



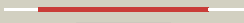







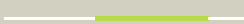










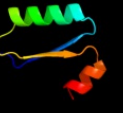

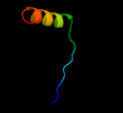







#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3eyeA_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: pts system n-acetylgalactosamine-specific iib PDBTitle: crystal structure of pts system n-acetylgalactosamine-2 specific iib component 1 from escherichia coli
2	d1nrza_	 Alignment		100.0	30	Fold: PTS Iib component Superfamily: PTS Iib component Family: PTS Iib component
3	d1blea_	 Alignment		100.0	28	Fold: PTS Iib component Superfamily: PTS Iib component Family: PTS Iib component
4	c3lfjB_	 Alignment		100.0	25	PDB header: transferase Chain: B: PDB Molecule: phosphotransferase system, mannose/fructose/n- PDBTitle: crystal structure of manxb from thermoanaerobacter tengcongensis
5	c3p3vB_	 Alignment		100.0	34	PDB header: transferase Chain: B: PDB Molecule: pts system, n-acetylgalactosamine-specific iib component; PDBTitle: crystal structure of a pts dependent n-acetyl-galactosamine-iib2 component (agav, spy_0631) from streptococcus pyogenes at 1.65 a3 resolution
6	c1vsqC_	 Alignment		100.0	34	PDB header: transferase Chain: C: PDB Molecule: mannose-specific phosphotransferase enzyme iib PDBTitle: solution nmr structure of the productive complex between2 iiamannose and iibmannose of the mannose transporter of3 the e. coli phosphotransferase system
7	c3l0gD_	 Alignment		66.3	16	PDB header: transferase Chain: D: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
8	c1qapA_	 Alignment		64.2	8	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid PDBTitle: phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
9	d1r8ja2	 Alignment		44.8	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: N-terminal domain of the circadian clock protein KaiA
10	c3rfaA_	 Alignment		38.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
11	d1qpoa1	 Alignment		34.4	11	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like

12	c3pm7A_	Alignment		32.2	3	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ef_3132 protein from enterococcus faecalis at the2 resolution 2a, northeast structural genomics consortium target efr184
13	c3ilhA_	Alignment		29.4	9	PDB header: transcription regulator Chain: A: PDB Molecule: two component response regulator; PDBTitle: crystal structure of two component response regulator from cytophaga2 hutchinsonii
14	c1qpoA_	Alignment		28.4	11	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
15	c2k1oA_	Alignment		26.8	22	PDB header: gene regulation Chain: A: PDB Molecule: putative; PDBTitle: nmr structure of helicobacter pylori jhp0511 (hp0564).
16	d1k68a_	Alignment		25.7	9	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
17	d1qapa1	Alignment		25.3	6	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
18	c3gl9B_	Alignment		23.3	15	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
19	c3pajA_	Alignment		22.5	11	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase, carboxylating; PDBTitle: 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
20	c3obhA_	Alignment		20.9	4	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: x-ray crystal structure of protein sp_0782 (7-79) from streptococcus2 pneumoniae. northeast structural genomics consortium target spr104
21	c3khtA_	Alignment	not modelled	19.6	10	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator from hahella chejuensis
22	d1t0kb_	Alignment	not modelled	18.8	10	Fold: Bacillus chorillus mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
23	c2yxxA_	Alignment	not modelled	18.1	16	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure analysis of diaminopimelate decarboxylate (lysa)
24	c3eqzB_	Alignment	not modelled	17.7	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from colwellia2 psychrerythraea
25	d1mb3a_	Alignment	not modelled	16.3	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
26	c2oqrA_	Alignment	not modelled	15.8	20	PDB header: transcription,signaling protein Chain: A: PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis
27	d2pl1a1	Alignment	not modelled	15.2	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
28	c3n53B_	Alignment	not modelled	14.2	9	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
						PDB header: transcription

29	c2qv0A_	Alignment	not modelled	14.1	11	Chain: A: PDB Molecule: protein mrke; PDBTitle: crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
30	c3h5iA_	Alignment	not modelled	13.6	13	PDB header: transcription Chain: A: PDB Molecule: response regulator/sensory box protein/ggdef PDBTitle: crystal structure of the n-terminal domain of a response2 regulator/sensory box/ggdef 3-domain protein from3 carboxydotherrus hydrogenoformans
31	d1ajza_	Alignment	not modelled	13.6	19	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
32	c2a5hC_	Alignment	not modelled	13.3	15	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
33	d1k66a_	Alignment	not modelled	12.8	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
34	c1rn1A_	Alignment	not modelled	12.8	15	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
35	d1kgsa1	Alignment	not modelled	12.4	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
36	d2i7pa1	Alignment	not modelled	11.8	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
37	c3cnbC_	Alignment	not modelled	11.7	9	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
38	d1bs0a_	Alignment	not modelled	11.5	13	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
39	c2y5sA_	Alignment	not modelled	11.3	16	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
40	d1t6t1_	Alignment	not modelled	11.1	11	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
41	c3btnA_	Alignment	not modelled	11.0	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: antizyme inhibitor 1; PDBTitle: crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein
42	c3m6mF_	Alignment	not modelled	10.9	18	PDB header: lyase/transferase Chain: F: PDB Molecule: sensory/regulatory protein rpfc; PDBTitle: crystal structure of rpff complexed with rec domain of rpfc
43	d2f1fa1	Alignment	not modelled	10.8	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
44	d1a04a2	Alignment	not modelled	10.7	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
45	c3cz5B_	Alignment	not modelled	10.1	12	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
46	c3cg4A_	Alignment	not modelled	10.0	22	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
47	d1ad1a_	Alignment	not modelled	9.9	24	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
48	d1dbwa_	Alignment	not modelled	9.8	6	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
49	d2fgca2	Alignment	not modelled	9.8	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
50	c3hebB_	Alignment	not modelled	9.7	16	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
51	d1oqya2	Alignment	not modelled	9.6	18	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
52	d1u0sy_	Alignment	not modelled	9.5	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
						PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-

53	c2rjnA	Alignment	not modelled	9.5	13	dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
54	d1xxaa	Alignment	not modelled	9.3	33	Fold: DCoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
55	d2obba1	Alignment	not modelled	9.3	7	Fold: HAD-like Superfamily: HAD-like Family: BT0820-like
56	c3hv2B	Alignment	not modelled	9.3	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
57	d2i7na2	Alignment	not modelled	9.1	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
58	d2pc6a2	Alignment	not modelled	8.8	8	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
59	c3c3wB	Alignment	not modelled	8.7	15	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
60	c2yr1B	Alignment	not modelled	8.6	19	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426
61	d2p5ma1	Alignment	not modelled	8.5	29	Fold: DCoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
62	c3cg0A	Alignment	not modelled	8.4	12	PDB header: lyase Chain: A: PDB Molecule: response regulator receiver modulated diguanylate cyclase PDBTitle: crystal structure of signal receiver domain of modulated diguanylate2 cyclase from desulfovibrio desulfuricans g20, an example of alternate3 folding
63	c3khdC	Alignment	not modelled	8.3	15	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
64	c3kyiB	Alignment	not modelled	8.3	12	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
65	c2y7eA	Alignment	not modelled	8.3	12	PDB header: lyase Chain: A: PDB Molecule: 3-keto-5-aminoheptanoate cleavage enzyme; PDBTitle: crystal structure of the 3-keto-5-aminoheptanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
66	c3hzhA	Alignment	not modelled	8.1	14	PDB header: signaling protein Chain: A: PDB Molecule: chemotaxis response regulator (chey-3); PDBTitle: crystal structure of the cheX-cheY-bef3-mg+2 complex from2 borrelia burgdorferi
67	c2qxyB	Alignment	not modelled	8.1	18	PDB header: transcription Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from thermotoga2 maritima
68	d1b4ba	Alignment	not modelled	8.0	29	Fold: DCoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
69	c3c3mA	Alignment	not modelled	8.0	23	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
70	c3icuA	Alignment	not modelled	8.0	16	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase rnf128; PDBTitle: protease-associated domain of the e3 ligase gra1
71	c3cagF	Alignment	not modelled	7.8	29	PDB header: dna binding protein Chain: F: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines.
72	d2guka1	Alignment	not modelled	7.8	17	Fold: PG1857-like Superfamily: PG1857-like Family: PG1857-like
73	c1a2oB	Alignment	not modelled	7.8	15	PDB header: bacterial chemotaxis Chain: B: PDB Molecule: cheb methyltransferase; PDBTitle: structural basis for methyltransferase cheb regulation by a2 phosphorylation-activated domain
74	d1a2oa1	Alignment	not modelled	7.8	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
75	d1o57a2	Alignment	not modelled	7.7	6	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
76	c3eywA	Alignment	not modelled	7.6	19	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
77	d1i3ca	Alignment	not modelled	7.2	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
						PDB header: structural genomics, unknown function

78	c1k3rA	Alignment	not modelled	7.2	10	Chain: A: PDB Molecule: conserved protein mt0001; PDBTitle: crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
79	c2zayA	Alignment	not modelled	7.2	23	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator from desulfuromonas2 acetoxidans
80	c1dd9A	Alignment	not modelled	7.0	12	PDB header: transferase Chain: A: PDB Molecule: dna primase; PDBTitle: structure of the dnag catalytic core
81	d1dd9a	Alignment	not modelled	7.0	12	Fold: DNA primase core Superfamily: DNA primase core Family: DNA primase DnaG catalytic core
82	c3eulB	Alignment	not modelled	7.0	16	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
83	d1dcfa	Alignment	not modelled	6.7	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: Receiver domain of the ethylene receptor
84	c2q97T	Alignment	not modelled	6.5	20	PDB header: structural protein/cell invasion Chain: T: PDB Molecule: toxofilin; PDBTitle: complex of mammalian actin with toxofilin from toxoplasma gondii
85	c3f6cB	Alignment	not modelled	6.4	9	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
86	c1o57A	Alignment	not modelled	6.4	6	PDB header: dna binding protein Chain: A: PDB Molecule: pur operon repressor; PDBTitle: crystal structure of the purine operon repressor of2 bacillus subtilis
87	c3luaA	Alignment	not modelled	6.1	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
88	c3jpyA	Alignment	not modelled	6.1	15	PDB header: transport protein Chain: A: PDB Molecule: glutamate [nmda] receptor subunit epsilon-2; PDBTitle: crystal structure of the zinc-bound amino terminal domain of the nmda2 receptor subunit nr2b
89	c2b7pA	Alignment	not modelled	6.1	20	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
90	c2jrlA	Alignment	not modelled	6.0	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: solution structure of the beryll fluoride-activated ntrc4 receiver2 domain dimer
91	c3lteH	Alignment	not modelled	6.0	13	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
92	d1mzva	Alignment	not modelled	6.0	23	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
93	c2is8A	Alignment	not modelled	6.0	12	PDB header: structural protein Chain: A: PDB Molecule: molybdopterin biosynthesis enzyme, moab; PDBTitle: crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus thermophilus hb8
94	c3jteA	Alignment	not modelled	6.0	10	PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
95	c1b4aA	Alignment	not modelled	5.9	29	PDB header: repressor Chain: A: PDB Molecule: arginine repressor; PDBTitle: structure of the arginine repressor from bacillus stearothermophilus
96	d1k3ra2	Alignment	not modelled	5.8	11	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Hypothetical protein MTH1 (MT0001), dimerisation domain
97	c2hvvA	Alignment	not modelled	5.8	11	PDB header: transcription Chain: A: PDB Molecule: dna-binding response regulator vicr; PDBTitle: crystal structure of an essential response regulator dna binding2 domain, vicrc in enterococcus faecalis, a member of the yycf3 subfamily.
98	c2k5jB	Alignment	not modelled	5.7	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
99	d1dz3a	Alignment	not modelled	5.7	6	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related