Phyre2

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Description	Q47151
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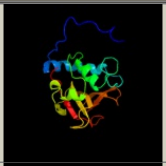
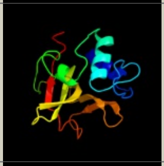
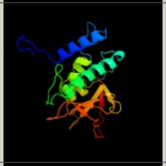
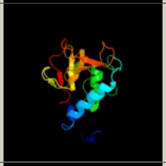
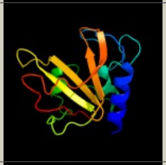
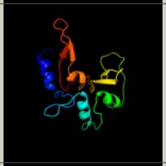
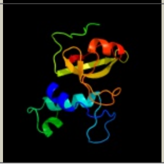
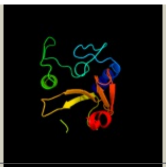
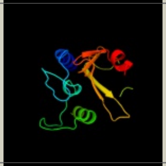
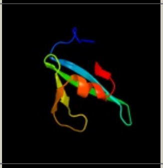
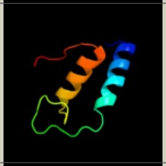
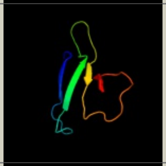
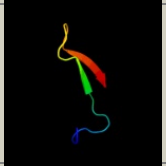
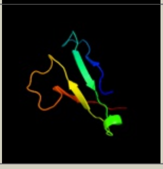
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fg0B_	Alignment		100.0	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
2	c3h41A_	Alignment		100.0	31	**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
3	c2k1gA_	Alignment		100.0	31	**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
4	c3npfB_	Alignment		100.0	33	**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
5	d2evra2	Alignment		100.0	30	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
6	c2xivA_	Alignment		100.0	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
7	c3pbiA_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invasion protein; **PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
8	c3i86A_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204
9	c3gt2A_	Alignment		100.0	33	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
10	c3m1uB_	Alignment		99.9	25	**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
11	c2p1gA_	Alignment		99.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative xylanase; **PDBTitle:** crystal structure of a putative xylanase from bacteroides fragilis

12	c2im9A_	Alignment		98.4	19	**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
13	d2im9a1	Alignment		98.4	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Lpg0564-like
14	c2kytA_	Alignment		98.2	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**group xvi phospholipase a2; **PDBTitle:** solution struture of the h-rev107 n-terminal domain
15	c3kw0D_	Alignment		97.8	28	**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
16	d2if6a1	Alignment		97.4	20	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**YiiX-like
17	d2io8a2	Alignment		85.7	11	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**CHAP domain
18	c2k3aA_	Alignment		84.3	15	**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
19	d2ar1a1	Alignment		80.0	15	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
20	c2vpmB_	Alignment		78.6	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**trypanothione synthetase; **PDBTitle:** trypanothione synthetase
21	d2g2xa1	Alignment	not modelled	78.6	23	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
22	c2ioaA_	Alignment	not modelled	78.1	11	**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
23	d2gbsa1	Alignment	not modelled	77.7	28	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
24	c3eopB_	Alignment	not modelled	76.1	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**thymocyte nuclear protein 1; **PDBTitle:** crystal structure of the duf55 domain of human thymocyte nuclear2 protein 1
25	d2evea1	Alignment	not modelled	75.5	23	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
26	c3nnlB_	Alignment	not modelled	75.4	19	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** halogenase domain from cura module (crystal form iii)
27	d1zcea1	Alignment	not modelled	74.1	24	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
28	c3kopB_	Alignment	not modelled	58.9	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution

29	d2eyqa1	Alignment	not modelled	50.3	26	**Fold:**SH3-like barrel **Superfamily:**CarD-like **Family:**CarD-like
30	d1jr7a_	Alignment	not modelled	45.7	14	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Gab protein (hypothetical protein YgaT)
31	c2wbqA_	Alignment	not modelled	43.4	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-arginine beta-hydroxylase; **PDBTitle:** crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
32	c2nnzA_	Alignment	not modelled	41.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus
33	d2ba0a2	Alignment	not modelled	38.0	33	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
34	c2og5A_	Alignment	not modelled	36.8	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxygenase; **PDBTitle:** crystal structure of asparagine oxygenase (asno)
35	d1o6aa_	Alignment	not modelled	35.5	8	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)
36	d1ds1a_	Alignment	not modelled	35.4	38	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Clavaminate synthase
37	d1vrba1	Alignment	not modelled	33.4	15	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
38	d1o9ya_	Alignment	not modelled	32.4	20	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)
39	c3emrA_	Alignment	not modelled	31.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ectd; **PDBTitle:** crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens
40	d1otja_	Alignment	not modelled	31.0	7	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
41	d1nx4a_	Alignment	not modelled	30.3	29	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**gamma-Butyrobetaine hydroxylase
42	d1wpga1	Alignment	not modelled	30.3	16	**Fold:**Double-stranded beta-helix **Superfamily:**Calcium ATPase, transduction domain A **Family:**Calcium ATPase, transduction domain A
43	c3r1jB_	Alignment	not modelled	29.0	14	**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
44	d1we3o_	Alignment	not modelled	28.8	25	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
45	c3eatX_	Alignment	not modelled	28.5	21	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**pyoverdine biosynthesis protein pvcb; **PDBTitle:** crystal structure of the pvcb (pa2255) protein from2 pseudomonas aeruginosa
46	c3d79A_	Alignment	not modelled	27.7	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph0734; **PDBTitle:** crystal structure of hypothetical protein ph0734.1 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
47	c2xdvA_	Alignment	not modelled	27.2	26	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**myc-induced nuclear antigen; **PDBTitle:** crystal structure of the catalytic domain of flj14393
48	c2dbiA_	Alignment	not modelled	26.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ybiu; **PDBTitle:** crystal structure of a hypothetical protein jw0805 from2 escherichia coli
49	c3pvjB_	Alignment	not modelled	26.4	14	**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
50	d2csga1	Alignment	not modelled	26.1	28	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**YbiU-like
51	d1oiha_	Alignment	not modelled	26.1	15	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
52	c3ms5A_	Alignment	not modelled	25.3	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gamma-butyrobetaine dioxygenase; **PDBTitle:** crystal structure of human gamma-butyrobetaine,2-oxoglutarate2 dioxygenase 1 (bbox1)
53	c3al6A_	Alignment	not modelled	25.2	30	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**jmjc domain-containing protein c2orf60; **PDBTitle:** crystal structure of human tyw5
54	c2opwA_	Alignment	not modelled	25.1	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phyhd1 protein; **PDBTitle:** crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
55	d1p3ha_	Alignment	not modelled	24.5	20	**Fold:**GroES-like **Superfamily:**GroES-like

						Family: GroES
56	d2jfga2	Alignment	not modelled	24.3	11	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
57	c1yy3A_	Alignment	not modelled	22.8	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:trna ribosyltransferase- **PDBTitle:** structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
58	d1c0aa2	Alignment	not modelled	22.5	40	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
59	c3b8eC_	Alignment	not modelled	22.0	12	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
60	d1l0wa2	Alignment	not modelled	21.8	50	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
61	d1y0za_	Alignment	not modelled	21.1	29	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**gamma-Butyrobetaine hydroxylase
62	c2eyqA_	Alignment	not modelled	20.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of escherichia coli transcription-repair2 coupling factor
63	d2fcta1	Alignment	not modelled	20.8	17	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
64	d1wida_	Alignment	not modelled	20.8	22	**Fold:**DNA-binding pseudobarrel domain **Superfamily:**DNA-binding pseudobarrel domain **Family:**B3 DNA binding domain
65	c2hc8A_	Alignment	not modelled	20.7	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
66	c3gjbA_	Alignment	not modelled	18.4	30	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cytc3; **PDBTitle:** cytc3 with fe(ii) and alpha-ketoglutarate
67	d1yela1	Alignment	not modelled	18.2	22	**Fold:**DNA-binding pseudobarrel domain **Superfamily:**DNA-binding pseudobarrel domain **Family:**B3 DNA binding domain
68	d1knwa1	Alignment	not modelled	17.8	26	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
69	d2a1xa1	Alignment	not modelled	17.6	28	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
70	d1vkya_	Alignment	not modelled	17.3	36	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
71	c2zxeA_	Alignment	not modelled	17.1	12	**PDB header:**hydrolase/transport protein **Chain:** A: **PDB Molecule:**na, k-atpase alpha subunit; **PDBTitle:** crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
72	c3uyjA_	Alignment	not modelled	16.9	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 8; **PDBTitle:** crystal structure of jmjd5 catalytic core domain in complex with2 nickle and alpha-kg
73	c2kijA_	Alignment	not modelled	16.5	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the actuator domain of the copper-2 transporting atpase atp7a
74	d2z1ea2	Alignment	not modelled	16.0	23	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
75	c2x35A_	Alignment	not modelled	15.9	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**peregrin; **PDBTitle:** molecular basis of histone h3k36me3 recognition by the pwwp2 domain of brpf1.
76	c2rdsA_	Alignment	not modelled	15.8	41	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxypentalenic acid 11-beta hydroxylase; fe(ii)/alpha- **PDBTitle:** crystal structure of ptlh with fe/oxalylglycine and ent-1-2 deoxypentalenic acid bound
77	d1iyca_	Alignment	not modelled	15.6	67	**Fold:**Invertebrate chitin-binding proteins **Superfamily:**Invertebrate chitin-binding proteins **Family:**Antifungal peptide scarabaecin
78	c3j09A_	Alignment	not modelled	15.4	15	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
79	d1njjb1	Alignment	not modelled	15.2	20	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
80	c3rfuC_	Alignment	not modelled	14.7	20	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
81	d1aono_	Alignment	not modelled	14.1	18	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES

82	d2phla2	Alignment	not modelled	13.7	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
83	d1wdia_	Alignment	not modelled	13.7	43	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
84	c2q1dX_	Alignment	not modelled	13.7	17	**PDB header:**lyase **Chain:** X: **PDB Molecule:**2-keto-3-deoxy-d-arabinonate dehydratase; **PDBTitle:** 2-keto-3-deoxy-d-arabinonate dehydratase complexed with magnesium and2 2,5-dioxopentanoate
85	d1hkva1	Alignment	not modelled	13.4	31	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
86	c3ixzA_	Alignment	not modelled	13.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
87	c1q7hA_	Alignment	not modelled	13.0	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** structure of a conserved pua domain protein from thermoplasma2 acidophilum
88	c3j08A_	Alignment	not modelled	12.8	15	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
89	d2ey4a1	Alignment	not modelled	12.6	17	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
90	d1gtta1	Alignment	not modelled	12.5	16	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
91	c2r32A_	Alignment	not modelled	12.1	23	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gcn4-pii/tumor necrosis factor ligand **PDBTitle:** crystal structure of human gitrl variant
92	d1hyoa2	Alignment	not modelled	12.0	38	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
93	c3r6oA_	Alignment	not modelled	11.7	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2-hydroxyhepta-2,4-diene-1, 7-dioateisomerase; **PDBTitle:** crystal structure of a probable 2-hydroxyhepta-2,4-diene-1, 7-2 dioateisomerase from mycobacterium abscessus
94	d2zoda2	Alignment	not modelled	11.5	21	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
95	d1s04a_	Alignment	not modelled	11.0	21	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
96	c3ibmB_	Alignment	not modelled	10.9	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of cupin 2 domain-containing protein hhal_0468 from2 halorhodospira halophila
97	d2hd9a1	Alignment	not modelled	10.9	21	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
98	d1bg6a1	Alignment	not modelled	10.9	11	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**N-(1-D-carboxylethyl)-L-norvaline dehydrogenase
99	d2apoa1	Alignment	not modelled	10.7	13	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain