















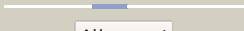


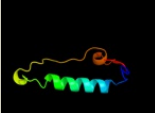






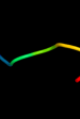






Phyre2

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Description	P30744
Date	Thu Jan 5 11:46:19 GMT 2012
Unique Job ID	2a2a5520d19e26d9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2iafa1	 Alignment		100.0	42	Fold: FwdE/GAPDH domain-like Superfamily: Serine metabolism enzymes domain Family: Serine dehydratase beta chain-like
2	c1ygyA_	 Alignment		99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
3	d1ygya4	 Alignment		99.3	19	Fold: FwdE/GAPDH domain-like Superfamily: Serine metabolism enzymes domain Family: SerA intervening domain-like
4	c2hp0A_	 Alignment		98.0	14	PDB header: isomerase Chain: A: PDB Molecule: ids-epimerase; PDBTitle: crystal structure of iminodisuccinate epimerase
5	d1szqa_	 Alignment		97.8	17	Fold: 2-methylcitrate dehydratase PrpD Superfamily: 2-methylcitrate dehydratase PrpD Family: 2-methylcitrate dehydratase PrpD
6	c3u4gA_	 Alignment		60.3	34	PDB header: transferase Chain: A: PDB Molecule: namn:dmb phosphoribosyltransferase; PDBTitle: the structure of cobt from pyrococcus horikoshii
7	c3s1sA_	 Alignment		44.0	31	PDB header: hydrolase, transferase Chain: A: PDB Molecule: restriction endonuclease bpusi; PDBTitle: characterization and crystal structure of the type iig restriction2 endonuclease bpusi
8	c2kelB_	 Alignment		27.4	21	PDB header: transcription repressor Chain: B: PDB Molecule: uncharacterized protein 56b; PDBTitle: structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
9	d1ug2a_	 Alignment		26.3	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
10	c1knyA_	 Alignment		26.2	22	PDB header: transferase Chain: A: PDB Molecule: kanamycin nucleotidyltransferase; PDBTitle: kanamycin nucleotidyltransferase
11	d1g64b_	 Alignment		23.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)

12	d1no5a_	Alignment		22.4	22	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Catalytic subunit of bi-partite nucleotidyltransferase
13	d1g5ta_	Alignment		19.1	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
14	c2rkbE_	Alignment		18.0	20	PDB header: lyase Chain: E: PDB Molecule: serine dehydratase-like; PDBTitle: serine dehydratase like-1 from human cancer cells
15	d1pwha_	Alignment		18.0	21	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
16	c1yy3A_	Alignment		14.5	57	PDB header: isomerase Chain: A: PDB Molecule: s-adenosylmethionine:trna ribosyltransferase- PDBTitle: structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
17	d2gkea2	Alignment		13.8	32	Fold: Diaminopimelate epimerase-like Superfamily: Diaminopimelate epimerase-like Family: Diaminopimelate epimerase
18	c2iifA_	Alignment		13.7	21	PDB header: recombination/dna Chain: A: PDB Molecule: integration host factor; PDBTitle: single chain integration host factor mutant protein (scihf2-2 k45ae) in complex with dna
19	d1knya2	Alignment		13.2	22	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
20	d1rypa_	Alignment		13.1	13	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
21	d1ee8a1	Alignment	not modelled	12.3	23	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
22	d1p5dx3	Alignment	not modelled	12.0	23	Fold: Phosphoglucomutase, first 3 domains Superfamily: Phosphoglucomutase, first 3 domains Family: Phosphoglucomutase, first 3 domains
23	c1u9pA_	Alignment	not modelled	11.8	17	PDB header: unknown function Chain: A: PDB Molecule: parc; PDBTitle: permuted single-chain arc
24	d2i7na2	Alignment	not modelled	10.7	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
25	d1h72c1	Alignment	not modelled	10.3	27	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
26	c2k9iB_	Alignment	not modelled	10.0	25	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid prn1, complete sequence; PDBTitle: nmr structure of plasmid copy control protein orf56 from2 sulfolobus islandicus
27	c3lr6A_	Alignment	not modelled	9.7	30	PDB header: structural protein Chain: A: PDB Molecule: major ampullate spidroin 1; PDBTitle: self-assembly of spider silk proteins is controlled by a ph-sensitive2 relay
28	d1jb0I_	Alignment	not modelled	9.6	26	Fold: Photosystem I reaction center subunit XI, PsaL Superfamily: Photosystem I reaction center subunit XI, PsaL Family: Photosystem I reaction center subunit XI, PsaL
29	d1ncfb3	Alignment	not modelled	9.6	40	Fold: TNF receptor-like Superfamily: TNF receptor-like

						Family: TNF receptor-like
30	c2ddhA	Alignment	not modelled	9.4	38	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa oxidase; PDBTitle: crystal structure of acyl-coa oxidase complexed with 3-oh-dodecanoate
31	c3ibqA	Alignment	not modelled	9.2	26	PDB header: transferase Chain: A: PDB Molecule: pyridoxal kinase; PDBTitle: crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp
32	c2k3qA	Alignment	not modelled	9.0	22	PDB header: structural protein Chain: A: PDB Molecule: tusp1; PDBTitle: solution structure of the n-terminal domain (tusp1-n) of the2 egg case silk from nephila antipodiana
33	d1j6ua3	Alignment	not modelled	9.0	33	Fold: Ribokinese-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
34	d2nrha1	Alignment	not modelled	8.8	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like
35	c3sz8D	Alignment	not modelled	8.6	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
36	d1b65a	Alignment	not modelled	8.5	20	Fold: DmpA/Argj-like Superfamily: DmpA/Argj-like Family: DmpA-like
37	d1fi6a	Alignment	not modelled	8.4	20	Fold: EF Hand-like Superfamily: EF-hand Family: Eps15 homology domain (EH domain)
38	d2i7pa1	Alignment	not modelled	8.4	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
39	c2fonA	Alignment	not modelled	8.4	25	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxisomal acyl-coa oxidase 1a; PDBTitle: x-ray crystal structure of leacx1, an acyl-coa oxidase from2 lycopersicon esculentum (tomato)
40	d1jswa	Alignment	not modelled	7.9	26	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
41	c1p5jA	Alignment	not modelled	7.8	16	PDB header: lyase Chain: A: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure analysis of human serine dehydratase
42	d1p5ja	Alignment	not modelled	7.8	16	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
43	c2fkka	Alignment	not modelled	7.8	42	PDB header: viral protein Chain: A: PDB Molecule: baseplate structural protein gp10; PDBTitle: crystal structure of the c-terminal domain of the bacteriophage t42 gene product 10
44	d1h0ha2	Alignment	not modelled	7.7	23	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
45	c2revA	Alignment	not modelled	7.6	12	PDB header: hydrolase Chain: A: PDB Molecule: type ii restriction enzyme sau3ai; PDBTitle: crystal structure of the c-terminal of sau3ai fragment
46	d1gg2g	Alignment	not modelled	7.5	42	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Transducin (heterotrimeric G protein), gamma chain Family: Transducin (heterotrimeric G protein), gamma chain
47	d2raqa1	Alignment	not modelled	7.5	11	Fold: Ferredoxin-like Superfamily: MTH889-like Family: MTH889-like
48	c2x3dC	Alignment	not modelled	7.4	16	PDB header: unknown function Chain: C: PDB Molecule: sso6206; PDBTitle: crystal structure of sso6206 from sulfolobus solfataricus p2
49	c3l0zC	Alignment	not modelled	7.3	13	PDB header: transferase Chain: C: PDB Molecule: putative nicotinate-nucleotide-dimethylbenzimidazole PDBTitle: crystal structure of a putative nicotinate-nucleotide-2 dimethylbenzimidazole phosphoribosyltransferase from3 methanocaldococcus jannaschii dsm 2661
50	d1omwg	Alignment	not modelled	7.1	42	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Transducin (heterotrimeric G protein), gamma chain Family: Transducin (heterotrimeric G protein), gamma chain
51	c2zfdB	Alignment	not modelled	7.1	23	PDB header: signaling protein/transferase Chain: B: PDB Molecule: putative uncharacterized protein t2015_90; PDBTitle: the crystal structure of plant specific calcium binding protein atcb122 in complex with the regulatory domain of atcpk14
52	c2fgyA	Alignment	not modelled	7.0	14	PDB header: lyase Chain: A: PDB Molecule: carboxysome shell polypeptide; PDBTitle: beta carbonic anhydrase from the carboxysomal shell of2 halothiobacillus neapolitanus (csosca)
53	c2iirJ	Alignment	not modelled	7.0	15	PDB header: transferase Chain: J: PDB Molecule: acetate kinase; PDBTitle: acetate kinase from a hypothermophile thermotoga maritima
54	c2i7pa	Alignment	not modelled	6.9	19	PDB header: transferase Chain: A: PDB Molecule: pantothenate kinase 3; PDBTitle: crystal structure of human pank3 in complex with accoa

55	d1ylqa1	Alignment	not modelled	6.8	16	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Catalytic subunit of bi-partite nucleotidyltransferase
56	d1k47a1	Alignment	not modelled	6.8	24	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
57	d1exta3	Alignment	not modelled	6.8	40	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
58	d1p3da3	Alignment	not modelled	6.8	22	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
59	d1wota_	Alignment	not modelled	6.6	29	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Catalytic subunit of bi-partite nucleotidyltransferase
60	c2rffA_	Alignment	not modelled	6.6	16	PDB header: transferase Chain: A: PDB Molecule: putative nucleotidyltransferase; PDBTitle: crystal structure of a putative nucleotidyltransferase2 (np_343093.1) from <i>Sulfolobus solfataricus</i> at 1.40 Å resolution
61	d3clsc1	Alignment	not modelled	6.2	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
62	d1gg4a4	Alignment	not modelled	6.1	26	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
63	c3eagA_	Alignment	not modelled	6.1	22	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- PDBTitle: the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from <i>Neisseria meningitidis</i>
64	d1k61a_	Alignment	not modelled	6.1	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
65	d1xhmb1	Alignment	not modelled	6.1	45	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Transducin (heterotrimeric G protein), gamma chain Family: Transducin (heterotrimeric G protein), gamma chain
66	c1xhmB_	Alignment	not modelled	6.0	45	PDB header: signaling protein Chain: B: PDB Molecule: guanine nucleotide-binding protein g(i)/g(s) PDBTitle: the crystal structure of a biologically active peptide2 (sigk) bound to a g protein beta:gamma heterodimer
67	c1w07A_	Alignment	not modelled	6.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa oxidase; PDBTitle: arabidopsis thaliana acyl-coa oxidase 1
68	d3bpda1	Alignment	not modelled	5.9	5	Fold: Ferredoxin-like Superfamily: MTH889-like Family: MTH889-like
69	d2o16a3	Alignment	not modelled	5.9	12	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
70	d1gotg_	Alignment	not modelled	5.9	8	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Transducin (heterotrimeric G protein), gamma chain Family: Transducin (heterotrimeric G protein), gamma chain
71	d1n93x_	Alignment	not modelled	5.9	30	Fold: P40 nucleoprotein Superfamily: P40 nucleoprotein Family: P40 nucleoprotein
72	c1n93X_	Alignment	not modelled	5.9	30	PDB header: viral protein Chain: X: PDB Molecule: p40 nucleoprotein; PDBTitle: crystal structure of the borna disease virus nucleoprotein
73	d1whqa_	Alignment	not modelled	5.7	25	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
74	c2fl8N_	Alignment	not modelled	5.7	56	PDB header: virus/viral protein Chain: N: PDB Molecule: baseplate structural protein gp10; PDBTitle: fitting of the gp10 trimer structure into the cryoem map of the2 bacteriophage t4 baseplate in the hexagonal conformation.
75	c2cosA_	Alignment	not modelled	5.7	17	PDB header: transferase Chain: A: PDB Molecule: serine/threonine protein kinase lats2; PDBTitle: solution structure of rsg1 ruh-038, a uba domain from mouse2 lats2 (large tumor suppressor homolog 2)
76	d1huua_	Alignment	not modelled	5.7	16	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
77	d2ar0a1	Alignment	not modelled	5.6	19	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: N-6 DNA Methylase-like
78	c3g2bA_	Alignment	not modelled	5.6	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: coenzyme pqq synthesis protein d; PDBTitle: crystal structure of pqqd from <i>Xanthomonas campestris</i>
79	d1k82a1	Alignment	not modelled	5.6	29	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
80	d1tbge_	Alignment	not modelled	5.6	8	Fold: Non-globular all-alpha subunits of globular proteins Superfamily: Transducin (heterotrimeric G protein), gamma chain Family: Transducin (heterotrimeric G protein), gamma chain
						PDB header: transferase

81	c2vg2C_	Alignment	not modelled	5.5	21	Chain: C: PDB Molecule: undecaprenyl pyrophosphate synthetase; PDBTitle: rv2361 with ipp
82	d1gkma_	Alignment	not modelled	5.5	16	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: HAL/PAL-like
83	d2jfga3	Alignment	not modelled	5.5	29	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
84	d1d5ra2	Alignment	not modelled	5.4	18	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
85	c3no9C_	Alignment	not modelled	5.4	20	PDB header: lyase Chain: C: PDB Molecule: fumarate hydratase class ii; PDBTitle: crystal structure of apo fumarate hydratase from mycobacterium2 tuberculosis
86	c2xa0A_	Alignment	not modelled	5.3	26	PDB header: apoptosis Chain: A: PDB Molecule: apoptosis regulator bcl-2; PDBTitle: crystal structure of bcl-2 in complex with a bax bh32 peptide
87	d1j09a1	Alignment	not modelled	5.3	19	Fold: An anticodon-binding domain of class I aminoacyl-tRNA synthetases Superfamily: An anticodon-binding domain of class I aminoacyl-tRNA synthetases Family: C-terminal domain of glutamyl-tRNA synthetase (GluRS)
88	d2cxaa1	Alignment	not modelled	5.3	11	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: LFTR-like
89	c2cxaA_	Alignment	not modelled	5.3	11	PDB header: transferase Chain: A: PDB Molecule: leucyl/phenylalanyl-trna-protein transferase; PDBTitle: crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
90	c3ugsB_	Alignment	not modelled	5.2	18	PDB header: transferase Chain: B: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
91	c3a24A_	Alignment	not modelled	5.2	7	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of bt1871 retaining glycosidase
92	c3dwgA_	Alignment	not modelled	5.2	17	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
93	d2r5yb1	Alignment	not modelled	5.1	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
94	d1x2na1	Alignment	not modelled	5.1	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
95	c2gefA_	Alignment	not modelled	5.1	50	PDB header: hydrolase Chain: A: PDB Molecule: protease vp4; PDBTitle: crystal structure of a novel viral protease with a2 serine/lysine catalytic dyad mechanism
96	c1qoyA_	Alignment	not modelled	5.0	12	PDB header: toxin Chain: A: PDB Molecule: hemolysin e; PDBTitle: e.coli hemolysin e (hlye, clya, shea)
97	d2sici_	Alignment	not modelled	5.0	63	Fold: Subtilisin inhibitor Superfamily: Subtilisin inhibitor Family: Subtilisin inhibitor
98	c3a05A_	Alignment	not modelled	5.0	19	PDB header: ligase Chain: A: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: crystal structure of tryptophanyl-trna synthetase from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan