














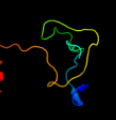
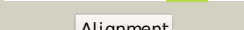
















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qgpA_	 Alignment		98.9	26	PDB header: hydrolase Chain: A: PDB Molecule: hnh endonuclease; PDBTitle: x-ray structure of the nhn endonuclease from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr87.
2	d2gykb1	 Alignment		96.1	34	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
3	c7ceiB_	 Alignment		88.4	31	PDB header: immune system Chain: B: PDB Molecule: protein (colicin e7 immunity protein); PDBTitle: the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein
4	c2qnfB_	 Alignment		82.7	20	PDB header: hydrolase/dna Chain: B: PDB Molecule: recombination endonuclease vii; PDBTitle: crystal structure of t4 endonuclease vii h43n mutant in2 complex with heteroduplex dna containing base mismatches
5	d1e7la2	 Alignment		80.3	22	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: Recombination endonuclease VII, N-terminal domain
6	c2orvB_	 Alignment		76.1	32	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: human thymidine kinase 1 in complex with tp4a
7	c1w4rC_	 Alignment		72.2	30	PDB header: transferase Chain: C: PDB Molecule: thymidine kinase; PDBTitle: structure of a type ii thymidine kinase with bound dtp
8	c2b8tA_	 Alignment		69.9	26	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from u.urealyticum in2 complex with thymidine
9	c2qq0B_	 Alignment		66.5	32	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from thermotoga maritima in complex with2 thymidine + appnhp
10	d2jb0b1	 Alignment		63.0	32	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
11	d2b8ta2	 Alignment		59.5	22	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger

12	d1xbta2	Alignment		50.8	29	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
13	c3goxB_	Alignment		44.7	20	PDB header: hydrolase/dna Chain: B: PDB Molecule: restriction endonuclease hpy99i; PDBTitle: crystal structure of the beta-beta-alpha-me type ii restriction2 endonuclease hpy99i in the absence of edta
14	d1jhfa1	Alignment		42.6	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
15	c1xx6B_	Alignment		40.5	24	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
16	c2iqjB_	Alignment		38.4	31	PDB header: protein transport Chain: B: PDB Molecule: stromal membrane-associated protein 1-like; PDBTitle: crystal structure of the gap domain of smap1l (loc64744)2 stromal membrane-associated protein 1-like
17	c3e2iA_	Alignment		37.7	20	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from s. aureus
18	c2vr0A_	Alignment		34.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c nitrite reductase, catalytic subunit nfra; PDBTitle: crystal structure of cytochrome c nitrite reductase nrhfa2 complex bound to the hqno inhibitor
19	d1qdba_	Alignment		29.4	24	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Di-heme elbow motif
20	c1vtA_	Alignment		27.3	22	PDB header: transcription regulation Chain: A: PDB Molecule: transactivator protein; PDBTitle: structure of the equine infectious anemia virus tat protein
21	c3h7hA_	Alignment	not modelled	24.2	26	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt4; PDBTitle: crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
22	d1vp8a_	Alignment	not modelled	23.8	28	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
23	d2dj7a1	Alignment	not modelled	23.3	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
24	c3lvrE_	Alignment	not modelled	23.1	36	PDB header: protein transport Chain: E: PDB Molecule: arf-gap with sh3 domain, ank repeat and ph domain- PDBTitle: the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium
25	c2ju5A_	Alignment	not modelled	22.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin disulfide isomerase; PDBTitle: dsbh oxidoreductase
26	c2p57A_	Alignment	not modelled	21.7	29	PDB header: metal binding protein Chain: A: PDB Molecule: gtpase-activating protein znf289; PDBTitle: gap domain of znf289, an id1-regulated zinc finger protein
27	d2glia5	Alignment	not modelled	21.5	46	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
28	d1jx6a_	Alignment	not modelled	21.5	22	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
						PDB header: immune system/viral protein

29	c2wy3B_	Alignment	not modelled	21.0	48	Chain: B: PDB Molecule: uncharacterized protein ul16; PDBTitle: structure of the hcmv ul16-micb complex elucidates select2 binding of a viral immunoevasin to diverse nkg2d ligands
30	c2f3oB_	Alignment	not modelled	20.2	24	PDB header: unknown function Chain: B: PDB Molecule: pyruvate formate-lyase 2; PDBTitle: crystal structure of a glycy radical enzyme from archaeoglobus2 fulgidus
31	d1xx6a2	Alignment	not modelled	19.8	29	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
32	c3hcvB_	Alignment	not modelled	19.8	25	PDB header: rna binding protein Chain: B: PDB Molecule: maltose operon transcriptional repressor; PDBTitle: crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus aureus
33	c2ja1A_	Alignment	not modelled	19.3	21	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
34	c3m7kA_	Alignment	not modelled	18.9	22	PDB header: hydrolase/dna Chain: A: PDB Molecule: restriction endonuclease paci; PDBTitle: crystal structure of paci-dna enzyme product complex
35	c3na7A_	Alignment	not modelled	17.9	34	PDB header: gene regulation, chaperone Chain: A: PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
36	d1x3ha2	Alignment	not modelled	17.7	35	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
37	d2jneal	Alignment	not modelled	17.5	54	Fold: Rubredoxin-like Superfamily: Yfgj-like Family: Yfgj-like
38	c2jneA_	Alignment	not modelled	17.5	54	PDB header: metal binding protein Chain: A: PDB Molecule: hypothetical protein yfgj; PDBTitle: nmr structure of e.coli yfgj modelled with two zn+2 bound.2 northeast structural genomics consortium target er317.
39	c3iraA_	Alignment	not modelled	17.1	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
40	c1yshD_	Alignment	not modelled	16.9	53	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
41	d1jj2y_	Alignment	not modelled	16.5	26	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
42	d1r9da_	Alignment	not modelled	16.1	22	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: PFL-like
43	c2x41A_	Alignment	not modelled	16.1	42	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase; PDBTitle: structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
44	c2d9lA_	Alignment	not modelled	16.0	24	PDB header: gene regulation Chain: A: PDB Molecule: nucleoporin-like protein rip; PDBTitle: solution structure of the arfgap domain of human rip
45	c2zkrz_	Alignment	not modelled	16.0	41	PDB header: ribosomal protein/rna Chain: Z: PDB Molecule: e site t-rna; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
46	c2j7aE_	Alignment	not modelled	15.3	18	PDB header: oxidoreductase Chain: E: PDB Molecule: cytochrome c nitrite reductase nrfa; PDBTitle: crystal structure of cytochrome c nitrite reductase nrfa2 complex from desulfovibrio vulgaris
47	c2jrpA_	Alignment	not modelled	15.2	46	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cytoplasmic c protein; PDBTitle: solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86
48	c3dwdB_	Alignment	not modelled	15.0	31	PDB header: transport protein Chain: B: PDB Molecule: adp-ribosylation factor gtpase-activating protein 1; PDBTitle: crystal structure of the arfgap domain of human arfgap1
49	d1vqoz1	Alignment	not modelled	14.8	21	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
50	c1fs9A_	Alignment	not modelled	14.7	33	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c nitrite reductase; PDBTitle: cytochrome c nitrite reductase from wolinetella succinogenes-azide2 complex
51	c2b0oF_	Alignment	not modelled	14.5	38	PDB header: metal binding protein Chain: F: PDB Molecule: uplc1; PDBTitle: crystal structure of uplc1 gap domain
52	c2joxA_	Alignment	not modelled	14.1	28	PDB header: transcription Chain: A: PDB Molecule: churchill protein; PDBTitle: embryonic neural inducing factor churchill is not a dna-2 binding zinc finger protein: solution structure reveals a3 solvent-exposed beta-sheet and zinc binuclear cluster
53	c1i6hA_	Alignment	not modelled	14.0	17	PDB header: transcription/dna-rna hybrid Chain: A: PDB Molecule: dna-directed rna polymerase ii largest subunit; PDBTitle: rna polymerase ii elongation complex
54	d2ic1a1	Alignment	not modelled	13.9	26	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins

						Family: Cysteine dioxygenase type I
55	c3qqcA	Alignment	not modelled	13.8	21	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase subunit b, dna-directed rna PDBTitle: crystal structure of archaeal spt4/5 bound to the rnap clamp domain
56	d3elna1	Alignment	not modelled	13.6	26	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Cysteine dioxygenase type I
57	c2y8nC	Alignment	not modelled	13.5	20	PDB header: lyase Chain: C: PDB Molecule: 4-hydroxyphenylacetate decarboxylase large subunit; PDBTitle: crystal structure of glycyl radical enzyme
58	d1fs7a	Alignment	not modelled	13.3	33	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Di-heme elbow motif
59	c3cc4Z	Alignment	not modelled	13.3	24	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
60	c4a17Y	Alignment	not modelled	13.2	47	PDB header: ribosome Chain: Y: PDB Molecule: rpl37a; PDBTitle: t thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
61	d1vh3a	Alignment	not modelled	12.8	21	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidyltransferase
62	d1ubdc1	Alignment	not modelled	12.6	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
63	d1weoa	Alignment	not modelled	12.5	21	Fold: RING/U-box Superfamily: RING/U-box Family: RING finger domain, C3HC4
64	d1ffkw	Alignment	not modelled	12.4	19	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
65	d1inza	Alignment	not modelled	11.6	31	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: ENTH domain
66	c3f9uA	Alignment	not modelled	11.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative exported cytochrome c biogenesis-related protein; PDBTitle: crystal structure of c-terminal domain of putative exported cytochrome2 c biogenesis-related protein from bacteroides fragilis
67	d1twfa	Alignment	not modelled	10.9	17	Fold: beta and beta-prime subunits of DNA dependent RNA-polymerase Superfamily: beta and beta-prime subunits of DNA dependent RNA-polymerase Family: RNA-polymerase beta-prime
68	c3jyw9	Alignment	not modelled	10.9	29	PDB header: ribosome Chain: 9: PDB Molecule: 60s ribosomal protein l43; PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
69	c1rika	Alignment	not modelled	10.6	38	PDB header: de novo protein Chain: A: PDB Molecule: e6apc1 peptide; PDBTitle: e6-binding zinc finger (e6apc1)
70	d1hs5a	Alignment	not modelled	10.6	100	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
71	d1n5ga	Alignment	not modelled	10.5	33	Fold: Zinc finger domain of DNA polymerase-alpha Superfamily: Zinc finger domain of DNA polymerase-alpha Family: Zinc finger domain of DNA polymerase-alpha
72	d2fiya1	Alignment	not modelled	10.4	32	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
73	c1x4lA	Alignment	not modelled	10.2	28	PDB header: metal binding protein Chain: A: PDB Molecule: skeletal muscle lim-protein 3; PDBTitle: solution structure of lim domain in four and a half lim2 domains protein 2
74	c3cueH	Alignment	not modelled	9.9	25	PDB header: protein transport Chain: H: PDB Molecule: transport protein particle 31 kda subunit; PDBTitle: crystal structure of a trapp subassembly activating the rab2 yptlp
75	c2qu7B	Alignment	not modelled	9.8	21	PDB header: transcription Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcription regulator2 from staphylococcus saprophyticus subsp. saprophyticus
76	d1h16a	Alignment	not modelled	9.6	20	Fold: PFL-like glycyl radical enzymes Superfamily: PFL-like glycyl radical enzymes Family: PFL-like
77	c2l4zA	Alignment	not modelled	9.5	26	PDB header: hydrolase, metal binding protein Chain: A: PDB Molecule: dna endonuclease rbbp8, lim domain transcription factor PDBTitle: nmr structure of fusion of ctip (641-685) to lmo4-lim1 (18-82)
78	c3pnnA	Alignment	not modelled	9.2	22	PDB header: transferase Chain: A: PDB Molecule: conserved domain protein; PDBTitle: the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
79	c3c2kA	Alignment	not modelled	9.1	20	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase;

79	c3c3A_	Alignment	not modelled	9.1	20	PDBTitle: crystal structure of an uncharacterized protein from actinobacillus2 succinogenes PDB header: transcription regulator Chain: B: PDB Molecule: putative lacI-family transcriptional regulator;
80	c3gbvB_	Alignment	not modelled	9.1	13	PDBTitle: crystal structure of a putative lacI transcriptional regulator from2 bacteroides fragilis PDB header: metal binding protein Chain: A: PDB Molecule: fusion of the lim interacting domain of ldb1 and
81	c1m3vA_	Alignment	not modelled	9.1	15	PDBTitle: flin4: fusion of the lim binding domain of ldb1 and the n-2 terminal lim domain of lmo4 PDB header: hydrolase, hydrolase activator Chain: A: PDB Molecule: adp-ribosylation factor gtpase-activating protein 1, adp-
82	c3o47A_	Alignment	not modelled	9.1	28	PDBTitle: crystal structure of arfgap1-arf1 fusion protein PDB header: ribosome Chain: Y: PDB Molecule: 60s ribosomal protein l37(a);
83	c3jywY_	Alignment	not modelled	9.0	38	PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein;
84	c2qh8A_	Alignment	not modelled	8.9	10	PDBTitle: crystal structure of conserved domain protein from vibrio2 cholerae o1 biovar eltor str. n16961 PDB header: contractile Chain: A: PDB Molecule: protein (crp1);
85	c1b8tA_	Alignment	not modelled	8.9	32	PDBTitle: solution structure of the chicken crp1 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ygeu;
86	c1vhkA_	Alignment	not modelled	8.8	24	PDBTitle: crystal structure of an hypothetical protein PDB header: structural genomics, unknown function Chain: A: PDB Molecule: integron gene cassette protein hfx_cass2;
87	c3fxhA_	Alignment	not modelled	8.8	58	PDBTitle: crystal structure from the mobile metagenome of halifax2 harbour sewage outfall: integron cassette protein hfx_cass2 PDB header: ribosomal protein/rna Chain: 2: PDB Molecule: 60s ribosomal protein l37e;
88	c2zkr2_	Alignment	not modelled	8.7	38	PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map PDB header: viral protein Chain: L: PDB Molecule: l1 protein;
89	c2r5iL_	Alignment	not modelled	8.7	33	PDBTitle: pentamer structure of major capsid protein l1 of human2 papilloma virus type 18 PDB header: transcription Chain: H: PDB Molecule: catabolite control protein a;
90	c2o20H_	Alignment	not modelled	8.5	30	PDBTitle: crystal structure of transcription regulator ccpa of lactococcus2 lactis PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase i;
91	c3ac0B_	Alignment	not modelled	8.4	35	PDBTitle: crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose PDB header: ribosome Chain: Y: PDB Molecule: 60s ribosomal protein l37-a;
92	c1s1iY_	Alignment	not modelled	8.3	38	PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h. Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
93	d1qcva_	Alignment	not modelled	8.3	20	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021);
94	c3gn5B_	Alignment	not modelled	8.3	15	PDBTitle: structure of the e. coli protein mqsa (ygit/b3021) PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator protein, lacI
95	c3mizB_	Alignment	not modelled	8.1	14	PDBTitle: crystal structure of a putative transcriptional regulator2 protein, lacI family from rhizobium etli Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
96	d2yt9a2	Alignment	not modelled	8.0	83	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein;
97	c3e56A_	Alignment	not modelled	8.0	19	PDBTitle: the 2.0 angstrom resolution crystal structure of npr1517, a putative2 heterocyst differentiation inhibitor from nostoc punctiforme Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
98	d2dlqa4	Alignment	not modelled	7.8	67	PDB header: transcription Chain: D: PDB Molecule: dnak suppressor protein;
99	c1tjID_	Alignment	not modelled	7.8	56	PDBTitle: crystal structure of transcription factor dkxa from e. coli