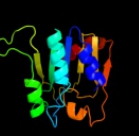
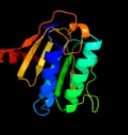


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wjyA_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
2	c2xzlA_	 Alignment		100.0	23	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent helicase nam7; PDBTitle: upf1-rna complex
3	c2gk7A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: regulator of nonsense transcripts 1; PDBTitle: structural and functional insights into the human upf1 helicase core
4	c3hsiC_	 Alignment		99.9	11	PDB header: transferase Chain: C: PDB Molecule: phosphatidylserine synthase; PDBTitle: crystal structure of phosphatidylserine synthase haemophilus2 influenzae rd kw20
5	d1byra_	 Alignment		99.8	16	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Nuclease
6	d1v0wa2	 Alignment		99.8	16	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Phospholipase D
7	c1v0sA_	 Alignment		99.8	17	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase d; PDBTitle: uninhibited form of phospholipase d from streptomyces sp.2 strain pmf
8	d1xdpa3	 Alignment		99.8	22	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
9	d1v0wa1	 Alignment		99.8	15	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Phospholipase D
10	c3e1sA_	 Alignment		99.6	20	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease v, subunit recd; PDBTitle: structure of an n-terminal truncation of deinococcus radiodurans recd2
11	c1w36G_	 Alignment		99.5	17	PDB header: recombination Chain: G: PDB Molecule: exodeoxyribonuclease v alpha chain; PDBTitle: recbcd:dna complex

12	c3lfuA_	Alignment		99.4	16	PDB header: hydrolase Chain: A: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of e. coli uvrD
13	c1pjrA_	Alignment		99.3	19	PDB header: helicase Chain: A: PDB Molecule: pcra; PDBTitle: structure of dna helicase
14	c3dmnA_	Alignment		99.2	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dna helicase; PDBTitle: the crystal structure of the c-terminal domain of a possilbe dna2 helicase from lactobacillus plantarun wcfs1
15	c1xdoB_	Alignment		99.1	16	PDB header: transferase Chain: B: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of escherichia coli polyphosphate kinase
16	c2is6B_	Alignment		99.0	21	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna helicase ii; PDBTitle: crystal structure of uvrD-dna-adpmg3 ternary complex
17	d1w36d2	Alignment		99.0	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
18	c1uaaB_	Alignment		98.9	16	PDB header: hydrolase/dna Chain: B: PDB Molecule: protein (atp-dependent dna heli case rep.); PDBTitle: e. coli rep helicase/dna complex
19	c2o8rA_	Alignment		98.6	15	PDB header: transferase Chain: A: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of polyphosphate kinase from2 porphyromonas gingivalis
20	d1xdpa4	Alignment		98.5	20	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
21	d2o8ra3	Alignment	not modelled	98.4	15	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
22	d2o8ra4	Alignment	not modelled	98.2	15	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
23	c1qhhD_	Alignment	not modelled	98.1	14	PDB header: hydrolase Chain: D: PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adnp
24	c2pjrB_	Alignment	not modelled	97.9	18	PDB header: hydrolase/dna Chain: B: PDB Molecule: protein (helicase pcra); PDBTitle: helicase product complex
25	d1uaaa2	Alignment	not modelled	97.9	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
26	d1w36b2	Alignment	not modelled	97.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
27	d1pjrA2	Alignment	not modelled	97.7	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
28	c1w36E_	Alignment	not modelled	97.1	19	PDB header: recombination Chain: E: PDB Molecule: exodeoxyribonuclease v beta chain; PDBTitle: recbcd:dna complex
						PDB header: hydrolase

29	c2c1lA_	Alignment	not modelled	97.0	22	Chain: A: PDB Molecule: restriction endonuclease; PDBTitle: structure of the bfiI restriction endonuclease
30	dlw36c2	Alignment	not modelled	96.5	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
31	c1nopB_	Alignment	not modelled	95.6	20	PDB header: hydrolase/dna Chain: B: PDB Molecule: tyrosyl-dna phosphodiesterase 1; PDBTitle: crystal structure of human tyrosyl-dna phosphodiesterase2 (tdp1) in complex with vanadate, dna and a human3 topoisomerase i-derived peptide
32	dlq32a2	Alignment	not modelled	95.5	26	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Tyrosyl-DNA phosphodiesterase TDP1
33	dljy1a2	Alignment	not modelled	95.3	17	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Tyrosyl-DNA phosphodiesterase TDP1
34	c1w36F_	Alignment	not modelled	94.8	13	PDB header: recombination Chain: F: PDB Molecule: exodeoxyribonuclease v gamma chain; PDBTitle: recbcd:dna complex
35	c1q32C_	Alignment	not modelled	94.3	29	PDB header: replication,transcription,hydrolase Chain: C: PDB Molecule: tyrosyl-dna phosphodiesterase; PDBTitle: crystal structure analysis of the yeast tyrosyl-dna2 phosphodiesterase
36	c3sq3C_	Alignment	not modelled	93.7	29	PDB header: hydrolase Chain: C: PDB Molecule: tyrosyl-dna phosphodiesterase 1; PDBTitle: crystal structure analysis of the yeast tyrosyl-dna phosphodiesterase2 h182a mutant
37	d2f5bx2	Alignment	not modelled	91.3	13	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: TrmB middle domain-like
38	c2pjrF_	Alignment	not modelled	91.1	20	PDB header: hydrolase/dna Chain: F: PDB Molecule: protein (helicase pcra); PDBTitle: helicase product complex
39	c2f5tX_	Alignment	not modelled	88.6	13	PDB header: transcription Chain: X: PDB Molecule: archaeal transcriptional regulator trmb; PDBTitle: crystal structure of the sugar binding domain of the archaeal2 transcriptional regulator trmb
40	dlpztA_	Alignment	not modelled	87.7	25	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: beta 1,4 galactosyltransferase (b4GalT1)
41	c3lw6A_	Alignment	not modelled	80.9	17	PDB header: transferase Chain: A: PDB Molecule: beta-4-galactosyltransferase 7; PDBTitle: crystal structure of drosophila beta1,4-galactosyltransferase-7
42	c1qhhA_	Alignment	not modelled	66.1	13	PDB header: hydrolase Chain: A: PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
43	dljy1a1	Alignment	not modelled	57.9	17	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Tyrosyl-DNA phosphodiesterase TDP1
44	c1t3gB_	Alignment	not modelled	33.0	9	PDB header: membrane protein Chain: B: PDB Molecule: x-linked interleukin-1 receptor accessory PDBTitle: crystal structure of the toll/interleukin-1 receptor (tir)2 domain of human il-1rapl
45	c1qhhB_	Alignment	not modelled	29.4	21	PDB header: hydrolase Chain: B: PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
46	dlgz0a2	Alignment	not modelled	23.9	15	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain
47	dlS2da_	Alignment	not modelled	23.6	21	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: N-deoxyribosyltransferase
48	dlf8ya_	Alignment	not modelled	22.1	13	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: N-deoxyribosyltransferase
49	c3oziB_	Alignment	not modelled	21.9	13	PDB header: plant protein Chain: B: PDB Molecule: l6tr; PDBTitle: crystal structure of the tir domain from the flax disease resistance2 protein l6
50	dlqzqa1	Alignment	not modelled	20.9	19	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Tyrosyl-DNA phosphodiesterase TDP1
51	c3fniA_	Alignment	not modelled	17.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (al13895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
52	c3dy0B_	Alignment	not modelled	17.4	33	PDB header: blood clotting, hydrolase inhibitor Chain: B: PDB Molecule: c-terminus plasma serine protease inhibitor; PDBTitle: crystal structure of cleaved pci bound to heparin
53	c3p1wA_	Alignment	not modelled	16.6	20	PDB header: protein transport Chain: A: PDB Molecule: rabgdi protein; PDBTitle: crystal structure of rab gdi from plasmodium falciparum, pfl2060c
54	dlq32a1	Alignment	not modelled	16.5	24	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Tyrosyl-DNA phosphodiesterase TDP1
55	c1lq8H_	Alignment	not modelled	16.3	33	PDB header: blood clotting Chain: H: PDB Molecule: plasma serine protease inhibitor;

						PDBTitle: crystal structure of cleaved protein c inhibitor
56	c3cqiD	Alignment	not modelled	16.2	21	PDB header: unknown function Chain: D: PDB Molecule: propanediol utilization protein pduu; PDBTitle: crystal structure of the pduu shell protein from the pdu2 microcompartment
57	d1gz0f2	Alignment	not modelled	15.8	15	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain
58	c3mpbA	Alignment	not modelled	15.6	24	PDB header: isomerase Chain: A: PDB Molecule: sugar isomerase; PDBTitle: z5688 from e. coli o157:h7 bound to fructose
59	d1o98a1	Alignment	not modelled	14.5	18	Fold: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Superfamily: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
60	c3pstA	Alignment	not modelled	12.6	20	PDB header: nuclear protein Chain: A: PDB Molecule: protein doa1; PDBTitle: crystal structure of pul and pfu(mutate) domain
61	d1r89a1	Alignment	not modelled	12.5	24	Fold: PAP/OAS1 substrate-binding domain Superfamily: PAP/OAS1 substrate-binding domain Family: Archaeal tRNA CCA-adding enzyme substrate-binding domain
62	c3ia0c	Alignment	not modelled	12.4	18	PDB header: structural protein Chain: C: PDB Molecule: ethanolamine utilization protein euts; PDBTitle: ethanolamine utilization microcompartment shell subunit,2 euts-g39v mutant
63	c3fd0B	Alignment	not modelled	12.1	12	PDB header: lyase Chain: B: PDB Molecule: putative cystathionine beta-lyase involved in aluminum PDBTitle: crystal structure of putative cystathionine beta-lyase involved in2 aluminum resistance (np_470671.1) from listeria innocua at 2.12 a3 resolution
64	c3l3fx	Alignment	not modelled	12.1	20	PDB header: protein binding Chain: X: PDB Molecule: protein doa1; PDBTitle: crystal structure of a pfu-pul domain pair of saccharomyces cerevisiae2 doa1/ufd3
65	c2l82A	Alignment	not modelled	12.1	14	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or32; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32
66	c2a5hC	Alignment	not modelled	12.0	8	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
67	d1xo1a2	Alignment	not modelled	12.0	15	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
68	c3ktbD	Alignment	not modelled	11.5	19	PDB header: transcription regulator Chain: D: PDB Molecule: arsenical resistance operon trans-acting repressor; PDBTitle: crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
69	c2y0oA	Alignment	not modelled	10.9	28	PDB header: isomerase Chain: A: PDB Molecule: probable d-lyxose ketol-isomerase; PDBTitle: the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis
70	c2z86D	Alignment	not modelled	10.8	15	PDB header: transferase Chain: D: PDB Molecule: chondroitin synthase; PDBTitle: crystal structure of chondroitin polymerase from2 escherichia coli strain k4 (k4cp) complexed with udp-glucua3 and udp
71	d1utaa	Alignment	not modelled	9.5	21	Fold: Ferredoxin-like Superfamily: Sporulation related repeat Family: Sporulation related repeat
72	c3ckvA	Alignment	not modelled	9.5	16	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a mycobacterial protein
73	d1x94a	Alignment	not modelled	8.9	17	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
74	d1vmea1	Alignment	not modelled	8.8	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
75	d1j5pa4	Alignment	not modelled	8.7	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
76	c3kgkA	Alignment	not modelled	8.5	15	PDB header: chaperone Chain: A: PDB Molecule: arsenical resistance operon trans-acting repressor arsd; PDBTitle: crystal structure of arsd
77	c2r60A	Alignment	not modelled	8.4	9	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase, group 1; PDBTitle: structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
78	c3iabB	Alignment	not modelled	8.3	25	PDB header: hydrolase/rna Chain: B: PDB Molecule: ribonucleases p/mrp protein subunit pop7; PDBTitle: crystal structure of rnase p/rnase mrp proteins pop6, pop72 in a complex with the p3 domain of rnase mrp rna
						PDB header: ribosome Chain: C: PDB Molecule: elongation factor g;

79	c2bcwC_	Alignment	not modelled	8.2	13	PDBTitle: coordinates of the n-terminal domain of ribosomal protein2 l11,c-terminal domain of ribosomal protein l7/l12 and a3 portion of the g' domain of elongation factor g, as fitted4 into cryo-em map of an escherichia coli 70s*ef-5 g*gdp*fusidic acid complex
80	c2x0dA_	Alignment	not modelled	7.9	7	PDB header: transferase Chain: A: PDB Molecule: wsaf; PDBTitle: apo structure of wsaf
81	d1o0sa2	Alignment	not modelled	7.6	12	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain
82	d1fyva_	Alignment	not modelled	7.5	11	Fold: Flavodoxin-like Superfamily: Toll/Interleukin receptor TIR domain Family: Toll/Interleukin receptor TIR domain
83	c2zrrA_	Alignment	not modelled	7.5	30	PDB header: antimicrobial protein Chain: A: PDB Molecule: mundticin ks immunity protein; PDBTitle: crystal structure of an immunity protein that contributes2 to the self-protection of bacteriocin-producing3 enterococcus mundtii 15-1a
84	d1w36d1	Alignment	not modelled	7.5	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
85	c3h16A_	Alignment	not modelled	6.1	16	PDB header: signaling protein Chain: A: PDB Molecule: tir protein; PDBTitle: crystal structure of a bacteria tir domain, pdtir from2 paracoccus denitrificans
86	c2dc1A_	Alignment	not modelled	6.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
87	c3cseA_	Alignment	not modelled	6.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: candida glabrata dihydrofolate reductase complexed with2 nadph and 2,4-diamino-5-(3-(2,5-dimethoxyphenyl)prop-1-3 ynyl)-6-ethylpyrimidine (ucp120b)
88	c3nklA_	Alignment	not modelled	5.9	15	PDB header: oxidoreductase/lyase Chain: A: PDB Molecule: udp-d-quinovosamine 4-dehydrogenase; PDBTitle: crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
89	c3cvjB_	Alignment	not modelled	5.7	17	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoheptose isomerase; PDBTitle: crystal structure of a putative phosphoheptose isomerase (bh3325) from2 bacillus halodurans c-125 at 2.00 a resolution
90	c2ihnA_	Alignment	not modelled	5.5	15	PDB header: hydrolase/dna Chain: A: PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
91	c3ht4B_	Alignment	not modelled	5.5	14	PDB header: lyase Chain: B: PDB Molecule: aluminum resistance protein; PDBTitle: crystal structure of the q81a77_baccr protein from bacillus2 cereus. northeast structural genomics consortium target3 bcr213
92	c3nkuA_	Alignment	not modelled	5.5	20	PDB header: protein transport Chain: A: PDB Molecule: drara; PDBTitle: crystal structure of the n-terminal domain of drara/sidm from2 legionella pneumophila
93	c2k19A_	Alignment	not modelled	5.4	30	PDB header: antimicrobial protein Chain: A: PDB Molecule: putative piscicolin 126 immunity protein; PDBTitle: nmr solution structure of pisi
94	c2bpbB_	Alignment	not modelled	5.3	20	PDB header: oxidoreductase Chain: B: PDB Molecule: sulfite\cytochrome c oxidoreductase subunit b; PDBTitle: sulfite dehydrogenase from starkeya novella
95	c1o98A_	Alignment	not modelled	5.2	18	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent PDBTitle: 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
96	c2x3yA_	Alignment	not modelled	5.2	20	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei