Phyre^2

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Description	P0A6C8
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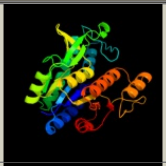
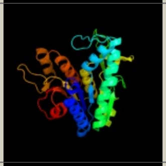
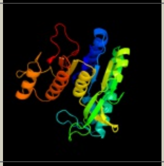
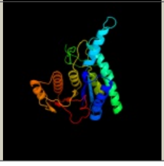
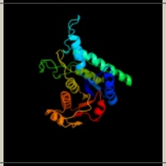
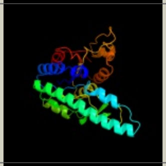
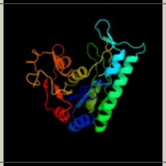
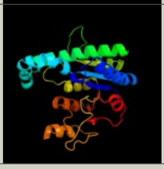
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gs5a_	Alignment		100.0	100	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
2	d2bufa1	Alignment		100.0	31	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
3	c2v5hB_	Alignment		100.0	33	**PDB header:**transcription **Chain:** B: **PDB Molecule:**acetylglutamate kinase; **PDBTitle:** controlling the storage of nitrogen as arginine: the2 complex of pii and acetylglutamate kinase from3 synechococcus elongatus pcc 7942
4	c2rd5A_	Alignment		100.0	34	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**acetylglutamate kinase-like protein; **PDBTitle:** structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
5	d2btya1	Alignment		100.0	33	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
6	d2ap9a1	Alignment		100.0	26	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
7	c2r98A_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetylglutamate synthase; **PDBTitle:** crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
8	c3l86A_	Alignment		100.0	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylglutamate kinase; **PDBTitle:** the crystal structure of smu.665 from streptococcus mutans ua159
9	c2egxA_	Alignment		100.0	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative acetylglutamate kinase; **PDBTitle:** crystal structure of the putative acetylglutamate kinase from thermus2 thermophilus
10	d1e19a_	Alignment		100.0	23	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**Carbamate kinase
11	d1b7ba_	Alignment		100.0	21	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**Carbamate kinase

12	c2j5tF_	Alignment		100.0	20	**PDB header:**transferase **Chain:** F: **PDB Molecule:**glutamate 5-kinase; **PDBTitle:** glutamate 5-kinase from escherichia coli complexed with2 glutamate
13	c3kzfC_	Alignment		100.0	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**carbamate kinase; **PDBTitle:** structure of giardia carbamate kinase
14	c2e9yA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbamate kinase; **PDBTitle:** crystal structure of project ape1968 from aeropyrum pernix k1
15	c2w21A_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate 5-kinase; **PDBTitle:** crystal structure of the aminoacid kinase domain of the2 glutamate 5 kinase of escherichia coli.
16	c3ll5C_	Alignment		100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**gamma-glutamyl kinase related protein; **PDBTitle:** crystal structure of t. acidophilum isopentenyl phosphate kinase2 product complex
17	c3ll9A_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isopentenyl phosphate kinase; **PDBTitle:** x-ray structures of isopentenyl phosphate kinase
18	c3k4yB_	Alignment		100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**isopentenyl phosphate kinase; **PDBTitle:** crystal structure of isopentenyl phosphate kinase from m. jannaschii2 in complex with ipp
19	d2bnea1	Alignment		100.0	17	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
20	d1ybda1	Alignment		100.0	15	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
21	d2akoa1	Alignment	not modelled	100.0	17	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
22	c3d40A_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**foma protein; **PDBTitle:** crystal structure of fosfomycin resistance kinase foma from2 streptomyces wedmorensis complexed with diphosphate
23	d2a1fa1	Alignment	not modelled	100.0	16	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
24	d2hmfa1	Alignment	not modelled	100.0	21	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
25	c3c1nA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable aspartokinase; **PDBTitle:** crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
26	d1z9da1	Alignment	not modelled	100.0	16	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
27	c3nwyB_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridylate kinase; **PDBTitle:** structure and allosteric regulation of the uridine monophosphate2 kinase from mycobacterium tuberculosis
28	c3l76B_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
						PDB header:transferase

29	c3ek5A_	Alignment	not modelled	100.0	16	**Chain:** A: **PDB Molecule:**uridylate kinase; **PDBTitle:** unique gtp-binding pocket and allostery of ump kinase from a gram-2 negative phytopathogen bacterium
30	d2j0wa1	Alignment	not modelled	100.0	19	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
31	c2jjxC_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridylate kinase; **PDBTitle:** the crystal structure of ump kinase from bacillus anthracis2 (ba1797)
32	d2cdqa1	Alignment	not modelled	100.0	16	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
33	c2cdqB_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
34	c2j0wA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lysine-sensitive aspartokinase 3; **PDBTitle:** crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
35	c2va1A_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridylate kinase; **PDBTitle:** crystal structure of ump kinase from ureaplasma parvum
36	c2ogxA_	Alignment	not modelled	100.0	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**molybdenum storage protein subunit alpha; **PDBTitle:** the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
37	d2brxa1	Alignment	not modelled	100.0	20	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
38	c2ogxB_	Alignment	not modelled	100.0	20	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**molybdenum storage protein subunit beta; **PDBTitle:** the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
39	c2j4kC_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridylate kinase; **PDBTitle:** crystal structure of uridylate kinase from sulfolobus2 solfataricus in complex with ump to 2.2 angstrom3 resolution
40	d2ij9a1	Alignment	not modelled	100.0	20	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
41	c3ab4K_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** K: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
42	c3gygA_	Alignment	not modelled	70.7	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ntd biosynthesis operon putative hydrolase ntdb; **PDBTitle:** crystal structure of yhjk (haloacid dehalogenase-like hydrolase2 protein) from bacillus subtilis
43	c2dlnA_	Alignment	not modelled	58.3	23	**PDB header:**ligase(peptidoglycan synthesis) **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution
44	d2zdra2	Alignment	not modelled	53.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
45	d1iowa1	Alignment	not modelled	51.6	23	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
46	d1xpja_	Alignment	not modelled	49.7	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
47	c2q4dB_	Alignment	not modelled	49.3	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lysine decarboxylase-like protein at5g11950; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
48	d1ydha_	Alignment	not modelled	45.3	16	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
49	d2rbka1	Alignment	not modelled	44.4	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
50	c3kv1A_	Alignment	not modelled	42.4	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional repressor; **PDBTitle:** crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
51	d1wzca1	Alignment	not modelled	42.2	7	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
52	c3daoB_	Alignment	not modelled	40.7	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phosphatse; **PDBTitle:** crystal structure of a putative phosphatse (eubrec_1417) from2 eubacterium rectale at 1.80 a resolution
53	c1xuzA_	Alignment	not modelled	40.2	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+,

						phosphoenolpyruvate, and n-3 acetyl mannosaminitol
54	d1ovma1	Alignment	not modelled	39.8	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
55	d2obba1	Alignment	not modelled	39.3	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
56	c3r4cA_	Alignment	not modelled	35.7	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, haloacid dehalogenase-like hydrolase; **PDBTitle:** divergence of structure and function among phosphatases of the2 haloalkanoate (had) enzyme superfamily: analysis of bt1666 from3 bacteroides thetaiotaomicron
57	c3ecsD_	Alignment	not modelled	35.7	10	**PDB header:**translation **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b subunit **PDBTitle:** crystal structure of human eif2b alpha
58	c3no4A_	Alignment	not modelled	35.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**creatinine amidohydrolase; **PDBTitle:** crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
59	d1zpda1	Alignment	not modelled	34.5	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
60	c3fzqA_	Alignment	not modelled	34.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
61	c2pvpB_	Alignment	not modelled	33.9	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
62	d1vlia2	Alignment	not modelled	31.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
63	d1rkqa_	Alignment	not modelled	29.9	19	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
64	c2pr7A_	Alignment	not modelled	26.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase/epoxide hydrolase family; **PDBTitle:** crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
65	c2p9jH_	Alignment	not modelled	26.1	26	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**hypothetical protein aq2171; **PDBTitle:** crystal structure of aq2171 from aquifex aeolicus
66	c2qniA_	Alignment	not modelled	25.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu0299; **PDBTitle:** crystal structure of uncharacterized protein atu0299
67	c2i55C_	Alignment	not modelled	24.9	26	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphomannomutase; **PDBTitle:** complex of glucose-1,6-bisphosphate with phosphomannomutase from2 leishmania mexicana
68	c2zqeA_	Alignment	not modelled	24.9	34	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**muts2 protein; **PDBTitle:** crystal structure of the smr domain of thermus thermophilus muts2
69	c3lubE_	Alignment	not modelled	24.5	18	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**putative creatinine amidohydrolase; **PDBTitle:** crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
70	d1v7za_	Alignment	not modelled	22.8	16	**Fold:**Creatininase **Superfamily:**Creatininase **Family:**Creatininase
71	d1vb5a_	Alignment	not modelled	21.5	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**IF2B-like
72	d2b30a1	Alignment	not modelled	21.0	24	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
73	d1nrwa_	Alignment	not modelled	20.6	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
74	c1vliA_	Alignment	not modelled	19.9	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
75	d1a9xa3	Alignment	not modelled	19.6	12	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
76	d1rlma_	Alignment	not modelled	19.4	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
77	d1nf2a_	Alignment	not modelled	18.5	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
						PDB header:hydrolase

78	c3mmzA_	Alignment	not modelled	18.2	19	**Chain:** A: **PDB Molecule:**putative had family hydrolase; **PDBTitle:** crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
79	c3niwA_	Alignment	not modelled	18.1	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron
80	d1xvia_	Alignment	not modelled	16.7	21	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
81	c1xviA_	Alignment	not modelled	16.7	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative mannosyl-3-phosphoglycerate phosphatase; **PDBTitle:** crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12
82	c2iz6A_	Alignment	not modelled	16.7	19	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**molybdenum cofactor carrier protein; **PDBTitle:** structure of the chlamydomonas rheinhardtii moco carrier2 protein
83	c1zjjA_	Alignment	not modelled	15.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein ph1952; **PDBTitle:** crystal structure of hypothetical protein ph1952 from pyrococcus2 horikoshii ot3
84	c3pgvB_	Alignment	not modelled	14.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**haloacid dehalogenase-like hydrolase; **PDBTitle:** crystal structure of a haloacid dehalogenase-like hydrolase2 (kpn_04322) from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at3 2.39 a resolution
85	c2hx1D_	Alignment	not modelled	13.5	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted sugar phosphatases of the had **PDBTitle:** crystal structure of possible sugar phosphatase, had2 superfamily (zp_00311070.1) from cytophaga hutchinsonii3 atcc 33406 at 2.10 a resolution
86	c3pkiF_	Alignment	not modelled	13.4	27	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
87	c3a11D_	Alignment	not modelled	13.3	13	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**translation initiation factor eif-2b, delta **PDBTitle:** crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
88	c3k35D_	Alignment	not modelled	13.0	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
89	c3qd7X_	Alignment	not modelled	13.0	31	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**uncharacterized protein ydal; **PDBTitle:** crystal structure of ydal, a stand-alone small muts-related protein2 from escherichia coli
90	c3nxkE_	Alignment	not modelled	12.6	22	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**cytoplasmic l-asparaginase; **PDBTitle:** crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
91	c3lklB_	Alignment	not modelled	12.5	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**antisigma-factor antagonist stas; **PDBTitle:** crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
92	c3dnpA_	Alignment	not modelled	12.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**stress response protein yhax; **PDBTitle:** crystal structure of stress response protein yhax from bacillus2 subtilis
93	c2vy9A_	Alignment	not modelled	12.2	13	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**anti-sigma-factor antagonist; **PDBTitle:** molecular architecture of the stressosome, a signal2 integration and transduction hub
94	d1l6ra_	Alignment	not modelled	12.1	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
95	d1ehia1	Alignment	not modelled	12.0	5	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
96	c1wnfA_	Alignment	not modelled	11.9	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**l-asparaginase; **PDBTitle:** crystal structure of ph0066 from pyrococcus horikoshii
97	c2qyhD_	Alignment	not modelled	11.5	20	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical conserved protein, gk1056; **PDBTitle:** crystal structure of the hypothetical protein (gk1056) from2 geobacillus kaustophilus hta426
98	d1nzya_	Alignment	not modelled	10.8	17	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Crotonase-like
99	d1wpga2	Alignment	not modelled	10.7	7	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P