Phyre2

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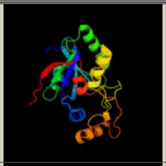
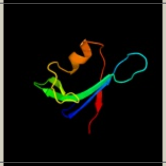
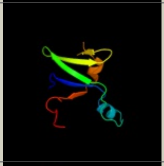
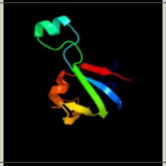
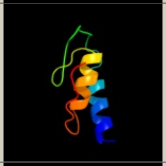
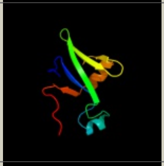
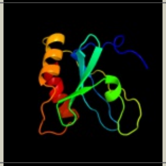
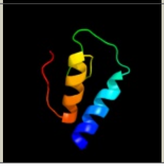
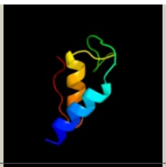
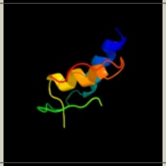
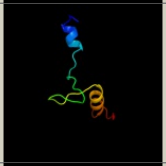
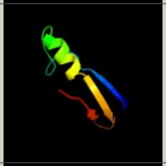
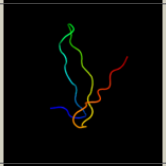
Description	P32167
Date	Thu Jan 5 11:49:44 GMT 2012
Unique Job ID	682bfd7af705ce4e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2if6a1	Alignment		100.0	98	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**YiiX-like
2	c3kw0D_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cysteine peptidase; **PDBTitle:** crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
3	c2p1gA_	Alignment		98.1	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative xylanase; **PDBTitle:** crystal structure of a putative xylanase from bacteroides fragilis
4	c2k1gA_	Alignment		97.8	15	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**lipoprotein spr; **PDBTitle:** solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162
5	c3npfB_	Alignment		97.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative dipeptidyl-peptidase vi; **PDBTitle:** crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
6	c2fg0B_	Alignment		97.6	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cog0791: cell wall-associated hydrolases (invasion- **PDBTitle:** crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
7	c3gt2A_	Alignment		97.5	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
8	c3h41A_	Alignment		97.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nlp/p60 family protein; **PDBTitle:** crystal structure of a nlpc/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
9	d2evra2	Alignment		97.5	20	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
10	c2kytA_	Alignment		97.5	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**group xvi phospholipase a2; **PDBTitle:** solution struture of the h-rev107 n-terminal domain
11	c2xivA_	Alignment		97.2	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis

12	c3pbiA_	Alignment		97.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invasion protein; **PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
13	c3i86A_	Alignment		97.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204
14	d2im9a1	Alignment		97.1	20	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Lpg0564-like
15	c2im9A_	Alignment		97.1	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein lpg0564 from legionella pneumophila str.2 philadelphia 1, pfam duf1460
16	c3m1uB_	Alignment		94.3	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative gamma-d-glutamyl-l-diamino acid endopeptidase; **PDBTitle:** crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dvu_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution
17	d2io8a2	Alignment		92.8	16	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**CHAP domain
18	c2ioaA_	Alignment		80.2	17	**PDB header:**ligase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional glutathionylspermidine **PDBTitle:** e. coli bifunctional glutathionylspermidine2 synthetase/amidase incomplex with mg2+ and adp and3 phosphinate inhibitor
19	c2k3aA_	Alignment		77.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chap domain protein; **PDBTitle:** nmr solution structure of staphylococcus saprophyticus chap2 (cysteine, histidine-dependent amidohydrolases/peptidases)3 domain protein. northeast structural genomics consortium4 target syr11
20	c2vpmB_	Alignment		77.2	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**trypanothione synthetase; **PDBTitle:** trypanothione synthetase
21	d1u5tb1	Alignment	not modelled	33.0	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
22	d1wh7a_	Alignment	not modelled	23.5	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
23	c3mvnA_	Alignment	not modelled	23.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamayl-medo- **PDBTitle:** crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamayl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
24	d1wfza_	Alignment	not modelled	20.6	19	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
25	d1zj8a1	Alignment	not modelled	19.9	27	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
26	c1wypA_	Alignment	not modelled	18.7	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**calponin 1; **PDBTitle:** solution structure of the ch domain of human calponin 1
27	c2z7eB_	Alignment	not modelled	17.9	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**nifu-like protein; **PDBTitle:** crystal structure of aquifex aeolicus iscu with bound [2fe-2 2s] cluster
28	d1jala2	Alignment	not modelled	13.6	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain

29	d1vbga2	Alignment	not modelled	13.3	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
30	d1ni3a2	Alignment	not modelled	13.1	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
31	d1knwa1	Alignment	not modelled	12.9	7	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
32	d1vcta2	Alignment	not modelled	12.7	9	**Fold:**TrkA C-terminal domain-like **Superfamily:**TrkA C-terminal domain-like **Family:**TrkA C-terminal domain-like
33	d1kbla2	Alignment	not modelled	12.1	11	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
34	d1e8ca2	Alignment	not modelled	11.8	14	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
35	c3a56B_	Alignment	not modelled	11.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein-glutaminase; **PDBTitle:** crystal structure of pro- protein-glutaminase
36	c3eatX_	Alignment	not modelled	11.5	13	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**pyoverdine biosynthesis protein pvcb; **PDBTitle:** crystal structure of the pvcb (pa2255) protein from2 pseudomonas aeruginosa
37	d2ptza1	Alignment	not modelled	11.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
38	c2wbqA_	Alignment	not modelled	10.7	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-arginine beta-hydroxylase; **PDBTitle:** crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
39	d2gdwa1	Alignment	not modelled	10.6	21	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Peptidyl carrier domain
40	c3da5A_	Alignment	not modelled	10.5	14	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**argonaute; **PDBTitle:** crystal structure of piwi/argonaute/zwille(paz) domain from2 thermococcus thioreducens
41	d1wpna_	Alignment	not modelled	10.3	10	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
42	d1vk3a3	Alignment	not modelled	10.2	15	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
43	c1wynA_	Alignment	not modelled	9.8	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**calponin-2; **PDBTitle:** solution structure of the ch domain of human calponin-2
44	d1k20a_	Alignment	not modelled	9.6	15	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
45	d2jfga2	Alignment	not modelled	9.5	19	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
46	d1h6za2	Alignment	not modelled	9.4	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
47	d1ds1a_	Alignment	not modelled	9.0	22	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Clavaminate synthase
48	c3pvjB_	Alignment	not modelled	8.9	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase; **PDBTitle:** crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440
49	c2og5A_	Alignment	not modelled	8.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxygenase; **PDBTitle:** crystal structure of asparagine oxygenase (asno)
50	d1twia1	Alignment	not modelled	8.9	9	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
51	c2cmpA_	Alignment	not modelled	8.3	19	**PDB header:**terminase **Chain:** A: **PDB Molecule:**terminase small subunit; **PDBTitle:** crystal structure of the dna binding domain of g1p small2 terminase subunit from bacteriophage sf6
52	d1otja_	Alignment	not modelled	8.3	27	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
53	c3r1jB_	Alignment	not modelled	8.1	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase; **PDBTitle:** crystal structure of alpha-ketoglutarate-dependent taurine dioxygenase2 from mycobacterium avium, native form
54	c2lc3A_	Alignment	not modelled	7.9	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase hectd1; **PDBTitle:** solution nmr structure of a helical bundle domain from human e3 ligase2 hectd1. northeast structural genomics consortium (nesg) target3 ht6305a
						Fold: Double-stranded beta-helix

55	d1oiha_	Alignment	not modelled	7.7	20	**Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
56	c2wawA_	Alignment	not modelled	7.6	7	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**moba relate protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis rv0371c2 homolog from mycobacterium sp. strain jc1
57	c3nnlB_	Alignment	not modelled	7.2	20	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** halogenase domain from cura module (crystal form iii)
58	c3n29A_	Alignment	not modelled	7.1	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carboxynorspermidine decarboxylase; **PDBTitle:** crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
59	c2pfrB_	Alignment	not modelled	7.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arylamine n-acetyltransferase 2; **PDBTitle:** human n-acetyltransferase 2
60	d1xjsa_	Alignment	not modelled	6.8	22	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
61	d1jr7a_	Alignment	not modelled	6.5	7	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Gab protein (hypothetical protein YgaT)
62	d2hawa1	Alignment	not modelled	6.4	10	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
63	c3bdeA_	Alignment	not modelled	6.4	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**mll5499 protein; **PDBTitle:** crystal structure of a dabb family protein with a ferredoxin-like fold2 (mll5499) from mesorhizobium loti maff303099 at 1.79 a resolution
64	d1hkva1	Alignment	not modelled	6.4	7	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
65	c3bguA_	Alignment	not modelled	6.4	7	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**ferredoxin-like protein of unknown function; **PDBTitle:** crystal structure of a dimeric ferredoxin-like protein of unknown2 function (tfu_0763) from thermobifida fusca yx at 1.50 a resolution
66	c3al6A_	Alignment	not modelled	6.2	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**jmjc domain-containing protein c2orf60; **PDBTitle:** crystal structure of human tyw5
67	d2bsza1	Alignment	not modelled	6.1	21	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
68	c3jxoB_	Alignment	not modelled	5.8	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**trka-n domain protein; **PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
69	d1w6va1	Alignment	not modelled	5.8	25	**Fold:**DUSP-like **Superfamily:**DUSP-like **Family:**DUSP, domain in ubiquitin-specific proteases
70	c2cr4A_	Alignment	not modelled	5.7	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sh3 domain-binding protein 2; **PDBTitle:** solution structure of the sh2 domain of human sh3bp2 protein
71	d1asua_	Alignment	not modelled	5.7	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
72	c3lybC_	Alignment	not modelled	5.7	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative endoribonuclease; **PDBTitle:** structure of putative endoribonuclease(kp1_3112) from2 klebsiella pneumoniae
73	d1w4ta1	Alignment	not modelled	5.5	13	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
74	c2r32A_	Alignment	not modelled	5.5	31	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gcn4-pii/tumor necrosis factor ligand **PDBTitle:** crystal structure of human gitrl variant
75	c3d01G_	Alignment	not modelled	5.5	23	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the protein atu1372 with unknown function from2 agrobacterium tumefaciens
76	c2zkqq_	Alignment	not modelled	5.4	25	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
77	d1hyoa2	Alignment	not modelled	5.4	23	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
78	c1nhgD_	Alignment	not modelled	5.3	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** crystal structure analysis of plasmodium falciparum enoyl-2 acyl-carrier-protein reductase with triclosan
79	c2eobA_	Alignment	not modelled	5.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1-phosphatidylinositol-4,5-bisphosphate **PDBTitle:** solution structure of the second sh2 domain from rat plc2 gamma-2
80	c1e8cB_	Alignment	not modelled	5.2	8	**PDB header:**ligase **Chain:** B: **PDB Molecule:**udp-n-acetylmuramoylalanyl-d-glutamate--2,6-

						PDBTitle: structure of mure the udp-n-acetylmuramyl tripeptide2 synthetase from e. coli
81	c2r8uA_	Alignment	not modelled	5.2	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**microtubule-associated protein rp/eb family **PDBTitle:** structure of fragment of human end-binding protein 1 (eb1)2 containing the n-terminal domain at 1.35 a resolution
82	d2hg6a1	Alignment	not modelled	5.2	67	**Fold:**PA1123-like **Superfamily:**PA1123-like **Family:**PA1123-like
83	d1r9pa_	Alignment	not modelled	5.1	19	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain