Phyre^2

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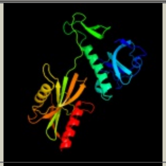
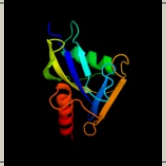
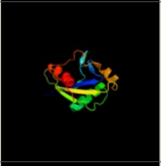
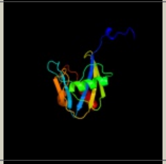
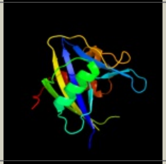
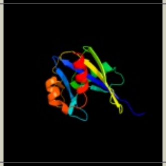
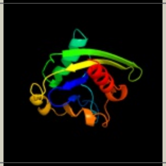
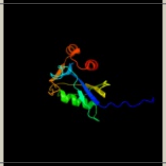
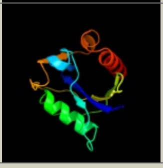
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gb5B_	Alignment		100.0	97	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nadh pyrophosphatase; **PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
2	c3cngC_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
3	d1vk6a2	Alignment		100.0	97	**Fold:**Nudix **Superfamily:**Nudix **Family:**NADH pyrophosphatase
4	c3q4iA_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohydrolase (mutt/nudix family protein); **PDBTitle:** crystal structure of cdp-chase in complex with gd3+
5	d2fb1a2	Alignment		99.9	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like
6	c3gz8C_	Alignment		99.9	17	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** cocrystal structure of nudix domain of shewanella oneidensis2 nrtr complexed with adp ribose
7	c2fb1A_	Alignment		99.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0354 from bacteroides thetaiotaomicron
8	c3h95A_	Alignment		99.9	20	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 6; **PDBTitle:** crystal structure of the nudix domain of nudt6
9	c3dkuB_	Alignment		99.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative phosphohydrolase; **PDBTitle:** crystal structure of nudix hydrolase orf153, ymfb, from2 escherichia coli k-1
10	d2b0va1	Alignment		99.9	24	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
11	d2fmla2	Alignment		99.9	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**BT0354 N-terminal domain-like

12	c3o8sA_	Alignment		99.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribose pyrophosphatase; **PDBTitle:** crystal structure of an adp-ribose pyrophosphatase (ssu98_1448) from2 streptococcus suis 89-1591 at 2.27 a resolution
13	c2pq1B_	Alignment		99.9	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ap4a hydrolase; **PDBTitle:** crystal structure of ap4a hydrolase complexed with amp and2 atp (aq_158) from aquifex aeolicus vf5
14	c3gg6A_	Alignment		99.9	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 18; **PDBTitle:** crystal structure of the nudix domain of human nudt18
15	c2qjoB_	Alignment		99.9	19	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional nmn adenylyltransferase/nudix hydrolase; **PDBTitle:** crystal structure of a bifunctional nmn adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
16	c3gz6A_	Alignment		99.8	18	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of shewanella oneidensis nrtr complexed2 with a 27mer dna
17	d1sjya_	Alignment		99.8	24	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
18	c3rh7A_	Alignment		99.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical oxidoreductase; **PDBTitle:** crystal structure of a hypothetical oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution
19	c3ef5A_	Alignment		99.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable pyrophosphohydrolase; **PDBTitle:** structure of the rna pyrophosphohydrolase bdrpph in complex with dgtp
20	c3grnB_	Alignment		99.8	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt related protein; **PDBTitle:** crystal structure of mutt protein from methanosarcina mazei go1
21	c2yyhC_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**8-oxo-dgtpase domain; **PDBTitle:** crystal structure of nudix family protein from aquifex aeolicus
22	c2r5wA_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**nicotinamide-nucleotide adenylyltransferase; **PDBTitle:** crystal structure of a bifunctional nmn2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
23	d1vhza_	Alignment	not modelled	99.8	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
24	c3fk9B_	Alignment	not modelled	99.8	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mmutator mutt protein from bacillus2 halodurans
25	d1vk6a3	Alignment	not modelled	99.8	98	**Fold:**Nudix **Superfamily:**Nudix **Family:**NADH pyrophosphatase
26	c3f6aA_	Alignment	not modelled	99.8	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a hydrolase, nudix family from2 clostridium perfringens
27	d1ryaa_	Alignment	not modelled	99.8	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**GDP-mannose mannosyl hydrolase NudD
28	c3gwyA_	Alignment	not modelled	99.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ctp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ctp pyrophosphohydrolase from2 bacteroides fragilis
						PDB header:structural genomics, unknown function

29	c2fmlB_	Alignment	not modelled	99.8	22	**Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of mutt/nudix family protein from enterococcus2 faecalis
30	c2kdvA_	Alignment	not modelled	99.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna pyrophosphohydrolase; **PDBTitle:** solution structure of rna pyrophosphohydrolase rpph from2 escherichia coli
31	c3i9xA_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from listeria innocua
32	d2azwa1	Alignment	not modelled	99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
33	d1irya_	Alignment	not modelled	99.8	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
34	c3e57A_	Alignment	not modelled	99.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein tm1382; **PDBTitle:** crystal structure of tm1382, a putative nudix hydrolase
35	d1k2ea_	Alignment	not modelled	99.8	23	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
36	c3r03B_	Alignment	not modelled	99.8	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nudix hydrolase; **PDBTitle:** the crystal structure of nudix hydrolase from rhodospirillum rubrum
37	d2b06a1	Alignment	not modelled	99.8	23	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
38	c3hhjA_	Alignment	not modelled	99.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutator mutt protein; **PDBTitle:** crystal structure of mutator mutt from bartonella henselae
39	c2w4eA_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
40	d1v8ya_	Alignment	not modelled	99.8	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
41	d2fkba1	Alignment	not modelled	99.8	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
42	c2yvoA_	Alignment	not modelled	99.8	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of ndx2 in complex with mg2+ and amp from thermus2 thermophilus hb8
43	d1vcda1	Alignment	not modelled	99.8	21	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
44	d1g0sa_	Alignment	not modelled	99.8	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
45	c3id9B_	Alignment	not modelled	99.8	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mutt/nudix family protein from2 bacillus thuringiensis
46	c2jvbA_	Alignment	not modelled	99.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mrna-decapping enzyme subunit 2; **PDBTitle:** solution structure of catalytic domain of ydcp2
47	c2pqvA_	Alignment	not modelled	99.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of mutt/nudix family protein from streptococcus2 pneumoniae
48	c3n77B_	Alignment	not modelled	99.8	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nucleoside triphosphatase nudi; **PDBTitle:** crystal structure of idp01880, putative ntp pyrophosphohydrolase of2 salmonella typhimurium lt2
49	c3fjyB_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable mutt1 protein; **PDBTitle:** crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
50	d2fvva1	Alignment	not modelled	99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
51	c2fvvA_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diphosphoinositol polyphosphate phosphohydrolase **PDBTitle:** human diphosphoinositol polyphosphate phosphohydrolase 1
52	c3exqA_	Alignment	not modelled	99.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix family hydrolase; **PDBTitle:** crystal structure of a nudix family hydrolase from2 lactobacillus brevis
53	d1puna_	Alignment	not modelled	99.8	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
54	c3bm4B_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adp-sugar pyrophosphatase; **PDBTitle:** crystal structure of human adp-ribose pyrophosphatase nudt52 in complex with magnesium and ampcpr
55	c2o1cB_	Alignment	not modelled	99.7	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**datp pyrophosphohydrolase; **PDBTitle:** structure of the e. coli dihydroneopterin triphosphate2

						pyrophosphohydrolase
56	c3f13A_	Alignment	not modelled	99.7	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative nudix hydrolase family member; **PDBTitle:** crystal structure of putative nudix hydrolase family member2 from chromobacterium violaceum
57	d1ktga_	Alignment	not modelled	99.7	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
58	d1jkna_	Alignment	not modelled	99.7	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
59	d2a6ta2	Alignment	not modelled	99.7	15	**Fold:**Nudix **Superfamily:**Nudix **Family:**mRNA decapping enzyme-like
60	d1xsba_	Alignment	not modelled	99.7	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
61	d1nqza_	Alignment	not modelled	99.7	20	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
62	c3sonB_	Alignment	not modelled	99.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical nudix hydrolase; **PDBTitle:** crystal structure of a hypothetical nudix hydrolase (lmof2365_2679)2 from listeria monocytogenes (atcc 19115) at 1.70 a resolution
63	c2qkmF_	Alignment	not modelled	99.7	16	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**spac19a8.12 protein; **PDBTitle:** the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
64	d2o5fa1	Alignment	not modelled	99.7	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
65	c3edsA_	Alignment	not modelled	99.7	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of a mut/nudix family protein from bacillus2 thuringiensis
66	d1q33a_	Alignment	not modelled	99.7	22	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
67	d1ppva_	Alignment	not modelled	99.7	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
68	c3fcmA_	Alignment	not modelled	99.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, nudix family; **PDBTitle:** crystal structure of a nudix hydrolase from clostridium2 perfringens
69	d1hzta_	Alignment	not modelled	99.7	17	**Fold:**Nudix **Superfamily:**Nudix **Family:**IPP isomerase-like
70	d1mqea_	Alignment	not modelled	99.7	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
71	d1viua_	Alignment	not modelled	99.7	18	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
72	c3q91D_	Alignment	not modelled	99.6	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uridine diphosphate glucose pyrophosphatase; **PDBTitle:** crystal structure of human uridine diphosphate glucose pyrophosphatase2 (nudt14)
73	c1rrqA_	Alignment	not modelled	99.6	13	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
74	d1x51a1	Alignment	not modelled	99.6	12	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
75	d1rrqa2	Alignment	not modelled	99.6	13	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutY C-terminal domain-like
76	c2i6kA_	Alignment	not modelled	99.5	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 1; **PDBTitle:** crystal structure of human type i ipp isomerase complexed2 with a substrate analog
77	c3dupB_	Alignment	not modelled	99.4	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mutt/nudix family protein; **PDBTitle:** crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
78	c2pnyA_	Alignment	not modelled	99.3	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 2; **PDBTitle:** structure of human isopentenyl-diphosphate delta-isomerase 2
79	d1u20a1	Alignment	not modelled	99.3	19	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
80	c2j8qB_	Alignment	not modelled	99.2	16	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**cleavage and polyadenylation specificity factor 5; **PDBTitle:** crystal structure of human cleavage and polyadenylation2 specificity factor 5 (cpsf5) in complex with a sulphate3 ion.

81	c3qsjA_	Alignment	not modelled	98.9	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
82	c3couA_	Alignment	not modelled	98.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside diphosphate-linked moiety x motif 16; **PDBTitle:** crystal structure of human nudix motif 16 (nudt16)
83	c3kvhA_	Alignment	not modelled	97.9	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein syndesmos; **PDBTitle:** crystal structure of human protein syndesmos (nudt16-like protein)
84	c3p5tE_	Alignment	not modelled	95.2	17	**PDB header:**rna binding protein **Chain:** E: **PDB Molecule:**cleavage and polyadenylation specificity factor subunit 5; **PDBTitle:** cfim25-cfim68 complex
85	d2ct7a1	Alignment	not modelled	94.1	13	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**IBR domain
86	d2fiya1	Alignment	not modelled	93.2	23	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
87	c1i3ql_	Alignment	not modelled	93.0	21	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii 14.2kd **PDBTitle:** rna polymerase ii crystal form i at 3.1 a resolution
88	c1nnjA_	Alignment	not modelled	92.8	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
89	d2k4xa1	Alignment	not modelled	92.6	22	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27a
90	c2js4A_	Alignment	not modelled	92.5	15	**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
91	c2f5qA_	Alignment	not modelled	92.5	21	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
92	c2jr6A_	Alignment	not modelled	92.0	8	**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
93	c3h0gI_	Alignment	not modelled	92.0	25	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
94	c1k82D_	Alignment	not modelled	91.9	20	**PDB header:**hydrolase/dna **Chain:** D: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
95	c2opfA_	Alignment	not modelled	91.8	20	**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
96	d2jnya1	Alignment	not modelled	91.4	12	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
97	c2aklA_	Alignment	not modelled	90.6	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phna-like protein pa0128; **PDBTitle:** solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
98	d2pk7a1	Alignment	not modelled	90.0	15	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
99	c2kpiA_	Alignment	not modelled	89.2	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
100	c1ee8A_	Alignment	not modelled	89.1	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
101	d2hf1a1	Alignment	not modelled	88.9	19	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
102	d1pfta_	Alignment	not modelled	88.1	21	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
103	c2pziA_	Alignment	not modelled	87.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable serine/threonine-protein kinase pkng; **PDBTitle:** crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
104	c1hk8A_	Alignment	not modelled	87.4	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
105	d1hk8a_	Alignment	not modelled	87.4	25	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes

						Family: Class III anaerobic ribonucleotide reductase NRDD subunit
106	c2k5cA_	Alignment	not modelled	86.9	28	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
107	d2akla2	Alignment	not modelled	86.0	22	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
108	d1ee8a3	Alignment	not modelled	85.7	21	**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
109	c1vddC_	Alignment	not modelled	85.5	19	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
110	d1tdza3	Alignment	not modelled	85.2	21	**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
111	d1vdda_	Alignment	not modelled	85.1	15	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
112	d1x3za1	Alignment	not modelled	84.5	20	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
113	d1r2za3	Alignment	not modelled	84.4	21	**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
114	c2ba1B_	Alignment	not modelled	83.4	23	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
115	d2f4ma1	Alignment	not modelled	82.9	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
116	d1k82a3	Alignment	not modelled	82.1	21	**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
117	d1k3xa3	Alignment	not modelled	82.0	21	**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
118	c2owoA_	Alignment	not modelled	81.9	22	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
119	c3k7aM_	Alignment	not modelled	81.7	17	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
120	d1dl6a_	Alignment	not modelled	81.5	13	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain