Phyre2

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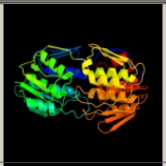
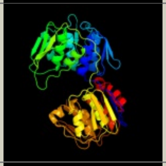
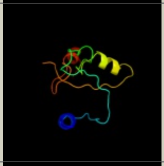
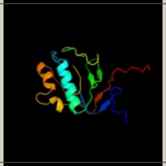
Description	P0A749
Date	Thu Jan 5 11:04:49 GMT 2012
Unique Job ID	fa0fa1805224f8bc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1uaea_	Alignment		100.0	100	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
2	d1ejda_	Alignment		100.0	93	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
3	c3r38A_	Alignment		100.0	50	**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
4	c2yvwA_	Alignment		100.0	44	**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
5	d1g6sa_	Alignment		100.0	22	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
6	c3rmtB_	Alignment		100.0	22	**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
7	c3roiA_	Alignment		100.0	23	**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
8	c2o0zA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase; **PDBTitle:** mycobacterium tuberculosis epsp synthase in complex with2 product (eps)
9	c2pqdA_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**3-phosphoshikimate 1-carboxyvinyltransferase; **PDBTitle:** a100g cp4 epsps liganded with (r)-difluoromethyl tetrahedral reaction2 intermediate analog
10	d1rf6a_	Alignment		100.0	24	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT
11	d1p88a_	Alignment		100.0	23	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**Enolpyruvate transferase, EPT

12	c1qmiC_	Alignment		95.9	14	**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
13	d1qmha2	Alignment		95.9	12	**Fold:**IF3-like **Superfamily:**EPT/RTPC-like **Family:**RNA 3'-terminal phosphate cyclase, RPTC
14	c3pqvD_	Alignment		95.3	15	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**rcl1 protein; **PDBTitle:** cyclase homolog
15	c1v8gB_	Alignment		50.8	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** crystal structure of anthranilate phosphoribosyltransferase2 (trpd) from thermus thermophilus hb8
16	c2bpqB_	Alignment		30.5	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyltransferase (trpd) from2 mycobacterium tuberculosis (apo structure)
17	c1khdD_	Alignment		28.9	14	**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)
18	c3gmgB_	Alignment		28.3	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rv1825/mt1873; **PDBTitle:** crystal structure of an uncharacterized conserved protein2 from mycobacterium tuberculosis
19	c3ke2A_	Alignment		25.5	16	**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
20	c3pc3A_	Alignment		24.4	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cg1753, isoform a; **PDBTitle:** full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
21	d1v8za1	Alignment	not modelled	19.7	15	**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
22	d2bhsa1	Alignment	not modelled	18.9	12	**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
23	c3h5qA_	Alignment	not modelled	18.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
24	c2dsjA_	Alignment	not modelled	17.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
25	d2ex2a1	Alignment	not modelled	17.3	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
26	c1otpA_	Alignment	not modelled	16.2	20	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
27	d1x9za_	Alignment	not modelled	13.7	11	**Fold:**DNA mismatch repair protein MutL **Superfamily:**DNA mismatch repair protein MutL

						Family:DNA mismatch repair protein MutL
28	d1jjcb2	Alignment	not modelled	13.7	16	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT
29	d1ml4a2	Alignment	not modelled	13.5	17	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
30	c2pqmA_	Alignment	not modelled	13.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cysteine synthase; **PDBTitle:** crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
31	c1o17A_	Alignment	not modelled	12.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyl-transferase (trpd)
32	d1w5da1	Alignment	not modelled	12.5	22	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
33	d1in0a2	Alignment	not modelled	12.0	19	**Fold:**Ferredoxin-like **Superfamily:**YajQ-like **Family:**YajQ-like
34	c2eguA_	Alignment	not modelled	11.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase; **PDBTitle:** crystal structure of o-acetylserine sulfhydrase from geobacillus2 kaustophilus hta426
35	c3nr6A_	Alignment	not modelled	11.4	17	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**protease p14; **PDBTitle:** crystal structure of xenotropic murine leukemia virus-related virus2 (xmrv) protease
36	c2j0fC_	Alignment	not modelled	11.2	20	**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
37	d1wkva1	Alignment	not modelled	10.7	22	**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
38	d2dy1a4	Alignment	not modelled	10.7	18	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
39	c3dwgA_	Alignment	not modelled	10.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase b; **PDBTitle:** crystal structure of a sulfur carrier protein complex found in the2 cysteine biosynthetic pathway of mycobacterium tuberculosis
40	c2cxiA_	Alignment	not modelled	10.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phenylalanyl-trna synthetase beta chain; **PDBTitle:** crystal structure of an n-terminal fragment of the phenylalanyl-trna2 synthetase beta-subunit from pyrococcus horikoshii
41	c1brwB_	Alignment	not modelled	9.9	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
42	c3dinB_	Alignment	not modelled	9.3	14	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
43	c3mjsA_	Alignment	not modelled	8.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**amphb; **PDBTitle:** structure of a-type ketoreductases from modular polyketide synthase
44	d1ekxa2	Alignment	not modelled	8.1	19	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
45	d1z7me1	Alignment	not modelled	8.1	32	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
46	d1o17a2	Alignment	not modelled	7.8	12	**Fold:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
47	d1w79a1	Alignment	not modelled	7.8	19	**Fold:**beta-lactamase/transpeptidase-like **Superfamily:**beta-lactamase/transpeptidase-like **Family:**Dac-like
48	c2vdaA_	Alignment	not modelled	7.7	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**translocase subunit seca; **PDBTitle:** solution structure of the seca-signal peptide complex
49	c2jwlB_	Alignment	not modelled	7.7	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**protein tolr; **PDBTitle:** solution structure of periplasmic domain of tolr from h.2 influenzae with saxs data
50	d2atca2	Alignment	not modelled	6.9	23	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
51	c1in0B_	Alignment	not modelled	6.8	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yajq protein; **PDBTitle:** yajq protein (hi1034)
52	c1f7uA_	Alignment	not modelled	6.5	17	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**arginyl-trna synthetase;

52	c1f7uA_	Alignment	not modelled	6.5	17	**PDBTitle:** crystal structure of the arginyl-trna synthetase complexed with the2 trna(arg) and l-arg
53	c3g0tA_	Alignment	not modelled	6.3	15	**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
54	c3juxA_	Alignment	not modelled	6.1	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** structure of the translocation atpase seca from thermotoga2 maritima
55	d1nh2a1	Alignment	not modelled	6.1	13	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
56	c2hzfA_	Alignment	not modelled	6.1	13	**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
57	d1z7wa1	Alignment	not modelled	6.0	17	**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
58	c3ihjA_	Alignment	not modelled	6.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine aminotransferase 2; **PDBTitle:** human alanine aminotransferase 2 in complex with plp
59	d2ftxb1	Alignment	not modelled	6.0	8	**Fold:**Kinetochore globular domain-like **Superfamily:**Kinetochore globular domain **Family:**Spc24-like
60	d1uc8a1	Alignment	not modelled	6.0	13	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Lysine biosynthesis enzyme LysX, N-terminal domain
61	c2ipcB_	Alignment	not modelled	5.9	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of the translocation atpase seca from thermus2 thermophilus reveals a parallel, head-to-head dimer
62	d1y7la1	Alignment	not modelled	5.8	14	**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
63	c2fv4B_	Alignment	not modelled	5.6	8	**PDB header:**structural protein, protein binding **Chain:** B: **PDB Molecule:**hypothetical 24.6 kda protein in ilv2-ade17 **PDBTitle:** nmr solution structure of the yeast kinetochore spc24/spc252 globular domain
64	d1p5ja_	Alignment	not modelled	5.4	17	**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
65	c1p5jA_	Alignment	not modelled	5.4	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-serine dehydratase; **PDBTitle:** crystal structure analysis of human serine dehydratase
66	c2o2jA_	Alignment	not modelled	5.3	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** mycobacterium tuberculosis tryptophan synthase beta chain2 dimer (apoform)
67	c3r0zA_	Alignment	not modelled	5.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**d-serine dehydratase; **PDBTitle:** crystal structure of apo d-serine deaminase from salmonella2 typhimurium
68	d1qnaa1	Alignment	not modelled	5.2	24	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain