Phyre2

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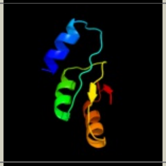
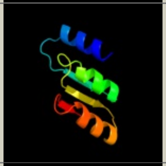
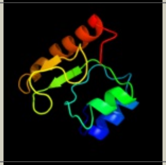
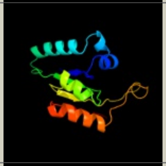
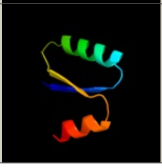
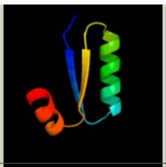
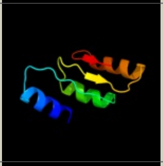
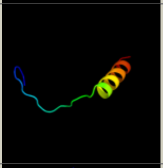
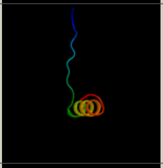
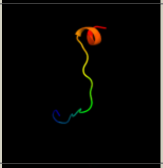
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nrza_	Alignment		100.0	35	**Fold:**PTS IIb component **Superfamily:**PTS IIb component **Family:**PTS IIb component
2	c1vsqC_	Alignment		100.0	37	**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
3	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
4	d1blea_	Alignment		100.0	33	**Fold:**PTS IIb component **Superfamily:**PTS IIb component **Family:**PTS IIb component
5	c3p3vB_	Alignment		100.0	42	**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	c3eyeA_	Alignment		100.0	46	**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
7	c1qapA_	Alignment		65.0	8	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**quinolinic acid phosphoribosyltransferase; **PDBTitle:** quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
8	c3l0gD_	Alignment		62.3	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
9	d1r8ja2	Alignment		54.3	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**N-terminal domain of the circadian clock protein KaiA
10	c3rfaA_	Alignment		52.2	14	**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	d1k68a_	Alignment		48.1	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related

12	c3ilhA_	Alignment		44.9	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** crystal structure of two component response regulator from cytophaga2 hutchinsonii
13	d1qapa1	Alignment		44.5	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
14	c3pm7A_	Alignment		42.5	13	**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
15	c2k1oA_	Alignment		37.7	19	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**putative; **PDBTitle:** nmr structure of helicobacter pylori jhp0511 (hp0564).
16	c2yxxA_	Alignment		35.7	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure analysis of diaminopimelate decarboxylate (lysa)
17	c3btnA_	Alignment		35.1	11	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**antizyme inhibitor 1; **PDBTitle:** crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein
18	c3obhA_	Alignment		33.1	9	**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
19	c3pajA_	Alignment		33.0	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	d1qpoa1	Alignment		30.9	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
21	c2y5sA_	Alignment	not modelled	30.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
22	d1t0kb_	Alignment	not modelled	30.2	10	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
23	c3gl9B_	Alignment	not modelled	30.2	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
24	c3eqzB_	Alignment	not modelled	29.7	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from colwellia2 psychrerythraea
25	d1k66a_	Alignment	not modelled	29.2	17	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
26	d1ajza_	Alignment	not modelled	27.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
27	d2obba1	Alignment	not modelled	27.2	7	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
28	c3khtA_	Alignment	not modelled	26.5	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator from hahella chejuensis

29	c3eywA_	Alignment	not modelled	25.8	18	**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
30	c2qv0A_	Alignment	not modelled	25.1	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein mrke; **PDBTitle:** crystal structure of the response regulatory domain of2 protein mrke from klebsiella pneumoniae
31	c3cz5B_	Alignment	not modelled	24.7	8	**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
32	c3n53B_	Alignment	not modelled	24.6	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator receiver modulated diguanylate cyclase; **PDBTitle:** crystal structure of a response regulator receiver modulated2 diguanylate cyclase from pelobacter carbinolicus
33	d1d7ka2	Alignment	not modelled	23.4	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
34	c1qpoA_	Alignment	not modelled	22.2	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**quinolinate acid phosphoribosyl transferase; **PDBTitle:** quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
35	d2i7pa1	Alignment	not modelled	21.6	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
36	c3cnbC_	Alignment	not modelled	20.2	11	**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
37	c3m6mF_	Alignment	not modelled	19.8	25	**PDB header:**lyase/transferase **Chain:** F: **PDB Molecule:**sensory/regulatory protein rpfc; **PDBTitle:** crystal structure of rpff complexed with rec domain of rpfc
38	c3q41B_	Alignment	not modelled	19.4	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**glutamate [nmda] receptor subunit zeta-1; **PDBTitle:** crystal structure of the glun1 n-terminal domain (ntd)
39	d1kgsa1	Alignment	not modelled	18.4	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**PhoB-like
40	d1a04a2	Alignment	not modelled	17.3	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
41	c3hebB_	Alignment	not modelled	16.9	13	**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
42	c2on3A_	Alignment	not modelled	16.8	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminooxy-3 1-aminopropane
43	d2i7na2	Alignment	not modelled	16.7	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
44	d1hkva2	Alignment	not modelled	16.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
45	c2qvgA_	Alignment	not modelled	16.4	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component response regulator; **PDBTitle:** the crystal structure of a two-component response regulator2 from legionella pneumophila
46	d1ad1a_	Alignment	not modelled	16.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
47	d1dd9a_	Alignment	not modelled	15.5	17	**Fold:**DNA primase core **Superfamily:**DNA primase core **Family:**DNA primase DnaG catalytic core
48	c1dd9A_	Alignment	not modelled	15.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** structure of the dnag catalytic core
49	c3cg0A_	Alignment	not modelled	15.4	13	**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
50	c2bmbA_	Alignment	not modelled	15.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**folic acid synthesis protein fol1; **PDBTitle:** x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase3 from saccharomyces cerevisiae
51	c1x1oC_	Alignment	not modelled	14.9	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of project id tt0268 from thermus thermophilus hb8
						PDB header:transcription

52	c2qsjB_	Alignment	not modelled	14.8	12	**Chain:** B: **PDB Molecule:**dna-binding response regulator, luxr family; **PDBTitle:** crystal structure of a luxr family dna-binding response2 regulator from silicibacter pomeroyi
53	d1i3ca_	Alignment	not modelled	14.4	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
54	c2is8A_	Alignment	not modelled	13.5	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
55	c2oqrA_	Alignment	not modelled	13.0	19	**PDB header:**transcription,signaling protein **Chain:** A: **PDB Molecule:**sensory transduction protein regx3; **PDBTitle:** the structure of the response regulator regx3 from mycobacterium2 tuberculosis
56	c3eulB_	Alignment	not modelled	13.0	9	**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
57	d1k3ra2	Alignment	not modelled	13.0	9	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**Hypothetical protein MTH1 (MT0001), dimerisation domain
58	c3q9vB_	Alignment	not modelled	12.8	8	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra c-terminal domain(123-221) from deinococcus2 radiodurans
59	d1oqya2	Alignment	not modelled	12.7	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
60	d2r25b1	Alignment	not modelled	12.6	19	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
61	c2zkr6_	Alignment	not modelled	12.5	10	**PDB header:**ribosomal protein/rna **Chain:** 6: **PDB Molecule:**60s ribosomal protein l30e; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
62	d1o4ua1	Alignment	not modelled	12.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
63	c2dzaA_	Alignment	not modelled	12.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
64	c3c3wB_	Alignment	not modelled	12.3	8	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
65	c2o0tB_	Alignment	not modelled	12.3	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** the three dimensional structure of diaminopimelate decarboxylase from2 mycobacterium tuberculosis reveals a tetrameric enzyme organisation
66	c3kyiB_	Alignment	not modelled	12.1	13	**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
67	d1w41a1	Alignment	not modelled	12.0	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
68	d1t6t1_	Alignment	not modelled	11.9	17	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
69	c2qxyB_	Alignment	not modelled	11.9	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of a response regulator from thermotoga2 maritima
70	d1mb3a_	Alignment	not modelled	11.9	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
71	d2f1fa1	Alignment	not modelled	11.6	8	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
72	c3h5iA_	Alignment	not modelled	11.4	11	**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 carboxydothermus hydrogenoformans
73	c2a5hC_	Alignment	not modelled	11.2	25	**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).
74	d2fgca2	Alignment	not modelled	11.1	21	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
75	c3h6hB_	Alignment	not modelled	11.1	10	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**glutamate receptor, ionotropic kainate 2; **PDBTitle:** crystal structure of the glur6 amino terminal domain dimer assembly2 mpd form

76	d2bo1a1	Alignment	not modelled	10.9	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**L30e-like **Family:**L30e/L7ae ribosomal proteins
77	c2k5jB_	Alignment	not modelled	10.8	17	**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
78	c3cpqB_	Alignment	not modelled	10.7	14	**PDB header:**ribosomal protein **Chain:** B: **PDB Molecule:**50s ribosomal protein l30e; **PDBTitle:** crystal structure of l30e a ribosomal protein from2 methanocaldococcus jannaschii dsm2661 (mj1044)
79	c3luaA_	Alignment	not modelled	10.4	14	**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
80	c2zayA_	Alignment	not modelled	10.4	5	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
81	d1dz3a_	Alignment	not modelled	10.4	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
82	c2yr1B_	Alignment	not modelled	10.2	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426
83	c3n2bD_	Alignment	not modelled	10.2	14	**PDB header:**lyase **Chain:** D: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
84	c3cg4A_	Alignment	not modelled	10.2	14	**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
85	c1rnlA_	Alignment	not modelled	10.2	12	**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
86	c1k3rA_	Alignment	not modelled	10.1	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein mt0001; **PDBTitle:** crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
87	d1o57a2	Alignment	not modelled	10.1	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
88	c1a2oB_	Alignment	not modelled	10.0	12	**PDB header:**bacterial chemotaxis **Chain:** B: **PDB Molecule:**cheb methylesterase; **PDBTitle:** structural basis for methylesterase cheb regulation by a2 phosphorylation-activated domain
89	c3lufB_	Alignment	not modelled	10.0	7	**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
90	c3smpA_	Alignment	not modelled	9.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 1; **PDBTitle:** monoclinic crystal structure of human pantothenate kinase 1 alpha
91	d1nyra3	Alignment	not modelled	9.8	11	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**ThrRS/AlaRS common domain **Family:**Threonyl-tRNA synthetase (ThrRS), second 'additional' domain
92	c3c3mA_	Alignment	not modelled	9.7	14	**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
93	c3jteA_	Alignment	not modelled	9.6	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver domain2 protein from clostridium thermocellum
94	c2y7eA_	Alignment	not modelled	9.5	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme; **PDBTitle:** crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
95	c3t8yA_	Alignment	not modelled	9.5	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chemotaxis response regulator protein-glutamate **PDBTitle:** crystal structure of the response regulator domain of thermotoga2 maritima cheb
96	d1u0sy_	Alignment	not modelled	9.4	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
97	d1bs0a_	Alignment	not modelled	9.3	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
98	c2i7pA_	Alignment	not modelled	9.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 3; **PDBTitle:** crystal structure of human pank3 in complex with accoa
99	d2pc6a2	Alignment	not modelled	9.1	6	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like