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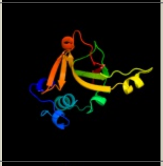
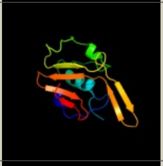
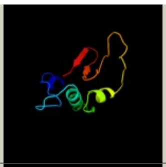
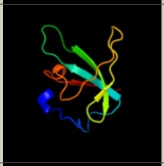
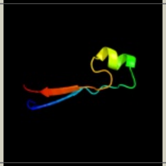
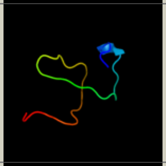
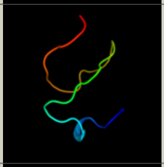
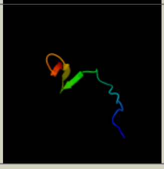
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kw0D_	Alignment		99.9	27	**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
2	c2fg0B_	Alignment		99.9	20	**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
3	d2if6a1	Alignment		99.9	28	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**YiiX-like
4	d2evra2	Alignment		99.9	21	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
5	c2xivA_	Alignment		99.9	23	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
6	c3npfB_	Alignment		99.9	19	**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
7	c3pbiA_	Alignment		99.9	25	**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	c3h41A_	Alignment		99.9	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
9	c3gt2A_	Alignment		99.9	25	**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	c2k1gA_	Alignment		99.9	21	**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
11	c3i86A_	Alignment		99.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204

12	c3m1uB_	Alignment		99.5	18	**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
13	c2p1gA_	Alignment		98.9	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative xylanase; **PDBTitle:** crystal structure of a putative xylanase from bacteroides fragilis
14	c2kytA_	Alignment		98.5	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**group xvi phospholipase a2; **PDBTitle:** solution struture of the h-rev107 n-terminal domain
15	d2im9a1	Alignment		95.7	17	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Lpg0564-like
16	c2im9A_	Alignment		95.7	17	**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
17	d2io8a2	Alignment		63.9	36	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**CHAP domain
18	d1wpga1	Alignment		50.0	29	**Fold:**Double-stranded beta-helix **Superfamily:**Calcium ATPase, transduction domain A **Family:**Calcium ATPase, transduction domain A
19	c2hc8A_	Alignment		43.0	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
20	d1o9ya_	Alignment		41.7	25	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)
21	c3kopB_	Alignment	not modelled	40.0	33	**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
22	c3b8eC_	Alignment	not modelled	39.2	20	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
23	d1gtta1	Alignment	not modelled	37.5	16	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
24	c3nnlB_	Alignment	not modelled	37.4	23	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** halogenase domain from cura module (crystal form iii)
25	c3b9bA_	Alignment	not modelled	36.8	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
26	d2evra1	Alignment	not modelled	36.3	23	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**Spr N-terminal domain-like
27	c3j08A_	Alignment	not modelled	36.3	9	**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
28	d2z1ea2	Alignment	not modelled	35.7	24	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like

29	d1ixda_	Alignment	not modelled	34.0	11	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
30	c2vpmB_	Alignment	not modelled	32.8	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**trypanothione synthetase; **PDBTitle:** trypanothione synthetase
31	c2kijA_	Alignment	not modelled	31.7	18	**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
32	d2jfga2	Alignment	not modelled	31.1	38	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
33	d1we3o_	Alignment	not modelled	30.5	20	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
34	d2zoda2	Alignment	not modelled	30.1	29	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
35	d2gbsa1	Alignment	not modelled	29.9	27	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
36	d2nqra2	Alignment	not modelled	29.9	14	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
37	c3qdfA_	Alignment	not modelled	29.7	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; **PDBTitle:** crystal structure of 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from mycobacterium marinum
38	c1mhsA_	Alignment	not modelled	29.4	30	**PDB header:**membrane protein, proton transport **Chain:** A: **PDB Molecule:**plasma membrane atpase; **PDBTitle:** model of neurospora crassa proton atpase
39	d2eyqa1	Alignment	not modelled	29.1	26	**Fold:**SH3-like barrel **Superfamily:**CarD-like **Family:**CarD-like
40	c3j09A_	Alignment	not modelled	28.8	9	**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
41	c1i7oC_	Alignment	not modelled	28.6	16	**PDB header:**isomerase, lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate degradation bifunctional **PDBTitle:** crystal structure of hpce
42	c2q1dX_	Alignment	not modelled	27.9	22	**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
43	c3ixzA_	Alignment	not modelled	27.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
44	c3mvnA_	Alignment	not modelled	27.7	28	**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
45	c3b8cB_	Alignment	not modelled	27.6	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atpase 2, plasma membrane-type; **PDBTitle:** crystal structure of a plasma membrane proton pump
46	c2zxeA_	Alignment	not modelled	27.1	20	**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
47	c2kbzA_	Alignment	not modelled	26.8	23	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**15 protein (bacteriophage spp1 complete **PDBTitle:** nmr structure of protein gp15 of bacteriophage spp1
48	d1y7ma2	Alignment	not modelled	26.0	8	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
49	d1ltqa1	Alignment	not modelled	26.0	22	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
50	d1uz5a2	Alignment	not modelled	25.7	20	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
51	d1nkqa_	Alignment	not modelled	25.6	22	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
52	c2ioaA_	Alignment	not modelled	24.8	32	**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
53	d2ftsa2	Alignment	not modelled	24.6	20	**Fold:**MoeA N-terminal region -like **Superfamily:**MoeA N-terminal region -like **Family:**MoeA N-terminal region -like
54	d1aono_	Alignment	not modelled	24.2	11	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES

55	d1hyoa2	Alignment	not modelled	23.4	54	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
56	d1vrba1	Alignment	not modelled	23.4	27	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Asparaginyl hydroxylase-like
57	d1k20a_	Alignment	not modelled	23.1	18	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
58	d2fcta1	Alignment	not modelled	22.8	23	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
59	d1p3ha_	Alignment	not modelled	22.7	23	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
60	d3c9ua2	Alignment	not modelled	22.0	21	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
61	d1zcea1	Alignment	not modelled	21.8	36	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
62	d1khia1	Alignment	not modelled	21.7	20	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**eIF5a N-terminal domain-like
63	c3rfuC_	Alignment	not modelled	20.9	19	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
64	d2ar1a1	Alignment	not modelled	20.8	14	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
65	d1gtta2	Alignment	not modelled	20.7	31	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
66	d1c0aa2	Alignment	not modelled	19.8	30	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
67	c1wzoC_	Alignment	not modelled	19.7	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hpce; **PDBTitle:** crystal structure of the hpce from thermus thermophilus hb8
68	d1l0wa2	Alignment	not modelled	19.5	40	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
69	d1jr7a_	Alignment	not modelled	19.1	18	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Gab protein (hypothetical protein YgaT)
70	c2wbqA_	Alignment	not modelled	18.8	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-arginine beta-hydroxylase; **PDBTitle:** crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
71	d1in0a1	Alignment	not modelled	18.4	23	**Fold:**Ferredoxin-like **Superfamily:**YajQ-like **Family:**YajQ-like
72	d1e8ca2	Alignment	not modelled	18.2	20	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
73	c2nqqA_	Alignment	not modelled	17.7	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
74	c3fd5B_	Alignment	not modelled	17.6	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**selenide, water dikinase 1; **PDBTitle:** crystal structure of human selenophosphate synthetase 12 complex with ampcp
75	d1sawa_	Alignment	not modelled	17.6	26	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
76	d2g2xa1	Alignment	not modelled	17.0	25	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
77	c2l8kA_	Alignment	not modelled	16.9	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 7; **PDBTitle:** nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
78	c2nnzA_	Alignment	not modelled	16.5	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus
79	c2og5A_	Alignment	not modelled	16.5	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxygenase; **PDBTitle:** crystal structure of asparagine oxygenase (asno)
80	d1ds1a_	Alignment	not modelled	16.5	55	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Clavaminate synthase
81	c3lzkC_	Alignment	not modelled	16.4	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fumarylacetoacetate hydrolase family protein; **PDBTitle:** the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021

82	d1foea2	Alignment	not modelled	16.3	38	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
83	d1o6aa_	Alignment	not modelled	16.1	7	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)
84	c1hyoB_	Alignment	not modelled	16.1	54	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fumarylacetoacetate hydrolase; **PDBTitle:** crystal structure of fumarylacetoacetate hydrolase2 complexed with 4-(hydroxymethylphosphinoyl)-3-oxo-butanoic3 acid
85	d1njjb1	Alignment	not modelled	16.1	19	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
86	d2hawa1	Alignment	not modelled	16.0	0	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)
87	d1koha2	Alignment	not modelled	15.9	13	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Non-canonical RBD domain
88	d1knwa1	Alignment	not modelled	15.9	36	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
89	d1clia2	Alignment	not modelled	15.8	21	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
90	d2evea1	Alignment	not modelled	15.7	24	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
91	c3ebrA_	Alignment	not modelled	15.6	7	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized rmlc-like cupin; **PDBTitle:** crystal structure of an rmlc-like cupin protein (reut_a0381) from2 ralstonia eutropha jmp134 at 2.60 a resolution
92	d1f3ta1	Alignment	not modelled	15.4	11	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
93	c1khiA_	Alignment	not modelled	15.3	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hex1; **PDBTitle:** crystal structure of hex1
94	d1g8aa_	Alignment	not modelled	15.1	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Fibrillarin homologue
95	c3l53F_	Alignment	not modelled	15.1	31	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative fumarylacetoacetate isomerase/hydrolase; **PDBTitle:** crystal structure of a putative fumarylacetoacetate2 isomerase/hydrolase from oleispira antarctica
96	c3al6A_	Alignment	not modelled	14.7	26	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**jmjc domain-containing protein c2orf60; **PDBTitle:** crystal structure of human tyw5
97	c2x35A_	Alignment	not modelled	14.7	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**peregrin; **PDBTitle:** molecular basis of histone h3k36me3 recognition by the pwwp2 domain of brpf1.
98	c2dfuB_	Alignment	not modelled	14.7	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; **PDBTitle:** crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from thermus thermophilus hb8
99	c3lkxA_	Alignment	not modelled	14.6	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**transcription factor btf3; **PDBTitle:** human nac dimerization domain