Phyre^2

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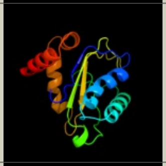
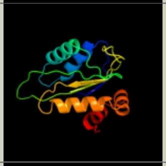
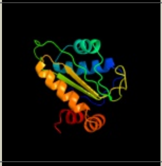
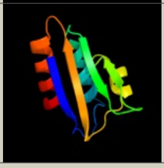
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1a3aa_	Alignment		100.0	47	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
2	c3bjvA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpa; **PDBTitle:** the crystal structure of a putative pts iia(ptxa) from streptococcus2 mutans
3	c2oqtD_	Alignment		100.0	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein spy0176; **PDBTitle:** structural genomics, the crystal structure of a putative2 pts iia domain from streptococcus pyogenes m1 gas
4	c3oxpB_	Alignment		100.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase enzyme ii, a component; **PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
5	c3oxpA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphotransferase enzyme ii, a component; **PDBTitle:** structure of phosphotransferase enzyme ii, a component from yersinia2 pestis co92 at 1.2 a resolution
6	c2oq3A_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific cryptic phosphotransferase **PDBTitle:** solution structure of the mannitol- specific cryptic2 phosphotransferase enzyme iia cmtb from escherichia coli
7	c3urrB_	Alignment		100.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts iia-like nitrogen-regulatory protein ptsn; **PDBTitle:** structure of pts iia-like nitrogen-regulatory protein ptsn (bth_i0484)2 (ptsn)
8	c2a0jA_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, nitrogen regulatory iia protein; **PDBTitle:** crystal structure of nitrogen regulatory protein iia-ntr from2 neisseria meningitidis
9	d1a6ja_	Alignment		100.0	23	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
10	d2hpra_	Alignment		99.9	40	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
11	d1pcha_	Alignment		99.9	35	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like

12	d1ka5a_	Alignment		99.9	41	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
13	d1qr5a_	Alignment		99.9	41	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
14	d1xiza_	Alignment		99.9	23	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**IIA domain of mannitol-specific and ntr phosphotransferase EII
15	c3ihsB_	Alignment		99.9	29	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**phosphocarrier protein hpr; **PDBTitle:** crystal structure of a phosphocarrier protein hpr from2 bacillus anthracis str. ames
16	d1mo1a_	Alignment		99.9	28	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
17	c3le1B_	Alignment		99.9	36	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase system, hpr-related proteins; **PDBTitle:** crystal structure of apohpr monomer from thermoanaerobacter2 tengcongensis
18	d2nzul1	Alignment		99.9	40	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
19	d1cm3a_	Alignment		99.9	33	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
20	d1ptfa_	Alignment		99.9	40	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
21	d1zvvj1	Alignment	not modelled	99.9	30	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
22	c1hynQ_	Alignment	not modelled	95.5	13	**PDB header:**membrane protein **Chain:** Q: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** crystal structure of the cytoplasmic domain of human2 erythrocyte band-3 protein
23	d1hynp_	Alignment	not modelled	95.5	14	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**Anion transport protein, cytoplasmic domain
24	c2jpiA_	Alignment	not modelled	43.7	14	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
25	c2dgbA_	Alignment	not modelled	29.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein purs; **PDBTitle:** structure of thermus thermophilus purs in the p21 form
26	d2vo1a1	Alignment	not modelled	28.9	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
27	c3bmbB_	Alignment	not modelled	26.9	21	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase; **PDBTitle:** crystal structure of a new rna polymerase interacting2 protein
28	d1gtda_	Alignment	not modelled	24.9	16	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase

29	d2ihta1	Alignment	not modelled	24.2	31	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
30	c2p73A_	Alignment	not modelled	20.8	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative glycosyltransferase (mannosyltransferase) involved **PDBTitle:** crystal structure of a glycosyltransferase involved in the2 glycosylation of the major capsid of pbcv-1
31	d5csma_	Alignment	not modelled	19.7	16	**Fold:**Chorismate mutase II **Superfamily:**Chorismate mutase II **Family:**Allosteric chorismate mutase
32	d2mhra_	Alignment	not modelled	18.3	24	**Fold:**Four-helical up-and-down bundle **Superfamily:**Hemerythrin-like **Family:**Hemerythrin-like
33	c3citB_	Alignment	not modelled	17.6	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of the gaf domain of a putative sensor histidine2 kinase from pseudomonas syringae pv. tomato
34	d1vq3a_	Alignment	not modelled	15.4	16	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
35	d1zpda1	Alignment	not modelled	13.5	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
36	d1r11a3	Alignment	not modelled	13.1	18	**Fold:**MutS N-terminal domain-like **Superfamily:**tRNA-intron endonuclease N-terminal domain-like **Family:**tRNA-intron endonuclease N-terminal domain-like
37	d1xi3a_	Alignment	not modelled	12.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
38	d1umdb2	Alignment	not modelled	11.8	22	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
39	c2zw2B_	Alignment	not modelled	11.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
40	c2d5wA_	Alignment	not modelled	10.6	17	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**peptide abc transporter, peptide-binding protein; **PDBTitle:** the crystal structure of oligopeptide binding protein from thermus2 thermophilus hb8 complexed with pentapeptide
41	d2ifea_	Alignment	not modelled	10.1	18	**Fold:**IF3-like **Superfamily:**Translation initiation factor IF3, C-terminal domain **Family:**Translation initiation factor IF3, C-terminal domain
42	d1pvda1	Alignment	not modelled	8.6	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
43	c3m8uA_	Alignment	not modelled	8.4	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**heme-binding protein a; **PDBTitle:** crystal structure of glutathione-binding protein a (gbpa) from2 haemophilus parasuis sh0165 in complex with glutathione disulfide3 (gssg)
44	d1hrba_	Alignment	not modelled	8.4	20	**Fold:**Four-helical up-and-down bundle **Superfamily:**Hemerythrin-like **Family:**Hemerythrin-like
45	d1aopa2	Alignment	not modelled	7.7	29	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
46	d1a04a2	Alignment	not modelled	7.4	18	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
47	c3kt9A_	Alignment	not modelled	7.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aprataxin; **PDBTitle:** aprataxin fha domain
48	d1i4ya_	Alignment	not modelled	7.2	20	**Fold:**Four-helical up-and-down bundle **Superfamily:**Hemerythrin-like **Family:**Hemerythrin-like
49	c1yj5C_	Alignment	not modelled	7.1	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase fha domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
50	d1dpea_	Alignment	not modelled	7.0	23	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
51	c3hzhA_	Alignment	not modelled	7.0	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**chemotaxis response regulator (chey-3); **PDBTitle:** crystal structure of the chex-chey-bef3-mg+2 complex from2 borrelia burgdorferi
52	d1zlqa1	Alignment	not modelled	6.9	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
53	d1yjma1	Alignment	not modelled	6.8	14	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
54	c1ibaA_	Alignment	not modelled	6.8	14	**PDB header:**phoshphotransferase **Chain:** A: **PDB Molecule:**glucose permease; **PDBTitle:** glucose permease (domain iib), nmr, 11 structures

55	d1us7b_	Alignment	not modelled	6.5	38	**Fold:**Hsp90 co-chaperone CDC37 **Superfamily:**Hsp90 co-chaperone CDC37 **Family:**Hsp90 co-chaperone CDC37
56	c1us7B_	Alignment	not modelled	6.5	38	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**hsp90 co-chaperone cdc37; **PDBTitle:** complex of hsp90 and p50
57	d1fmfa_	Alignment	not modelled	6.3	14	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
58	d1mzha_	Alignment	not modelled	6.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
59	d1ccwa_	Alignment	not modelled	6.2	14	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
60	d1grja2	Alignment	not modelled	6.1	23	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
61	c3nvaB_	Alignment	not modelled	6.1	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
62	d1m2ka_	Alignment	not modelled	5.8	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
63	d2hmza_	Alignment	not modelled	5.8	18	**Fold:**Four-helical up-and-down bundle **Superfamily:**Hemerythrin-like **Family:**Hemerythrin-like
64	d1tiga_	Alignment	not modelled	5.7	18	**Fold:**IF3-like **Superfamily:**Translation initiation factor IF3, C-terminal domain **Family:**Translation initiation factor IF3, C-terminal domain