Phyre^2

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Description	P0ABW0
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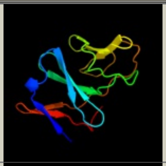
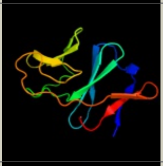
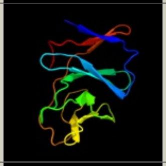
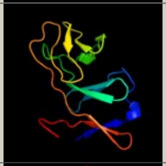
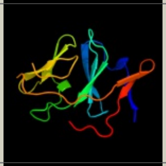
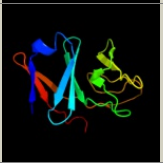
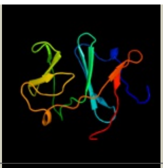
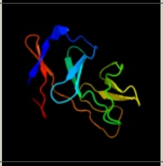
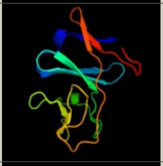
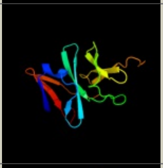
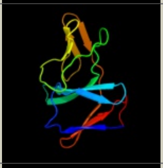
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fqta_	Alignment		100.0	39	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
2	c2qpzA_	Alignment		100.0	45	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**naphthalene 1,2-dioxygenase system ferredoxin **PDBTitle:** naphthalene 1,2-dioxygenase rieske ferredoxin
3	c2i7fB_	Alignment		100.0	40	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin component of dioxygenase; **PDBTitle:** sphingomonas yanoikuyae b1 ferredoxin
4	c2de7E_	Alignment		100.0	34	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ferredoxin component of carbazole; **PDBTitle:** the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
5	c3gceA_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin component of carbazole 1,9a- **PDBTitle:** ferredoxin of carbazole 1,9a-dioxygenase from nocardioides2 aromaticivorans ic177
6	d3c0da1	Alignment		100.0	25	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
7	c3dqyA_	Alignment		100.0	39	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**toluene 1,2-dioxygenase system ferredoxin **PDBTitle:** crystal structure of toluene 2,3-dioxygenase ferredoxin
8	d2de6a1	Alignment		99.9	24	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
9	d1z01a1	Alignment		99.9	31	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
10	d1vm9a_	Alignment		99.9	27	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
11	c3d89A_	Alignment		99.9	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rieske domain-containing protein; **PDBTitle:** crystal structure of a soluble rieske ferredoxin from mus musculus

12	d2jzaa1	Alignment		99.9	25	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
13	c2de7B_	Alignment		99.9	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**terminal oxygenase component of carbazole; **PDBTitle:** the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
14	c3gkqB_	Alignment		99.9	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**terminal oxygenase component of carbazole 1,9a- **PDBTitle:** terminal oxygenase of carbazole 1,9a-dioxygenase from2 novosphingobium sp. ka1
15	d2jo6a1	Alignment		99.9	17	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
16	c3gcfC_	Alignment		99.9	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**terminal oxygenase component of carbazole 1,9a- **PDBTitle:** terminal oxygenase of carbazole 1,9a-dioxygenase from2 nocardioides aromaticivorans ic177
17	c2zylA_	Alignment		99.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**possible oxidoreductase; **PDBTitle:** crystal structure of 3-ketosteroid-9-alpha-hydroxylase2 (ksha) from m. tuberculosis
18	c1z01D_	Alignment		99.9	32	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**2-oxo-1,2-dihydroquinoline 8-monooxygenase, **PDBTitle:** 2-oxoquinoline 8-monooxygenase component: active site2 modulation by rieske-[2fe-2s] center oxidation/reduction
19	c3n0qA_	Alignment		99.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative aromatic-ring hydroxylating dioxygenase; **PDBTitle:** crystal structure of a putative aromatic-ring hydroxylating2 dioxygenase (tm1040_3219) from silicibacter sp. tm1040 at 1.80 a3 resolution
20	c3gteB_	Alignment		99.9	23	**PDB header:**electron transport, oxidoreductase **Chain:** B: **PDB Molecule:**ddmc; **PDBTitle:** crystal structure of dicamba monooxygenase with non-heme2 iron
21	d1ulia1	Alignment	not modelled	99.9	16	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
22	d1wqla1	Alignment	not modelled	99.9	14	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
23	d2bmoa1	Alignment	not modelled	99.9	14	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
24	c1uljA_	Alignment	not modelled	99.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**biphenyl dioxygenase large subunit; **PDBTitle:** biphenyl dioxygenase (bpha1a2) in complex with the substrate
25	d2b1xa1	Alignment	not modelled	99.9	23	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
26	c1wqlA_	Alignment	not modelled	99.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-sulfur protein large subunit of cumene dioxygenase; **PDBTitle:** cumene dioxygenase (cuma1a2) from pseudomonas fluorescens ip01
27	d1o7na1	Alignment	not modelled	99.9	18	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
28	d1g8kb_	Alignment	not modelled	99.9	22	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
						PDB header:oxidoreductase

29	c2gbxE_	Alignment	not modelled	99.9	19	**Chain:** E: **PDB Molecule:**biphenyl 2,3-dioxygenase alpha subunit; **PDBTitle:** crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl
30	c2hmnA_	Alignment	not modelled	99.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**naphthalene 1,2-dioxygenase alpha subunit; **PDBTitle:** crystal structure of the naphthalene 1,2-dioxygenase f352v2 mutant bound to anthracene.
31	c2b1xE_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**naphthalene dioxygenase large subunit; **PDBTitle:** crystal structure of naphthalene 1,2-dioxygenase from rhodococcus sp.
32	d3cx5e1	Alignment	not modelled	99.9	16	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
33	d1rfsa_	Alignment	not modelled	99.8	17	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
34	d1q90c_	Alignment	not modelled	99.8	19	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
35	d1riea_	Alignment	not modelled	99.8	19	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
36	d1nyka_	Alignment	not modelled	99.8	19	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
37	d2e74d1	Alignment	not modelled	99.8	20	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
38	c2e76D_	Alignment	not modelled	99.7	19	**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
39	c1p84E_	Alignment	not modelled	99.7	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
40	c2nvgA_	Alignment	not modelled	99.7	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit; **PDBTitle:** soluble domain of rieske iron sulfur protein.
41	c2fyuE_	Alignment	not modelled	99.7	18	**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
42	d1jm1a_	Alignment	not modelled	99.6	28	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
43	c2fynO_	Alignment	not modelled	99.6	20	**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
44	d2hf1a1	Alignment	not modelled	69.9	14	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
45	d2jnya1	Alignment	not modelled	69.8	14	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
46	c2jr6A_	Alignment	not modelled	62.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein nma0874; **PDBTitle:** solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32
47	d2pk7a1	Alignment	not modelled	62.9	9	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
48	c2js4A_	Alignment	not modelled	60.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein bb2007; **PDBTitle:** solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
49	c2kpiA_	Alignment	not modelled	56.1	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sco3027; **PDBTitle:** solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58
50	c2w3nA_	Alignment	not modelled	36.3	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase 2; **PDBTitle:** structure and inhibition of the co2-sensing carbonic2 anhydrase can2 from the pathogenic fungus cryptococcus3 neoformans
51	c3lasA_	Alignment	not modelled	32.8	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution
52	d1ddza2	Alignment	not modelled	30.5	14	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
53	c1ylkA_	Alignment	not modelled	28.9	31	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv1284/mt1322; **PDBTitle:** crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate

54	c1ddzA_	Alignment	not modelled	28.9	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1
55	c3ucoB_	Alignment	not modelled	28.8	25	**PDB header:**lyase/lyase inhibitor **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** coccomyxa beta-carbonic anhydrase in complex with iodide
56	c3eyxB_	Alignment	not modelled	28.7	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
57	c2a8cE_	Alignment	not modelled	27.5	15	**PDB header:**lyase **Chain:** E: **PDB Molecule:**carbonic anhydrase 2; **PDBTitle:** haemophilus influenzae beta-carbonic anhydrase
58	d1ekja_	Alignment	not modelled	26.5	8	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
59	d1ddza1	Alignment	not modelled	26.4	18	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
60	c2a5vB_	Alignment	not modelled	24.9	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase (carbonate dehydratase) (carbonic **PDBTitle:** crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c,2 tetrameric form
61	d1i6pa_	Alignment	not modelled	24.8	14	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
62	d1g5ca_	Alignment	not modelled	23.2	21	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
63	c3eoiB_	Alignment	not modelled	12.6	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**pilm; **PDBTitle:** crystal structure of putative protein pilm from escherichia coli b7a
64	c2k5rA_	Alignment	not modelled	12.6	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein xf2673; **PDBTitle:** solution nmr structure of xf2673 from xylella fastidiosa.2 northeast structural genomics consortium target xfr39
65	c2xk0A_	Alignment	not modelled	12.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb protein pcl; **PDBTitle:** solution structure of the tudor domain from drosophila2 polycomblike (pcl)
66	d2j7ja2	Alignment	not modelled	11.0	33	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
67	d1ubdc1	Alignment	not modelled	10.6	33	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
68	d1r2za3	Alignment	not modelled	10.2	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
69	c3hg9B_	Alignment	not modelled	10.1	5	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**pilm; **PDBTitle:** crystal structure of putative pilm protein from pseudomonas aeruginosa2 2192
70	d1l1ta3	Alignment	not modelled	8.8	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
71	d1tdza3	Alignment	not modelled	8.8	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
72	d2c42a2	Alignment	not modelled	8.1	8	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**PFOR PP module
73	d1h7va_	Alignment	not modelled	7.9	15	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
74	d1e44b_	Alignment	not modelled	7.6	38	**Fold:**Ribonuclease domain of colicin E3 **Superfamily:**Ribonuclease domain of colicin E3 **Family:**Ribonuclease domain of colicin E3
75	c2w8xB_	Alignment	not modelled	7.6	15	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**ion-channel modulator raklp; **PDBTitle:** structure of the tick ion-channel modulator ra-klp
76	d2aqaa1	Alignment	not modelled	7.5	17	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
77	c2opfA_	Alignment	not modelled	7.5	18	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**endonuclease viii; **PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
78	c3izbP_	Alignment	not modelled	7.3	40	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**40s ribosomal protein rps11 (s17p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
79	d1dgwa_	Alignment	not modelled	7.2	14	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein

80	c2kn9A_	Alignment	not modelled	7.2	15	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin; **PDBTitle:** solution structure of zinc-substituted rubredoxin b (rv3250c) from2 mycobacterium tuberculosis. seattle structural genomics center for3 infectious disease target mytud.01635.a
81	c2j6aA_	Alignment	not modelled	7.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein trm112; **PDBTitle:** crystal structure of s. cerevisiae ynr046w, a zinc finger2 protein from the erf1 methyltransferase complex.
82	c2eqjA_	Alignment	not modelled	6.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metal-response element-binding transcription **PDBTitle:** solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
83	d1ee8a3	Alignment	not modelled	6.6	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
84	c3e59A_	Alignment	not modelled	6.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyoverdine biosynthesis protein pvca; **PDBTitle:** crystal structure of the pvca (pa2254) protein from pseudomonas2 aeruginosa
85	d1ibia1	Alignment	not modelled	6.5	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
86	d1k3xa3	Alignment	not modelled	6.4	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
87	c2e5pA_	Alignment	not modelled	6.3	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 1 (phf1 protein)
88	d1k82a3	Alignment	not modelled	6.2	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
89	d1dl6a_	Alignment	not modelled	6.2	25	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
90	c3iz6P_	Alignment	not modelled	6.2	40	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**40s ribosomal protein s11 (s17p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
91	d2apob1	Alignment	not modelled	6.1	23	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
92	d2dara1	Alignment	not modelled	5.8	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
93	d1hq0a_	Alignment	not modelled	5.8	19	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**Type 1 cytotoxic necrotizing factor, catalytic domain
94	c2xznQ_	Alignment	not modelled	5.6	40	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**ribosomal protein s17 containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
95	d1uika1	Alignment	not modelled	5.5	23	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
96	c3dkqB_	Alignment	not modelled	5.5	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pkhd-type hydroxylase sbal_3634; **PDBTitle:** crystal structure of putative oxygenase (yp_001051978.1) from2 shewanella baltica os155 at 2.26 a resolution
97	d2ey4e1	Alignment	not modelled	5.3	23	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
98	c2e5qA_	Alignment	not modelled	5.2	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 19; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 19, isoform b [homo sapiens]