Phyre^2

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Description	RVBD0253_(nirD)_305453_305809
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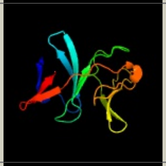
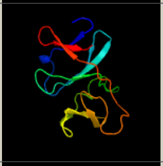
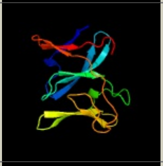
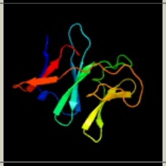
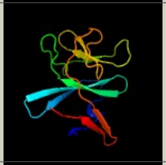
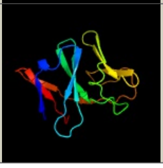
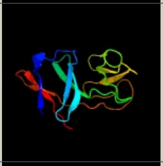
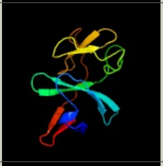
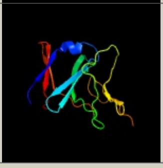
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4aivA_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nitrite reductase [nad(p)h] small subunit nird; **PDBTitle:** crystal structure of putative nadh-dependent nitrite reductase small2 subunit from mycobacterium tuberculosis
2	d2jo6a1	Alignment		100.0	41	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
3	d3c0da1	Alignment		100.0	38	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
4	d2jzaa1	Alignment		100.0	44	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
5	d1vm9a_	Alignment		100.0	18	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
6	c3gceA_	Alignment		99.9	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin component of carbazole 1,9a- **PDBTitle:** ferredoxin of carbazole 1,9a-dioxygenase from nocardioides2 aromaticivorans ic177
7	c2de7E_	Alignment		99.9	24	**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
8	c4qdfA_	Alignment		99.9	17	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** A: **PDB Molecule:**3-ketosteroid 9alpha-hydroxylase oxygenase; **PDBTitle:** crystal structure of apo ksha5 and ksha1 in complex with 1,4-30q-coa2 from r. rhodochrous
9	c4qdfB_	Alignment		99.9	15	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** B: **PDB Molecule:**3-ketosteroid 9alpha-hydroxylase oxygenase; **PDBTitle:** crystal structure of apo ksha5 and ksha1 in complex with 1,4-30q-coa2 from r. rhodochrous
10	c2qpzA_	Alignment		99.9	24	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**naphthalene 1,2-dioxygenase system ferredoxin **PDBTitle:** naphthalene 1,2-dioxygenase rieske ferredoxin
11	d1fqta_	Alignment		99.9	19	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)

12	c2zylA_	Alignment		99.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**possible oxidoreductase; **PDBTitle:** crystal structure of 3-ketosteroid-9-alpha-hydroxylase2 (ksha) from m. tuberculosis
13	c2de7B_	Alignment		99.9	16	**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	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**terminal oxygenase component of carbazole 1,9a-dioxygenase; **PDBTitle:** terminal oxygenase of carbazole 1,9a-dioxygenase from novosphingobium2 sp. ka1
15	c3d89A_	Alignment		99.9	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rieske domain-containing protein; **PDBTitle:** crystal structure of a soluble rieske ferredoxin from mus musculus
16	d2de6a1	Alignment		99.9	15	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
17	d1z01a1	Alignment		99.9	20	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
18	c3gcfC_	Alignment		99.9	24	**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
19	c3n0qA_	Alignment		99.9	19	**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	c3vcaA_	Alignment		99.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ring-hydroxylating dioxygenase; **PDBTitle:** quaternary ammonium oxidative demethylation: x-ray crystallographic,2 resonance raman and uv-visible spectroscopic analysis of a rieske-3 type demethylase
21	c1z01D_	Alignment	not modelled	99.9	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**2-oxo-1,2-dihydroquinoline 8-monooxygenase, oxygenase **PDBTitle:** 2-oxoquinoline 8-monooxygenase component: active site modulation by2 rieske-[2fe-2s] center oxidation/reduction
22	c3gteB_	Alignment	not modelled	99.9	27	**PDB header:**electron transport, oxidoreductase **Chain:** B: **PDB Molecule:**ddmc; **PDBTitle:** crystal structure of dicamba monooxygenase with non-heme iron
23	c2i7fB_	Alignment	not modelled	99.9	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin component of dioxygenase; **PDBTitle:** sphingomonas yanoikuyae b1 ferredoxin
24	c3dqyA_	Alignment	not modelled	99.9	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**toluene 1,2-dioxygenase system ferredoxin **PDBTitle:** crystal structure of toluene 2,3-dioxygenase ferredoxin
25	d1ulia1	Alignment	not modelled	99.9	14	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
26	d1wqla1	Alignment	not modelled	99.9	14	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
27	c5cxmC_	Alignment	not modelled	99.9	15	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**cytochrome b6/f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cyanobacterial plasma membrane rieske protein2 petc3 from synechocystis pcc 6803
28	d2bmoa1	Alignment	not modelled	99.9	17	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain

29	c1uljA_	Alignment	not modelled	99.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**biphenyl dioxygenase large subunit; **PDBTitle:** biphenyl dioxygenase (bpha1a2) in complex with the substrate
30	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
31	d2b1xa1	Alignment	not modelled	99.9	17	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
32	d1o7na1	Alignment	not modelled	99.9	17	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
33	c2gbxE_	Alignment	not modelled	99.9	20	**PDB header:**oxidoreductase **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
34	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.
35	c2b1xE_	Alignment	not modelled	99.9	17	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**naphthalene dioxygenase large subunit; **PDBTitle:** crystal structure of naphthalene 1,2-dioxygenase from rhodococcus sp.
36	c4aayH_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**arob; **PDBTitle:** crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
37	d1rfsa_	Alignment	not modelled	99.8	14	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
38	d1g8kb_	Alignment	not modelled	99.8	14	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
39	d1q90c_	Alignment	not modelled	99.8	13	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
40	d3cx5e1	Alignment	not modelled	99.8	14	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
41	d2e74d1	Alignment	not modelled	99.8	14	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
42	d1riea_	Alignment	not modelled	99.7	14	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
43	d1nyka_	Alignment	not modelled	99.7	21	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
44	c2e76D_	Alignment	not modelled	99.6	14	**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
45	c2fyuE_	Alignment	not modelled	99.6	13	**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
46	c1p84E_	Alignment	not modelled	99.6	16	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
47	c2fynO_	Alignment	not modelled	99.5	19	**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
48	c2nvgA_	Alignment	not modelled	99.5	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit; **PDBTitle:** soluble domain of rieske iron sulfur protein.
49	d1jm1a_	Alignment	not modelled	99.4	22	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
50	c6hwhB_	Alignment	not modelled	99.4	13	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit; **PDBTitle:** structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
51	c6fo2R_	Alignment	not modelled	98.9	16	**PDB header:**membrane protein **Chain:** R: **PDB Molecule:**cytochrome b-c1 complex subunit rieske, mitochondrial; **PDBTitle:** cryoem structure of bovine cytochrome bc1 with no ligand bound
52	d2hf1a1	Alignment	not modelled	57.0	19	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
53	d2jnya1	Alignment	not modelled	56.9	19	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like

54	d2pk7a1	Alignment	not modelled	53.6	16	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
55	c2jr6A_	Alignment	not modelled	48.5	22	**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
56	c2kpiA_	Alignment	not modelled	46.9	19	**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
57	c2js4A_	Alignment	not modelled	46.0	22	**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
58	c6f5zC_	Alignment	not modelled	40.0	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**upf0434 family protein; **PDBTitle:** complex between the haloferax volcanii trm112 methyltransferase2 activator and the hvo_0019 putative methyltransferase
59	c3tenD_	Alignment	not modelled	33.5	0	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cs2 hydrolase; **PDBTitle:** holo form of carbon disulfide hydrolase
60	c4esjA_	Alignment	not modelled	31.0	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**type-2 restriction enzyme dpni; **PDBTitle:** restriction endonuclease dpni in complex with target dna
61	c3wwnB_	Alignment	not modelled	27.3	13	**PDB header:**metal binding protein/transferase **Chain:** B: **PDB Molecule:**orff; **PDBTitle:** crystal structure of lysz from thermus thermophilus complex with lysw
62	c3vrkA_	Alignment	not modelled	25.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carbonyl sulfide hydrolase; **PDBTitle:** crystal structutre of thiobacillus thioparus thi115 carbonyl sulfide2 hydrolase / thiocyanate complex
63	c3vpbF_	Alignment	not modelled	23.5	15	**PDB header:**ligase **Chain:** F: **PDB Molecule:**alpha-aminoadipate carrier protein lysw; **PDBTitle:** argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
64	c3lasA_	Alignment	not modelled	22.7	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution
65	c5ztpB_	Alignment	not modelled	22.2	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** carbonic anhydrase from glaciozyma antarctica
66	c2k5hA_	Alignment	not modelled	22.2	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
67	c2w3nA_	Alignment	not modelled	20.9	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase 2; **PDBTitle:** structure and inhibition of the co2-sensing carbonic anhydrase can22 from the pathogenic fungus cryptococcus neoformans
68	d2exda1	Alignment	not modelled	20.9	22	**Fold:**OB-fold **Superfamily:**NfeD domain-like **Family:**NfeD domain-like
69	d1ddza2	Alignment	not modelled	19.8	21	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
70	c6gwuB_	Alignment	not modelled	19.4	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** carbonic anhydrase cance103p from candida albicans
71	c6g4wr_	Alignment	not modelled	18.5	22	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**40s ribosomal protein s17; **PDBTitle:** cryo-em structure of a late human pre-40s ribosomal subunit - state a
72	c3cp0A_	Alignment	not modelled	18.4	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**membrane protein implicated in regulation of membrane **PDBTitle:** crystal structure of the soluble domain of membrane protein implicated2 in regulation of membrane protease activity from corynebacterium3 glutamicum
73	c2a8cE_	Alignment	not modelled	18.2	17	**PDB header:**lyase **Chain:** E: **PDB Molecule:**carbonic anhydrase 2; **PDBTitle:** haemophilus influenzae beta-carbonic anhydrase
74	d1ddza1	Alignment	not modelled	18.0	17	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
75	c1ylkA_	Alignment	not modelled	18.0	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv1284/mt1322; **PDBTitle:** crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate
76	c5cxkG_	Alignment	not modelled	18.0	17	**PDB header:**lyase **Chain:** G: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of beta carbonic anhydrase from vibrio cholerae
77	d2nn6g3	Alignment	not modelled	17.9	21	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
78	c3eyxB_	Alignment	not modelled	17.7	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase nce103 from2

						saccharomyces cerevisiae
79	c5swcE_	Alignment	not modelled	17.7	8	**PDB header:**lyase **Chain:** E: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** the structure of the beta-carbonic anhydrase ccaa
80	c1ddzA_	Alignment	not modelled	17.3	21	**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
81	c3ucoB_	Alignment	not modelled	17.0	8	**PDB header:**lyase/lyase inhibitor **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** coccomyxa beta-carbonic anhydrase in complex with iodide
82	c2a5vB_	Alignment	not modelled	16.7	33	**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
83	d2aqaa1	Alignment	not modelled	16.5	20	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
84	c2j6aA_	Alignment	not modelled	16.4	6	**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.
85	d1ekja_	Alignment	not modelled	16.0	17	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
86	c5cm2M_	Alignment	not modelled	16.0	0	**PDB header:**transferase **Chain:** M: **PDB Molecule:**trna methyltransferase activator subunit; **PDBTitle:** insights into molecular plasticity in protein complexes from trm9-2 trm112 trna modifying enzyme crystal structure
87	c4rxyA_	Alignment	not modelled	15.3	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of the beta carbonic anhydrase psca3 isolated from2 pseudomonas aeruginosa
88	d1i6pa_	Alignment	not modelled	15.2	25	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
89	d1g5ca_	Alignment	not modelled	14.4	8	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
90	c6g5iy_	Alignment	not modelled	14.3	13	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**40s ribosomal protein s24; **PDBTitle:** cryo-em structure of a late human pre-40s ribosomal subunit - state r
91	d2apob1	Alignment	not modelled	12.6	19	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
92	c3j20R_	Alignment	not modelled	12.6	20	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**30s ribosomal protein s17p; **PDBTitle:** promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
93	d2ey4e1	Alignment	not modelled	12.5	19	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
94	c4o1kA_	Alignment	not modelled	12.4	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structures of two tetrameric beta-carbonic anhydrases from the2 filamentous ascomycete sordaria macrospora.
95	d2j7ja2	Alignment	not modelled	12.0	33	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
96	c2jrrA_	Alignment	not modelled	11.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of q5lls5 from silicibacter2 pomeroyi. northeast structural genomics consortium target3 sir90
97	c4o1jB_	Alignment	not modelled	11.6	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structures of two tetrameric beta-carbonic anhydrases from the2 filamentous ascomycete sordaria macrospora.
98	d2c42a2	Alignment	not modelled	11.2	0	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**PFOR PP module
99	d1ubdc1	Alignment	not modelled	10.3	33	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2