Phyre2

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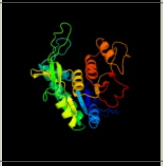
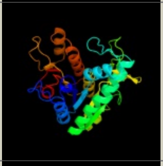
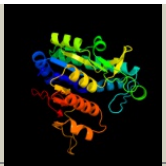
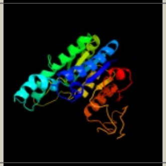
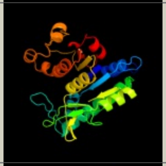
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1e19a_	Alignment		100.0	37	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**Carbamate kinase
2	c2e9yA_	Alignment		100.0	41	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbamate kinase; **PDBTitle:** crystal structure of project ape1968 from aeropyrum pernix k1
3	d1b7ba_	Alignment		100.0	40	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**Carbamate kinase
4	c3kzfC_	Alignment		100.0	39	**PDB header:**transferase **Chain:** C: **PDB Molecule:**carbamate kinase; **PDBTitle:** structure of giardia carbamate kinase
5	c2rd5A_	Alignment		100.0	26	**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
6	d2ap9a1	Alignment		100.0	20	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
7	c2r98A_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetylglutamate synthase; **PDBTitle:** crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
8	d2bufa1	Alignment		100.0	21	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
9	c2v5hB_	Alignment		100.0	23	**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
10	d2btya1	Alignment		100.0	24	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
11	d1gs5a_	Alignment		100.0	24	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase

12	c3l86A_	Alignment		100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylglutamate kinase; **PDBTitle:** the crystal structure of smu.665 from streptococcus mutans ua159
13	c2j5tF_	Alignment		100.0	24	**PDB header:**transferase **Chain:** F: **PDB Molecule:**glutamate 5-kinase; **PDBTitle:** glutamate 5-kinase from escherichia coli complexed with2 glutamate
14	c2egxA_	Alignment		100.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative acetylglutamate kinase; **PDBTitle:** crystal structure of the putative acetylglutamate kinase from thermus2 thermophilus
15	c2w21A_	Alignment		100.0	25	**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	d2hmfa1	Alignment		100.0	17	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
17	d1ybda1	Alignment		100.0	20	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
18	d2bnea1	Alignment		100.0	21	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
19	d1z9da1	Alignment		100.0	19	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
20	c3ll5C_	Alignment		100.0	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**gamma-glutamyl kinase related protein; **PDBTitle:** crystal structure of t. acidophilum isopentenyl phosphate kinase2 product complex
21	c2jjxC_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridylate kinase; **PDBTitle:** the crystal structure of ump kinase from bacillus anthracis2 (ba1797)
22	d2akoa1	Alignment	not modelled	100.0	19	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
23	c3c1nA_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable aspartokinase; **PDBTitle:** crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
24	c3ek5A_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridylate kinase; **PDBTitle:** unique gtp-binding pocket and allostery of ump kinase from a gram-2 negative phytopathogen bacterium
25	c3nwyB_	Alignment	not modelled	100.0	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridylate kinase; **PDBTitle:** structure and allosteric regulation of the uridine monophosphate2 kinase from mycobacterium tuberculosis
26	c3ll9A_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isopentenyl phosphate kinase; **PDBTitle:** x-ray structures of isopentenyl phosphate kinase
27	c3l76B_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
28	c3k4yB_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**isopentenyl phosphate kinase; **PDBTitle:** crystal structure of isopentenyl phosphate kinase from m. jannaschii2 in complex with ipp

29	d2j0wa1	Alignment	not modelled	100.0	16	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
30	d2cdqa1	Alignment	not modelled	100.0	14	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
31	d2ij9a1	Alignment	not modelled	100.0	26	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
32	c3d40A_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**foma protein; **PDBTitle:** crystal structure of fosfomycin resistance kinase foma from2 streptomyces wedmorensis complexed with diphosphate
33	c2cdqB_	Alignment	not modelled	100.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
34	d2a1fa1	Alignment	not modelled	100.0	20	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
35	d2brxa1	Alignment	not modelled	100.0	24	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
36	c2ogxB_	Alignment	not modelled	100.0	22	**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)
37	c2ogxA_	Alignment	not modelled	100.0	24	**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)
38	c2j0wA_	Alignment	not modelled	100.0	15	**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)
39	c3ab4K_	Alignment	not modelled	100.0	22	**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
40	c2va1A_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridylate kinase; **PDBTitle:** crystal structure of ump kinase from ureaplasma parvum
41	c2j4kC_	Alignment	not modelled	100.0	27	**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
42	c2vcbA_	Alignment	not modelled	72.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylglucosaminidase; **PDBTitle:** family 89 glycoside hydrolase from clostridium perfringens2 in complex with pugnac
43	d2nx2a1	Alignment	not modelled	67.0	20	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**YpsA-like
44	c3bq9A_	Alignment	not modelled	63.4	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted rossmann fold nucleotide-binding domain- **PDBTitle:** crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
45	d1ydha_	Alignment	not modelled	52.5	21	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
46	c2q4dB_	Alignment	not modelled	49.6	21	**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
47	d2q4oa1	Alignment	not modelled	42.4	17	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
48	c2q4oA_	Alignment	not modelled	42.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein at2g37210/t2n18.3; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
49	d1xpja_	Alignment	not modelled	42.1	17	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
50	d2b0ja2	Alignment	not modelled	31.4	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
51	c2ejbA_	Alignment	not modelled	25.4	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
52	c3f46A_	Alignment	not modelled	22.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methenyltetrahydromethanopterin hydrogenase; **PDBTitle:** the crystal structure of c176a mutated [fe]-hydrogenase (hmd)2 holoenzyme from methanocaldococcus jannaschii
						PDB header:hydrolase

53	c3mmzA_	Alignment	not modelled	22.2	17	**Chain:** A: **PDB Molecule:**putative had family hydrolase; **PDBTitle:** crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
54	c3gk0H_	Alignment	not modelled	19.9	26	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
55	d1u02a_	Alignment	not modelled	18.8	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Trehalose-phosphatase
56	d1k1ea_	Alignment	not modelled	18.0	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Probable phosphatase YrbI
57	c3o6cA_	Alignment	not modelled	16.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** pyridoxal phosphate biosynthetic protein pdxj from campylobacter2 jejuni
58	c2w6rA_	Alignment	not modelled	16.7	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**imidazole glycerol phosphate synthase subunit **PDBTitle:** crystal structure of an artificial (ba)8-barrel protein2 designed from identical half barrels
59	d1m5wa_	Alignment	not modelled	16.2	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
60	c3e8mD_	Alignment	not modelled	14.9	29	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acylneuraminate cytidylyltransferase; **PDBTitle:** structure-function analysis of 2-keto-3-deoxy-d-glycero-d-galacto-2 nononate-9-phosphate (kdn) phosphatase defines a new clad within the3 type c0 had subfamily
61	c2iz6A_	Alignment	not modelled	14.0	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**molybdenum cofactor carrier protein; **PDBTitle:** structure of the chlamydomonas rheinhardtii moco carrier2 protein
62	d1q0qa2	Alignment	not modelled	13.0	60	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
63	c3ewiB_	Alignment	not modelled	12.5	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**n-acylneuraminate cytidylyltransferase; **PDBTitle:** structural analysis of the c-terminal domain of murine cmp-2 sialic acid synthetase
64	c3mn1B_	Alignment	not modelled	12.1	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable yrbi family phosphatase; **PDBTitle:** crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
65	d1weha_	Alignment	not modelled	11.7	7	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
66	d1ecfa1	Alignment	not modelled	11.6	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
67	c3etjB_	Alignment	not modelled	10.9	35	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure e. coli purk in complex with mg, adp, and2 pi
68	c3gygA_	Alignment	not modelled	10.7	14	**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
69	d1yzfa1	Alignment	not modelled	10.5	30	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**TAP-like
70	d1weka_	Alignment	not modelled	10.4	22	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
71	c1ecjB_	Alignment	not modelled	10.2	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
72	d1rcua_	Alignment	not modelled	9.3	20	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
73	c1rcuB_	Alignment	not modelled	9.3	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein vt76; **PDBTitle:** x-ray structure of tm1055 northeast structural genomics2 consortium target vt76
74	d2zdra2	Alignment	not modelled	8.5	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
75	c2kswA_	Alignment	not modelled	8.4	31	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**oryctin; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for oryctin
76	d1gph11	Alignment	not modelled	8.0	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
77	c2zakB_	Alignment	not modelled	8.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-asparaginase precursor; **PDBTitle:** orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (ecaiii) with active-site t179a mutation
						Fold:MCP/YpsA-like

78	d1t35a_	Alignment	not modelled	7.9	14	**Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
79	c3dhnA_	Alignment	not modelled	7.4	16	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
80	c2p9jH_	Alignment	not modelled	7.2	13	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**hypothetical protein aq2171; **PDBTitle:** crystal structure of aq2171 from aquifex aeolicus
81	c2qx0A_	Alignment	not modelled	7.1	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**7,8-dihydro-6-hydroxymethylpterin- **PDBTitle:** crystal structure of yersinia pestis hppk (ternary complex)
82	c1t3mA_	Alignment	not modelled	7.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
83	c3quaA_	Alignment	not modelled	6.9	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein and possible2 molybdenum cofactor protein from mycobacterium smegmatis
84	c2h29A_	Alignment	not modelled	6.7	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide **PDBTitle:** crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from staphylococcus aureus: product3 bound form 1
85	c3nd5D_	Alignment	not modelled	6.0	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** crystal structure of phosphopantetheine adenylyltransferase (ppat)2 from enterococcus faecalis
86	c3gh1A_	Alignment	not modelled	6.0	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted nucleotide-binding protein; **PDBTitle:** crystal structure of predicted nucleotide-binding protein from vibrio2 cholerae
87	d1wmaa1	Alignment	not modelled	5.9	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
88	c1gph1_	Alignment	not modelled	5.9	22	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
89	d3eeqa2	Alignment	not modelled	5.9	33	**Fold:**CbiG N-terminal domain-like **Superfamily:**CbiG N-terminal domain-like **Family:**CbiG N-terminal domain-like