Phyre2

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Description	P24238
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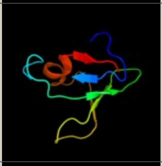
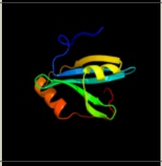
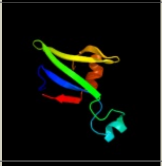
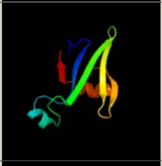
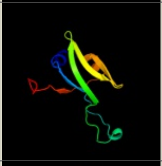
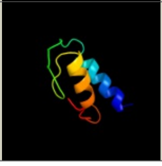
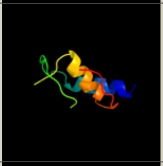
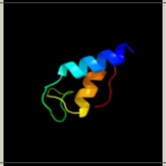
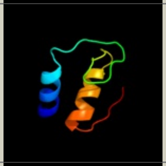
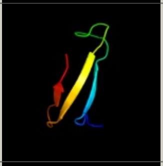
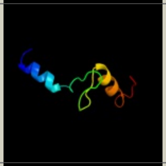
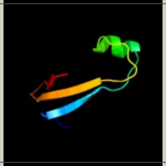
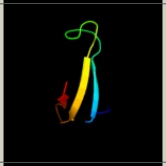
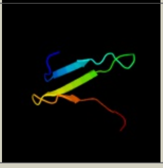
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2if6a1	Alignment		100.0	25	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**YiiX-like
2	c3kw0D_	Alignment		100.0	21	**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	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative xylanase; **PDBTitle:** crystal structure of a putative xylanase from bacteroides fragilis
4	c3h41A_	Alignment		97.5	19	**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
5	c2k1gA_	Alignment		97.5	22	**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
6	c2kytA_	Alignment		97.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**group xvi phospholipase a2; **PDBTitle:** solution struture of the h-rev107 n-terminal domain
7	c2fg0B_	Alignment		97.3	27	**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
8	d2evra2	Alignment		97.2	26	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
9	c2im9A_	Alignment		97.0	13	**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
10	d2im9a1	Alignment		97.0	13	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Lpg0564-like
11	c3gt2A_	Alignment		97.0	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c

12	c2xivA_	Alignment		96.7	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
13	c3i86A_	Alignment		96.7	12	**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	c3pbiA_	Alignment		96.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invasion protein; **PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
15	c3npfB_	Alignment		96.1	16	**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
16	d2io8a2	Alignment		93.0	25	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**CHAP domain
17	c3m1uB_	Alignment		91.0	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
18	c2vpmB_	Alignment		83.5	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**trypanothione synthetase; **PDBTitle:** trypanothione synthetase
19	c2ioaA_	Alignment		83.1	26	**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
20	c2k3aA_	Alignment		66.9	26	**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
21	d1wh7a_	Alignment	not modelled	44.2	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
22	d1igna2	Alignment	not modelled	41.0	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**DNA-binding domain of rap1
23	d1wfza_	Alignment	not modelled	29.0	35	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
24	c3nnlB_	Alignment	not modelled	27.2	33	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** halogenase domain from cura module (crystal form iii)
25	c2z7eB_	Alignment	not modelled	25.4	12	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**nifu-like protein; **PDBTitle:** crystal structure of aquifex aeolicus iscu with bound [2fe-2 2s] cluster
26	d2glza1	Alignment	not modelled	22.5	10	**Fold:**FwdE/GAPDH domain-like **Superfamily:**FwdE-like **Family:**FwdE-like
27	d2gy9q1	Alignment	not modelled	19.3	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
28	d1hkva1	Alignment	not modelled	18.0	20	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
29	d1wpna	Alignment	not modelled	17.1	15	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases

29	d1wpha_	Alignment	not modelled	17.1	15	**Family:**Manganese-dependent inorganic pyrophosphatase (family II)
30	d1vbga2	Alignment	not modelled	15.4	13	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
31	c1khiA_	Alignment	not modelled	15.2	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hex1; **PDBTitle:** crystal structure of hex1
32	d1h2ka_	Alignment	not modelled	14.7	24	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Hypoxia-inducible factor HIF ihhibitor (FIH1)
33	d2z1ea2	Alignment	not modelled	14.7	24	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
34	c2zkqq_	Alignment	not modelled	14.2	30	**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
35	d1khia1	Alignment	not modelled	13.5	15	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
36	d1zyma2	Alignment	not modelled	13.3	14	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
37	c3bbnQ_	Alignment	not modelled	13.3	15	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**ribosomal protein s17; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
38	c3zvmA_	Alignment	not modelled	13.0	19	**PDB header:**hydrolase/transferase/dna **Chain:** A: **PDB Molecule:**bifunctional polynucleotide phosphatase/kinase; **PDBTitle:** the structural basis for substrate recognition by mammalian2 polynucleotide kinase 3' phosphatase
39	d1r9pa_	Alignment	not modelled	12.7	29	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
40	c2obnA_	Alignment	not modelled	12.6	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a duf1611 family protein (ava_3511) from anabaena2 variabilis atcc 29413 at 2.30 a resolution
41	d1k20a_	Alignment	not modelled	12.4	26	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
42	d1asua_	Alignment	not modelled	12.4	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Retroviral integrase, catalytic domain
43	c3k1rA_	Alignment	not modelled	12.1	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
44	d1kbla2	Alignment	not modelled	11.8	13	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
45	c1s1hQ_	Alignment	not modelled	11.6	20	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**40s ribosomal protein s11; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
46	c3k2oB_	Alignment	not modelled	11.6	41	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional arginine demethylase and lysyl-hydroxylase **PDBTitle:** structure of an oxygenase
47	d1h6za2	Alignment	not modelled	11.6	13	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
48	c2x35A_	Alignment	not modelled	11.5	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**peregrin; **PDBTitle:** molecular basis of histone h3k36me3 recognition by the pwwp2 domain of brpf1.
49	c2zpmA_	Alignment	not modelled	11.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
50	d1xjsa_	Alignment	not modelled	11.3	12	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
51	c2opwA_	Alignment	not modelled	11.0	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phyhd1 protein; **PDBTitle:** crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
52	d2qamc2	Alignment	not modelled	10.8	28	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
53	d1rl2a2	Alignment	not modelled	10.7	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
54	c1zx6A_	Alignment	not modelled	10.5	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ypr154wp; **PDBTitle:** high-resolution crystal structure of yeast pin3 sh3 domain
						Fold:OB-fold

55	d2uubq1	Alignment	not modelled	10.3	20	**Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
56	d1vcta2	Alignment	not modelled	10.2	8	**Fold:**TrkA C-terminal domain-like **Superfamily:**TrkA C-terminal domain-like **Family:**TrkA C-terminal domain-like
57	d2hawa1	Alignment	not modelled	9.8	15	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
58	d1su0b_	Alignment	not modelled	9.5	35	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
59	d1i94q_	Alignment	not modelled	9.3	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
60	c1ezaA_	Alignment	not modelled	9.0	12	**PDB header:**phosphotransferase **Chain:** A: **PDB Molecule:**enzyme i; **PDBTitle:** amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
61	d2f4pa1	Alignment	not modelled	9.0	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**TM1287-like
62	d1ripa_	Alignment	not modelled	8.8	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
63	c2wkdA_	Alignment	not modelled	8.7	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**orf34p2; **PDBTitle:** crystal structure of a double ile-to-met mutant of protein2 orf34 from lactococcus phage p2
64	d2fcta1	Alignment	not modelled	8.7	13	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
65	d2hg6a1	Alignment	not modelled	8.6	50	**Fold:**PA1123-like **Superfamily:**PA1123-like **Family:**PA1123-like
66	d1i74a_	Alignment	not modelled	8.3	28	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
67	c3mt1B_	Alignment	not modelled	8.2	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative carboxynorspermidine decarboxylase protein; **PDBTitle:** crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
68	d1ntha_	Alignment	not modelled	8.1	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Monomethylamine methyltransferase MtmB **Family:**Monomethylamine methyltransferase MtmB
69	d1vrba1	Alignment	not modelled	8.0	6	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
70	d2nlua1	Alignment	not modelled	8.0	38	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**PWWP domain
71	d2zoda2	Alignment	not modelled	8.0	6	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
72	d1hyoa2	Alignment	not modelled	7.6	17	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
73	d1wpga1	Alignment	not modelled	7.4	28	**Fold:**Double-stranded beta-helix **Superfamily:**Calcium ATPase, transduction domain A **Family:**Calcium ATPase, transduction domain A
74	c3al6A_	Alignment	not modelled	7.3	41	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**jmjc domain-containing protein c2orf60; **PDBTitle:** crystal structure of human tyw5
75	c1nhgD_	Alignment	not modelled	7.2	9	**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
76	d1fc6a3	Alignment	not modelled	7.2	30	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**Tail specific protease PDZ domain
77	c1yj5B_	Alignment	not modelled	7.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase catalytic domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
78	c2yy8B_	Alignment	not modelled	7.0	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**upf0106 protein ph0461; **PDBTitle:** crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
79	d1sota1	Alignment	not modelled	6.9	18	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
80	d1h3za_	Alignment	not modelled	6.9	25	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**PWWP domain
81	d1cz5a1	Alignment	not modelled	6.8	38	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like

						Family: Cdc48 N-terminal domain-like
82	d1knwa1	Alignment	not modelled	6.8	20	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
83	c1i7oC_	Alignment	not modelled	6.8	17	**PDB header:**isomerase, lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate degradation bifunctional **PDBTitle:** crystal structure of hpce
84	d1d7ka1	Alignment	not modelled	6.7	21	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
85	c2hc8A_	Alignment	not modelled	6.6	33	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
86	c4a1bO_	Alignment	not modelled	6.5	24	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**rpl28; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 3.
87	c2p3wB_	Alignment	not modelled	6.4	27	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**probable serine protease htra3; **PDBTitle:** crystal structure of the htra3 pdz domain bound to a phage-derived2 ligand (fgrwv)
88	c3c9qA_	Alignment	not modelled	6.4	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein c8orf32; **PDBTitle:** crystal structure of the uncharacterized human protein c8orf32 with2 bound peptide
89	d1l0wa2	Alignment	not modelled	6.2	30	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
90	c3d3rA_	Alignment	not modelled	6.1	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hydrogenase assembly chaperone hypc/hupf; **PDBTitle:** crystal structure of the hydrogenase assembly chaperone hypc/hupf2 family protein from shewanella oneidensis mr-1
91	d1clia2	Alignment	not modelled	6.1	13	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
92	d2eyqa1	Alignment	not modelled	6.1	35	**Fold:**SH3-like barrel **Superfamily:**CarD-like **Family:**CarD-like
93	d1vi6a_	Alignment	not modelled	6.1	14	**Fold:**Flavodoxin-like **Superfamily:**Ribosomal protein S2 **Family:**Ribosomal protein S2
94	c2qniA_	Alignment	not modelled	6.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu0299; **PDBTitle:** crystal structure of uncharacterized protein atu0299
95	c1yfsB_	Alignment	not modelled	5.9	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** the crystal structure of alanyl-trna synthetase in complex2 with l-alanine
96	d1ky9a1	Alignment	not modelled	5.9	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
97	c2j5uB_	Alignment	not modelled	5.8	20	**PDB header:**cell shape regulation **Chain:** B: **PDB Molecule:**mrec protein; **PDBTitle:** mrec lysteria monocytogenes
98	c2qq4A_	Alignment	not modelled	5.8	29	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**iron-sulfur cluster biosynthesis protein iscu; **PDBTitle:** crystal structure of iron-sulfur cluster biosynthesis2 protein iscu (ttha1736) from thermus thermophilus hb8
99	c2hw2A_	Alignment	not modelled	5.8	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rifampin adp-ribosyl transferase; **PDBTitle:** crystal structure of rifampin adp-ribosyl transferase in2 complex with rifampin