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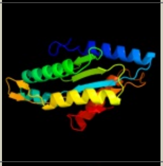
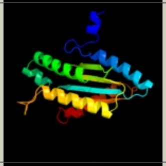
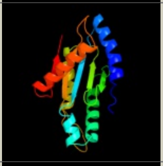
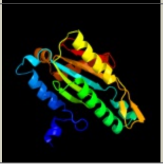
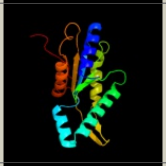
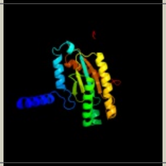
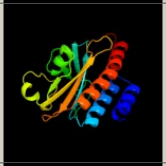
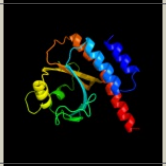
Description	P76245
Date	Thu Jan 5 12:21:11 GMT 2012
Unique Job ID	156713ed3463e27e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w25B_	Alignment		100.0	28	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**stalked-cell differentiation controlling protein; **PDBTitle:** response regulator pled in complex with c-digmp
2	c3ezuA_	Alignment		100.0	28	**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
3	c3breA_	Alignment		100.0	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**probable two-component response regulator; **PDBTitle:** crystal structure of p.aeruginosa pa3702
4	c3iclA_	Alignment		100.0	26	**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
5	c3ignA_	Alignment		100.0	24	**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
6	c3i5aA_	Alignment		100.0	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
7	c3hvaA_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
8	c3i5bA_	Alignment		100.0	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
9	d1w25a3	Alignment		100.0	30	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
10	c3i5cA_	Alignment		100.0	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**fusion of general control protein gcn4 and wspr response **PDBTitle:** crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wspr from pseudomonas aeruginosa
11	c3mtkA_	Alignment		100.0	21	**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

12	c3qyyB_	Alignment		100.0	29	**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
13	c3hvwA_	Alignment		100.0	13	**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
14	c3pjwA_	Alignment		100.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
15	c3gfzB_	Alignment		99.7	10	**PDB header:**hydrolase, signaling protein **Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1; **PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
16	c3ci6B_	Alignment		99.1	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase
17	c3trcA_	Alignment		99.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of the gaf domain from a phosphoenolpyruvate-protein2 phosphotransferase (ptsp) from coxiella burnetii
18	d2o9ca1	Alignment		99.0	16	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
19	c3k2nB_	Alignment		99.0	18	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**sigma-54-dependent transcriptional regulator; **PDBTitle:** the crystal structure of sigma-54-dependent transcriptional2 regulator domain from chlorobium tepidum tls
20	c3mmhA_	Alignment		98.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase; **PDBTitle:** x-ray structure of free methionine-r-sulfoxide reductase from2 neisseria meningitidis in complex with its substrate
21	c2zmfA_	Alignment		98.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**camp and camp-inhibited cgmp 3',5'-cyclic phosphodiesterase **PDBTitle:** crystal structure of the c-terminal gaf domain of human2 phosphodiesterase 10a
22	d2veaa1	Alignment	not modelled	98.9	14	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
23	c3p7nB_	Alignment	not modelled	98.9	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
24	d2oola1	Alignment	not modelled	98.8	16	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
25	c3oovA_	Alignment	not modelled	98.8	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein, putative; **PDBTitle:** crystal structure of a methyl-accepting chemotaxis protein, residues2 122 to 287
26	c3p01C_	Alignment	not modelled	98.7	12	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
27	c3o5yA_	Alignment	not modelled	98.7	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of the gaf domain of a two-component sensor2 histidine kinase from bacillus halodurans to

						2.45a
28	c2qybA_	Alignment	not modelled	98.7	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**membrane protein, putative; **PDBTitle:** crystal structure of the gaf domain region of putative membrane2 protein from geobacter sulfurreducens pca
29	c3p01A_	Alignment	not modelled	98.7	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
30	d3c2wa1	Alignment	not modelled	98.6	15	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
31	c1vhmB_	Alignment	not modelled	98.6	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein yebr; **PDBTitle:** crystal structure of an hypothetical protein
32	c3eeaB_	Alignment	not modelled	98.6	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**gaf domain/hd domain protein; **PDBTitle:** the crystal structure of the gaf domain/hd domain protein2 from geobacter sulfurreducens
33	c3ibjB_	Alignment	not modelled	98.6	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** x-ray structure of pde2a
34	d1vhma_	Alignment	not modelled	98.5	12	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
35	c1mc0A_	Alignment	not modelled	98.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3',5'-cyclic nucleotide phosphodiesterase 2a; **PDBTitle:** regulatory segment of mouse 3',5'-cyclic nucleotide phosphodiesterase2 2a, containing the gaf a and gaf b domains
36	d1mc0a1	Alignment	not modelled	98.5	12	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
37	c3hcyB_	Alignment	not modelled	98.5	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative two-component sensor histidine kinase protein; **PDBTitle:** the crystal structure of the domain of putative two-component sensor2 histidine kinase protein from sinorhizobium meliloti 1021
38	c2vjwA_	Alignment	not modelled	98.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gaf family protein; **PDBTitle:** crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
39	c3ksiA_	Alignment	not modelled	98.4	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of frmsr of staphylococcus aureus (complex with 2-propanol)
40	c3e0yA_	Alignment	not modelled	98.4	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a conserved domain from a protein of2 geobacter sulfurreducens pca
41	c3dbaB_	Alignment	not modelled	98.4	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cone cgmp-specific 3',5'-cyclic phosphodiesterase subunit **PDBTitle:** crystal structure of the cgmp-bound gaf a domain from the2 photoreceptor phosphodiesterase 6c
42	c2w3gA_	Alignment	not modelled	98.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component sensor histidine kinase devs (gaf **PDBTitle:** air-oxidized structure of the first gaf domain of2 mycobacterium tuberculosis doss
43	d2k2na1	Alignment	not modelled	98.3	19	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
44	c2lb5A_	Alignment	not modelled	98.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** refined structural basis for the photoconversion of a phytochrome to2 the activated far-red light-absorbing form
45	d1mc0a2	Alignment	not modelled	98.2	10	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
46	c3mf0A_	Alignment	not modelled	98.2	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of pde5a gaf domain (89-518)
47	c1ykdB_	Alignment	not modelled	98.2	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of the tandem gaf domains from a cyanobacterial2 adenylyl cyclase: novel modes of ligand-binding and dimerization
48	c3e98B_	Alignment	not modelled	98.1	12	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**gaf domain of unknown function; **PDBTitle:** crystal structure of a gaf domain containing protein that belongs to2 pfam duf484 family (pa5279) from pseudomonas aeruginosa at 2.43 a3 resolution
49	c2oolA_	Alignment	not modelled	98.1	16	**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
50	c3c2wB_	Alignment	not modelled	98.0	13	**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
51	c2k31A_	Alignment	not modelled	98.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphodiesterase 5a, cgmp-specific; **PDBTitle:** solution structure of cgmp-binding gaf domain of2 phosphodiesterase 5
						PDB header:transferase

52	c2o9bA_	Alignment	not modelled	97.9	16	**Chain:** A: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of bacteriophytochrome chromophore binding domain
53	c2qv6D_	Alignment	not modelled	97.7	21	**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
54	d1f5ma_	Alignment	not modelled	97.5	10	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
55	c2veaA_	Alignment	not modelled	97.5	13	**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.
56	c2xssB_	Alignment	not modelled	97.2	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-specific 3', 5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of gafb from the human phosphodiesterase 5
57	d1azsa_	Alignment	not modelled	89.9	15	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
58	d1fx2a_	Alignment	not modelled	89.0	12	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
59	c2aq4A_	Alignment	not modelled	87.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** ternary complex of the catalytic core of rev1 with dna and dctp.
60	c1cjkA_	Alignment	not modelled	86.4	17	**PDB header:**lyase/lyase/signaling protein **Chain:** A: **PDB Molecule:**adenylate cyclase, type v; **PDBTitle:** complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
61	c1ybuA_	Alignment	not modelled	84.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipj; **PDBTitle:** mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
62	d1fx4a_	Alignment	not modelled	84.2	16	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
63	c1wc6B_	Alignment	not modelled	84.2	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylate cyclase; **PDBTitle:** soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
64	d1wc1a_	Alignment	not modelled	83.6	16	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
65	c3mr7B_	Alignment	not modelled	81.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenylate/guanylate cyclase/hydrolase, alpha/beta fold **PDBTitle:** crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi
66	c3et6A_	Alignment	not modelled	80.9	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**soluble guanylyl cyclase beta; **PDBTitle:** the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
67	c2w01C_	Alignment	not modelled	76.5	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of the guanylyl cyclase cya2
68	c1yk9A_	Alignment	not modelled	72.7	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
69	c3gqcB_	Alignment	not modelled	71.8	21	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** structure of human rev1-dna-dntp ternary complex
70	c1y10C_	Alignment	not modelled	71.4	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
71	c3uvjC_	Alignment	not modelled	69.0	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**guanylate cyclase soluble subunit alpha-3; **PDBTitle:** crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
72	c2gx5B_	Alignment	not modelled	65.9	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**gtp-sensing transcriptional pleiotropic repressor cody; **PDBTitle:** n-terminal gaf domain of transcriptional pleiotropic repressor cody
73	c1s97D_	Alignment	not modelled	61.6	17	**PDB header:**transferase/dna **Chain:** D: **PDB Molecule:**dna polymerase iv; **PDBTitle:** dpo4 with gt mismatch
74	c3onqB_	Alignment	not modelled	58.5	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**regulator of polyketide synthase expression; **PDBTitle:** crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
75	c1k1qA_	Alignment	not modelled	51.4	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dbh protein; **PDBTitle:** crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
76	c3r5gB_	Alignment	not modelled	50.7	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cyab; **PDBTitle:** crystal structure of the adenylyl cyclase cyab from p. aeruginosa

77	c2r8kB_	Alignment	not modelled	50.2	29	**PDB header:**replication, transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase eta; **PDBTitle:** structure of the eukaryotic dna polymerase eta in complex with 1,2-2 d(gpg)-cisplatin containing dna
78	c3cloC_	Alignment	not modelled	49.2	12	**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
79	c1jihA_	Alignment	not modelled	47.0	29	**PDB header:**translation **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** yeast dna polymerase eta
80	d1l3la2	Alignment	not modelled	40.3	15	**Fold:**Profilin-like **Superfamily:**Pheromone-binding domain of LuxR-like quorum-sensing transcription factors **Family:**Pheromone-binding domain of LuxR-like quorum-sensing transcription factors
81	c3bwlA_	Alignment	not modelled	39.7	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of pas domain of htr-like protein from haloarcula2 marismortui
82	c3mfxA_	Alignment	not modelled	35.0	7	**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
83	c3mxqC_	Alignment	not modelled	35.0	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of sensory box sensor histidine kinase from vibrio2 cholerae
84	d1jx4a2	Alignment	not modelled	33.0	15	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
85	c2wz1B_	Alignment	not modelled	31.7	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**guanylate cyclase soluble subunit beta-1; **PDBTitle:** structure of the catalytic domain of human soluble2 guanylate cyclase 1 beta 3.
86	c2oh2B_	Alignment	not modelled	31.6	21	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase kappa; **PDBTitle:** ternary complex of human dna polymerase
87	d1im4a_	Alignment	not modelled	30.0	20	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
88	c2qkpD_	Alignment	not modelled	30.0	12	**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
89	c2w0nA_	Alignment	not modelled	28.7	10	**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
90	c3mr2A_	Alignment	not modelled	28.5	25	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm)
91	d1ew0a_	Alignment	not modelled	26.5	17	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
92	c2w1rA_	Alignment	not modelled	24.9	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of the c-terminal domain of b. subtilis2 spovt
93	d1jiha2	Alignment	not modelled	23.9	20	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
94	d1t0aa_	Alignment	not modelled	23.5	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
95	c3lyxA_	Alignment	not modelled	22.8	12	**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
96	c3oloB_	Alignment	not modelled	21.2	9	**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
97	d1azsb_	Alignment	not modelled	21.1	11	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
98	d1w55a2	Alignment	not modelled	20.8	9	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
99	d1iv3a_	Alignment	not modelled	18.6	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like