Phyre^2

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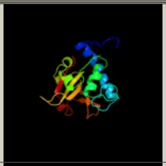
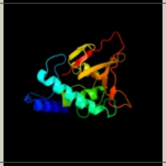
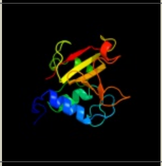
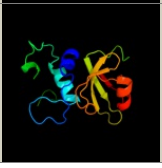
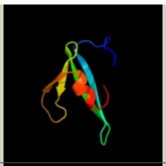
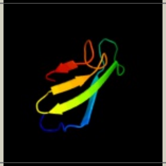
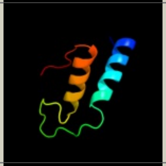
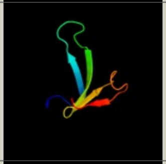
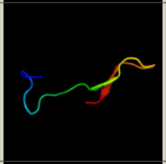
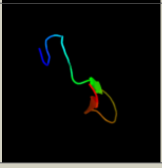
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fg0B_	Alignment		100.0	34	**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	c2xivA_	Alignment		100.0	27	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
3	d2evra2	Alignment		100.0	37	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**NlpC/P60
4	c3h41A_	Alignment		100.0	34	**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	c3npfB_	Alignment		100.0	30	**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	c3pbiA_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invasion protein; **PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
7	c2k1gA_	Alignment		100.0	35	**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
8	c3gt2A_	Alignment		100.0	34	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
9	c3i86A_	Alignment		100.0	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204
10	c3m1uB_	Alignment		99.8	21	**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	c2kytA_	Alignment		98.1	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**group xvi phospholipase a2; **PDBTitle:** solution struture of the h-rev107 n-terminal domain
13	c3kw0D_	Alignment		98.0	24	**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
14	d2if6a1	Alignment		97.3	18	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**YiiX-like
15	c2k3aA_	Alignment		93.3	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
16	c2im9A_	Alignment		91.8	23	**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	d2im9a1	Alignment		91.8	23	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Lpg0564-like
18	d2io8a2	Alignment		87.8	21	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**CHAP domain
19	d2ar1a1	Alignment		85.2	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
20	d2g2xa1	Alignment		83.8	22	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
21	d2gbsa1	Alignment	not modelled	83.7	21	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
22	d1zcea1	Alignment	not modelled	83.1	38	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
23	c3eopB_	Alignment	not modelled	82.7	22	**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
24	d2evea1	Alignment	not modelled	82.3	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Atu2648/PH1033-like
25	c2vpmB_	Alignment	not modelled	75.4	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**trypanothione synthetase; **PDBTitle:** trypanothione synthetase
26	c3kopB_	Alignment	not modelled	74.3	23	**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
27	c3nnlB_	Alignment	not modelled	66.3	27	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** halogenase domain from cura module (crystal form iii)
28	c2ioaA_	Alignment	not modelled	65.3	21	**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

29	d2eyqa1	Alignment	not modelled	65.2	35	**Fold:**SH3-like barrel **Superfamily:**CarD-like **Family:**CarD-like
30	c2wbqA_	Alignment	not modelled	64.3	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-arginine beta-hydroxylase; **PDBTitle:** crystal structure of vioc in complex with (2s,3s)-2 hydroxyarginine
31	c1i7oC_	Alignment	not modelled	62.7	27	**PDB header:**isomerase, lyase **Chain:** C: **PDB Molecule:**4-hydroxyphenylacetate degradation bifunctional **PDBTitle:** crystal structure of hpce
32	d1jr7a_	Alignment	not modelled	62.4	8	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Gab protein (hypothetical protein YgaT)
33	d1wpga1	Alignment	not modelled	59.7	21	**Fold:**Double-stranded beta-helix **Superfamily:**Calcium ATPase, transduction domain A **Family:**Calcium ATPase, transduction domain A
34	d1ds1a_	Alignment	not modelled	57.5	36	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Clavaminate synthase
35	c2og5A_	Alignment	not modelled	57.3	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxygenase; **PDBTitle:** crystal structure of asparagine oxygenase (asno)
36	d2ba0a2	Alignment	not modelled	55.1	28	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
37	d1otja_	Alignment	not modelled	54.4	12	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
38	d2fcta1	Alignment	not modelled	53.6	15	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
39	c3r1jB_	Alignment	not modelled	50.5	18	**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
40	d1nx4a_	Alignment	not modelled	49.8	27	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**gamma-Butyrobetaine hydroxylase
41	c3eatX_	Alignment	not modelled	49.6	25	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**pyoverdine biosynthesis protein pvcb; **PDBTitle:** crystal structure of the pvcb (pa2255) protein from2 pseudomonas aeruginosa
42	c3pvjB_	Alignment	not modelled	48.6	18	**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
43	d1oiha_	Alignment	not modelled	48.2	18	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**TauD/TfdA-like
44	d1o6aa_	Alignment	not modelled	47.5	15	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)
45	c2q1dX_	Alignment	not modelled	46.8	21	**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
46	d1zx8a1	Alignment	not modelled	44.7	25	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**TM1367-like
47	c2nnzA_	Alignment	not modelled	44.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus
48	c3b8eC_	Alignment	not modelled	44.0	27	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
49	d1o9ya_	Alignment	not modelled	43.8	18	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)
50	d1y0za_	Alignment	not modelled	42.0	18	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**gamma-Butyrobetaine hydroxylase
51	c2eyqA_	Alignment	not modelled	41.9	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of escherichia coli transcription-repair2 coupling factor
52	c3ms5A_	Alignment	not modelled	41.9	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**gamma-butyrobetaine dioxygenase; **PDBTitle:** crystal structure of human gamma-butyrobetaine,2-oxoglutarate2 dioxygenase 1 (bbox1)
53	d1c0aa2	Alignment	not modelled	41.3	40	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
54	c2hc8A_	Alignment	not modelled	41.2	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cation-transporting atpase, p-type; **PDBTitle:** structure of the a. fulgidus copa a-domain
						PDB header:hydrolase

55	c2kijA_	Alignment	not modelled	41.1	19	**Chain:** A: **PDB Molecule:**copper-transporting atpase 1; **PDBTitle:** solution structure of the actuator domain of the copper-2 transporting atpase atp7a
56	d1nkqa_	Alignment	not modelled	40.4	24	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
57	d2z1ea2	Alignment	not modelled	40.1	31	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
58	d1l0wa2	Alignment	not modelled	39.8	40	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
59	c2dbiA_	Alignment	not modelled	38.8	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ybiu; **PDBTitle:** crystal structure of a hypothetical protein jw0805 from2 escherichia coli
60	c3qdfA_	Alignment	not modelled	38.7	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
61	d2csga1	Alignment	not modelled	38.3	25	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**YbiU-like
62	c3b9bA_	Alignment	not modelled	37.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
63	d2jfga2	Alignment	not modelled	37.2	17	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
64	c2x35A_	Alignment	not modelled	37.0	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**peregrin; **PDBTitle:** molecular basis of histone h3k36me3 recognition by the pwwp2 domain of brpf1.
65	d1hyoa2	Alignment	not modelled	36.8	41	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
66	c2opwA_	Alignment	not modelled	36.8	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phyhd1 protein; **PDBTitle:** crystal structure of human phytanoyl-coa dioxygenase phyhd1 (apo)
67	c3d79A_	Alignment	not modelled	36.0	21	**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
68	c2zxeA_	Alignment	not modelled	33.5	23	**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
69	d1wida_	Alignment	not modelled	33.5	26	**Fold:**DNA-binding pseudobarrel domain **Superfamily:**DNA-binding pseudobarrel domain **Family:**B3 DNA binding domain
70	d1we3o_	Alignment	not modelled	32.8	31	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
71	c3lzkC_	Alignment	not modelled	32.4	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
72	c1yy3A_	Alignment	not modelled	31.9	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:trna ribosyltransferase- **PDBTitle:** structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
73	c3emrA_	Alignment	not modelled	31.9	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ectd; **PDBTitle:** crystal structure analysis of the ectoine hydroxylase ectd from2 salibacillus salexigens
74	d1p3ha_	Alignment	not modelled	31.8	24	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
75	c1mhsA_	Alignment	not modelled	31.8	22	**PDB header:**membrane protein, proton transport **Chain:** A: **PDB Molecule:**plasma membrane atpase; **PDBTitle:** model of neurospora crassa proton atpase
76	d2zoda2	Alignment	not modelled	31.4	31	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
77	c3r6oA_	Alignment	not modelled	31.3	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
78	d1knwa1	Alignment	not modelled	30.8	26	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
79	c2rdsA_	Alignment	not modelled	30.7	30	**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
						PDB header:hydrolase

80	c3ixzA_	Alignment	not modelled	29.4	30	**Chain:** A: **PDB Molecule:**potassium-transporting atpase alpha; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
81	c2de0X_	Alignment	not modelled	28.5	21	**PDB header:**transferase **Chain:** X: **PDB Molecule:**alpha-(1,6)-fucosyltransferase; **PDBTitle:** crystal structure of human alpha 1,6-fucosyltransferase, fut8
82	d2a1xa1	Alignment	not modelled	28.5	45	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**PhyH-like
83	c3gjbA_	Alignment	not modelled	28.4	50	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cytc3; **PDBTitle:** cytc3 with fe(ii) and alpha-ketoglutarate
84	c1wzoC_	Alignment	not modelled	28.2	21	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hpce; **PDBTitle:** crystal structure of the hpce from thermus thermophilus hb8
85	d1njjb1	Alignment	not modelled	27.6	29	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
86	d1vkya_	Alignment	not modelled	27.6	33	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
87	c3j09A_	Alignment	not modelled	27.3	21	**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
88	d1aono_	Alignment	not modelled	26.8	26	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
89	c2l8kA_	Alignment	not modelled	26.6	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 7; **PDBTitle:** nmr structure of the arterivirus nonstructural protein 7 alpha (nsp72 alpha)
90	c3ibmB_	Alignment	not modelled	25.6	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
91	d2ja9a1	Alignment	not modelled	25.3	41	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
92	c2qf4A_	Alignment	not modelled	25.0	33	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**cell shape determining protein mrec; **PDBTitle:** high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form)
93	d1hkva1	Alignment	not modelled	24.9	36	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
94	c3es4B_	Alignment	not modelled	24.6	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein duf861 with a rmlc-like cupin fold; **PDBTitle:** crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
95	d1y71a1	Alignment	not modelled	24.4	39	**Fold:**SH3-like barrel **Superfamily:**Kinase-associated protein B-like **Family:**Kinase-associated protein B-like
96	c3j08A_	Alignment	not modelled	24.4	21	**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
97	d1wdia_	Alignment	not modelled	24.3	29	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like
98	d1twia1	Alignment	not modelled	23.9	21	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
99	c2xxzA_	Alignment	not modelled	23.7	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysine-specific demethylase 6b; **PDBTitle:** crystal structure of the human jmjd3 jumonji domain
100	d3c9ua2	Alignment	not modelled	23.2	33	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
101	d2caya1	Alignment	not modelled	23.2	35	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**VPS36 N-terminal domain-like
102	c3anuA_	Alignment	not modelled	23.2	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**d-serine dehydratase; **PDBTitle:** crystal structure of d-serine dehydratase from chicken kidney
103	d1s04a_	Alignment	not modelled	23.0	36	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
104	c3lyiA_	Alignment	not modelled	22.9	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bromodomain-containing protein 1; **PDBTitle:** pwwp domain of human bromodomain-containing protein 1
105	d1xnea_	Alignment	not modelled	22.9	29	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
						Fold:PK beta-barrel domain-like

106	d1a3xa1	Alignment	not modelled	22.5	7	**Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
107	c2nn6H_	Alignment	not modelled	22.3	33	**PDB header:**hydrolase/transferase **Chain:** H: **PDB Molecule:**exosome complex exonuclease rrp4; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
108	c3tu8A_	Alignment	not modelled	21.9	41	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**burkholderia lethal factor 1 (blf1); **PDBTitle:** crystal structure of the burkholderia lethal factor 1 (blf1)
109	d1f3ta1	Alignment	not modelled	21.8	29	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
110	d2toda1	Alignment	not modelled	21.7	31	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
111	d7odca1	Alignment	not modelled	21.2	36	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
112	d1clia2	Alignment	not modelled	21.2	27	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
113	c2dfuB_	Alignment	not modelled	20.8	29	**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
114	c2p5dA_	Alignment	not modelled	20.7	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0310 protein mjecl36; **PDBTitle:** crystal structure of mjecl36 from methanocaldococcus2 jannaschii dsm 2661
115	c3rfuC_	Alignment	not modelled	20.5	18	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
116	d2grea1	Alignment	not modelled	20.5	31	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Aminopeptidase/glucanase lid domain **Family:**Aminopeptidase/glucanase lid domain
117	c3l53F_	Alignment	not modelled	20.3	35	**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