Phyre^2

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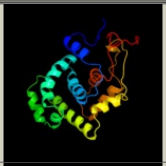
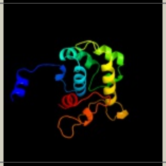
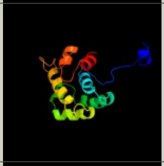
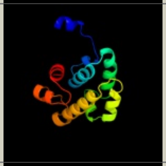
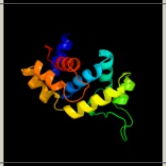
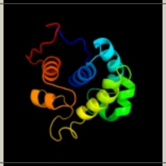
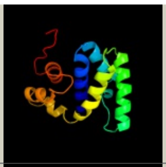
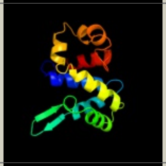
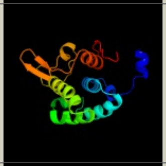
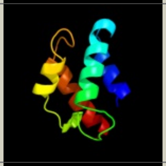
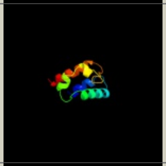
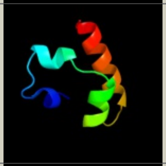
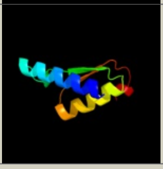
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nkua_	Alignment		100.0	98	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase I (Tag)
2	c2jg6A_	Alignment		100.0	43	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna-3-methyladenine glycosidase; **PDBTitle:** crystal structure of a 3-methyladenine dna glycosylase i2 from staphylococcus aureus
3	d1keaa_	Alignment		97.3	12	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
4	d1orna_	Alignment		96.5	18	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
5	c3n5nX_	Alignment		96.3	19	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**a/g-specific adenine dna glycosylase; **PDBTitle:** crystal structure analysis of the catalytic domain and interdomain2 connector of human muty homologue
6	d1rrqa1	Alignment		96.2	15	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
7	d1kg2a_	Alignment		96.0	18	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
8	d1pu6a_	Alignment		96.0	19	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**3-Methyladenine DNA glycosylase III (MagIII)
9	c3fhgA_	Alignment		94.8	13	**PDB header:**dna repair, hydrolase, lyase **Chain:** A: **PDB Molecule:**n-glycosylase/dna lyase; **PDBTitle:** crystal structure of sulfolobus solfataricus 8-oxoguanine dna2 glycosylase (ssogg)
10	d2abka_	Alignment		94.1	18	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
11	c2yg8B_	Alignment		91.6	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dna-3-methyladenine glycosidase ii, putative; **PDBTitle:** structure of an unusual 3-methyladenine dna glycosylase ii (2 alka) from deinococcus radiodurans

12	c3n0uB_	Alignment		91.2	16	**PDB header:**hydrolase, lyase **Chain:** B: **PDB Molecule:**probable n-glycosylase/dna lyase; **PDBTitle:** crystal structure of tm1821, the 8-oxoguanine dna glycosylase of2 thermotoga maritima
13	c3kntC_	Alignment		91.2	13	**PDB header:**hydrolase, lyase/dna **Chain:** C: **PDB Molecule:**n-glycosylase/dna lyase; **PDBTitle:** crystal structure of methanocaldococcus jannaschii 8-2 oxoguanine glycosylase/lyase in complex with 15mer dna3 containing 8-oxoguanine
14	c1rrqA_	Alignment		89.8	15	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**muty; **PDBTitle:** muty adenine glycosylase in complex with dna containing an2 a:oxog pair
15	d1ngna_	Alignment		89.1	14	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Mismatch glycosylase
16	c3s6iA_	Alignment		81.5	15	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**dna-3-methyladenine glycosylase 1; **PDBTitle:** schizosaccaromyces pombe 3-methyladenine dna glycosylase (mag1) in2 complex with abasic-dna.
17	d1mpga1	Alignment		75.7	24	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
18	c1oxjA_	Alignment		68.7	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna-binding protein smaug; **PDBTitle:** crystal structure of the smaug rna binding domain
19	d1oxja1	Alignment		62.4	14	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
20	c3hjzA_	Alignment		61.2	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transaldolase b; **PDBTitle:** the structure of an aldolase from prochlorococcus marinus
21	c2eseA_	Alignment	not modelled	59.4	18	**PDB header:**protein/rna complex **Chain:** A: **PDB Molecule:**vts1p; **PDBTitle:** structure of the sam domain of vts1p in complex with rna
22	c2vtgA_	Alignment	not modelled	55.2	13	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**ionized calcium-binding adapter molecule 2; **PDBTitle:** crystal structure of human iba2, trigonal crystal form
23	c2fe9A_	Alignment	not modelled	55.2	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein vts1; **PDBTitle:** solution structure of the vts1 sam domain in the presence2 of rna
24	c2b6gA_	Alignment	not modelled	54.7	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**vts1p; **PDBTitle:** rna recognition by the vts1 sam domain
25	d2noha1	Alignment	not modelled	51.2	18	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
26	c2g2bA_	Alignment	not modelled	50.0	15	**PDB header:**immune system **Chain:** A: **PDB Molecule:**allograft inflammatory factor 1; **PDBTitle:** nmr structure of the human allograft inflammatory factor 1
27	c2hjwA_	Alignment	not modelled	49.1	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** crystal structure of the bc domain of acc2
28	d1a9xa2	Alignment	not modelled	47.6	25	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
						PDB header:structural protein

29	c3k1rB_	Alignment	not modelled	46.7	19	**Chain:** B: **PDB Molecule:**usher syndrome type-1g protein; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
30	c2d58A_	Alignment	not modelled	46.1	16	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**allograft inflammatory factor 1; **PDBTitle:** human microglia-specific protein iba1
31	c2e8nA_	Alignment	not modelled	45.6	25	**PDB header:**transferase, signaling protein **Chain:** A: **PDB Molecule:**ephrin type-a receptor 2; **PDBTitle:** solution structure of the c-terminal sam-domain of ephaa2:2 ephrin type-a receptor 2 precursor (ec 2.7.10.1)
32	d1wg8a1	Alignment	not modelled	43.9	26	**Fold:**SAM domain-like **Superfamily:**Putative methyltransferase TM0872, insert domain **Family:**Putative methyltransferase TM0872, insert domain
33	c3m16A_	Alignment	not modelled	42.4	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transaldolase; **PDBTitle:** structure of a transaldolase from oleispira antarctica
34	d1coka_	Alignment	not modelled	41.7	14	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
35	d1onra_	Alignment	not modelled	41.7	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
36	c2yvqA_	Alignment	not modelled	41.4	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
37	c3igxA_	Alignment	not modelled	40.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transaldolase; **PDBTitle:** 1.85 angstrom resolution crystal structure of transaldolase b (tala)2 from francisella tularensis.
38	c2jhnB_	Alignment	not modelled	35.8	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna-glycosylase; **PDBTitle:** 3-methyladenine dna-glycosylase from archaeoglobus fulgidus
39	c2h56C_	Alignment	not modelled	31.3	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dna-3-methyladenine glycosidase; **PDBTitle:** crystal structure of dna-3-methyladenine glycosidase (10174367) from2 bacillus halodurans at 2.55 a resolution
40	d1zkda1	Alignment	not modelled	31.2	28	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**RPA4359-like
41	d1kjna_	Alignment	not modelled	30.3	36	**Fold:**Hypothetical protein MTH777 (MT0777) **Superfamily:**Hypothetical protein MTH777 (MT0777) **Family:**Hypothetical protein MTH777 (MT0777)
42	c2hnhA_	Alignment	not modelled	30.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit; **PDBTitle:** crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
43	d1f05a_	Alignment	not modelled	30.1	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
44	c2fe3B_	Alignment	not modelled	30.1	27	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**peroxide operon regulator; **PDBTitle:** the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
45	c2dl0A_	Alignment	not modelled	29.2	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sam and sh3 domain-containing protein 1; **PDBTitle:** solution structure of the sam-domain of the sam and sh32 domain containing protein 1
46	d1zcza1	Alignment	not modelled	29.2	14	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
47	c2uv1B_	Alignment	not modelled	28.9	45	**PDB header:**inhibitor **Chain:** B: **PDB Molecule:**host-nuclease inhibitor protein gam; **PDBTitle:** hexagonal crystal form of gams from bacteriophage lambda.
48	c2lc0A_	Alignment	not modelled	28.2	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** rv0020c_nter structure
49	d1wlza1	Alignment	not modelled	27.9	14	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
50	d1b0xa_	Alignment	not modelled	26.2	27	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
51	c1b0xA_	Alignment	not modelled	26.2	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (epha4 receptor tyrosine kinase); **PDBTitle:** the crystal structure of an eph receptor sam domain reveals2 a mechanism for modular dimerization.
52	c2remB_	Alignment	not modelled	25.7	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**disulfide oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase dsba from xylella2 fastidiosa
53	d1vpxa_	Alignment	not modelled	24.7	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
54	d1v38a_	Alignment	not modelled	24.7	10	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain
55	d2j9ga2	Alignment	not modelled	24.6	18	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like

56	c1wlzD_	Alignment	not modelled	24.5	14	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**cap-binding protein complex interacting protein **PDBTitle:** crystal structure of djbp fragment which was obtained by2 limited proteolysis
57	c3cq0B_	Alignment	not modelled	24.4	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative transaldolase ygr043c; **PDBTitle:** crystal structure of tal2_yeast
58	c2l98A_	Alignment	not modelled	23.3	15	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** structure of trans-resveratrol in complex with the cardiac regulatory2 protein troponin c
59	c3f10A_	Alignment	not modelled	23.2	18	**PDB header:**hydrolase, lyase **Chain:** A: **PDB Molecule:**8-oxoguanine-dna-glycosylase; **PDBTitle:** crystal structure of clostridium acetobutylicum 8-2 oxoguanine dna glycosylase in complex with 8-oxoguanosine
60	d1g8ma1	Alignment	not modelled	22.2	14	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
61	c1scvA_	Alignment	not modelled	21.6	16	**PDB header:**contractile protein, structural protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** nmr structure of the c terminal domain of cardiac troponin2 c bound to the n terminal domain of cardiac troponin i
62	c3l78A_	Alignment	not modelled	21.2	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein spx; **PDBTitle:** the crystal structure of smu.1142c from streptococcus mutans ua159
63	d1ulza2	Alignment	not modelled	20.8	21	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
64	d2e1da1	Alignment	not modelled	20.2	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
65	c3s1vD_	Alignment	not modelled	20.1	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**probable transaldolase; **PDBTitle:** transaldolase from thermoplasma acidophilum in complex with d-fructose2 6-phosphate schiff-base intermediate
66	d1pkxa1	Alignment	not modelled	19.0	17	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
67	c2b1uA_	Alignment	not modelled	18.5	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calmodulin-like protein 5; **PDBTitle:** solution structure of calmodulin-like skin protein c2 terminal domain
68	c2ktgA_	Alignment	not modelled	17.9	18	**PDB header:**ca-binding protein **Chain:** A: **PDB Molecule:**calmodulin, putative; **PDBTitle:** calmodulin like protein from entamoeba histolytica: solution structure2 and calcium binding properties of a partially folded protein
69	c2eaoA_	Alignment	not modelled	17.7	32	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**ephrin type-b receptor 1; **PDBTitle:** solution structure of the c-terminal sam-domain of mouse2 ephrin type-b receptor 1 precursor (ec 2.7.1.112)
70	c2jziB_	Alignment	not modelled	17.5	36	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase 2b **PDBTitle:** structure of calmodulin complexed with the calmodulin2 binding domain of calcineurin
71	c2kdhA_	Alignment	not modelled	17.1	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** the solution structure of human cardiac troponin c in2 complex with the green tea polyphenol; (-)-3 epigallocatechin-3-gallate
72	c1mpgB_	Alignment	not modelled	16.7	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3-methyladenine dna glycosylase ii; **PDBTitle:** 3-methyladenine dna glycosylase ii from escherichia coli
73	c3senD_	Alignment	not modelled	16.5	28	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**caskin-1; **PDBTitle:** structure of caskin1 tandem sams
74	c2ebuA_	Alignment	not modelled	16.3	24	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication factor c subunit 1; **PDBTitle:** solution structure of the brct domain from human2 replication factor c large subunit 1
75	d1wx0a1	Alignment	not modelled	16.3	36	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
76	c2l05A_	Alignment	not modelled	16.2	64	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase b-raf; **PDBTitle:** solution nmr structure of the ras-binding domain of serine/threonine-2 protein kinase b-raf from homo sapiens, northeast structural genomics3 consortium target hr4694f
77	c2o03A_	Alignment	not modelled	16.1	31	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable zinc uptake regulation protein furb; **PDBTitle:** crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
78	c1cjyB_	Alignment	not modelled	16.0	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (cytosolic phospholipase a2); **PDBTitle:** human cytosolic phospholipase a2
79	d2opoa1	Alignment	not modelled	15.4	9	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Polcalcin
						PDB header:hydrolase, oxidoreductase

80	c2o7pA_	Alignment	not modelled	14.9	31	**Chain:** A: **PDB Molecule:**riboflavin biosynthesis protein ribd; **PDBTitle:** the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain
81	c3gidB_	Alignment	not modelled	14.8	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** the biotin carboxylase (bc) domain of human acetyl-coa2 carboxylase 2 (acc2) in complex with soraphen a
82	c3mwmA_	Alignment	not modelled	14.7	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative metal uptake regulation protein; **PDBTitle:** graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
83	d1qjta_	Alignment	not modelled	14.4	15	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Eps15 homology domain (EH domain)
84	c1yqmA_	Alignment	not modelled	14.2	15	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**n-glycosylase/dna lyase; **PDBTitle:** catalytically inactive human 8-oxoguanine glycosylase2 crosslinked to 7-deazaguanine containing dna
85	c1rrbA_	Alignment	not modelled	14.2	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**raf proto-oncogene serine/threonine-protein **PDBTitle:** the ras-binding domain of raf-1 from rat, nmr, 1 structure
86	c1qzuB_	Alignment	not modelled	14.0	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical protein mds018; **PDBTitle:** crystal structure of human phosphopantothenoylcysteine decarboxylase
87	d1cjya2	Alignment	not modelled	13.9	10	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**Lysophospholipase
88	d1f54a_	Alignment	not modelled	13.9	9	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
89	d1fi5a_	Alignment	not modelled	13.8	17	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
90	c1fi5A_	Alignment	not modelled	13.8	17	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**protein (troponin c); **PDBTitle:** nmr structure of the c terminal domain of cardiac troponin2 c bound to the n terminal domain of cardiac troponin i.
91	c1ykuB_	Alignment	not modelled	13.6	9	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein pxo2-61; **PDBTitle:** crystal structure of a sensor domain homolog
92	c3kp9A_	Alignment	not modelled	13.6	20	**PDB header:**blood coagulation,oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** structure of a bacterial homolog of vitamin k epoxide reductase
93	d1jc2a_	Alignment	not modelled	13.5	17	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
94	c1jc2A_	Alignment	not modelled	13.5	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**troponin c, skeletal muscle; **PDBTitle:** complex of the c-domain of troponin c with residues 1-40 of2 troponin i
95	d1wrka1	Alignment	not modelled	12.9	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
96	c3gkxB_	Alignment	not modelled	12.9	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative arsc family related protein; **PDBTitle:** crystal structure of putative arsc family related protein from2 bacteroides fragilis
97	d1ap4a_	Alignment	not modelled	12.9	12	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
98	d1qzua_	Alignment	not modelled	12.9	10	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
99	d1l7ba_	Alignment	not modelled	12.9	24	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**DNA ligase