Phyre^2

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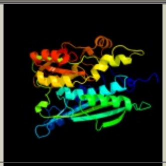
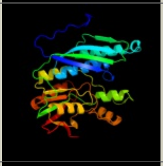
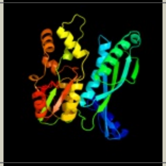
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fd5B_	Alignment		100.0	28	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase 1; **PDBTitle:** crystal structure of human selenophosphate synthetase 12 complex with ampcp
2	c2zodB_	Alignment		100.0	36	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of selenophosphate synthetase from2 aquifex aeolicus
3	c2zauB_	Alignment		100.0	37	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase; **PDBTitle:** crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus
4	c2btuB_	Alignment		100.0	20	**PDB header:**synthase **Chain:** B: **PDB Molecule:**phosphoribosyl-aminoimidazole synthetase; **PDBTitle:** crystal structure of phosphoribosylformylglycinamidine2 cyclo-ligase from bacillus anthracis at 2.3a resolution.
5	c1cliD_	Alignment		100.0	18	**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
6	c2rb9D_	Alignment		100.0	23	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hype protein; **PDBTitle:** crystal structure of e.coli hype
7	c3mcqA_	Alignment		100.0	20	**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
8	c2z1tA_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hype; **PDBTitle:** crystal structure of hydrogenase maturation protein hype
9	c2z1eA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hype; **PDBTitle:** crystal structure of hype from thermococcus kodakaraensis (outward2 form)
10	c3c9uB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiamine monophosphate kinase; **PDBTitle:** aathil complexed with adp and tpp
11	c1vqvB_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiamine monophosphate kinase; **PDBTitle:** crystal structure of thiamine monophosphate kinase (thil)2 from aquifex aeolicus

12	c2yxzA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thiamin-monophosphate kinase; **PDBTitle:** crystal structure of tt0281 from thermus thermophilus hb8
13	c2z01A_	Alignment		100.0	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole2 synthetase from geobacillus kaustophilus
14	c3m84A_	Alignment		100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole synthetase from2 francisella tularensis
15	c2v9yA_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine cyclo-ligase; **PDBTitle:** human aminoimidazole ribonucleotide synthetase
16	c3ac6A_	Alignment		100.0	23	**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	18	**PDB header:**ligase **Chain:** I: **PDB Molecule:**phosphoribosylformylglycinamidine synthase ii; **PDBTitle:** stucture of purlqs from thermotoga maritima
19	d2zoda2	Alignment		100.0	33	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
20	c3mdoB_	Alignment		100.0	17	**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
21	c1t3tA_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
22	d2zoda1	Alignment	not modelled	100.0	38	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
23	c3kizA_	Alignment	not modelled	100.0	18	**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
24	d2zaua1	Alignment	not modelled	100.0	42	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
25	d2z1ea2	Alignment	not modelled	100.0	21	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
26	d3c9ua1	Alignment	not modelled	100.0	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
27	d1clia2	Alignment	not modelled	100.0	15	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
28	d1clib1	Alignment	not modelled	100.0	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like

29	d1clia1	Alignment	not modelled	99.9	21	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
30	d3c9ua2	Alignment	not modelled	99.9	18	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
31	d1vk3a2	Alignment	not modelled	99.9	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
32	d2z1ea1	Alignment	not modelled	99.9	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
33	d1vk3a3	Alignment	not modelled	99.9	14	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
34	d1t3ta6	Alignment	not modelled	99.9	12	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
35	d1vk3a1	Alignment	not modelled	99.8	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
36	d1t3ta7	Alignment	not modelled	99.7	20	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
37	d1t3ta4	Alignment	not modelled	99.3	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
38	d1t3ta5	Alignment	not modelled	99.1	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
39	d3dhxa1	Alignment	not modelled	85.2	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
40	d1to3a_	Alignment	not modelled	80.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
41	c3jrkG_	Alignment	not modelled	77.3	11	**PDB header:**lyase **Chain:** G: **PDB Molecule:**tagatose 1,6-diphosphate aldolase 2; **PDBTitle:** a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
42	c3qi7A_	Alignment	not modelled	74.3	17	**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
43	d2qrra1	Alignment	not modelled	61.4	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
44	c3fokH_	Alignment	not modelled	55.0	11	**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
45	d1j2oa1	Alignment	not modelled	50.6	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
46	d1m3va1	Alignment	not modelled	37.0	60	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
47	c2a2cA_	Alignment	not modelled	36.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetylgalactosamine kinase; **PDBTitle:** x-ray structure of human n-acetyl galactosamine kinase2 complexed with mg-adp and n-acetyl galactosamine 1-3 phosphate
48	d1ujda_	Alignment	not modelled	35.8	20	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
49	d1oi7a1	Alignment	not modelled	34.0	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
50	d1wf8a1	Alignment	not modelled	31.9	11	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
51	c3eggC_	Alignment	not modelled	31.8	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
52	d1ihja_	Alignment	not modelled	29.9	14	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
53	d2byga1	Alignment	not modelled	29.2	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
54	c2dmzA_	Alignment	not modelled	28.0	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the third pdz domain of human inad-2 like protein
55	c3hmuA_	Alignment	not modelled	27.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, class iii;

55	c3hmdA_	Alignment	not modelled	27.5	15	**PDBTitle:** crystal structure of a class iii aminotransferase from2 silicibacter pomeroyi
56	c3shwA_	Alignment	not modelled	26.9	19	**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
57	c2jreA_	Alignment	not modelled	26.5	16	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**c60-1 pdz domain peptide; **PDBTitle:** c60-1, a pdz domain designed using statistical coupling2 analysis
58	d1ep3b1	Alignment	not modelled	26.2	39	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
59	d1x5qa1	Alignment	not modelled	25.9	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
60	c2qjhH_	Alignment	not modelled	25.8	19	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
61	d1fnda1	Alignment	not modelled	25.4	33	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
62	c2cjdA_	Alignment	not modelled	23.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**l-lysine-epsilon aminotransferase; **PDBTitle:** lysine aminotransferase from m. tuberculosis in external2 aldimine form
63	d2csua1	Alignment	not modelled	23.4	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
64	c1v9fA_	Alignment	not modelled	22.7	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase d; **PDBTitle:** crystal structure of catalytic domain of pseudouridine2 synthase rlud from escherichia coli
65	d1v9fa_	Alignment	not modelled	22.7	14	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
66	d2fe5a1	Alignment	not modelled	22.6	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
67	d1whaa_	Alignment	not modelled	22.5	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
68	d2bmwa1	Alignment	not modelled	22.1	27	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
69	c2dnrA_	Alignment	not modelled	21.8	11	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**synaptojanin-1; **PDBTitle:** solution structure of rna binding domain in synaptojanin 1
70	d2qswa1	Alignment	not modelled	21.4	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
71	d1gawa1	Alignment	not modelled	21.3	33	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
72	d1jyea_	Alignment	not modelled	20.9	9	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
73	c1jyeA_	Alignment	not modelled	20.9	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lactose operon repressor; **PDBTitle:** structure of a dimeric lac repressor with c-terminal deletion and k84l2 substitution
74	c2djtA_	Alignment	not modelled	20.6	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structures of the pdz domain of human unnamed2 protein product
75	d1wfga_	Alignment	not modelled	19.2	15	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
76	d1wh1a_	Alignment	not modelled	19.1	8	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
77	d1pcaa1	Alignment	not modelled	18.9	24	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
78	d2f0aa1	Alignment	not modelled	18.9	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
79	d1o6xa_	Alignment	not modelled	18.7	20	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
80	d1guda_	Alignment	not modelled	18.4	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
81	c3cs3A_	Alignment	not modelled	18.2	11	**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

82	d1rgra_	Alignment	not modelled	17.9	16	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
83	d2boaa2	Alignment	not modelled	17.6	16	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
84	d1krha1	Alignment	not modelled	17.2	44	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
85	d1kwma2	Alignment	not modelled	17.1	12	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
86	c3l49D_	Alignment	not modelled	17.0	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
87	c2jikB_	Alignment	not modelled	16.9	18	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**synaptojanin-2 binding protein; **PDBTitle:** crystal structure of pdz domain of synaptojanin-2 binding2 protein
88	d1pyta_	Alignment	not modelled	16.7	20	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
89	d1ayea2	Alignment	not modelled	16.6	20	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain
90	c2vk2A_	Alignment	not modelled	16.6	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**abc transporter periplasmic-binding protein ytfq; **PDBTitle:** crystal structure of a galactofuranose binding protein
91	d1tvca1	Alignment	not modelled	16.5	38	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
92	d1udxa3	Alignment	not modelled	16.5	14	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain
93	c2jilA_	Alignment	not modelled	16.4	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**glutamate receptor interacting protein-1; **PDBTitle:** crystal structure of 2nd pdz domain of glutamate receptor2 interacting protein-1 (grip1)
94	c2zplA_	Alignment	not modelled	16.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain a
95	c2fneB_	Alignment	not modelled	16.0	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 13th pdz domain of mpdz
96	c3bblA_	Alignment	not modelled	15.9	5	**PDB header:**regulatory protein **Chain:** A: **PDB Molecule:**regulatory protein of laci family; **PDBTitle:** crystal structure of a regulatory protein of laci family from2 chloroflexus aggregans
97	c3n5mD_	Alignment	not modelled	15.8	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**adenosylmethionine-8-amino-7-oxononanoate aminotransferase; **PDBTitle:** crystals structure of a bacillus anthracis aminotransferase
98	c3d8uA_	Alignment	not modelled	15.8	21	**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
99	d1nsaa2	Alignment	not modelled	15.3	12	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Pancreatic carboxypeptidase, activation domain