Phyre^2

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Description	P0A6D3
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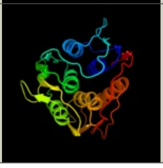
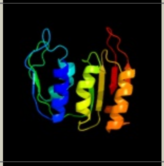
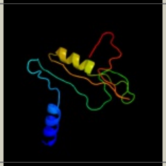
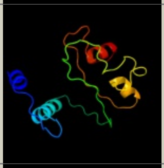
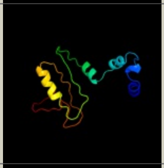
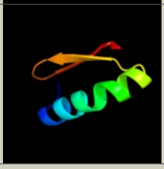
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1g6sa_	Alignment		100.0	100	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
2	c2o0zA_	Alignment		100.0	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase; **PDBTitle:** mycobacterium tuberculosis epsp synthase in complex with2 product (eps)
3	d1rf6a_	Alignment		100.0	26	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
4	c3r38A_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 1-carboxyvinyltransferase 1; **PDBTitle:** 2.23 angstrom resolution crystal structure of udp-n-acetylglucosamine2 1-carboxyvinyltransferase (mura) from listeria monocytogenes egd-e
5	c3roiA_	Alignment		100.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase; **PDBTitle:** 2.20 angstrom resolution structure of 3-phosphoshikimate 1-2 carboxyvinyltransferase (aroa) from coxiella burnetii
6	c2pqdA_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase; **PDBTitle:** a100g cp4 epsps liganded with (r)-difluoromethyl tetrahedral reaction2 intermediate analog
7	d1uaea_	Alignment		100.0	22	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
8	c3rmtB_	Alignment		100.0	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase 1; **PDBTitle:** crystal structure of putative 5-enolpyruvoylshikimate-3-phosphate2 synthase from bacillus halodurans c-125
9	d1ejda_	Alignment		100.0	22	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
10	c2yvwA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 1-carboxyvinyltransferase; **PDBTitle:** crystal structure of udp-n-acetylglucosamine 1-carboxyvinyltransferase2 from aquifex aeolicus vf5
11	d1p88a_	Alignment		100.0	100	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT

12	d1qmha2	Alignment		95.3	17	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**RNA 3'-terminal phosphate cyclase, RPTC
13	c1qmiC_	Alignment		95.3	21	**PDB header:**rna 3'-terminal phosphate cyclase **Chain:** C: **PDB Molecule:**rna 3'-terminal phosphate cyclase; **PDBTitle:** crystal structure of rna 3'-terminal phosphate cyclase, an2 ubiquitous enzyme with unusual topology
14	c3pqvD_	Alignment		84.0	16	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**rcl1 protein; **PDBTitle:** cyclase homolog
15	c2dsjA_	Alignment		60.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
16	c1v8gB_	Alignment		46.1	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
17	c3h5qA_	Alignment		46.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
18	c3g0tA_	Alignment		39.9	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative aminotransferase; **PDBTitle:** crystal structure of putative aspartate aminotransferase (np_905498.1)2 from porphyromonas gingivalis w83 at 1.75 a resolution
19	d1ni9a_	Alignment		38.6	20	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**GlpX-like bacterial fructose-1,6-bisphosphatase
20	d1x9za_	Alignment		30.3	14	**Fold:**DNA mismatch repair protein MutL **Superfamily:**DNA mismatch repair protein MutL **Family:**DNA mismatch repair protein MutL
21	c1khdD_	Alignment	not modelled	29.4	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure analysis of the anthranilate2 phosphoribosyltransferase from erwinia carotovora at 1.93 resolution (current name, pectobacterium carotovorum)
22	c1otpA_	Alignment	not modelled	28.0	19	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
23	d1a9xa1	Alignment	not modelled	27.2	5	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
24	c2ci6A_	Alignment	not modelled	26.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ng, ng-dimethylarginine dimethylaminohydrolase 1; **PDBTitle:** crystal structure of dimethylarginine2 dimethylaminohydrolase i bound with zinc low ph
25	d1p5ja_	Alignment	not modelled	23.9	24	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
26	c1p5jA_	Alignment	not modelled	23.9	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-serine dehydratase; **PDBTitle:** crystal structure analysis of human serine dehydratase
						Fold: Pentein, beta/alpha-propeller

27	d1h70a_	Alignment	not modelled	21.7	15	**Superfamily:**Pentein **Family:**Dimethylarginine dimethylaminohydrolase DDAH
28	c2hw4A_	Alignment	not modelled	18.3	14	**PDB header:**structural genomics, hydrolase **Chain:** A: **PDB Molecule:**14 kda phosphohistidine phosphatase; **PDBTitle:** crystal structure of human phosphohistidine phosphatase
29	c1brwB_	Alignment	not modelled	18.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
30	c2bpqB_	Alignment	not modelled	17.7	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
31	d2hw4a1	Alignment	not modelled	16.8	14	**Fold:**PHP14-like **Superfamily:**PHP14-like **Family:**Janus/Ocnus
32	c3i4aA_	Alignment	not modelled	14.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n(g),n(g)-dimethylarginine dimethylaminohydrolase **PDBTitle:** crystal structure of dimethylarginine2 dimethylaminohydrolase-1 (ddah-1) in complex with n5-(1-3 iminopropyl)-l-ornithine
33	c2j0fC_	Alignment	not modelled	13.5	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
34	c2jugB_	Alignment	not modelled	11.7	15	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**tubc protein; **PDBTitle:** multienzyme docking in hybrid megasynthetases
35	c3nfiB_	Alignment	not modelled	11.3	16	**PDB header:**dna binding protein, transcription **Chain:** B: **PDB Molecule:**dna-directed rna polymerase i subunit rpa49; **PDBTitle:** crystal structure of tandem winged helix domain of rna polymerase i2 subunit a49
36	c3czdA_	Alignment	not modelled	10.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaminase kidney isoform; **PDBTitle:** crystal structure of human glutaminase in complex with l-glutamate
37	c3uo9B_	Alignment	not modelled	10.8	26	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**glutaminase kidney isoform, mitochondrial; **PDBTitle:** crystal structure of human gac in complex with glutamate and bptes
38	d1d6za4	Alignment	not modelled	10.7	19	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Copper amine oxidase, domain N **Family:**Copper amine oxidase, domain N
39	c2ox1C_	Alignment	not modelled	10.6	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** archaeal dehydroquinase
40	c2hzfA_	Alignment	not modelled	10.1	16	**PDB header:**electron transport, oxidoreductase **Chain:** A: **PDB Molecule:**glutaredoxin-1; **PDBTitle:** crystal structures of a poxviral glutaredoxin in the oxidized and2 reduced states show redox-correlated structural changes
41	c3gkuB_	Alignment	not modelled	9.9	17	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**probable rna-binding protein; **PDBTitle:** crystal structure of a probable rna-binding protein from clostridium2 symbiosum atcc 14940
42	c3gabC_	Alignment	not modelled	9.8	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dna mismatch repair protein mutl; **PDBTitle:** c-terminal domain of bacillus subtilis mutl crystal form i
43	d2dy1a4	Alignment	not modelled	9.6	15	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
44	c3ss4C_	Alignment	not modelled	9.4	26	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glutaminase c; **PDBTitle:** crystal structure of mouse glutaminase c, phosphate-bound form
45	d1u60a_	Alignment	not modelled	9.4	15	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Glutaminase
46	d1jjcb2	Alignment	not modelled	9.3	30	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT
47	d1nh2a1	Alignment	not modelled	8.8	25	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
48	d1o17a2	Alignment	not modelled	8.4	33	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
49	c3ke2A_	Alignment	not modelled	8.2	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yp_928783.1; **PDBTitle:** crystal structure of a duf2131 family protein (sama_2911) from2 shewanella amazonensis sb2b at 2.50 a resolution
50	c2zxrA_	Alignment	not modelled	8.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**single-stranded dna specific exonuclease recj; **PDBTitle:** crystal structure of recj in complex with mg2+ from thermus2 thermophilus hb8
						Fold:ATC-like

51	d1ekxa2	Alignment	not modelled	7.6	17	**Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
52	c3nr6A_	Alignment	not modelled	7.3	17	**PDB header:**hydrolase/inhibitor **Chain: A: PDB Molecule:**protease p14; **PDBTitle:** crystal structure of xenotropic murine leukemia virus-related virus2 (xmrv) protease
53	c3gocB_	Alignment	not modelled	7.3	8	**PDB header:**hydrolase **Chain: B: PDB Molecule:**endonuclease v; **PDBTitle:** crystal structure of the endonuclease v (sav1684) from streptomyces2 avermitilis. northeast structural genomics consortium target svr196
54	c2pbyB_	Alignment	not modelled	7.2	15	**PDB header:**hydrolase **Chain: B: PDB Molecule:**glutaminase; **PDBTitle:** probable glutaminase from geobacillus kaustophilus hta426
55	c3kzpA_	Alignment	not modelled	7.2	17	**PDB header:**structural genomics, unknown function **Chain: A: PDB Molecule:**putative diguanylate cyclase/phosphodiesterase; **PDBTitle:** crystal structure of putative diguanylate cyclase/phosphodiesterase2 from listaria monocytigenes
56	d1mkia_	Alignment	not modelled	7.2	17	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Glutaminase
57	d1qnaa1	Alignment	not modelled	6.7	22	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
58	d2atca2	Alignment	not modelled	6.6	15	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
59	c3ih9A_	Alignment	not modelled	6.4	15	**PDB header:**hydrolase **Chain: A: PDB Molecule:**salt-tolerant glutaminase; **PDBTitle:** crystal structure analysis of mglu in its tris form
60	c2dfwA_	Alignment	not modelled	6.3	11	**PDB header:**hydrolase **Chain: A: PDB Molecule:**salt-tolerant glutaminase; **PDBTitle:** crystal structure of a major fragment of the salt-tolerant2 glutaminase from micrococcus luteus k-3
61	d1cdwa1	Alignment	not modelled	6.1	28	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
62	c3s8iA_	Alignment	not modelled	5.6	11	**PDB header:**hydrolase **Chain: A: PDB Molecule:**protein ddi1 homolog 1; **PDBTitle:** the retroviral-like protease (rvp) domain of human ddi1
63	c2fvgA_	Alignment	not modelled	5.5	4	**PDB header:**hydrolase **Chain: A: PDB Molecule:**endoglucanase; **PDBTitle:** crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution
64	d1ml4a2	Alignment	not modelled	5.5	10	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
65	d1nh8a2	Alignment	not modelled	5.4	18	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
66	d1vpka1	Alignment	not modelled	5.1	9	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase III, beta subunit