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Description	P75908
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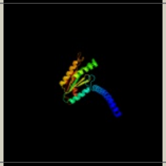
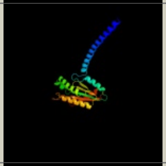
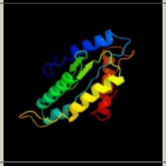
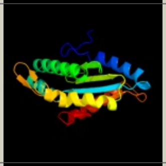
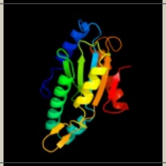
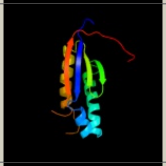
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w25B_	Alignment		100.0	32	**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	31	**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	c3i5aA_	Alignment		100.0	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator/ggdef domain protein; **PDBTitle:** crystal structure of full-length wpsr from pseudomonas syringae
5	c3i5cA_	Alignment		100.0	30	**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
6	c3i5bA_	Alignment		100.0	34	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wspr response regulator; **PDBTitle:** crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
7	c3ignA_	Alignment		100.0	39	**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
8	d1w25a3	Alignment		100.0	36	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**GGDEF domain
9	c3hvaA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein fimx; **PDBTitle:** crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
10	c3iclA_	Alignment		100.0	30	**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
11	c3qyyB_	Alignment		100.0	31	**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

12	c3mtkA_	Alignment		100.0	22	**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
13	c3pjwA_	Alignment		99.9	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cyclic dimeric gmp binding protein; **PDBTitle:** structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
14	c3hvwA_	Alignment		99.9	17	**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
15	c3gfzB_	Alignment		99.4	8	**PDB header:**hydrolase, signaling protein **Chain:** B: **PDB Molecule:**klebsiella pneumoniae blrp1; **PDBTitle:** klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
16	c3p7nB_	Alignment		98.2	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
17	c2qv6D_	Alignment		97.2	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
18	c1cjkA_	Alignment		95.6	11	**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
19	d1fx2a_	Alignment		95.4	15	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
20	d1wc1a_	Alignment		95.0	15	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
21	c3mr7B_	Alignment	not modelled	94.7	15	**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
22	c1wc6B_	Alignment	not modelled	94.5	14	**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
23	d1azsa_	Alignment	not modelled	94.4	11	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
24	c2w01C_	Alignment	not modelled	94.0	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of the guanylyl cyclase cya2
25	c1ybuA_	Alignment	not modelled	93.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipj; **PDBTitle:** mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
26	d1fx4a_	Alignment	not modelled	93.3	22	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
27	c3uvjC_	Alignment	not modelled	92.1	11	**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.
28	c2aq4A_	Alignment	not modelled	92.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** ternary complex of the catalytic core of rev1 with dna

						and dctp.
29	c1yk9A_	Alignment	not modelled	91.5	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
30	c1y10C_	Alignment	not modelled	89.8	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hypothetical protein rv1264/mt1302; **PDBTitle:** mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
31	c3gqcB_	Alignment	not modelled	85.9	27	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** structure of human rev1-dna-dntp ternary complex
32	c3et6A_	Alignment	not modelled	84.1	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**soluble guanylyl cyclase beta; **PDBTitle:** the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
33	d1azsb_	Alignment	not modelled	82.4	15	**Fold:**Ferredoxin-like **Superfamily:**Nucleotide cyclase **Family:**Adenylyl and guanylyl cyclase catalytic domain
34	d1im4a_	Alignment	not modelled	80.9	21	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
35	c1s97D_	Alignment	not modelled	79.1	19	**PDB header:**transferase/dna **Chain:** D: **PDB Molecule:**dna polymerase iv; **PDBTitle:** dpo4 with gt mismatch
36	c1k1qA_	Alignment	not modelled	76.8	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dbh protein; **PDBTitle:** crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
37	c3mr2A_	Alignment	not modelled	75.1	26	**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)
38	c2r8kB_	Alignment	not modelled	75.0	25	**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
39	d1k1sa2	Alignment	not modelled	74.1	20	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
40	c3onqB_	Alignment	not modelled	73.8	7	**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
41	c3l7xA_	Alignment	not modelled	71.0	27	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative hit-like protein involved in cell-cycle **PDBTitle:** the crystal structure of smu.412c from streptococcus mutans ua159
42	c1jihA_	Alignment	not modelled	70.5	25	**PDB header:**translation **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** yeast dna polymerase eta
43	c2oh2B_	Alignment	not modelled	68.7	23	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase kappa; **PDBTitle:** ternary complex of human dna polymerase
44	c3i24B_	Alignment	not modelled	67.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hit family hydrolase; **PDBTitle:** crystal structure of a hit family hydrolase protein from2 vibrio fischeri. northeast structural genomics consortium3 target id vfr176
45	c3l5aA_	Alignment	not modelled	64.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh/flavin oxidoreductase/nadh oxidase; **PDBTitle:** crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
46	d1jx4a2	Alignment	not modelled	62.9	20	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
47	d1jiha2	Alignment	not modelled	62.0	25	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
48	c3p0tB_	Alignment	not modelled	58.6	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an hit-like protein from mycobacterium2 paratuberculosis
49	c2wz1B_	Alignment	not modelled	54.8	12	**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.
50	c3l0oB_	Alignment	not modelled	53.3	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transcription termination factor rho; **PDBTitle:** structure of rna-free rho transcription termination factor from2 thermotoga maritima
51	c1t3nB_	Alignment	not modelled	50.2	25	**PDB header:**replication/dna **Chain:** B: **PDB Molecule:**polymerase (dna directed) iota; **PDBTitle:** structure of the catalytic core of dna polymerase iota in2 complex with dna and dttp
52	d2o5aa1	Alignment	not modelled	49.8	10	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Iojap/YbeB-like
53	c3nrdB_	Alignment	not modelled	49.0	22	**PDB header:**nucleotide binding protein **Chain:** B: **PDB Molecule:**histidine triad (hit) protein; **PDBTitle:** crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution

54	d1gx1a_	Alignment	not modelled	47.9	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
55	c3oheA_	Alignment	not modelled	47.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histidine triad (hit) protein; **PDBTitle:** crystal structure of a histidine triad protein (maqu_1709) from2 marinobacter aquaeolei vt8 at 1.20 a resolution
56	c3hf3A_	Alignment	not modelled	47.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
57	c1qgeE_	Alignment	not modelled	46.8	29	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**protein (triacylglycerol hydrolase); **PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
58	d1xxaa_	Alignment	not modelled	45.8	16	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
59	c3imiB_	Alignment	not modelled	44.0	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hit family protein; **PDBTitle:** 2.01 angstrom resolution crystal structure of a hit family protein2 from bacillus anthracis str. 'ames ancestor'
60	c2flIA_	Alignment	not modelled	42.6	23	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** ternary complex of human dna polymerase iota with dna and dttp
61	c2pmpA_	Alignment	not modelled	42.4	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana
62	d1t94a2	Alignment	not modelled	41.9	30	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
63	d1t0aa_	Alignment	not modelled	40.4	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
64	c1t94B_	Alignment	not modelled	40.1	26	**PDB header:**replication **Chain:** B: **PDB Molecule:**polymerase (dna directed) kappa; **PDBTitle:** crystal structure of the catalytic core of human dna2 polymerase kappa
65	c3f0gA_	Alignment	not modelled	39.4	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp
66	d1w55a2	Alignment	not modelled	39.2	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
67	d1gwja_	Alignment	not modelled	38.8	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
68	d1iv3a_	Alignment	not modelled	36.4	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
69	c2jroA_	Alignment	not modelled	33.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of so0334 from shewanella oneidensis. northeast2 structural genomics target sor75
70	c3k30B_	Alignment	not modelled	32.1	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex
71	d1y23a_	Alignment	not modelled	31.4	15	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**HIT (HINT, histidine triad) family of protein kinase-interacting proteins
72	c3af5A_	Alignment	not modelled	29.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1404; **PDBTitle:** the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
73	d1ps9a1	Alignment	not modelled	29.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
74	c3atyA_	Alignment	not modelled	28.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**prostaglandin f2a synthase; **PDBTitle:** crystal structure of tcoye
75	c3ksvA_	Alignment	not modelled	27.2	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** hypothetical protein from leishmania major
76	d2ox6a1	Alignment	not modelled	25.8	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**YdiL-like
77	c2zztA_	Alignment	not modelled	25.2	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein
78	c3nx3A_	Alignment	not modelled	24.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
79	c1ps9A_	Alignment	not modelled	24.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase

80	c3i4sB_	Alignment	not modelled	24.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidine triad protein; **PDBTitle:** crystal structure of histidine triad protein blr8122 from2 bradyrhizobium japonicum
81	d1vh8a_	Alignment	not modelled	24.5	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
82	c1xaxA_	Alignment	not modelled	24.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0054 protein hi0004; **PDBTitle:** nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
83	c3iyuY_	Alignment	not modelled	23.4	17	**PDB header:**virus **Chain:** Y: **PDB Molecule:**outer capsid protein vp4; **PDBTitle:** atomic model of an infectious rotavirus particle
84	c3b6nA_	Alignment	not modelled	22.4	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate **PDBTitle:** crystal structure of 2c-methyl-d-erythritol 2,4-2 cyclodiphosphate synthase pv003920 from plasmodium vivax
85	c2eh6A_	Alignment	not modelled	21.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase from aquifex2 aeolicus vf5
86	d1cm3a_	Alignment	not modelled	21.5	14	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
87	c3nuiA_	Alignment	not modelled	20.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate transaminase; **PDBTitle:** crystal structure of omega-transferase from vibrio fluvialis js17
88	d1z7da1	Alignment	not modelled	19.9	20	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
89	d1iwga2	Alignment	not modelled	19.6	17	**Fold:**Ferredoxin-like **Superfamily:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains **Family:**Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains
90	c1w57A_	Alignment	not modelled	19.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ispd/ispf bifunctional enzyme; **PDBTitle:** structure of the bifunctional ispdf from campylobacter2 jejuni containing zn
91	c3upsA_	Alignment	not modelled	19.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**iojap-like protein; **PDBTitle:** crystal structure of iojap-like protein from zymomonas mobilis
92	d1kdga2	Alignment	not modelled	19.1	46	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**GMC oxidoreductases
93	d1xpua3	Alignment	not modelled	18.5	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
94	c1z5wA_	Alignment	not modelled	18.3	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**tubulin gamma-1 chain; **PDBTitle:** crystal structure of gamma-tubulin bound to gtp
95	c2hl2A_	Alignment	not modelled	18.2	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** crystal structure of the editing domain of threonyl-trna2 synthetase from pyrococcus abyssi in complex with an3 analog of seryladenylate
96	d1b4ba_	Alignment	not modelled	18.0	9	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
97	c2ordA_	Alignment	not modelled	17.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylornithine aminotransferase; **PDBTitle:** crystal structure of acetylornithine aminotransferase (ec 2.6.1.11)2 (acoat) (tm1785) from thermotoga maritima at 1.40 a resolution
98	c2uzhB_	Alignment	not modelled	17.6	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2c-methyl-d-erythritol 2,4-cyclodiphosphate **PDBTitle:** mycobacterium smegmatis 2c-methyl-d-erythritol-2,4-2 cyclodiphosphate synthase (ispf)
99	c3anoA_	Alignment	not modelled	17.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ap-4-a phosphorylase; **PDBTitle:** crystal structure of a novel diadenosine 5',5'''-p1,p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv