Phyre^2

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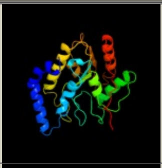
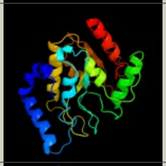
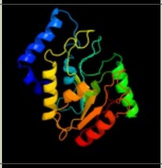
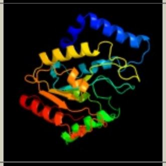
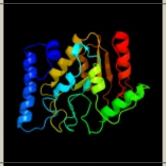
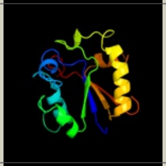
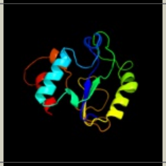
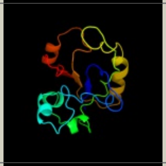
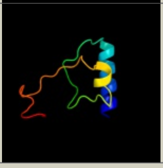
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3euga_	Alignment		100.0	99	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
2	c3tr7A_	Alignment		100.0	62	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** structure of a uracil-dna glycosylase (ung) from coxiella burnetii
3	d1okba_	Alignment		100.0	59	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
4	d2hxma1	Alignment		100.0	56	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
5	c2booA_	Alignment		100.0	55	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** the crystal structure of uracil-dna n-glycosylase (ung)2 from deinococcus radiodurans.
6	c3cxmA_	Alignment		100.0	48	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** leishmania naiffi uracil-dna glycosylase in complex with 5-bromouracil
7	d1laue_	Alignment		100.0	46	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
8	c2zhxG_	Alignment		100.0	38	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** G: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of uracil-dna glycosylase from mycobacterium2 tuberculosis in complex with a proteinaceous inhibitor
9	d2j8xa1	Alignment		100.0	48	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Uracil-DNA glycosylase
10	c2owrD_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of vaccinia virus uracil-dna glycosylase
11	c2rbaB_	Alignment		97.0	10	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**g/t mismatch-specific thymine dna glycosylase; **PDBTitle:** structure of human thymine dna glycosylase bound to abasic and2 undamaged dna

12	c2c2pA_	Alignment		95.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**g/u mismatch-specific dna glycosylase; **PDBTitle:** the crystal structure of mismatch specific uracil-dna2 glycosylase (mug) from deinococcus radiodurans
13	d1oe4a_	Alignment		94.7	17	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Single-strand selective monofunctional uracil-DNA glycosylase SMUG1
14	d1muga_	Alignment		94.7	13	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Mug-like
15	d1ui0a_	Alignment		94.3	18	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Mug-like
16	c3ikbB_	Alignment		93.6	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the structure of a conserved protein from streptococcus2 mutans ua159.
17	c2d3yA_	Alignment		92.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uracil-dna glycosylase; **PDBTitle:** crystal structure of uracil-dna glycosylase from thermus thermophilus2 hb8
18	d1vk2a_	Alignment		90.4	20	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Mug-like
19	c2h2wA_	Alignment		50.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-succinyltransferase; **PDBTitle:** crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
20	c3p9xB_	Alignment		35.1	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
21	d1meoa_	Alignment	not modelled	32.3	20	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
22	c2l3fA_	Alignment	not modelled	30.2	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a putative uracil dna glycosylase from2 methanosarcina acetivorans, northeast structural genomics consortium3 target mvr76
23	c2ywrA_	Alignment	not modelled	30.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of gar transformylase from aquifex2 aeolicus
24	c3tqrA_	Alignment	not modelled	25.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
25	d1jkxa_	Alignment	not modelled	22.1	25	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
26	c3dcjA_	Alignment	not modelled	19.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable 5'-phosphoribosylglycinamide **PDBTitle:** crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
27	c3t7hB_	Alignment	not modelled	15.6	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** atg8 transfer from atg7 to atg3: a distinctive e1-e2

						architecture and2 mechanism in the autophagy pathway
28	c1fmtA_	Alignment	not modelled	15.1	21	**PDB header:**formyltransferase **Chain:** A: **PDB Molecule:**methionyl-trna fmet formyltransferase; **PDBTitle:** methionyl-trnafmet formyltransferase from escherichia coli
29	d2ghra1	Alignment	not modelled	14.4	11	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**HTS-like
30	c3nrbD_	Alignment	not modelled	13.4	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
31	d2blna2	Alignment	not modelled	12.8	21	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
32	d1fmta2	Alignment	not modelled	12.3	18	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
33	c2yqsA_	Alignment	not modelled	12.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
34	c3o1lB_	Alignment	not modelled	11.8	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
35	d1maba2	Alignment	not modelled	11.7	29	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
36	d2bw0a2	Alignment	not modelled	10.7	27	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
37	c3n0vD_	Alignment	not modelled	10.5	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
38	c3oc9A_	Alignment	not modelled	10.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine pyrophosphorylase; **PDBTitle:** crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
39	c2p2gD_	Alignment	not modelled	10.4	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
40	d1skyb2	Alignment	not modelled	9.8	33	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
41	c3ogzA_	Alignment	not modelled	9.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-sugar pyrophosphorylase; **PDBTitle:** protein structure of usp from l. major in apo-form
42	c3obiC_	Alignment	not modelled	9.4	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
43	d1fx0a2	Alignment	not modelled	9.4	29	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
44	c1yrwA_	Alignment	not modelled	9.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of e.coli arna transformylase domain
45	c2xrfA_	Alignment	not modelled	8.9	54	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridine phosphorylase 2; **PDBTitle:** crystal structure of human uridine phosphorylase 2
46	c3e35A_	Alignment	not modelled	8.5	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sco1997; **PDBTitle:** actinobacteria-specific protein of unknown function, sco1997
47	d1pj3a1	Alignment	not modelled	8.5	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
48	d2jdia2	Alignment	not modelled	8.3	29	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
49	d1q3qa2	Alignment	not modelled	8.1	26	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
50	c3kcqA_	Alignment	not modelled	8.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase; **PDBTitle:** crystal structure of phosphoribosylglycinamide formyltransferase from2 anaplasma phagocytophilum
						Fold:ATC-like

51	d1ekxa2	Alignment	not modelled	7.9	26	**Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
52	d2j13a1	Alignment	not modelled	7.8	9	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
53	c1z7eC_	Alignment	not modelled	7.6	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of full length arna
54	c2k3mA_	Alignment	not modelled	7.2	70	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**rv1761c; **PDBTitle:** rv1761c
55	c2iw0A_	Alignment	not modelled	7.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitin deacetylase; **PDBTitle:** structure of the chitin deacetylase from the fungal2 pathogen colletotrichum lindemuthianum
56	d1r2aa_	Alignment	not modelled	7.0	25	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
57	c3eufC_	Alignment	not modelled	6.7	54	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridine phosphorylase 1; **PDBTitle:** crystal structure of bau-bound human uridine phosphorylase 1
58	d1jv1a_	Alignment	not modelled	6.6	14	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
59	d1s3ia2	Alignment	not modelled	6.6	26	**Fold:**Formyltransferase **Superfamily:**Formyltransferase **Family:**Formyltransferase
60	c1w4xA_	Alignment	not modelled	6.4	27	**PDB header:**oxygenase **Chain:** A: **PDB Molecule:**phenylacetone monooxygenase; **PDBTitle:** phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
61	d2f4za1	Alignment	not modelled	6.4	31	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
62	d1vm8a_	Alignment	not modelled	6.3	17	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
63	c2i5kB_	Alignment	not modelled	6.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of ugp1p
64	d1w4xa1	Alignment	not modelled	6.3	29	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
65	c3q0iA_	Alignment	not modelled	6.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from vibrio cholerae
66	d2icya2	Alignment	not modelled	6.2	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**UDP-glucose pyrophosphorylase
67	d1vl6a1	Alignment	not modelled	6.0	42	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
68	c2yr6A_	Alignment	not modelled	6.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pro-enzyme of l-phenylalanine oxidase; **PDBTitle:** crystal structure of l-phenylalanine oxidase from psuedomonas sp.p501
69	d1o0sa1	Alignment	not modelled	5.9	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
70	c1zghA_	Alignment	not modelled	5.8	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** methionyl-trna formyltransferase from clostridium thermocellum
71	d2vgna2	Alignment	not modelled	5.7	29	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**ERF1/Dom34 middle domain-like
72	c3rf1B_	Alignment	not modelled	5.7	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**glycyl-trna synthetase alpha subunit; **PDBTitle:** the crystal structure of glycyl-trna synthetase subunit alpha from2 campylobacter jejuni subsp. jejuni nctc 11168
73	d1gq2a1	Alignment	not modelled	5.6	37	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
74	c3tqqA_	Alignment	not modelled	5.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionyl-trna formyltransferase; **PDBTitle:** structure of the methionyl-trna formyltransferase (fmt) from coxiella2 burnetii
75	c2vkzH_	Alignment	not modelled	5.6	13	**PDB header:**transferase **Chain:** H: **PDB Molecule:**fatty acid synthase subunit beta; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
76	d1w44a_	Alignment	not modelled	5.5	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
77	d2igsa1	Alignment	not modelled	5.5	41	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like

						Family:PA2222-like
78	c3louB_	Alignment	not modelled	5.1	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution