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Description	P03841
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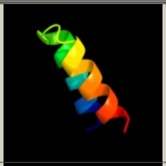
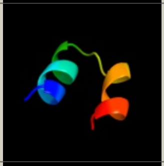
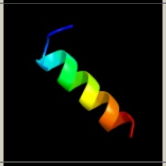
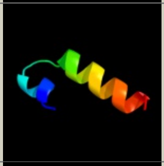
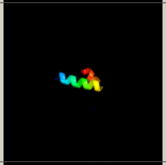
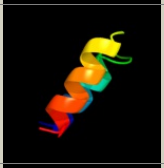
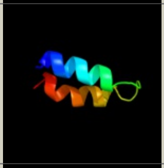
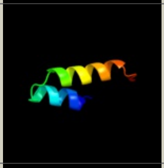
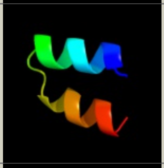
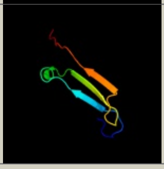
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1wcrA_	Alignment		57.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, n, n'-diacetylchitobiose-specific **PDBTitle:** trimeric structure of the enzyme iia from escherichia coli2 phosphotransferase system specific for n,n'-3 diacetylchitobiose
2	c2x0kB_	Alignment		53.4	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribf; **PDBTitle:** crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
3	c3op1A_	Alignment		53.1	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
4	c1t6zB_	Alignment		45.4	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin kinase/fmn adenylyltransferase; **PDBTitle:** crystal structure of riboflavin bound tm379
5	c1vliA_	Alignment		40.4	39	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
6	d1mrza2	Alignment		39.2	32	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
7	c1xuzA_	Alignment		39.2	28	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
8	c3dzaB_	Alignment		37.5	41	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized putative membrane protein; **PDBTitle:** crystal structure of a putative membrane protein of unknown function2 (yfdx) from klebsiella pneumoniae subsp. at 1.65 a resolution
9	c3rjvA_	Alignment		37.2	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative sel1 repeat protein; **PDBTitle:** crystal structure of a putative sel1 repeat protein (kpn_04481) from2 klebsiella pneumoniae subsp. pneumoniae at 1.65 a resolution
10	d2zdra2	Alignment		34.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
11	d1vlia2	Alignment		33.9	39	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like

12	d2e2aa_	Alignment		33.7	40	**Fold:**Spectrin repeat-like **Superfamily:**Enzyme IIa from lactose specific PTS, IIa-lac **Family:**Enzyme IIa from lactose specific PTS, IIa-lac
13	c3l8rA_	Alignment		33.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative pts system, cellobiose-specific iia **PDBTitle:** the crystal structure of ptca from s. mutans
14	c3k1sE_	Alignment		33.0	20	**PDB header:**transferase **Chain:** E: **PDB Molecule:**pts system, cellobiose-specific iia component; **PDBTitle:** crystal structure of the pts cellobiose specific enzyme iia2 from bacillus anthracis
15	d2b4jc1	Alignment		24.8	32	**Fold:**N-cbl like **Superfamily:**HIV integrase-binding domain **Family:**HIV integrase-binding domain
16	c1z9eA_	Alignment		23.9	32	**PDB header:**protein binding/transcription **Chain:** A: **PDB Molecule:**pc4 and sfrs1 interacting protein 2; **PDBTitle:** solution structure of the hiv-1 integrase-binding domain in2 ledgf/p75
17	d1klxa_	Alignment		23.7	31	**Fold:**alpha-alpha superhelix **Superfamily:**HCP-like **Family:**HCP-like
18	d1hw1a2	Alignment		23.1	13	**Fold:**GntR ligand-binding domain-like **Superfamily:**GntR ligand-binding domain-like **Family:**GntR ligand-binding domain-like
19	c1xb2B_	Alignment		21.7	30	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor ts, mitochondrial; **PDBTitle:** crystal structure of bos taurus mitochondrial elongation2 factor tu/ts complex
20	c2v43A_	Alignment		20.5	15	**PDB header:**regulator **Chain:** A: **PDB Molecule:**sigma-e factor regulatory protein rseb; **PDBTitle:** crystal structure of rseb: a sensor for periplasmic stress2 response in e. coli
21	d3bula1	Alignment	not modelled	19.6	17	**Fold:**Methionine synthase domain-like **Superfamily:**Methionine synthase domain **Family:**Methionine synthase domain
22	d2gy9t1	Alignment	not modelled	18.8	29	**Fold:**Spectrin repeat-like **Superfamily:**Ribosomal protein S20 **Family:**Ribosomal protein S20
23	c2wtoB_	Alignment	not modelled	18.2	10	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**orf131 protein; **PDBTitle:** crystal structure of apo-form czce from c. metallidurans ch34
24	d1aipc1	Alignment	not modelled	17.7	46	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
25	d2cp9a1	Alignment	not modelled	17.5	31	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
26	d1jr3d1	Alignment	not modelled	17.5	26	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
27	c1o7dC_	Alignment	not modelled	17.0	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**lysosomal alpha-mannosidase; **PDBTitle:** the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
28	d1efub3	Alignment	not modelled	15.7	23	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
						Fold:alpha-alpha superhelix

29	d1ouva_	Alignment	not modelled	15.6	19	**Superfamily:**HCP-like **Family:**HCP-like
30	d2a2pa1	Alignment	not modelled	15.2	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
31	d1xb2b1	Alignment	not modelled	14.8	31	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TS-N domain
32	d2uubt1	Alignment	not modelled	14.8	21	**Fold:**Spectrin repeat-like **Superfamily:**Ribosomal protein S20 **Family:**Ribosomal protein S20
33	d1nqja_	Alignment	not modelled	13.6	23	**Fold:**CUB-like **Superfamily:**Collagen-binding domain **Family:**Collagen-binding domain
34	d2ve8a1	Alignment	not modelled	13.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FtsK C-terminal domain-like
35	c3pnxF_	Alignment	not modelled	12.3	14	**PDB header:**transferase **Chain:** F: **PDB Molecule:**putative sulfurtransferase dsre; **PDBTitle:** crystal structure of a putative sulfurtransferase dsre (swol_2425)2 from syntrophomonas wolfei str. goettingen at 1.92 a resolution
36	d2fzta1	Alignment	not modelled	12.0	31	**Fold:**Methionine synthase domain-like **Superfamily:**TM0693-like **Family:**TM0693-like
37	c2kc7A_	Alignment	not modelled	11.8	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**bfr218_protein; **PDBTitle:** solution nmr structure of bacteroides fragilis protein2 bf1650. northeast structural genomics consortium target3 bfr218
38	d2j5pa1	Alignment	not modelled	11.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FtsK C-terminal domain-like
39	d2a4ha1	Alignment	not modelled	11.5	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
40	d1q98a_	Alignment	not modelled	11.1	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
41	d1jr3a1	Alignment	not modelled	10.9	16	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
42	c3fgaD_	Alignment	not modelled	10.8	25	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**shugoshin-like 1; **PDBTitle:** structural basis of pp2a and sgo interaction
43	c3s9jA_	Alignment	not modelled	10.6	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**member of duf4221 family; **PDBTitle:** crystal structure of a member of duf4221 family (bvu_1028) from2 bacteroides vulgatus atcc 8482 at 1.75 a resolution
44	c2hs5A_	Alignment	not modelled	10.5	35	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator gntr; **PDBTitle:** structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1
45	c3eyiB_	Alignment	not modelled	10.4	20	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**z-dna-binding protein 1; **PDBTitle:** the crystal structure of the second z-dna binding domain of2 human dai (zbp1) in complex with z-dna
46	d1wtea_	Alignment	not modelled	10.4	26	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease EcoO109IR
47	c2dbaA_	Alignment	not modelled	10.3	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**smooth muscle cell associated protein-1, isoform **PDBTitle:** the solution structure of the tetratrico peptide repeat of2 human smooth muscle cell associated protein-1, isoform 2
48	c2kjfA_	Alignment	not modelled	10.0	47	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**carnocyclin-a; **PDBTitle:** the solution structure of the circular bacteriocin2 carnocyclin a (ccla)
49	d2csfa1	Alignment	not modelled	9.6	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
50	d2q07a1	Alignment	not modelled	9.3	29	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
51	c2yfrA_	Alignment	not modelled	9.3	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**levansucrase; **PDBTitle:** crystal structure of inulosucrase from lactobacillus2 johnsonii ncc533
52	c2f06B_	Alignment	not modelled	9.0	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
53	c3dwlG_	Alignment	not modelled	8.9	26	**PDB header:**structural protein **Chain:** G: **PDB Molecule:**actin-related protein 2/3 complex subunit 5; **PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
54	d2ey4e1	Alignment	not modelled	8.8	16	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
						Fold: Thioredoxin fold

55	d1z5ye1	Alignment	not modelled	8.7	22	**Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
56	d1w96c1	Alignment	not modelled	8.7	5	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
57	d1zhva2	Alignment	not modelled	8.4	38	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
58	c3bx6A_	Alignment	not modelled	8.3	6	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**alpha-1-acid glycoprotein; **PDBTitle:** crystal structure of human alpha 1 acid glycoprotein
59	d1st9a_	Alignment	not modelled	8.1	6	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
60	c3do9C_	Alignment	not modelled	8.1	27	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**upf0302 protein ba_1542/gbaa1542/bas1430; **PDBTitle:** crystal structure of protein ba1542 from bacillus anthracis2 str.ames
61	d1a9xa1	Alignment	not modelled	7.8	29	**Fold:**Carbamoyl phosphate synthetase, large subunit connection domain **Superfamily:**Carbamoyl phosphate synthetase, large subunit connection domain **Family:**Carbamoyl phosphate synthetase, large subunit connection domain
62	c3b5nC_	Alignment	not modelled	7.8	32	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**protein transport protein sec9; **PDBTitle:** structure of the yeast plasma membrane snare complex
63	d2hs5a2	Alignment	not modelled	7.7	36	**Fold:**GntR ligand-binding domain-like **Superfamily:**GntR ligand-binding domain-like **Family:**GntR ligand-binding domain-like
64	d1td6a_	Alignment	not modelled	7.6	17	**Fold:**Hypothetical protein MPN330 **Superfamily:**Hypothetical protein MPN330 **Family:**Hypothetical protein MPN330
65	c2r73C_	Alignment	not modelled	7.5	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**trichosurin; **PDBTitle:** crystal structure of the possum milk whey lipocalin2 trichosurin at ph 8.2
66	d1seda_	Alignment	not modelled	7.4	16	**Fold:**Hypothetical protein YhaI **Superfamily:**Hypothetical protein YhaI **Family:**Hypothetical protein YhaI
67	d1sena_	Alignment	not modelled	7.3	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
68	c1senA_	Alignment	not modelled	7.3	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**thioredoxin-like protein p19; **PDBTitle:** endoplasmic reticulum protein rp19 o95881
69	c2l57A_	Alignment	not modelled	7.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
70	c1mh3A_	Alignment	not modelled	7.1	21	**PDB header:**sugar binding, dna binding protein **Chain:** A: **PDB Molecule:**maltose binding-a1 homeodomain protein chimera; **PDBTitle:** maltose binding-a1 homeodomain protein chimera, crystal2 form i
71	c2z4hB_	Alignment	not modelled	6.8	14	**PDB header:**signaling protein activator **Chain:** B: **PDB Molecule:**copper homeostasis protein cutf; **PDBTitle:** crystal structure of the cpx pathway activator nlpe from2 escherichia coli
72	c3sxkB_	Alignment	not modelled	6.7	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** zn2+-bound fcd domain of tm0439, a putative transcriptional regulator
73	d1ulza1	Alignment	not modelled	6.6	14	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
74	c1aipG_	Alignment	not modelled	6.6	46	**PDB header:**complex of two elongation factors **Chain:** G: **PDB Molecule:**elongation factor ts; **PDBTitle:** ef-tu ef-ts complex from thermus thermophilus
75	d1rsoa_	Alignment	not modelled	6.3	50	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
76	c2kckA_	Alignment	not modelled	6.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tpr repeat; **PDBTitle:** nmr solution structure of the northeast structural genomics2 consortium (nesg) target mrr121a
77	d2f06a1	Alignment	not modelled	6.2	25	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
78	d2aqaa1	Alignment	not modelled	6.1	26	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
79	d1vqqa1	Alignment	not modelled	6.1	6	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Penicillin binding protein 2a (PBP2A), N-terminal domain
80	c1ztyA_	Alignment	not modelled	6.0	20	**PDB header:**sugar binding protein, signaling protein **Chain:** A: **PDB Molecule:**chitin oligosaccharide binding protein; **PDBTitle:** crystal structure of the chitin oligasaccharide binding2 protein
						PDB header:protein binding

81	c3isyA_	Alignment	not modelled	5.9	5	**Chain:** A: **PDB Molecule:**intracellular proteinase inhibitor; **PDBTitle:** crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
82	d1veja1	Alignment	not modelled	5.9	36	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
83	d2k0bx1	Alignment	not modelled	5.8	33	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
84	c3fmsA_	Alignment	not modelled	5.8	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** crystal structure of tm0439, a gntr transcriptional2 regulator
85	c3eiqC_	Alignment	not modelled	5.7	20	**PDB header:**hydrolase/antitumor protein **Chain:** C: **PDB Molecule:**programmed cell death protein 4; **PDBTitle:** crystal structure of pdcd4-eif4a
86	c2ju5A_	Alignment	not modelled	5.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin disulfide isomerase; **PDBTitle:** dsbh oxidoreductase
87	c3nztA_	Alignment	not modelled	5.6	8	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase; **PDBTitle:** 2.0 angstrom crystal structure of glutamate--cysteine ligase (gsha)2 ftom francisella tularensis in complex with amp
88	c3fk8A_	Alignment	not modelled	5.6	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**disulphide isomerase; **PDBTitle:** the crystal structure of disulphide isomerase from xylella fastidiosa2 temecula1
89	d1w96a1	Alignment	not modelled	5.5	5	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
90	c2yruA_	Alignment	not modelled	5.5	11	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**steroid receptor rna activator 1; **PDBTitle:** solution structure of mouse steroid receptor rna activator2 1 (sra1) protein
91	d1ppya_	Alignment	not modelled	5.3	18	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Pyruvoyl dependent aspartate decarboxylase, ADC
92	d1d9ea_	Alignment	not modelled	5.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
93	c1efuB_	Alignment	not modelled	5.3	23	**PDB header:**complex (two elongation factors) **Chain:** B: **PDB Molecule:**elongation factor ts; **PDBTitle:** elongation factor complex ef-tu/ef-ts from escherichia coli
94	c3msvB_	Alignment	not modelled	5.2	23	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**nuclear import adaptor, nro1; **PDBTitle:** the hypoxic regulator of sterol synthesis nro1 is a nuclear import2 adaptor
95	c2qyxB_	Alignment	not modelled	5.1	32	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein mj0159; **PDBTitle:** crystal structure of uncharacterized protein mj0159 from2 methanocaldococcus jannaschii
96	c3ia1A_	Alignment	not modelled	5.1	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thio-disulfide isomerase/thioredoxin; **PDBTitle:** crystal structure of thio-disulfide isomerase from thermus2 thermophilus
97	d3d4ub1	Alignment	not modelled	5.1	19	**Fold:**Defensin-like **Superfamily:**Defensin-like **Family:**Tick carboxypeptidase inhibitor-like
98	c2jy5A_	Alignment	not modelled	5.0	36	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquilin-1; **PDBTitle:** nmr structure of ubiquilin 1 uba domain
99	c3kcmC_	Alignment	not modelled	5.0	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thioredoxin family protein; **PDBTitle:** the crystal structure of thioredoxin protein from geobacter2 metallireducens