Phyre^2

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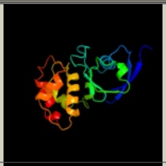
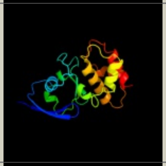
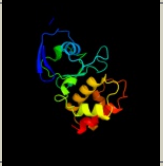
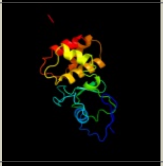
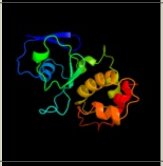
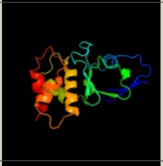
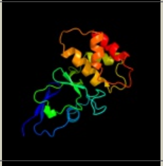
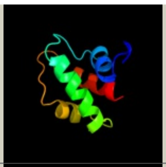
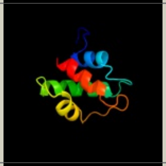
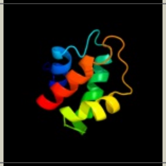
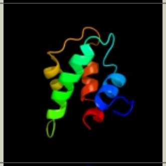
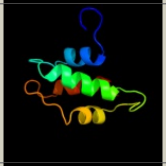
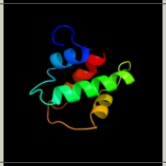
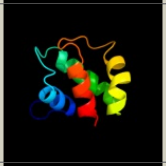
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1t3qD_	Alignment		100.0	42	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
2	c1vlbA_	Alignment		100.0	37	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
3	c3hrdH_	Alignment		100.0	46	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
4	c1rm6F_	Alignment		100.0	44	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
5	c1wygA_	Alignment		100.0	37	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
6	c1ffuA_	Alignment		100.0	43	**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
7	c1dgjA_	Alignment		100.0	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
8	c1n60D_	Alignment		100.0	44	**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
9	c3eubJ_	Alignment		100.0	37	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
10	c3b9jI_	Alignment		100.0	36	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine
11	c2w3rG_	Alignment		100.0	41	**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

12	d1ffva1	Alignment		100.0	46	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
13	d1n62a1	Alignment		100.0	44	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
14	d1rm6c1	Alignment		100.0	47	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
15	d1zxia1	Alignment		100.0	44	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
16	d1t3qa1	Alignment		100.0	36	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
17	d1v97a1	Alignment		100.0	41	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
18	d1dgja1	Alignment		100.0	38	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
19	d1vlba1	Alignment		100.0	33	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
20	d1jroa1	Alignment		100.0	41	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
21	d1t3qa2	Alignment	not modelled	100.0	46	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
22	d1jroa2	Alignment	not modelled	99.9	41	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
23	d1n62a2	Alignment	not modelled	99.9	45	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
24	d1v97a2	Alignment	not modelled	99.9	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
25	d1ffva2	Alignment	not modelled	99.9	40	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
26	d1rm6c2	Alignment	not modelled	99.9	41	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
27	d1vlba2	Alignment	not modelled	99.9	40	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
28	d1dgja2	Alignment	not modelled	99.9	42	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
29	d2bs2b2	Alignment	not modelled	99.4	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like

						Family:2Fe-2S ferredoxin domains from multidomain proteins
30	d1nekb2	Alignment	not modelled	99.3	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
31	d3c8ya2	Alignment	not modelled	99.2	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
32	d1kf6b2	Alignment	not modelled	99.2	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
33	c2b76N_	Alignment	not modelled	99.1	19	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
34	c2bs2E_	Alignment	not modelled	98.8	21	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
35	d2fug33	Alignment	not modelled	98.8	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
36	c1c4cA_	Alignment	not modelled	98.8	23	**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
37	c2h89B_	Alignment	not modelled	98.8	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
38	c1nekB_	Alignment	not modelled	98.5	18	**PDB header:**oxidoreductase/electron transport **Chain:** B: **PDB Molecule:**succinate dehydrogenase iron-sulfur protein; **PDBTitle:** complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
39	c2fugC_	Alignment	not modelled	98.5	21	**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
40	d1frra_	Alignment	not modelled	98.1	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
41	d1fxia_	Alignment	not modelled	98.0	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
42	d1wria_	Alignment	not modelled	97.9	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
43	d1awda_	Alignment	not modelled	97.9	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
44	d1a70a_	Alignment	not modelled	97.8	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
45	d1iuea_	Alignment	not modelled	97.8	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
46	d1czpa_	Alignment	not modelled	97.7	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
47	d2cjoa_	Alignment	not modelled	97.6	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
48	d1l5pa_	Alignment	not modelled	97.6	31	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
49	d1jq4a_	Alignment	not modelled	97.5	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
50	d1offa_	Alignment	not modelled	97.5	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
51	c1krhA_	Alignment	not modelled	97.5	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
52	d1gaqb_	Alignment	not modelled	97.5	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
53	d2piaa3	Alignment	not modelled	97.4	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
54	d1krha3	Alignment	not modelled	97.4	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
55	d1pfda_	Alignment	not modelled	97.4	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
56	d1frda_	Alignment	not modelled	97.4	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like

							Family:2Fe-2S ferredoxin-related
57	c2wlbB_		Alignment	not modelled	97.3	20	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**electron transfer protein 1, mitochondrial; **PDBTitle:** adrenodoxin-like ferredoxin etp1fd(516-618) of2 schizosaccharomyces pombe mitochondria
58	c3lxfC_		Alignment	not modelled	97.3	36	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**ferredoxin; **PDBTitle:** crystal structure of [2fe-2s] ferredoxin arx from novosphingobium2 aromaticivorans
59	c3huiA_		Alignment	not modelled	97.3	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** crystal structure of the mutant a105r of [2fe-2s] ferredoxin2 in the class i cyp199a2 system from rhodopseudomonas3 palustris
60	d4fxca_		Alignment	not modelled	97.3	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
61	c2piaA_		Alignment	not modelled	97.2	20	**PDB header:**reductase **Chain:** A: **PDB Molecule:**phthalate dioxygenase reductase; **PDBTitle:** phthalate dioxygenase reductase: a modular structure for2 electron transfer from pyridine nucleotides to [2fe-2s]
62	d1e9ma_		Alignment	not modelled	97.1	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
63	d1xlqa1		Alignment	not modelled	97.0	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
64	c3ah7A_		Alignment	not modelled	97.0	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**[2fe-2s]ferredoxin; **PDBTitle:** crystal structure of the isc-like [2fe-2s] ferredoxin (fdxb) from2 pseudomonas putida jcm 20004
65	d2bt6a1		Alignment	not modelled	97.0	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
66	d1doia_		Alignment	not modelled	96.7	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
67	c1x31A_		Alignment	not modelled	96.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sarcosine oxidase alpha subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
68	d1b9ra_		Alignment	not modelled	96.6	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
69	d1e0za_		Alignment	not modelled	96.3	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
70	d1i7ha_		Alignment	not modelled	96.1	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
71	c1y56A_		Alignment	not modelled	95.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1363; **PDBTitle:** crystal structure of l-proline dehydrogenase from p.horikoshii
72	c1l6vA_		Alignment	not modelled	93.4	15	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**adrenodoxin 1; **PDBTitle:** structure of reduced bovine adrenodoxin
73	c3cwiA_		Alignment	not modelled	84.5	25	**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
74	c2kd0A_		Alignment	not modelled	83.4	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
75	d1zud21		Alignment	not modelled	83.0	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
76	c2kl0A_		Alignment	not modelled	82.9	18	**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
77	d1ep3b2		Alignment	not modelled	79.9	28	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Dihydroorotate dehydrogenase B, PyrK subunit
78	d1v86a_		Alignment	not modelled	76.2	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
79	c2kk8A_		Alignment	not modelled	75.5	20	**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
80	c1ep3B_		Alignment	not modelled	73.6	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydroorotate dehydrogenase b (pyrk subunit); **PDBTitle:** crystal structure of lactococcus lactis dihydroorotate dehydrogenase2 b. data collected under cryogenic conditions.
							Fold:beta-Grasp (ubiquitin-like)

81	d1v2ya_	Alignment	not modelled	65.1	18	**Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
82	c2nnzA_	Alignment	not modelled	65.0	3	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus
83	c1tygG_	Alignment	not modelled	64.0	15	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
84	d1v5oa_	Alignment	not modelled	63.1	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
85	c2kanA_	Alignment	not modelled	62.1	13	**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
86	d2cu3a1	Alignment	not modelled	61.1	34	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
87	d1wh3a_	Alignment	not modelled	58.0	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
88	d1tygb_	Alignment	not modelled	54.6	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
89	c2dziA_	Alignment	not modelled	54.3	16	**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)
90	d1oqya4	Alignment	not modelled	53.9	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
91	d1p1aa_	Alignment	not modelled	52.7	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
92	c2ojrA_	Alignment	not modelled	52.6	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin; **PDBTitle:** structure of ubiquitin solved by sad using the lanthanide-2 binding tag
93	d2al3a1	Alignment	not modelled	51.0	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
94	d1z2ma2	Alignment	not modelled	50.4	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
95	d2znvb1	Alignment	not modelled	49.7	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
96	d1v5ta_	Alignment	not modelled	48.4	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
97	d1uela_	Alignment	not modelled	47.2	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
98	d1wiaa_	Alignment	not modelled	46.9	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
99	d1bt0a_	Alignment	not modelled	45.0	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
100	c1qzeA_	Alignment	not modelled	43.5	22	**PDB header:**replication **Chain:** A: **PDB Molecule:**uv excision repair protein rad23 homolog a; **PDBTitle:** hhr23a protein structure based on residual dipolar coupling2 data
101	d1wx8a1	Alignment	not modelled	42.3	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
102	d1ndda_	Alignment	not modelled	40.3	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
103	d1sifa_	Alignment	not modelled	40.2	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
104	d1wx9a1	Alignment	not modelled	39.8	4	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
105	c1yx5B_	Alignment	not modelled	39.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ubiquitin; **PDBTitle:** solution structure of s5a uim-1/ubiquitin complex
106	d1wgga_	Alignment	not modelled	37.4	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
107	d2bwfa1	Alignment	not modelled	37.0	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
						PDB header:structural genomics unknown function

108	c2dzmA_	Alignment	not modelled	35.6	3	**Chain:** A: **PDB Molecule:**fas-associated factor 1; **PDBTitle:** solution structure of the ubiquitin-like domain in human2 fas-associated factor 1 (hfaf1)
109	c3cvoA_	Alignment	not modelled	34.1	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase-like protein of unknown function; **PDBTitle:** crystal structure of a methyltransferase-like protein (spo2022) from2 silicibacter pomeroyi dss-3 at 1.80 a resolution
110	d1iyfa_	Alignment	not modelled	34.0	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
111	d1z2ma1	Alignment	not modelled	32.7	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
112	d1ogwa_	Alignment	not modelled	31.6	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
113	d1wx7a1	Alignment	not modelled	30.7	6	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
114	d1ud7a_	Alignment	not modelled	29.8	7	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
115	d1t3ua_	Alignment	not modelled	29.6	11	**Fold:**Cell division protein ZapA-like **Superfamily:**Cell division protein ZapA-like **Family:**Cell division protein ZapA-like
116	d1wgha_	Alignment	not modelled	28.8	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
117	d1c3ta_	Alignment	not modelled	28.7	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
118	c2jerG_	Alignment	not modelled	27.1	21	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**agmatine deiminase; **PDBTitle:** agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
119	d2jera1	Alignment	not modelled	26.5	21	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
120	d1vjka_	Alignment	not modelled	26.1	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**MoaD