Phyre^2

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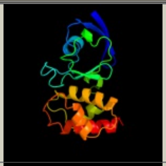
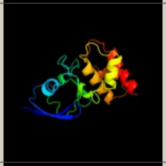
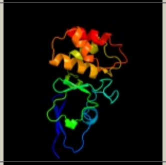
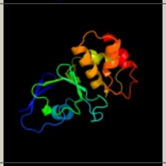
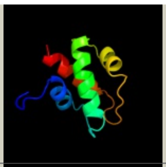
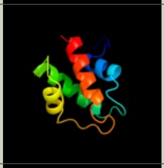
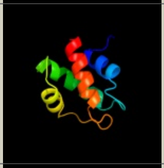
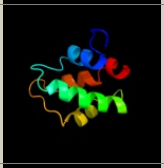
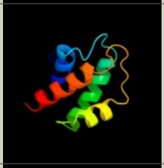
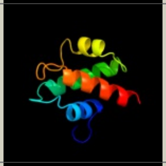
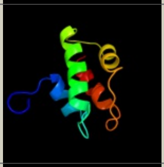
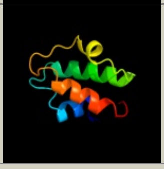
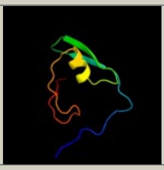
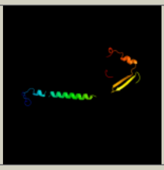
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vlbA_	Alignment		100.0	42	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
2	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
3	c3hrdH_	Alignment		100.0	37	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
4	c1dgjA_	Alignment		100.0	42	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
5	c1t3qD_	Alignment		100.0	43	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
6	c1wygA_	Alignment		100.0	43	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
7	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
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	c3b9jI_	Alignment		100.0	42	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine
10	c3eubJ_	Alignment		100.0	43	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
11	c2w3rG_	Alignment		100.0	44	**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	41	**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	43	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
14	d1zxia1	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
15	d1dgja1	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
16	d1t3qa1	Alignment		100.0	40	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
17	d1rm6c1	Alignment		100.0	40	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
18	d1vlba1	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	d1v97a1	Alignment		100.0	39	**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	45	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
21	d1v97a2	Alignment	not modelled	100.0	44	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
22	d1jroa2	Alignment	not modelled	100.0	42	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
23	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
24	d1n62a2	Alignment	not modelled	100.0	41	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
25	d1ffva2	Alignment	not modelled	100.0	45	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
26	d1rm6c2	Alignment	not modelled	100.0	46	**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	46	**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	43	**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	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like

						Family:2Fe-2S ferredoxin domains from multidomain proteins
30	d1nekb2	Alignment	not modelled	99.2	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
31	d1kf6b2	Alignment	not modelled	99.2	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
32	d3c8ya2	Alignment	not modelled	99.1	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
33	c2b76N_	Alignment	not modelled	98.6	25	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
34	d2fug33	Alignment	not modelled	98.5	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
35	c2bs2E_	Alignment	not modelled	98.5	26	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
36	c1c4cA_	Alignment	not modelled	98.5	30	**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	98.5	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
38	c1nekB_	Alignment	not modelled	98.2	32	**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	d1frra_	Alignment	not modelled	97.8	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
40	d1fxia_	Alignment	not modelled	97.8	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
41	d1wria_	Alignment	not modelled	97.7	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
42	d1awda_	Alignment	not modelled	97.7	31	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
43	d1iuea_	Alignment	not modelled	97.6	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
44	d1a70a_	Alignment	not modelled	97.6	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
45	c2fugC_	Alignment	not modelled	97.5	20	**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
46	d1l5pa_	Alignment	not modelled	97.5	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
47	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
48	d2cjoa_	Alignment	not modelled	97.3	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
49	d1czpa_	Alignment	not modelled	97.3	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
50	c1krhA_	Alignment	not modelled	97.3	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
51	d1offa_	Alignment	not modelled	97.2	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
52	c2piaA_	Alignment		97.2	22	**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]
53	d1jq4a_	Alignment	not modelled	97.1	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
54	d1frda_	Alignment	not modelled	97.1	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
						Fold:beta-Grasp (ubiquitin-like)

55	d1gaqb_	Alignment	not modelled	97.1	23	**Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
56	d1krha3	Alignment	not modelled	97.0	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
57	d1pfda_	Alignment	not modelled	97.0	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
58	c3huiA_	Alignment	not modelled	97.0	25	**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
59	c2wlbB_	Alignment	not modelled	97.0	22	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**electron transfer protein 1, mitochondrial; **PDBTitle:** adrenodoxin-like ferredoxin etp1fd(516-618) of2 schizosaccharomyces pombe mitochondria
60	c3ah7A_	Alignment	not modelled	97.0	24	**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
61	d4fxca_	Alignment	not modelled	96.9	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
62	c3lxfC_	Alignment	not modelled	96.8	20	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**ferredoxin; **PDBTitle:** crystal structure of [2fe-2s] ferredoxin arx from novosphingobium2 aromaticivorans
63	d1e9ma_	Alignment	not modelled	96.7	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
64	d1xlqa1	Alignment	not modelled	96.5	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
65	d2bt6a1	Alignment	not modelled	96.4	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
66	d1doia_	Alignment	not modelled	96.4	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
67	d1b9ra_	Alignment	not modelled	96.1	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
68	c1x31A_	Alignment	not modelled	96.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sarcosine oxidase alpha subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
69	d1i7ha_	Alignment	not modelled	95.8	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
70	d1e0za_	Alignment	not modelled	95.5	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
71	c1y56A_	Alignment	not modelled	93.2	25	**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	92.6	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**adrenodoxin 1; **PDBTitle:** structure of reduced bovine adrenodoxin
73	d1ep3b2	Alignment	not modelled	86.9	21	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Dihydroorotate dehydrogenase B, PyrK subunit
74	c2kl0A_	Alignment	not modelled	78.5	16	**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
75	c1p84E_	Alignment		77.1	17	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
76	c2kd0A_	Alignment	not modelled	76.4	30	**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
77	c1ep3B_	Alignment	not modelled	75.5	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.
78	c3cwiA_	Alignment	not modelled	73.0	22	**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
						Fold:beta-Grasp (ubiquitin-like)

79	d1v86a_	Alignment	not modelled	65.6	13	**Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
80	d1oqya4	Alignment	not modelled	61.1	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
81	d1wh3a_	Alignment	not modelled	60.8	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
82	d1zud21	Alignment	not modelled	59.3	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
83	d1v5oa_	Alignment	not modelled	58.6	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
84	c2dziA_	Alignment	not modelled	58.4	18	**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)
85	c2kk8A_	Alignment	not modelled	53.5	41	**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
86	d2al3a1	Alignment	not modelled	53.3	31	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
87	d1wiaa_	Alignment	not modelled	52.5	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
88	d1p1aa_	Alignment	not modelled	49.9	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
89	d1uela_	Alignment	not modelled	49.8	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
90	c1tygG_	Alignment	not modelled	49.7	26	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
91	d1v2ya_	Alignment	not modelled	48.6	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
92	d2znvb1	Alignment	not modelled	41.4	36	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
93	d1bt0a_	Alignment	not modelled	40.2	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
94	d2cu3a1	Alignment	not modelled	39.8	38	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
95	c2kanA_	Alignment	not modelled	39.4	24	**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
96	c2klcA_	Alignment	not modelled	38.8	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ubiquilin-1; **PDBTitle:** nmr solution structure of human ubiquitin-like domain of2 ubiquilin 1, northeast structural genomics consortium3 (nesg) target ht5a
97	c3itcA_	Alignment	not modelled	37.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**renal dipeptidase; **PDBTitle:** crystal structure of sco3058 with bound citrate and glycerol
98	c3cvoA_	Alignment	not modelled	36.8	16	**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
99	d1dusa_	Alignment	not modelled	36.7	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical protein MJ0882
100	d1tygb_	Alignment	not modelled	36.3	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
101	c3kdvB_	Alignment	not modelled	35.8	27	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna damage response b protein; **PDBTitle:** crystal structure of dna damage response b (ddrb) from deinococcus2 geothermalis
102	d1itua_	Alignment	not modelled	35.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Renal dipeptidase
103	c2e76D_	Alignment	not modelled	34.6	25	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
104	d1j8ca_	Alignment	not modelled	34.5	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related

105	d1erda_	Alignment	not modelled	34.5	19	**Fold:**Protozoan pheromone-like **Superfamily:**Protozoan pheromone proteins **Family:**Protozoan pheromone proteins
106	d1wx7a1	Alignment	not modelled	34.0	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
107	c1qzeA_	Alignment	not modelled	32.6	19	**PDB header:**replication **Chain:** A: **PDB Molecule:**uv excision repair protein rad23 homolog a; **PDBTitle:** hhr23a protein structure based on residual dipolar coupling2 data
108	c2nnzA_	Alignment	not modelled	32.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus
109	d1ndda_	Alignment	not modelled	32.2	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
110	c2pq4B_	Alignment	not modelled	31.3	30	**PDB header:**chaperone/oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic nitrate reductase precursor; **PDBTitle:** nmr solution structure of napd in complex with napa1-352 signal peptide
111	c3kbgA_	Alignment	not modelled	31.3	31	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s4e; **PDBTitle:** crystal structure of the 30s ribosomal protein s4e from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar28.
112	c2jv8A_	Alignment	not modelled	30.6	34	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ne1242; **PDBTitle:** solution structure of protein ne1242 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net4
113	c2fynO_	Alignment	not modelled	30.6	31	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
114	d1v7wa1	Alignment	not modelled	29.8	17	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
115	d1sifa_	Alignment	not modelled	29.6	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
116	c1yx5B_	Alignment	not modelled	28.5	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ubiquitin; **PDBTitle:** solution structure of s5a uim-1/ubiquitin complex
117	d1wx9a1	Alignment	not modelled	28.1	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
118	c2ojrA_	Alignment	not modelled	27.9	31	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ubiquitin; **PDBTitle:** structure of ubiquitin solved by sad using the lanthanide-2 binding tag
119	d1iyfa_	Alignment	not modelled	27.0	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
120	c2fyuE_	Alignment	not modelled	24.7	21	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor