

Phyre2

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 Description RVBD0416_(thiS)_502170_502376
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ki0A_	Alignment		99.9	37	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	25	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	d1tygb_	Alignment		99.8	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
5	d2cu3a1	Alignment		99.8	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
6	c1tygG_	Alignment		99.8	24	PDB header: biosynthetic protein Chain: G: PDB Molecule: yjbs; PDBTitle: structure of the thiazole synthase/thiS complex
7	c6jzbD_	Alignment		98.2	22	PDB header: transferase Chain: D: PDB Molecule: moad/thiS family protein; PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
8	c6jc0A_	Alignment		98.2	21	PDB header: transferase Chain: A: PDB Molecule: putative molybdenum cofactor biosynthesis protein d2 PDBTitle: structural analysis of molybdopterin synthases from two mycobacteria2 pathogens
9	c2g1eA_	Alignment		98.2	15	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ta0895; PDBTitle: solution structure of ta0895
10	c2qieB_	Alignment		98.2	18	PDB header: transferase Chain: B: PDB Molecule: molybdopterin synthase small subunit; PDBTitle: staphylococcus aureus molybdopterin synthase in complex with precursor2 z
11	c2m19A_	Alignment		97.9	29	PDB header: protein binding Chain: A: PDB Molecule: molybdopterin converting factor subunit 1; PDBTitle: solution structure of the haloferax volcanii hvo 2177 protein

12	c4n6eB_	Alignment		97.9	28	PDB header: lyase/biosynthetic protein Chain: B: PDB Molecule: this/moad family protein; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
13	c3po0A_	Alignment		97.9	29	PDB header: protein binding Chain: A: PDB Molecule: small archaeal modifier protein 1; PDBTitle: crystal structure of samp1 from haloferax volcanii
14	c3rpfC_	Alignment		97.8	24	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
15	c5mpoA_	Alignment		97.8	14	PDB header: transferase Chain: A: PDB Molecule: molybdopterin synthase sulfur carrier subunit; PDBTitle: crystal structure of human molybdopterin synthase complex
16	d1v8ca1	Alignment		97.8	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: MoadD
17	d1ryja_	Alignment		97.7	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
18	c2qjlA_	Alignment		97.6	16	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin-related modifier 1; PDBTitle: crystal structure of urm1
19	d1fm0d_	Alignment		97.5	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: MoadD
20	c2l52A_	Alignment		97.5	17	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
21	c2kmmA_	Alignment	not modelled	97.4	26	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)
22	d1xo3a_	Alignment	not modelled	97.3	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: C9orf74 homolog
23	d1rwsa_	Alignment	not modelled	97.3	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: ThiS
24	d1vjka_	Alignment	not modelled	97.3	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: MoadD
25	c2k9xA_	Alignment	not modelled	97.3	24	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of urm1 from trypanosoma brucei
26	c1v8cA_	Alignment	not modelled	97.3	17	PDB header: protein binding Chain: A: PDB Molecule: moad related protein; PDBTitle: crystal structure of moad related protein from thermus2 thermophilus hb8
27	d1wgka_	Alignment	not modelled	97.2	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: C9orf74 homolog
28	c3dwmA_	Alignment	not modelled	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 PDB header: structural genomics, unknown function

29	c3hvvB_	Alignment	not modelled	96.8	15	Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the tgs domain of the clolep_03100 protein from 2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
30	d1tkea1	Alignment	not modelled	96.1	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
31	c5xf9F_	Alignment	not modelled	96.1	13	PDB header: oxidoreductase Chain: F: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
32	c5ldxG_	Alignment	not modelled	95.7	25	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class3.
33	c5ldwG_	Alignment	not modelled	95.7	25	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class1
34	c5ghaF_	Alignment	not modelled	95.6	27	PDB header: transferase/transport protein Chain: F: PDB Molecule: sulfur carrier ttub; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
35	d3c8ya2	Alignment	not modelled	95.3	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
36	c1wwtA_	Alignment	not modelled	95.1	22	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase, cytoplasmic; PDBTitle: solution structure of the tgs domain from human threonyl-2 trna synthetase
37	c1c4cA_	Alignment	not modelled	95.0	17	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
38	c5lc5G_	Alignment	not modelled	94.9	25	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class2
39	c6gcsA_	Alignment	not modelled	94.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
40	c5lnk3_	Alignment	not modelled	94.7	27	PDB header: oxidoreductase Chain: 3: PDB Molecule: mitochondrial complex i, 75 kda subunit; PDBTitle: entire ovine respiratory complex i
41	d1vlba2	Alignment	not modelled	93.9	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
42	d2hj1a1	Alignment	not modelled	93.8	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Moad/ThiS Family: HI0395-like
43	c2hj1A_	Alignment	not modelled	93.8	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 from 2 haemophilus influenzae
44	d1wxqa2	Alignment	not modelled	93.2	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: G domain-linked domain
45	c1nyqA_	Alignment	not modelled	91.4	21	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
46	c2fugC_	Alignment	not modelled	91.3	19	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
47	d1c3ta_	Alignment	not modelled	91.0	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
48	c1yx5B_	Alignment	not modelled	90.9	18	PDB header: hydrolase Chain: B: PDB Molecule: ubiquitin; PDBTitle: solution structure of s5a uim-1/ubiquitin complex
49	d1n62a2	Alignment	not modelled	90.9	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
50	d1t3qa2	Alignment	not modelled	90.4	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
51	d1nyra2	Alignment	not modelled	90.2	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
52	d2fug33	Alignment	not modelled	90.2	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
53	d1ud7a_	Alignment	not modelled	89.7	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
54	c5g5gA_	Alignment	not modelled	89.5	23	PDB header: oxidoreductase Chain: A: PDB Molecule: putative xanthine dehydrogenase yagt iron-sulfur-binding PDBTitle: escherichia coli periplasmic aldehyde oxidase
55	c1tkaA_	Alignment	not modelled	89.4	21	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase;

55	c1rkaA	Alignment	not modelled	85.4	41	PDBTitle: crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
56	d1rm6c2	Alignment	not modelled	88.5	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
57	c2ekiA	Alignment	not modelled	87.7	13	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
58	d1dgja2	Alignment	not modelled	86.9	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
59	c2lrwA	Alignment	not modelled	86.2	21	PDB header: cell cycle Chain: A: PDB Molecule: ubiquitin, putative; PDBTitle: solution structure of a ubiquitin-like protein from trypanosoma brucei
60	d1ogwa	Alignment	not modelled	85.5	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
61	d1wh3a	Alignment	not modelled	85.1	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
62	c4zohC	Alignment	not modelled	84.3	24	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase iron-sulfur subunit; PDBTitle: crystal structure of glyceraldehyde oxidoreductase
63	d1bt0a	Alignment	not modelled	83.7	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
64	d1euvb	Alignment	not modelled	83.2	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
65	c1n60D	Alignment	not modelled	82.7	11	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
66	c5gjlA	Alignment	not modelled	81.9	10	PDB header: protein binding Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of sumo from plasmodium falciparum
67	d1ffva2	Alignment	not modelled	81.9	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
68	c1vlbA	Alignment	not modelled	80.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
69	c3tixA	Alignment	not modelled	79.5	10	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
70	d1wm3a	Alignment	not modelled	78.0	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
71	c1qf6A	Alignment	not modelled	77.9	18	PDB header: ligase/rna Chain: A: PDB Molecule: threonyl-trna synthetase; PDBTitle: structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
72	c5jp1B	Alignment	not modelled	77.3	14	PDB header: hydrolase Chain: B: PDB Molecule: small ubiquitin-related modifier; PDBTitle: structure of xanthomonas campestris effector protein xopd bound to2 tomato sumo
73	c5xqmA	Alignment	not modelled	77.1	20	PDB header: signaling protein Chain: A: PDB Molecule: small ubiquitin-related modifier; PDBTitle: nmr solution structure of smo1, sumo homologue in caenorhabditis2 elegans
74	c3a4rB	Alignment	not modelled	77.1	11	PDB header: transcription Chain: B: PDB Molecule: nfatc2-interacting protein; PDBTitle: the crystal structure of sumo-like domain 2 in nip45
75	d1uela	Alignment	not modelled	76.8	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
76	d1ndda	Alignment	not modelled	76.5	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
77	c1t3qD	Alignment	not modelled	75.1	15	PDB header: oxidoreductase Chain: D: PDB Molecule: quinoline 2-oxidoreductase small subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
78	c3v7oB	Alignment	not modelled	74.9	10	PDB header: transcription Chain: B: PDB Molecule: minor nucleoprotein vp30; PDBTitle: crystal structure of the c-terminal domain of ebola virus vp30 (strain2 reston-89)
79	c5y6qA	Alignment	not modelled	74.4	24	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase small subunit; PDBTitle: crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
80	c2kanA	Alignment	not modelled	73.4	16	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 PDB header: protein binding

81	c2jxxA_	Alignment	not modelled	73.0	13	Chain: A: PDB Molecule: nfatc2-interacting protein; PDBTitle: nmr solution structure of ubiquitin-like domain of2 nfatc2ip. northeast structural genomics consortium target3 hr5627
82	c1ffuA_	Alignment	not modelled	71.3	16	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
83	d1we7a_	Alignment	not modelled	70.1	6	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
84	c2ekeC_	Alignment	not modelled	69.9	8	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
85	c3hrdH_	Alignment	not modelled	69.2	15	PDB header: oxidoreductase Chain: H: PDB Molecule: nicotinate dehydrogenase small fes subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
86	d1v97a2	Alignment	not modelled	68.1	32	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
87	c2kk8A_	Alignment	not modelled	67.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein at4g05270; PDBTitle: nmr solution structure of a putative uncharacterized protein2 obtained from arabidopsis thaliana: northeast structural3 genomics consortium target ar3449a
88	d1v86a_	Alignment	not modelled	67.6	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
89	c3pgeA_	Alignment	not modelled	67.0	10	PDB header: dna binding protein Chain: A: PDB Molecule: sumo-modified proliferating cell nuclear antigen; PDBTitle: structure of sumoylated pcna
90	d2io3b1	Alignment	not modelled	66.7	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
91	d1jroa2	Alignment	not modelled	66.0	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
92	c2l76A_	Alignment	not modelled	66.0	13	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
93	d2uyzb1	Alignment	not modelled	65.9	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
94	d2faza1	Alignment	not modelled	63.8	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
95	c1dgiA_	Alignment	not modelled	63.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
96	d1sifa_	Alignment	not modelled	63.0	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
97	c3goeA_	Alignment	not modelled	62.9	17	PDB header: recombination, replication Chain: A: PDB Molecule: dna repair protein rad60; PDBTitle: molecular mimicry of sumo promotes dna repair
98	c2kd0A_	Alignment	not modelled	62.9	15	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
99	c4k95G_	Alignment	not modelled	62.7	27	PDB header: ligase Chain: G: PDB Molecule: e3 ubiquitin-protein ligase parkin; PDBTitle: crystal structure of parkin
100	c2k8hA_	Alignment	not modelled	60.7	10	PDB header: signaling protein Chain: A: PDB Molecule: small ubiquitin protein; PDBTitle: solution structure of sumo from trypanosoma brucei
101	c5ogxA_	Alignment	not modelled	59.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 reductase; PDBTitle: crystal structure of amycolatopsis cytochrome p450 reductase gcob.
102	d1wy8a1	Alignment	not modelled	59.1	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
103	d1p9ka_	Alignment	not modelled	59.0	16	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Ybcj-like
104	d1wgga_	Alignment	not modelled	58.5	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
105	c3q3fA_	Alignment	not modelled	57.9	15	PDB header: hydrolase, protein binding Chain: A: PDB Molecule: ribonuclease/ubiquitin chimeric protein; PDBTitle: engineering domain-swapped binding interfaces by mutually exclusive2 folding: insertion of ubiquitin into position 103 of barnase

106	d1z2ma2	Alignment	not modelled	57.5	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
107	c1gxcA	Alignment	not modelled	56.6	8	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
108	d1gxca	Alignment	not modelled	56.6	8	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
109	d1wz0a1	Alignment	not modelled	55.2	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
110	d2piea1	Alignment	not modelled	55.1	17	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
111	d1yjma1	Alignment	not modelled	53.4	17	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
112	c3kt9A	Alignment	not modelled	53.2	17	PDB header: hydrolase Chain: A; PDB Molecule: aprataxin; PDBTitle: aprataxin fha domain
113	d1a5ra	Alignment	not modelled	52.4	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
114	c2dziA	Alignment	not modelled	52.3	15	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)
115	c4jonA	Alignment	not modelled	51.6	17	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: centrosomal protein of 170 kda; PDBTitle: crystal structure of a centrosomal protein 170kda, transcript variant2 beta (cep170) from homo sapiens at 2.15 a resolution (psi community3 target, sundstrom)
116	d1v5oa	Alignment	not modelled	51.5	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
117	c1oqyA	Alignment	not modelled	51.2	13	PDB header: replication Chain: A; PDB Molecule: uv excision repair protein rad23 homolog a; PDBTitle: structure of the dna repair protein hhr23a
118	d1g3ga	Alignment	not modelled	50.7	17	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
119	c2l7rA	Alignment	not modelled	50.2	29	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
120	c2ojrA	Alignment	not modelled	49.7	15	PDB header: protein binding Chain: A; PDB Molecule: ubiquitin; PDBTitle: structure of ubiquitin solved by sad using the lanthanide-binding tag