Phyre^2

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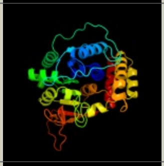
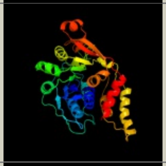
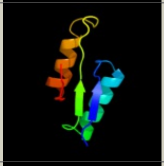
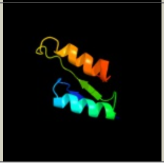
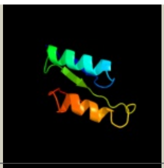
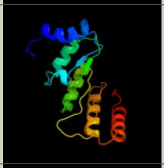
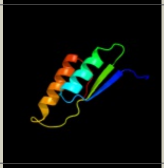
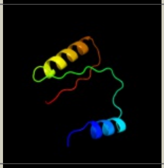
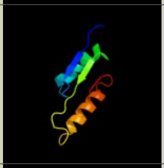
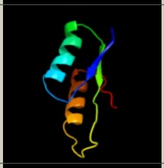
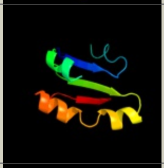
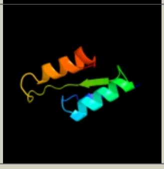
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3b9xA_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrimidine-specific ribonucleoside hydrolase rihb; **PDBTitle:** crystal structure of the e. coli pyrimidine nucleoside hydrolase yeik2 in complex with inosine
2	d1q8fa_	Alignment		100.0	100	**Fold:**Nucleoside hydrolase **Superfamily:**Nucleoside hydrolase **Family:**Nucleoside hydrolase
3	d2masa_	Alignment		100.0	39	**Fold:**Nucleoside hydrolase **Superfamily:**Nucleoside hydrolase **Family:**Nucleoside hydrolase
4	d1ezra_	Alignment		100.0	41	**Fold:**Nucleoside hydrolase **Superfamily:**Nucleoside hydrolase **Family:**Nucleoside hydrolase
5	c1yoeA_	Alignment		100.0	39	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein ybek; **PDBTitle:** crystal structure of a the e. coli pyrimidine nucleoside hydrolase2 ybek with bound ribose
6	c3fz0C_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nucleoside hydrolase, putative; **PDBTitle:** inosine-guanosine nucleoside hydrolase (ig-nh)
7	c2c40B_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inosine-uridine preferring nucleoside hydrolase family **PDBTitle:** crystal structure of inosine-uridine preferring nucleoside2 hydrolase from bacillus anthracis at 2.2a resolution
8	d1kica_	Alignment		100.0	21	**Fold:**Nucleoside hydrolase **Superfamily:**Nucleoside hydrolase **Family:**Nucleoside hydrolase
9	c2yhgA_	Alignment		99.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellulose-binding protein; **PDBTitle:** ab initio phasing of a nucleoside hydrolase-related hypothetical2 protein from saccharophagus degradans that is associated with3 carbohydrate metabolism
10	d1gpma1	Alignment		81.5	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
11	c2dplA_	Alignment		65.5	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing] subunit b; **PDBTitle:** crystal structure of the gmp synthase from pyrococcus horikoshii ot3

12	c3tqiB_	Alignment		51.6	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii
13	c2hmaA_	Alignment		42.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable trna (5-methylaminomethyl-2-thiouridylate)- **PDBTitle:** the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
14	d1f74a_	Alignment		39.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
15	c3fiuD_	Alignment		39.0	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis
16	d1o5za2	Alignment		37.7	15	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**Folylpolyglutamate synthetase
17	c3uowB_	Alignment		32.9	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
18	c2derA_	Alignment		31.3	20	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna-specific 2-thiouridylase mnma; **PDBTitle:** cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
19	d1ccwa_	Alignment		30.1	25	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
20	c1gpmD_	Alignment		25.8	16	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate
21	c3p52B_	Alignment	not modelled	23.7	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion
22	d2c5sa1	Alignment	not modelled	22.4	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
23	c2zyiB_	Alignment	not modelled	19.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipase, putative; **PDBTitle:** a. fulgidus lipase with fatty acid fragment and calcium
24	d2ocda1	Alignment	not modelled	18.8	16	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
25	c3bl5E_	Alignment	not modelled	18.4	17	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**queuosine biosynthesis protein quec; **PDBTitle:** crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
26	d2b3ya2	Alignment	not modelled	18.1	17	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
27	d3bula2	Alignment	not modelled	17.7	20	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
28	c3dlaD_	Alignment	not modelled	17.5	19	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don

29	d1nnsa_	Alignment	not modelled	16.0	15	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
30	d1e0ta3	Alignment	not modelled	15.9	16	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
31	d1xnga1	Alignment	not modelled	15.2	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
32	d7reqa2	Alignment	not modelled	13.9	12	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
33	c2ehhE_	Alignment	not modelled	13.7	12	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
34	c3si9B_	Alignment	not modelled	13.5	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
35	d2gc6a2	Alignment	not modelled	13.3	15	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**Folylpolyglutamate synthetase
36	c2yxgD_	Alignment	not modelled	12.9	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihyrodipicolinate synthase (dapa)
37	d1vbka1	Alignment	not modelled	12.7	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
38	c2vosA_	Alignment	not modelled	12.4	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase protein folc; **PDBTitle:** mycobacterium tuberculosis folylpolyglutamate synthase2 complexed with adp
39	c3cseA_	Alignment	not modelled	12.1	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** candida glabrata dihydrofolate reductase complexed with2 nadph and 2,4-diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-3 ynyl)-6-ethylpyrimidine (ucp120b)
40	d1tcaa_	Alignment	not modelled	11.6	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
41	c3r79B_	Alignment	not modelled	11.6	8	**PDB header:**structure genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharactertized protein from agrobacterium2 tumefaciens
42	c2eapA_	Alignment	not modelled	10.7	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**lymphocyte cytosolic protein 2; **PDBTitle:** solution structure of the n-terminal sam-domain of human2 lymphocyte cytosolic protein 2
43	d1o94c_	Alignment	not modelled	10.2	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
44	d1lw7a1	Alignment	not modelled	9.7	8	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
45	c2ywcC_	Alignment	not modelled	9.1	20	**PDB header:**ligase **Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
46	d2vk9a1	Alignment	not modelled	8.9	20	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycosylating toxin catalytic domain-like
47	d1kqpa_	Alignment	not modelled	8.9	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
48	c1xtyD_	Alignment	not modelled	8.9	45	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of sulfolobus solfataricus peptidyl-trna2 hydrolase
49	d4pgaa_	Alignment	not modelled	8.6	27	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
50	c2d3kA_	Alignment	not modelled	8.4	45	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** structural study on project id ph1539 from pyrococcus2 horikoshii ot3
51	c1w78A_	Alignment	not modelled	8.1	16	**PDB header:**synthase **Chain:** A: **PDB Molecule:**folc bifunctional protein; **PDBTitle:** e.coli folc in complex with dhpp and adp
52	d3cx5a2	Alignment	not modelled	8.1	23	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
53	c2zv3E_	Alignment	not modelled	8.1	45	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
54	c3rg9A_	Alignment	not modelled	8.0	22	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** A: **PDB Molecule:**bifunctional dihydrofolate reductase-thymidylate synthase; **PDBTitle:** trypanosoma brucei dihydrofolate reductase (tbdhfr) in complex with2 wr99210
						Fold: Adenine nucleotide alpha hydrolase-like

55	d2pg3a1	Alignment	not modelled	7.6	19	**Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
56	c3bjqA_	Alignment	not modelled	7.4	12	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**phage-related protein; **PDBTitle:** crystal structure of a phage-related protein (bb3626) from bordetella2 bronchiseptica rb50 at 2.05 a resolution
57	d1q7sa_	Alignment	not modelled	7.4	36	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
58	d1agxa_	Alignment	not modelled	7.3	15	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
59	d2nu7b1	Alignment	not modelled	7.1	17	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
60	d3erja1	Alignment	not modelled	7.0	55	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
61	c3sz8D_	Alignment	not modelled	7.0	7	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 2; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
62	c1wnfA_	Alignment	not modelled	7.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**l-asparaginase; **PDBTitle:** crystal structure of ph0066 from pyrococcus horikoshii
63	c1bmtB_	Alignment	not modelled	7.0	20	**PDB header:**methyltransferase **Chain:** B: **PDB Molecule:**methionine synthase; **PDBTitle:** how a protein binds b12: a 3.o angstrom x-ray structure of2 the b12-binding domains of methionine synthase
64	c2dy3B_	Alignment	not modelled	6.9	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from corynebacterium glutamicum
65	c2nu9E_	Alignment	not modelled	6.5	17	**PDB header:**ligase **Chain:** E: **PDB Molecule:**succinyl-coa synthetase beta chain; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
66	d1rlka_	Alignment	not modelled	6.5	45	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
67	d1xcra1	Alignment	not modelled	6.3	25	**Fold:**AF0104/ALDC/Ptd012-like **Superfamily:**AF0104/ALDC/Ptd012-like **Family:**PTD012-like
68	c1k98A_	Alignment	not modelled	6.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionine synthase; **PDBTitle:** adomet complex of meth c-terminal fragment
69	d1liua3	Alignment	not modelled	6.1	15	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
70	d1ik6a2	Alignment	not modelled	6.0	25	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
71	d2bvla1	Alignment	not modelled	5.9	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Glycosylating toxin catalytic domain-like
72	d1o7ja_	Alignment	not modelled	5.9	12	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
73	c2vxoB_	Alignment	not modelled	5.9	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
74	c3lciA_	Alignment	not modelled	5.6	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
75	d1kmva_	Alignment	not modelled	5.3	26	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
76	c3llxA_	Alignment	not modelled	5.3	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**predicted amino acid aldolase or racemase; **PDBTitle:** crystal structure of an ala racemase-like protein (il1761) from2 idiomarina loihiensis at 1.50 a resolution
77	d1ru8a_	Alignment	not modelled	5.3	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
78	c2e18B_	Alignment	not modelled	5.2	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of project ph0182 from pyrococcus horikoshii ot3
79	d1qf5a_	Alignment	not modelled	5.2	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like