Phyre^{2}

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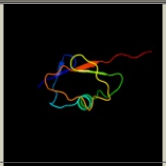
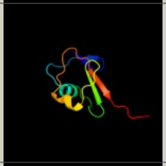
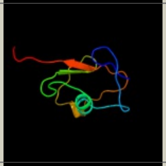
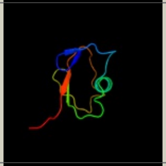
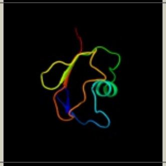
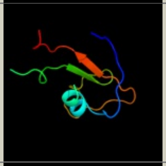
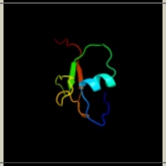
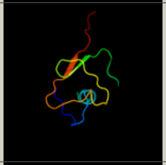
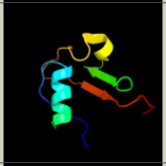
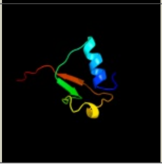
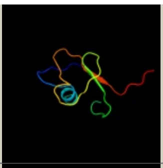
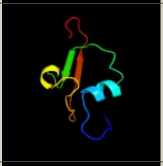
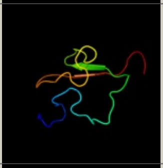
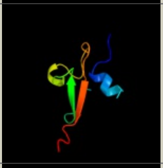
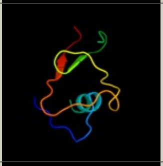
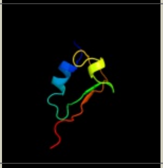
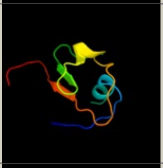
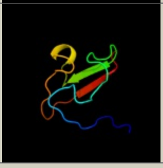
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kl0A_	Alignment		99.9	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
2	d1zud21	Alignment		99.9	100	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
3	c3cwiA_	Alignment		99.8	24	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this; **PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
4	d2cu3a1	Alignment		99.8	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
5	d1tygb_	Alignment		99.8	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
6	c1tygG_	Alignment		99.8	16	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
7	c2g1eA_	Alignment		98.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ta0895; **PDBTitle:** solution structure of ta0895
8	c2qieB_	Alignment		98.2	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase small subunit; **PDBTitle:** staphylococcus aureus molybdopterin synthase in complex2 with precursor z
9	c3po0A_	Alignment		97.9	22	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small archaeal modifier protein 1; **PDBTitle:** crystal structure of samp1 from haloferax volcanii
10	d1v8ca1	Alignment		97.8	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
11	c3rpfC_	Alignment		97.7	26	**PDB header:**transferase **Chain:** C: **PDB Molecule:**molybdopterin converting factor, subunit 1 (moad); **PDBTitle:** protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695

12	d1fm0d_	Alignment		97.6	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
13	c2qjlA_	Alignment		97.6	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin-related modifier 1; **PDBTitle:** crystal structure of urm1
14	c2l52A_	Alignment		97.5	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**methanosarcina acetivorans samp1 homolog; **PDBTitle:** solution structure of the small archaeal modifier protein 1 (samp1)2 from methanosarcina acetivorans
15	d1xo3a_	Alignment		97.4	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
16	d1vjka_	Alignment		97.4	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD
17	c2k9xA_	Alignment		97.4	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of urm1 from trypanosoma brucei
18	d1wgka_	Alignment		97.3	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
19	c1v8cA_	Alignment		97.3	28	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**moad related protein; **PDBTitle:** crystal structure of moad related protein from thermus2 thermophilus hb8
20	c3dwmA_	Alignment		97.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**9.5 kda culture filtrate antigen cfp10a; **PDBTitle:** crystal structure of mycobacterium tuberculosis cyso, an antigen
21	d1ryja_	Alignment	not modelled	97.2	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
22	c2kmmA_	Alignment	not modelled	97.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**guanosine-3',5'-bis(diphosphate) 3'- **PDBTitle:** solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
23	d1rwsa_	Alignment	not modelled	96.9	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
24	c3hvzB_	Alignment	not modelled	96.1	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
25	d1tkea1	Alignment	not modelled	95.3	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
26	d3c8ya2	Alignment	not modelled	94.9	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
27	d1vlba2	Alignment	not modelled	94.8	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
28	c1wwtA_	Alignment	not modelled	94.4	5	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase, cytoplasmic; **PDBTitle:** solution structure of the tgs domain from human threonyl-2 trna synthetase

29	c1c4cA_	Alignment	not modelled	93.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (fe-only hydrogenase); **PDBTitle:** binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
30	c2hj1A_	Alignment	not modelled	93.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
31	d2hj1a1	Alignment	not modelled	93.5	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**HI0395-like
32	c1nyqA_	Alignment	not modelled	92.6	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase 1; **PDBTitle:** structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
33	d1dgja2	Alignment	not modelled	91.9	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
34	d1t3qa2	Alignment	not modelled	91.4	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
35	d1n62a2	Alignment	not modelled	91.2	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
36	d1ffva2	Alignment	not modelled	89.9	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
37	d2fug33	Alignment	not modelled	89.7	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
38	d1rm6c2	Alignment	not modelled	89.0	7	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
39	d1ud7a_	Alignment	not modelled	88.0	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
40	d1wxqa2	Alignment	not modelled	88.0	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**G domain-linked domain
41	c1tkeA_	Alignment	not modelled	87.8	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
42	c1yx5B_	Alignment	not modelled	86.1	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ubiquitin; **PDBTitle:** solution structure of s5a uim-1/ubiquitin complex
43	d1c3ta_	Alignment	not modelled	85.7	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
44	c2ekiA_	Alignment	not modelled	84.2	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**developmentally-regulated gtp-binding protein 1; **PDBTitle:** solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1
45	c1n60D_	Alignment	not modelled	83.8	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**carbon monoxide dehydrogenase small chain; **PDBTitle:** crystal structure of the cu,mo-co dehydrogenase (codh); cyanide-2 inactivated form
46	c1t3qD_	Alignment	not modelled	82.9	7	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
47	d1nyra2	Alignment	not modelled	80.7	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
48	c2fugC_	Alignment	not modelled	79.1	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
49	c1ffuA_	Alignment	not modelled	78.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cuts, iron-sulfur protein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
50	c3hrdH_	Alignment	not modelled	78.5	15	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
51	d1euvb_	Alignment	not modelled	76.3	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
52	c1rm6F_	Alignment	not modelled	75.5	7	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
53	c1qf6A_	Alignment	not modelled	73.4	13	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna

54	d1uela_	Alignment	not modelled	72.8	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
55	c1vlbA_	Alignment	not modelled	72.8	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
56	d1ogwa_	Alignment	not modelled	72.1	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
57	d1wm3a_	Alignment	not modelled	71.5	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
58	c2kd0A_	Alignment	not modelled	70.9	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**lrr repeats and ubiquitin-like domain-containing **PDBTitle:** nmr solution structure of o64736 protein from arabidopsis2 thaliana. northeast structural genomics consortium mega3 target ar3445a
59	d1wgga_	Alignment	not modelled	69.7	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
60	d1jroa2	Alignment	not modelled	69.4	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
61	d1v97a2	Alignment	not modelled	69.4	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
62	d1v86a_	Alignment	not modelled	66.5	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
63	c3tixA_	Alignment	not modelled	64.4	12	**PDB header:**gene regulation/protein binding **Chain:** A: **PDB Molecule:**ubiquitin-like protein smt3, rna-induced transcriptional **PDBTitle:** crystal structure of the chp1-tas3 complex core
64	d1bt0a_	Alignment	not modelled	63.2	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
65	c3a4rB_	Alignment	not modelled	63.0	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nfatc2-interacting protein; **PDBTitle:** the crystal structure of sumo-like domain 2 in nip45
66	d2io3b1	Alignment	not modelled	60.7	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
67	d1we7a_	Alignment	not modelled	59.8	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
68	d1ndda_	Alignment	not modelled	59.3	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
69	c1dgjA_	Alignment	not modelled	59.3	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
70	c2jxxA_	Alignment	not modelled	58.1	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**nfatc2-interacting protein; **PDBTitle:** nmr solution structure of ubiquitin-like domain of2 nfatc2ip. northeast structural genomics consortium target3 hr5627
71	d1wh3a_	Alignment	not modelled	57.8	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
72	c3pgeA_	Alignment	not modelled	57.1	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**sumo-modified proliferating cell nuclear antigen; **PDBTitle:** structure of sumoylated pcna
73	c3goeA_	Alignment	not modelled	54.6	17	**PDB header:**recombination, replication **Chain:** A: **PDB Molecule:**dna repair protein rad60; **PDBTitle:** molecular mimicry of sumo promotes dna repair
74	c3eubJ_	Alignment	not modelled	53.7	18	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
75	c3b9jI_	Alignment	not modelled	52.8	18	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine
76	d2faza1	Alignment	not modelled	52.6	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
77	d1sifa_	Alignment	not modelled	52.5	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
78	c2kanA_	Alignment	not modelled	51.6	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ar3433a; **PDBTitle:** solution nmr structure of ubiquitin-like domain of2 arabidopsis thaliana protein at2g32350. northeast3 structural genomics consortium target ar3433a
79	d2uyzb1	Alignment	not modelled	51.6	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
						PDB header:signaling protein

80	c2k8hA_	Alignment	not modelled	51.2	10	**Chain:** A: **PDB Molecule:**small ubiquitin protein; **PDBTitle:** solution structure of sumo from trypanosoma brucei
81	c2ekeC_	Alignment	not modelled	51.1	10	**PDB header:**ligase/protein binding **Chain:** C: **PDB Molecule:**ubiquitin-like protein smt3; **PDBTitle:** structure of a sumo-binding-motif mimic bound to smt3p-2 ubc9p: conservation of a noncovalent ubiquitin-like3 protein-e2 complex as a platform for selective4 interactions within a sumo pathway
82	d2piea1	Alignment	not modelled	47.7	21	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
83	d2g1la1	Alignment	not modelled	47.3	23	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
84	d1a5ra_	Alignment	not modelled	46.6	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
85	d1gxca_	Alignment	not modelled	46.6	17	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
86	c1gxcA_	Alignment	not modelled	46.6	17	**PDB header:**phosphoprotein-binding domain **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase chk2; **PDBTitle:** fha domain from human chk2 kinase in complex with a2 synthetic phosphopeptide
87	c2l76A_	Alignment	not modelled	46.4	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nfatc2-interacting protein; **PDBTitle:** solution nmr structure of human nfatc2ip ubiquitin-like domain,2 nfatc2ip_244_338, nesg target ht65a/ocsp target hs00387_244_338/sgc-3 toronto
88	d1wz0a1	Alignment	not modelled	45.4	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
89	d1v5oa_	Alignment	not modelled	44.1	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
90	d1yfba1	Alignment	not modelled	44.0	14	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
91	c2l7rA_	Alignment	not modelled	43.3	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin-like protein fubi; **PDBTitle:** solution nmr structure of n-terminal ubiquitin-like domain of fubi, a2 ribosomal protein s30 precursor from homo sapiens. northeast3 structural genomics consortium (nesg) target hr6166
92	d1j8ca_	Alignment	not modelled	42.8	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
93	c3dh3C_	Alignment	not modelled	42.7	12	**PDB header:**isomerase/rna **Chain:** C: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f; **PDBTitle:** crystal structure of rluf in complex with a 22 nucleotide2 rna substrate
94	d1g3ga_	Alignment	not modelled	42.4	25	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
95	c2eh0A_	Alignment	not modelled	41.0	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**kinesin-like protein kif1b; **PDBTitle:** solution structure of the fha domain from human kinesin-2 like protein kif1b
96	c3lzkC_	Alignment	not modelled	40.8	10	**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
97	c3kt9A_	Alignment	not modelled	40.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aprataxin; **PDBTitle:** aprataxin fha domain
98	d2fy9a1	Alignment	not modelled	40.2	23	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**AbrB N-terminal domain-like
99	d1iyfa_	Alignment	not modelled	40.0	7	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
100	c3hx1B_	Alignment	not modelled	39.4	30	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**slr1951 protein; **PDBTitle:** crystal structure of the slr1951 protein from synechocystis sp.2 northeast structural genomics consortium target sgr167a
101	c2w3rG_	Alignment	not modelled	38.5	18	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
102	d1yjma1	Alignment	not modelled	38.4	13	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
103	c3jxoB_	Alignment	not modelled	37.0	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**trka-n domain protein; **PDBTitle:** crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
104	c2w1tB_	Alignment	not modelled	37.0	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt

105	d1wy8a1	Alignment	not modelled	36.8	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
106	d1p9ka_	Alignment	not modelled	36.7	18	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**YbcJ-like
107	c3fm8A_	Alignment	not modelled	36.4	27	**PDB header:**transport protein/hydrolase activator **Chain:** A: **PDB Molecule:**kinesin-like protein kif13b; **PDBTitle:** crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
108	c2ro5B_	Alignment	not modelled	36.4	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** rdc-refined solution structure of the n-terminal dna2 recognition domain of the bacillus subtilis transition-3 state regulator spovt
109	c2glwA_	Alignment	not modelled	35.3	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**92aa long hypothetical protein; **PDBTitle:** the solution structure of phs018 from pyrococcus horikoshii
110	d1dm9a_	Alignment	not modelled	33.5	24	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
111	c1dm9A_	Alignment	not modelled	33.5	24	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
112	d1zkha1	Alignment	not modelled	33.2	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
113	c2bknA_	Alignment	not modelled	33.0	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein ph0236; **PDBTitle:** structure analysis of unknown function protein
114	c2jqlA_	Alignment	not modelled	31.2	26	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna damage response protein kinase dun1; **PDBTitle:** nmr structure of the yeast dun1 fha domain in complex with2 a doubly phosphorylated (pt) peptide derived from rad533 scd1
115	c3m62B_	Alignment	not modelled	31.1	15	**PDB header:**ligase/protein binding **Chain:** B: **PDB Molecule:**uv excision repair protein rad23; **PDBTitle:** crystal structure of ufd2 in complex with the ubiquitin-like (ubl)2 domain of rad23
116	c2dziA_	Alignment	not modelled	31.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquitin-like protein 4a; **PDBTitle:** 2dzi/solution structure of the n-terminal ubiquitin-like2 domain in human ubiquitin-like protein 4a (gdx)
117	c1yj5C_	Alignment	not modelled	28.5	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase fha domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
118	c2kdiA_	Alignment	not modelled	27.8	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquitin, vacuolar protein sorting-associated **PDBTitle:** solution structure of a ubiquitin/uim fusion protein
119	d1vcta2	Alignment	not modelled	27.4	16	**Fold:**TrkA C-terminal domain-like **Superfamily:**TrkA C-terminal domain-like **Family:**TrkA C-terminal domain-like
120	d1oqya4	Alignment	not modelled	27.4	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related