Phyre^{2}

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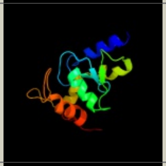
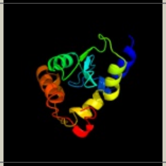
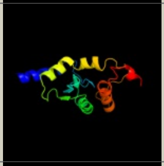
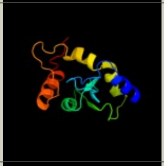
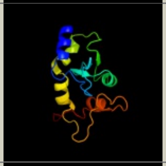
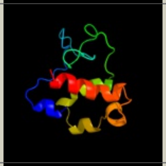
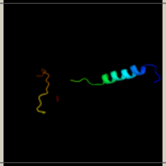
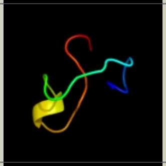
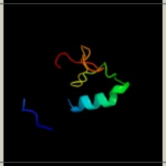
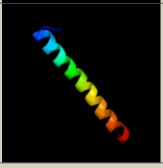
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d9lA_	Alignment		100.0	95	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**nucleoporin-like protein rip; **PDBTitle:** solution structure of the arfgap domain of human rip
2	c3lvrE_	Alignment		100.0	19	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**arf-gap with sh3 domain, ank repeat and ph domain- **PDBTitle:** the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium
3	c2iqjB_	Alignment		100.0	25	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**stromal membrane-associated protein 1-like; **PDBTitle:** crystal structure of the gap domain of smap1l (loc64744)2 stromal membrane-associated protein 1-like
4	c3fehA_	Alignment		100.0	24	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**centaurin-alpha-1; **PDBTitle:** crystal structure of full length centaurin alpha-1
5	d1dcqa2	Alignment		100.0	21	**Fold:**ArfGap/RecO-like zinc finger **Superfamily:**ArfGap/RecO-like zinc finger **Family:**Pyk2-associated protein beta ARF-GAP domain
6	c3jueA_	Alignment		100.0	20	**PDB header:**protein transport/endocytosis **Chain:** A: **PDB Molecule:**arfgap with coiled-coil, ank repeat and ph domain- **PDBTitle:** crystal structure of arfgap and ank repeat domain of acap1
7	c1dcqA_	Alignment		100.0	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**pyk2-associated protein beta; **PDBTitle:** crystal structure of the arf-gap domain and ankyrin repeats2 of papbeta.
8	c2b0oF_	Alignment		100.0	19	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**uplc1; **PDBTitle:** crystal structure of uplc1 gap domain
9	c2owaB_	Alignment		100.0	21	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**arfgap-like finger domain containing protein; **PDBTitle:** crystal structure of putative gtpase activating protein for2 adp ribosylation factor from cryptosporidium parvum3 (cgd5_1040)
10	c2p57A_	Alignment		100.0	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**gtpase-activating protein znf289; **PDBTitle:** gap domain of znf289, an id1-regulated zinc finger protein
11	c3o47A_	Alignment		100.0	23	**PDB header:**hydrolase, hydrolase activator **Chain:** A: **PDB Molecule:**adp-ribosylation factor gtpase-activating protein 1, adp- **PDBTitle:** crystal structure of arfgap1-arf1 fusion protein

12	c3dwdB_	Alignment		100.0	23	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**adp-ribosylation factor gtpase-activating protein 1; **PDBTitle:** crystal structure of the arfgap domain of human arfgap1
13	d1u5ka2	Alignment		96.4	18	**Fold:**ArfGap/RecO-like zinc finger **Superfamily:**ArfGap/RecO-like zinc finger **Family:**RecO C-terminal domain-like
14	c1u5kA_	Alignment		95.9	16	**PDB header:**recombination,replication **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** recombinational repair protein reco
15	c3bjiA_	Alignment		92.3	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** structural basis of promiscuous guanine nucleotide exchange2 by the t-cell essential vav1
16	c1y1yS_	Alignment		73.8	17	**PDB header:**transferase/transcription/dna-rna hybrid **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis-dna/rna complex
17	d1y0ja1	Alignment		67.5	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
18	c1d4uA_	Alignment		66.8	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**nucleotide excision repair protein xpa (xpa-mbd); **PDBTitle:** interactions of human nucleotide excision repair protein2 xpa with rpa70 and dna: chemical shift mapping and 15n nmr3 relaxation studies
19	c3a1bA_	Alignment		60.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna (cytosine-5)-methyltransferase 3a, histone h3.1; **PDBTitle:** crystal structure of the dnmt3a add domain in complex with histone h3
20	d2je6b2	Alignment		57.4	21	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
21	c3ihpB_	Alignment	not modelled	57.1	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** covalent ubiquitin-usp5 complex
22	c2zetD_	Alignment	not modelled	54.1	29	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**melanophilin; **PDBTitle:** crystal structure of the small gtpase rab27b complexed with2 the slp homology domain of slac2-a/melanophilin
23	d2ba0d2	Alignment	not modelled	53.8	15	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
24	c1pqvS_	Alignment	not modelled	53.5	17	**PDB header:**transferase/transcription **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis complex
25	d2crga1	Alignment	not modelled	53.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
26	d2br2b2	Alignment	not modelled	51.9	18	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
27	d1vqoz1	Alignment	not modelled	51.8	15	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
28	d1jj2y_	Alignment	not modelled	51.7	23	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
29	c1vshD	Alignment	not modelled	50.7	21	**PDB header:**structural protein/rna **Chain:** D: **PDB Molecule:**ribosomal protein l37a;

29	c1yshD_	Alignment	not modelled	50.7	21	**PDBTitle:** localization and dynamic behavior of ribosomal protein l30e
30	d1gnfa_	Alignment	not modelled	50.6	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
31	c2zkrz_	Alignment	not modelled	50.2	23	**PDB header:**ribosomal protein/rna **Chain:** Z: **PDB Molecule:**e site t-rna; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
32	c2qa4Z_	Alignment	not modelled	50.1	15	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
33	d1pjua1	Alignment	not modelled	48.9	44	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
34	c4a17Y_	Alignment	not modelled	48.4	18	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**rpl37a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
35	d5gata_	Alignment	not modelled	48.0	22	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
36	d2idaa1	Alignment	not modelled	47.8	31	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**Zf-UBP
37	c3f4yF_	Alignment	not modelled	47.5	36	**PDB header:**viral protein **Chain:** F: **PDB Molecule:**mutant peptide derived from hiv gp41 chr domain; **PDBTitle:** hiv gp41 six-helix bundle containing a mutant chr alpha-2 peptide sequence
38	d1ffkw_	Alignment	not modelled	46.4	26	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
39	d2vuti1	Alignment	not modelled	46.3	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
40	c3auoB_	Alignment	not modelled	45.1	9	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase beta family (x family); **PDBTitle:** dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp
41	d1zbdb_	Alignment	not modelled	44.8	18	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
42	c2hr5B_	Alignment	not modelled	44.5	13	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
43	c3h00A_	Alignment	not modelled	44.4	25	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** structure of the c-terminal domain of a putative hiv-1 gp412 fusion intermediate
44	c2kgoA_	Alignment	not modelled	44.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ybii; **PDBTitle:** solution nmr structure of zn finger protein ybil from escherichia2 coli. nesg target et107, ocsp target ec0402
45	c2i50A_	Alignment	not modelled	43.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 16; **PDBTitle:** solution structure of ubp-m znf-ubp domain
46	c2d8uA_	Alignment	not modelled	43.8	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin ligase trim63; **PDBTitle:** solution structure of the b-box domain of the human2 tripartite motif-containing 63 protein
47	c3cc4Z_	Alignment	not modelled	42.3	15	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** co-crystal structure of anisomycin bound to the 50s ribosomal subunit
48	d3gata_	Alignment	not modelled	42.2	16	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Erythroid transcription factor GATA-1
49	c3c65A_	Alignment	not modelled	41.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uvrabc system protein c; **PDBTitle:** crystal structure of bacillus stearothermophilus uvrc 5'2 endonuclease domain
50	d2nllb_	Alignment	not modelled	40.2	24	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
51	d1v6za2	Alignment	not modelled	39.9	9	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
52	d1hcqa_	Alignment	not modelled	39.8	22	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
53	c4a5bA_	Alignment	not modelled	38.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside-triphosphatase 2; **PDBTitle:** crystal structure of the c258s/c268s variant of toxoplasma gondii2 nucleoside triphosphate diphosphohydrolase 1 (ntpdase1)
54	c2yusA_	Alignment	not modelled	38.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin- **PDBTitle:** solution structure of the sant domain of human swi/snf-2 related matrix-associated actin-dependent regulator of3 chromatin subfamily c member 1

55	c2kdxA_	Alignment	not modelled	38.0	21	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
56	c2junA_	Alignment	not modelled	37.9	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**midline-1; **PDBTitle:** structure of the mid1 tandem b-boxes reveals an interaction2 reminiscent of intermolecular ring heterodimers
57	d2a2pa1	Alignment	not modelled	37.3	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
58	c1kxuA_	Alignment	not modelled	37.2	16	**PDB header:**regulatory protein **Chain:** A: **PDB Molecule:**cyclin h; **PDBTitle:** cyclin h, a positive regulatory subunit of cdk activating kinase
59	d1cjya2	Alignment	not modelled	37.1	19	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**Lysophospholipase
60	d2g45a1	Alignment	not modelled	36.6	35	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**Zf-UBP
61	c3k7aM_	Alignment	not modelled	36.1	32	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
62	c1dvbA_	Alignment	not modelled	35.9	29	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
63	d2dq5a1	Alignment	not modelled	35.5	23	**Fold:**B-box zinc-binding domain **Superfamily:**B-box zinc-binding domain **Family:**B-box zinc-binding domain
64	d2cora1	Alignment	not modelled	34.8	17	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
65	c1oahA_	Alignment	not modelled	34.3	17	**PDB header:**reductase **Chain:** A: **PDB Molecule:**cytochrome c nitrite reductase; **PDBTitle:** cytochrome c nitrite reductase from desulfovibrio2 desulfuricans atcc 27774: the relevance of the two3 calcium sites in the structure of the catalytic subunit4 (nrfa).
66	d1oaha_	Alignment	not modelled	34.3	17	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Di-heme elbow motif
67	c2vr0A_	Alignment	not modelled	34.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c nitrite reductase, catalytic subunit nfra; **PDBTitle:** crystal structure of cytochrome c nitrite reductase nrfha2 complex bound to the hqno inhibitor
68	d1dl6a_	Alignment	not modelled	33.8	13	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
69	c2egmA_	Alignment	not modelled	33.5	17	**PDB header:**transcription/metal binding protein **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 41; **PDBTitle:** solution structure of the zf-b_box domain from human2 tripartite motif protein 41
70	c1yuzB_	Alignment	not modelled	32.6	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
71	c2cszA_	Alignment	not modelled	32.6	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**synaptotagmin-like protein 4; **PDBTitle:** solution structure of the ring domain of the synaptotagmin-2 like protein 4
72	c2p3xA_	Alignment	not modelled	32.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**polyphenol oxidase, chloroplast; **PDBTitle:** crystal structure of grenache (vitis vinifera) polyphenol2 oxidase
73	d1glua_	Alignment	not modelled	32.3	22	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
74	c3agrB_	Alignment	not modelled	32.2	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoside triphosphate hydrolase; **PDBTitle:** crystal structure of nucleoside triphosphate hydrolases from neospora2 caninum
75	d2djaa1	Alignment	not modelled	32.1	20	**Fold:**B-box zinc-binding domain **Superfamily:**B-box zinc-binding domain **Family:**B-box zinc-binding domain
76	c1qh2B_	Alignment	not modelled	32.0	41	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**protein (trypsin inhibitor c2); **PDBTitle:** chymotrypsin inhibitor (c2) from nicotiana alata
77	c3ky9B_	Alignment	not modelled	31.8	13	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** autoinhibited vav1
78	c3jyw9_	Alignment	not modelled	31.8	13	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**60s ribosomal protein l43; **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
79	d1p6oa_	Alignment	not modelled	31.7	24	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
80	d1unld_	Alignment	not modelled	31.3	31	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin

81	d2bkra1	Alignment	not modelled	31.3	13	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Adenain-like
82	c1tjlD_	Alignment	not modelled	31.3	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** crystal structure of transcription factor dksa from e. coli
83	d1fyba1	Alignment	not modelled	31.2	43	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
84	c2w9mB_	Alignment	not modelled	31.1	7	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
85	d1ce3a_	Alignment	not modelled	30.7	42	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
86	c1unhD_	Alignment	not modelled	30.7	31	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**cyclin-dependent kinase 5 activator 1; **PDBTitle:** structural mechanism for the inhibition of cdk5-p25 by2 roscovitine, aloisine and indirubin.
87	d1ynwa1	Alignment	not modelled	30.7	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
88	d1pfta_	Alignment	not modelled	30.5	24	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
89	c2gb5B_	Alignment	not modelled	30.1	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nadh pyrophosphatase; **PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
90	c3c5kA_	Alignment	not modelled	29.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histone deacetylase 6; **PDBTitle:** crystal structure of human hdac6 zinc finger domain
91	c3pihA_	Alignment	not modelled	29.6	15	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
92	d2k2na1	Alignment	not modelled	29.1	20	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
93	d1kb2a_	Alignment	not modelled	27.9	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
94	c3o5aB_	Alignment	not modelled	27.9	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diheme cytochrome c napb; **PDBTitle:** crystal structure of partially reduced periplasmic nitrate reductase2 from cupriavidus necator using ionic liquids
95	d1rg6a_	Alignment	not modelled	27.6	18	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
96	d1dszb_	Alignment	not modelled	27.4	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
97	d1ik7a_	Alignment	not modelled	27.0	22	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
98	c2kq9A_	Alignment	not modelled	26.9	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** solution structure of dnak suppressor protein from agrobacterium2 tumefaciens c58. northeast structural genomics consortium target3 att12/ontario center for structural proteomics target atc0888
99	c1l4aE_	Alignment	not modelled	26.9	21	**PDB header:**endocytosis/exocytosis **Chain:** E: **PDB Molecule:**synaphin a; **PDBTitle:** x-ray structure of the neuronal complexin/snare complex2 from the squid loligo pealei
100	d1tiha_	Alignment	not modelled	26.6	43	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
101	c2eqrA_	Alignment	not modelled	26.3	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear receptor corepressor 1; **PDBTitle:** solution structure of the first sant domain from human2 nuclear receptor corepressor 1
102	c2eblA_	Alignment	not modelled	25.9	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**coup transcription factor 1; **PDBTitle:** solution structure of the zinc finger, c4-type domain of2 human coup transcription factor 1
103	c2j7aE_	Alignment	not modelled	25.7	17	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**cytochrome c nitrite reductase nrfa; **PDBTitle:** crystal structure of cytochrome c nitrite reductase nrfha2 complex from desulfovibrio vulgaris
104	c1x6iB_	Alignment	not modelled	25.0	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ygfy; **PDBTitle:** crystal structure of ygfy from escherichia coli
105	d2d8ua1	Alignment	not modelled	24.6	18	**Fold:**B-box zinc-binding domain **Superfamily:**B-box zinc-binding domain **Family:**B-box zinc-binding domain
106	d1gff1_	Alignment	not modelled	24.4	26	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Microviridae-like VP
107	d1oyvi_	Alignment	not modelled	24.3	44	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors

						Family: Plant proteinase inhibitors
108	d1b8ta2	Alignment	not modelled	24.0	24	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
109	d1lo1a_	Alignment	not modelled	24.0	24	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
110	c3f29A_	Alignment	not modelled	23.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**eight-heme nitrite reductase; **PDBTitle:** structure of the thioalkalivibrio nitratireducens2 cytochrome c nitrite reductase in complex with sulfite
111	c3dzuD_	Alignment	not modelled	23.8	27	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**peroxisome proliferator-activated receptor gamma; **PDBTitle:** intact ppar gamma - rxr alpha nuclear receptor complex on dna bound2 with bvt.13, 9-cis retinoic acid and ncoa2 peptide
112	d1kb6b_	Alignment	not modelled	23.5	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
113	c2pv0A_	Alignment	not modelled	23.1	10	**PDB header:**transferase regulator **Chain:** A: **PDB Molecule:**dna (cytosine-5)-methyltransferase 3-like; **PDBTitle:** dna methyltransferase 3 like protein (dnmt3l)
114	c3izci_	Alignment	not modelled	22.8	35	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein rpl10 (l10e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
115	c1fybA_	Alignment	not modelled	21.9	43	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**proteinase inhibitor; **PDBTitle:** solution structure of c1-t1, a two-domain proteinase2 inhibitor derived from the circular precursor protein na-3 propi from nicotiana alata
116	d1r4ra_	Alignment	not modelled	21.8	25	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
117	d1m06f_	Alignment	not modelled	21.7	21	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**ssDNA viruses **Family:**Microviridae-like VP
118	c2xssB_	Alignment	not modelled	21.5	7	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-specific 3', 5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of gafb from the human phosphodiesterase 5
119	d1r4ia_	Alignment	not modelled	21.1	21	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
120	c1r4iA_	Alignment	not modelled	21.1	21	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**androgen receptor; **PDBTitle:** crystal structure of androgen receptor dna-binding domain2 bound to a direct repeat response element