Phyre2

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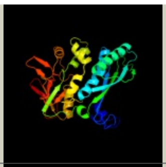
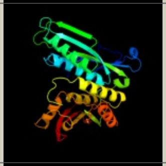
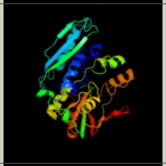
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rb9D_	Alignment		100.0	98	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hype protein; **PDBTitle:** crystal structure of e.coli hype
2	c2z1tA_	Alignment		100.0	48	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hype; **PDBTitle:** crystal structure of hydrogenase maturation protein hype
3	c2z1eA_	Alignment		100.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hype; **PDBTitle:** crystal structure of hype from thermococcus kodakaraensis (outward2 form)
4	c3fd5B_	Alignment		100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase 1; **PDBTitle:** crystal structure of human selenophosphate synthetase 12 complex with ampcp
5	c2btuB_	Alignment		100.0	21	**PDB header:**synthase **Chain:** B: **PDB Molecule:**phosphoribosyl-aminoimidazole synthetase; **PDBTitle:** crystal structure of phosphoribosylformylglycinamidine2 cyclo-ligase from bacillus anthracis at 2.3a resolution.
6	c3mcqA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamine-monophosphate kinase; **PDBTitle:** crystal structure of thiamine-monophosphate kinase (mfla_0573) from2 methylobacillus flagellatus kt at 1.91 a resolution
7	c2zodB_	Alignment		100.0	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of selenophosphate synthetase from2 aquifex aeolicus
8	c1cliD_	Alignment		100.0	19	**PDB header:**ligase **Chain:** D: **PDB Molecule:**protein (phosphoribosyl-aminoimidazole synthetase); **PDBTitle:** x-ray crystal structure of aminoimidazole ribonucleotide synthetase2 (purm), from the e. coli purine biosynthetic pathway, at 2.5 a3 resolution
9	c2zauB_	Alignment		100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus
10	c3c9uB_	Alignment		100.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiamine monophosphate kinase; **PDBTitle:** aathil complexed with adp and tpp
11	c2z01A_	Alignment		100.0	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole2 synthetase from geobacillus kaustophilus

12	c1vqvB_	Alignment		100.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiamine monophosphate kinase; **PDBTitle:** crystal structure of thiamine monophosphate kinase (thil)2 from aquifex aeolicus
13	c2v9yA_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** human aminoimidazole ribonucleotide synthetase
14	c3m84A_	Alignment		100.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole synthetase from2 francisella tularensis
15	c2yxzA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamin-monophosphate kinase; **PDBTitle:** crystal structure of tt0281 from thermus thermophilus hb8
16	c3ac6A_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 2; **PDBTitle:** crystal structure of purl from thermus thermophilus
17	c2hs0A_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase ii; **PDBTitle:** t. maritima purl complexed with atp
18	c3d54I_	Alignment		100.0	17	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phosphoribosylformylglycinamidine synthase ii; **PDBTitle:** stucture of purlqs from thermotoga maritima
19	c3mdoB_	Alignment		100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of a putative phosphoribosylformylglycinamidine2 cyclo-ligase (bdi_2101) from parabacteroides distasonis atcc 8503 at3 1.91 a resolution
20	c3kizA_	Alignment		100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of putative phosphoribosylformylglycinamidine cyclo-2 ligase (yp_676759.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
21	c1t3tA_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
22	d2z1ea2	Alignment	not modelled	100.0	36	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
23	d3c9ua1	Alignment	not modelled	100.0	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
24	d1clia1	Alignment	not modelled	100.0	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
25	d2zoda2	Alignment	not modelled	100.0	13	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
26	d1clib1	Alignment	not modelled	100.0	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
27	d2z1ea1	Alignment	not modelled	100.0	48	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
28	d3c9ua2	Alignment	not modelled	100.0	25	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
29	d2zoda1	Alignment	not modelled	99.9	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like

						Family: PurM N-terminal domain-like
30	d2zaua1	Alignment	not modelled	99.9	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
31	d1clia2	Alignment	not modelled	99.9	20	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
32	d1vk3a3	Alignment	not modelled	99.9	18	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
33	d1t3ta6	Alignment	not modelled	99.9	17	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
34	d1vk3a2	Alignment	not modelled	99.9	10	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
35	d1vk3a1	Alignment	not modelled	99.8	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
36	d1t3ta7	Alignment	not modelled	99.8	21	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
37	d1t3ta4	Alignment	not modelled	99.2	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
38	d1t3ta5	Alignment	not modelled	98.9	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
39	d3dhxa1	Alignment	not modelled	86.8	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
40	d1to3a_	Alignment	not modelled	71.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
41	d2qrra1	Alignment	not modelled	56.5	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
42	d1w5fa2	Alignment	not modelled	46.7	9	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
43	c3g85A_	Alignment	not modelled	37.0	0	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (laci family); **PDBTitle:** crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
44	c3jrkG_	Alignment	not modelled	30.7	16	**PDB header:**lyase **Chain:** G: **PDB Molecule:**tagatose 1,6-diphosphate aldolase 2; **PDBTitle:** a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
45	d2qswa1	Alignment	not modelled	28.1	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
46	c3shwA_	Alignment	not modelled	27.5	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of zo-1 pdz3-sh3-guk supramodule complex with2 connexin-45 peptide
47	d2csua1	Alignment	not modelled	26.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
48	c3d02A_	Alignment	not modelled	25.8	0	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative laci-type transcriptional regulator; **PDBTitle:** crystal structure of periplasmic sugar-binding protein2 (yp_001338366.1) from klebsiella pneumoniae subsp. pneumoniae mgh3 78578 at 1.30 a resolution
49	d1jyea_	Alignment	not modelled	25.5	21	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
50	c1jyeA_	Alignment	not modelled	25.5	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lactose operon repressor; **PDBTitle:** structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
51	c3rotA_	Alignment	not modelled	25.4	7	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc sugar transporter, periplasmic sugar binding protein; **PDBTitle:** crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
52	c3gbvB_	Alignment	not modelled	24.9	16	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative laci-family transcriptional regulator; **PDBTitle:** crystal structure of a putative laci transcriptional regulator from2 bacteroides fragilis
53	c3eggC_	Alignment	not modelled	23.3	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**spinophilin; **PDBTitle:** crystal structure of a complex between protein phosphatase 1 alpha2 (pp1) and the pp1 binding and pdz domains of spinophilin
54	c3o1hB_	Alignment	not modelled	23.0	18	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**periplasmic protein tort; **PDBTitle:** crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
						Fold:NAD(P)-binding Rossmann-fold domains

55	d1oi7a1	Alignment	not modelled	23.0	24	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
56	c3mizB_	Alignment	not modelled	23.0	21	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator protein, laci **PDBTitle:** crystal structure of a putative transcriptional regulator2 protein, lacI family from rhizobium etli
57	c2qjhH_	Alignment	not modelled	21.6	15	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
58	c2vk2A_	Alignment	not modelled	21.4	24	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter periplasmic-binding protein ytfq; **PDBTitle:** crystal structure of a galactofuranose binding protein
59	c3qi7A_	Alignment	not modelled	20.0	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
60	c2hqbA_	Alignment	not modelled	19.3	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional activator of comk gene; **PDBTitle:** crystal structure of a transcriptional activator of comk2 gene from bacillus halodurans
61	c3d8uA_	Alignment	not modelled	19.2	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**purr transcriptional regulator; **PDBTitle:** the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
62	c2zplA_	Alignment	not modelled	18.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain a
63	c3cs3A_	Alignment	not modelled	17.4	6	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sugar-binding transcriptional regulator, laci family; **PDBTitle:** crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis
64	c3diwB_	Alignment	not modelled	17.4	15	**PDB header:**signaling protein/cell adhesion **Chain:** B: **PDB Molecule:**tax1-binding protein 3; **PDBTitle:** c-terminal beta-catenin bound tip-1 structure
65	d1fnda1	Alignment	not modelled	17.3	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
66	c3h75A_	Alignment	not modelled	17.2	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**periplasmic sugar-binding domain protein; **PDBTitle:** crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
67	d1q3oa_	Alignment	not modelled	17.2	9	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
68	d1tjya_	Alignment	not modelled	17.0	13	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
69	c3lukB_	Alignment	not modelled	16.9	20	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**protein argonaute-2; **PDBTitle:** crystal structure of mid domain from hago2
70	d1x5qa1	Alignment	not modelled	16.9	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
71	c2q6tB_	Alignment	not modelled	16.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
72	c3fokH_	Alignment	not modelled	16.4	19	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**uncharacterized protein cgl0159; **PDBTitle:** crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
73	c3jy6B_	Alignment	not modelled	15.7	9	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci transcriptional regulator from lactobacillus2 brevis
74	d1ekqa_	Alignment	not modelled	15.2	20	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
75	d2dria_	Alignment	not modelled	15.1	12	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
76	c3g1wB_	Alignment	not modelled	15.0	9	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**sugar abc transporter; **PDBTitle:** crystal structure of sugar abc transporter (sugar-binding protein)2 from bacillus halodurans
77	c3k1rA_	Alignment	not modelled	14.3	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
78	d1gsoa2	Alignment	not modelled	14.1	39	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
79	c3l4fD_	Alignment	not modelled	13.5	9	**PDB header:**signaling protein/protein binding **Chain:** D: **PDB Molecule:**sh3 and multiple ankyrin repeat domains protein **PDBTitle:** crystal structure of betapix coiled-coil domain and shank2 pdz complex
						PDB header:transport protein **Chain:** A: **PDB Molecule:**abc-type sugar transport system,

80	c3ksmA_	Alignment	not modelled	13.4	16	periplasmic component; **PDBTitle:** crystal structure of abc-type sugar transport system, periplasmic2 component from hahella chejuensis
81	c3egcF_	Alignment	not modelled	13.1	18	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative ribose operon repressor; **PDBTitle:** crystal structure of a putative ribose operon repressor from2 burkholderia thailandensis
82	d1htwa_	Alignment	not modelled	13.1	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**YjeE-like
83	d1e8ca2	Alignment	not modelled	12.9	42	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
84	d1whaa_	Alignment	not modelled	12.8	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
85	c3kkeA_	Alignment	not modelled	12.8	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**laci family transcriptional regulator; **PDBTitle:** crystal structure of a laci family transcriptional regulator2 from mycobacterium smegmatis
86	c2rjoA_	Alignment	not modelled	12.8	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal protein; **PDBTitle:** crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
87	c3l49D_	Alignment	not modelled	12.7	6	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**abc sugar (ribose) transporter, periplasmic **PDBTitle:** crystal structure of abc sugar transporter subunit from2 rhodobacter sphaeroides 2.4.1
88	d1kona_	Alignment	not modelled	12.6	15	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
89	d1jx6a_	Alignment	not modelled	12.5	9	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
90	d1udxa3	Alignment	not modelled	12.2	29	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
91	d2ok5a4	Alignment	not modelled	11.9	29	**Fold:**Complement control module/SCR domain **Superfamily:**Complement control module/SCR domain **Family:**Complement control module/SCR domain
92	c3dzvB_	Alignment	not modelled	11.9	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-methyl-5-(beta-hydroxyethyl)thiazole kinase; **PDBTitle:** crystal structure of 4-methyl-5-(beta- hydroxyethyl)thiazole2 kinase (np_816404.1) from enterococcus faecalis v583 at3 2.57 a resolution
93	d2nzug1	Alignment	not modelled	11.5	12	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
94	d1ep3b1	Alignment	not modelled	11.5	38	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
95	c3h5oB_	Alignment	not modelled	11.4	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator gntr; **PDBTitle:** the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
96	d2byga1	Alignment	not modelled	11.1	28	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
97	c3l6uA_	Alignment	not modelled	11.1	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc-type sugar transport system periplasmic **PDBTitle:** crystal structure of abc-type sugar transport system,2 periplasmic component from exiguobacterium sibiricum
98	c3bilA_	Alignment	not modelled	11.0	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable laci-family transcriptional regulator; **PDBTitle:** crystal structure of a probable laci family transcriptional2 regulator from corynebacterium glutamicum
99	c2ka9A_	Alignment	not modelled	10.9	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**disks large homolog 4; **PDBTitle:** solution structure of psd-95 pdz12 complexed with cypin2 peptide