molecule: protein rv1364c/mtl410; PDBTitle: the n-terminal pas domain crystal structure of rv1364c from2 mycobacterium tuberculosis at 2.3 angstrom
59	c3fg8B_	Alignment	not modelled	99.5	17 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein rha05790; PDBTitle: crystal structure of pas domain of rha05790
60	c2z6dB_	Alignment	not modelled	99.5	19 PDB header: transferase Chain: B: PDB Molecule: phototropin-2; PDBTitle: crystal structure of lov1 domain of phototropin2 from2 arabidopsis thaliana
61	d1l18a_	Alignment	not modelled	99.4	13 Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: N-terminal PAS domain of Pas kinase
62	c2kdkA_	Alignment	not modelled	99.4	12 PDB header: transcription regulator Chain: A: PDB Molecule: aryl hydrocarbon receptor nuclear translocator-like protein PDBTitle: structure of human circadian clock protein bmal2 c-terminal pas domain
63	c3kx0X_	Alignment	not modelled	99.4	13 PDB header: signaling protein Chain: X: PDB Molecule: uncharacterized protein rv1364c/mtl410; PDBTitle: crystal structure of the pas domain of rv1364c
64	c3eehA_	Alignment	not modelled	99.4	17 PDB header: transferase Chain: A: PDB Molecule: putative light and redox sensing histidine kinase; PDBTitle: the crystal structure of the domain of the putative light and redox2 sensing histidine kinase from haloarcula marismortui
65	d1nwza_	Alignment	not modelled	99.4	14 Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
66	c3h9wA_	Alignment	not modelled	99.4	16 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: diguanylate cyclase with pas/pac sensor; PDBTitle: crystal structure of the n-terminal domain of diguanylate cyclase with2 pas/pac sensor (maqu_2914) from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr66c
67	c3fc7B_	Alignment	not modelled	99.3	16 PDB header: transferase Chain: B: PDB Molecule: htr-like protein; PDBTitle: the crystal structure of a domain of htr-like protein from haloarcula2 marismortui atcc 43049
68	c3icyB_	Alignment	not modelled	99.3	11 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: sensory protein; PDBTitle: the crystal structure of sensory box histidine2 kinase/response regulator domain from chlorobium tepidum3 tfs
69	c2qkpD_	Alignment	not modelled	99.3	11 PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of c-terminal domain of smu_1151c from streptococcus2 mutans
70	d1mzua_	Alignment	not modelled	99.3	15 Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like

71	d1otda_	Alignment	not modelled	99.3	15	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
72	c2jheB_	Alignment	not modelled	99.2	12	PDB header: transcription Chain: B: PDB Molecule: transcription regulator tyrr; PDBTitle: n-terminal domain of tyrr transcription factor (residues 1 -2 190)
73	d1oj5a_	Alignment	not modelled	99.1	9	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PAS domain of steroid receptor coactivator 1A, NCoA1
74	c2pdtD_	Alignment	not modelled	99.1	17	PDB header: circadian clock protein Chain: D: PDB Molecule: vivid pas protein vvd; PDBTitle: 2.3 angstrom structure of phosphodiesterase treated vivid
75	c3njaC_	Alignment	not modelled	99.1	10	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: probable ggdef family protein; PDBTitle: the crystal structure of the pas domain of a ggdef family protein from2 chromobacterium violaceum atcc 12472.
76	d1xfna1	Alignment	not modelled	99.0	13	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: PYP-like
77	c3a0vA_	Alignment	not modelled	99.0	15	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: pas domain of histidine kinase thka (tm1359) (semet,2 f486m/f489m)
78	c2o9bA_	Alignment	not modelled	99.0	10	PDB header: transferase Chain: A: PDB Molecule: bacteriophytochrome; PDBTitle: crystal structure of bacteriophytochrome chromophore binding domain
79	c3a0rA_	Alignment	not modelled	98.9	17	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)
80	c2veaA_	Alignment	not modelled	98.9	7	PDB header: transferase Chain: A: PDB Molecule: phytochrome-like protein cph1; PDBTitle: the complete sensory module of the cyanobacterial2 phytochrome cph1 in the pr-state.
81	c2oolA_	Alignment	not modelled	98.9	11	PDB header: signaling protein Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of the chromophore-binding domain of an unusual2 bacteriophytochrome rpbphp3 from r. palustris
82	c2w0nA_	Alignment	not modelled	98.9	18	PDB header: transferase Chain: A: PDB Molecule: sensor protein dcus; PDBTitle: plasticity of pas domain and potential role for signal2 transduction in the histidine-kinase dcus
83	c3cloC_	Alignment	not modelled	98.8	13	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
84	c3c2wB_	Alignment	not modelled	97.7	11	PDB header: signaling protein Chain: B: PDB Molecule: bacteriophytochrome; PDBTitle: crystal structure of the photosensory core domain of p.2 aeruginosa bacteriophytochrome pabphp in the pfr state
85	c2qv6D_	Alignment	not modelled	97.3	17	PDB header: hydrolase Chain: D: PDB Molecule: gtp cyclohydrolase iii; PDBTitle: gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
86	d2o9ca2	Alignment	not modelled	95.8	12	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: BphP N-terminal domain-like
87	d1mvoa_	Alignment	not modelled	95.7	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
88	c3khtA_	Alignment	not modelled	95.7	10	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
89	d2oola2	Alignment	not modelled	95.6	6	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: BphP N-terminal domain-like
90	c3hebB_	Alignment	not modelled	95.4	14	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
91	d1krwa_	Alignment	not modelled	95.0	16	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
92	c2zayA_	Alignment	not modelled	94.8	15	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans
93	c2ayxA_	Alignment	not modelled	94.7	15	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
94	d2veaa3	Alignment	not modelled	94.6	10	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: BphP N-terminal domain-like
95	c2jk1A_	Alignment	not modelled	94.5	8	PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein hupr1; PDBTitle: crystal structure of the wild-type hupr receiver domain
96	d1w25a1	Alignment	not modelled	94.4	10	Fold: Flavodoxin-like Superfamily: CheY-like

						Family: CheY-related
97	d1p6qa_	Alignment	not modelled	94.3	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
98	d3c2wa3	Alignment	not modelled	93.7	16	Fold: Profilin-like Superfamily: PYP-like sensor domain (PAS domain) Family: BphP N-terminal domain-like
99	d1u0sy_	Alignment	not modelled	93.6	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
100	c3crnA_	Alignment	not modelled	93.1	13	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
101	d1jbea_	Alignment	not modelled	93.0	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
102	c2rjnA_	Alignment	not modelled	93.0	12	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
103	c3b2nA_	Alignment	not modelled	93.0	12	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein q99uf4; PDBTitle: crystal structure of dna-binding response regulator, luxr family, from2 staphylococcus aureus
104	d2r25b1	Alignment	not modelled	92.6	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
105	c3nhzA_	Alignment	not modelled	92.4	13	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
106	c2j48A_	Alignment	not modelled	92.4	16	PDB header: transferase Chain: A: PDB Molecule: two-component sensor kinase; PDBTitle: nmr structure of the pseudo-receiver domain of the cika2 protein.
107	d1ny5a1	Alignment	not modelled	92.2	18	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
108	d1dz3a_	Alignment	not modelled	92.1	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
109	c2zwmA_	Alignment	not modelled	92.0	11	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein yycf; PDBTitle: crystal structure of yycf receiver domain from bacillus2 subtilis
110	c3gt7A_	Alignment	not modelled	92.0	13	PDB header: hydrolase Chain: A: PDB Molecule: sensor protein; PDBTitle: crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
111	d1yioa2	Alignment	not modelled	91.8	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
112	d1nvma2	Alignment	not modelled	91.7	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
113	c3c97A_	Alignment	not modelled	91.7	11	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
114	c3eulB_	Alignment	not modelled	91.4	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
115	d1h5ya_	Alignment		91.2	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
116	c3gl9B_	Alignment	not modelled	91.2	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
117	d1k68a_	Alignment	not modelled	91.0	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
118	c3i42A_	Alignment	not modelled	90.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (chey-like)2 from methylobacillus flagellatus
119	c3hv2B_	Alignment	not modelled	90.7	14	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
120	d1zesa1	Alignment	not modelled	90.6	11	Fold: Flavodoxin-like Superfamily: CheY-like

