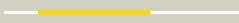
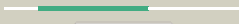
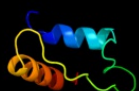
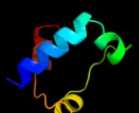
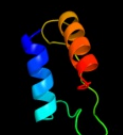
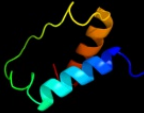
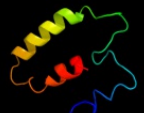


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2rfpA_	 Alignment		75.8	24	PDB header: hydrolase Chain: A: PDB Molecule: putative ntp pyrophosphohydrolase; PDBTitle: crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exigubacterium sibiricum 255-15 at 1.74 a3 resolution
2	c1vgmB_	 Alignment		46.4	16	PDB header: transferase Chain: B: PDB Molecule: 378aa long hypothetical citrate synthase; PDBTitle: crystal structure of an isozyme of citrate synthase from sulfolbus2 tokodaii strain7
3	dlhw1a1	 Alignment		44.4	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
4	c2r26C_	 Alignment		37.1	13	PDB header: transferase Chain: C: PDB Molecule: citrate synthase; PDBTitle: the structure of the ternary complex of carboxymethyl2 coenzyme a and oxalateacetate with citrate synthase from3 the thermophilic archaeonthermoplasma acidophilum
5	c3ic7A_	 Alignment		36.8	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator of gntR family2 from bacteroides thetaiotaomicron
6	c2wv0H_	 Alignment		34.4	21	PDB header: transcription Chain: H: PDB Molecule: hth-type transcriptional repressor yvoa; PDBTitle: crystal structure of the gntR-hutC family member yvoa from2 bacillus subtilis
7	dl07xa_	 Alignment		34.0	11	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
8	c1e2xA_	 Alignment		33.4	25	PDB header: transcriptional regulation Chain: A: PDB Molecule: fatty acid metabolism regulator protein; PDBTitle: fadr, fatty acid responsive transcription factor from e.2 coli
9	c3neuA_	 Alignment		30.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1836 protein; PDBTitle: the crystal structure of a functionally-unknown protein lin1836 from2 listeria innocua clip11262
10	dlv4ra1	 Alignment		28.7	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
11	c2vcbA_	 Alignment		28.4	30	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylglucosaminidase; PDBTitle: family 89 glycoside hydrolase from clostridium perfringens2 in complex with pugnac

12	d1ioma_	Alignment		27.7	15	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
13	c3by6C_	Alignment		26.4	12	PDB header: transcription regulator Chain: C: PDB Molecule: predicted transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator from oenococcus oeni
14	d1k3pa_	Alignment		25.2	19	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
15	c3eetA_	Alignment		24.6	9	PDB header: transcription regulator Chain: A: PDB Molecule: putative gntr-family transcriptional regulator; PDBTitle: crystal structure of putative gntr-family transcriptional2 regulator
16	c3bwgA_	Alignment		22.8	13	PDB header: transcription regulator Chain: A: PDB Molecule: uncharacterized hth-type transcriptional regulator yydk; PDBTitle: the crystal structure of possible transcriptional regulator yydk from2 bacillus subtilis subsp. subtilis str. 168
17	c2p2wA_	Alignment		22.7	14	PDB header: transferase Chain: A: PDB Molecule: citrate synthase; PDBTitle: crystal structure of citrate synthase from thermotoga maritima msb8
18	c3edpB_	Alignment		22.6	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lin2111 protein; PDBTitle: the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
19	c3tqnC_	Alignment		22.1	20	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, gntr family; PDBTitle: structure of the transcriptional regulator of the gntr family, from2 coxiella burnetii.
20	d1a59a_	Alignment		22.0	18	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
21	d1r9la_	Alignment	not modelled	21.3	18	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
22	c3tqgA_	Alignment	not modelled	20.9	17	PDB header: transferase Chain: A: PDB Molecule: 2-methylcitrate synthase; PDBTitle: structure of the 2-methylcitrate synthase (prpc) from coxiella2 burnetii
23	c3o8jH_	Alignment	not modelled	20.6	19	PDB header: transferase Chain: H: PDB Molecule: 2-methylcitrate synthase; PDBTitle: crystal structure of 2-methylcitrate synthase (prpc) from salmonella2 typhimurium
24	c2du9A_	Alignment	not modelled	18.9	25	PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulators; PDBTitle: crystal structure of the transcriptional factor from c.glutamicum
25	c3fmsA_	Alignment	not modelled	18.5	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, gntr family; PDBTitle: crystal structure of tm0439, a gntr transcriptional2 regulator
26	c2h12C_	Alignment	not modelled	17.6	19	PDB header: transferase Chain: C: PDB Molecule: citrate synthase; PDBTitle: structure of acetobacter aceti citrate synthase complexed2 with oxaloacetate and carboxymethyl dethia coenzyme a (cmx)
27	d1csca_	Alignment	not modelled	15.9	13	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
28	d1hc1a2	Alignment	not modelled	15.8	21	Fold: Di-copper centre-containing domain Superfamily: Di-copper centre-containing domain Family: Hemocyanin middle domain

29	d2fzta1	Alignment	not modelled	15.7	41	Fold: Methionine synthase domain-like Superfamily: TM0693-like Family: TM0693-like
30	c3hhsA	Alignment	not modelled	15.6	35	PDB header: oxidoreductase Chain: A: PDB Molecule: phenoloxidase subunit 2; PDBTitle: crystal structure of manduca sexta prophenoloxidase
31	d3bwga1	Alignment	not modelled	15.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
32	d1l1aa2	Alignment	not modelled	13.9	15	Fold: Di-copper centre-containing domain Superfamily: Di-copper centre-containing domain Family: Hemocyanin middle domain
33	d1bh9b	Alignment	not modelled	13.1	27	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
34	c2i9nA	Alignment	not modelled	12.8	70	PDB header: de novo protein Chain: A: PDB Molecule: mhb4a peptide; PDBTitle: design of bivalent miniprotein consisting of two2 independent elements, a b-hairpin peptide and a-helix3 peptide, tethered by four glycines
35	c2i9oA	Alignment	not modelled	12.5	70	PDB header: de novo protein Chain: A: PDB Molecule: mhb8a peptide; PDBTitle: design of bivalent miniprotein consisting of two2 independent elements, a b-hairpin peptide and a-helix3 peptide, tethered by eight glycines
36	d1e8ca2	Alignment	not modelled	11.9	21	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
37	c3fkeB	Alignment	not modelled	11.5	40	PDB header: rna binding protein Chain: B: PDB Molecule: polymerase cofactor vp35; PDBTitle: structure of the ebola vp35 interferon inhibitory domain
38	c2ibpB	Alignment	not modelled	11.4	15	PDB header: transferase Chain: B: PDB Molecule: citrate synthase; PDBTitle: crystal structure of citrate synthase from pyrobaculum aerophilum
39	d2hs5a1	Alignment	not modelled	11.2	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators
40	cliq8B	Alignment	not modelled	11.1	26	PDB header: transferase Chain: B: PDB Molecule: archaeosine trna-guanine transglycosylase; PDBTitle: crystal structure of archaeosine trna-guanine2 transglycosylase from pyrococcus horikoshii
41	d1vi0a2	Alignment	not modelled	10.4	18	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
42	c3ks8D	Alignment	not modelled	9.2	40	PDB header: viral protein/rna Chain: D: PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of reston ebolavirus vp35 rna binding2 domain in complex with 18bp dsrna
43	d2g7sa2	Alignment	not modelled	8.4	20	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
44	c3f8mA	Alignment	not modelled	8.4	18	PDB header: transcription Chain: A: PDB Molecule: gntR-family protein transcriptional regulator; PDBTitle: crystal structure of phnF from mycobacterium smegmatis
45	d1rh7a	Alignment	not modelled	8.3	18	Fold: Resistin Superfamily: Resistin Family: Resistin
46	d1aj8a	Alignment	not modelled	8.0	18	Fold: Citrate synthase Superfamily: Citrate synthase Family: Citrate synthase
47	d1nb5i	Alignment	not modelled	7.9	40	Fold: Cystatin-like Superfamily: Cystatin/monellin Family: Cystatins
48	d1o98a1	Alignment	not modelled	7.8	40	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
49	c1nolA	Alignment	not modelled	7.5	18	PDB header: oxygen transport Chain: A: PDB Molecule: hemocyanin (subunit type ii); PDBTitle: oxygenated hemocyanin (subunit type ii)
50	d1atga	Alignment	not modelled	7.4	29	Fold: Periplasmic binding protein-like II Superfamily: Periplasmic binding protein-like II Family: Phosphate binding protein-like
51	c3mvnA	Alignment	not modelled	7.3	19	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-medo- PDBTitle: crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
52	d2i10a2	Alignment	not modelled	7.2	20	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
53	d1bysa2	Alignment	not modelled	7.1	21	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: DNA helicase RuvA subunit, middle domain
						PDB header: oxygen transport

54	c1hcyE_	Alignment	not modelled	7.0	25	Chain: E: PDB Molecule: arthropodan nemocyanin; PDBTitle: crystal structure of hexameric haemocyanin from panulirus interruptus2 refined at 3.2 angstroms resolution
55	d1fi4a2	Alignment	not modelled	6.7	10	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate 5-diphosphate decarboxylase
56	c3ajvA_	Alignment	not modelled	6.5	14	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: splicing endonuclease from aeropyrum pernix
57	d1z1za1	Alignment	not modelled	6.5	22	Fold: Phage tail protein-like Superfamily: Phage tail protein-like Family: Lambda phage gpU-like
58	d1dpya_	Alignment	not modelled	6.4	38	Fold: Phospholipase A2, PLA2 Superfamily: Phospholipase A2, PLA2 Family: Vertebrate phospholipase A2
59	d1g8fa3	Alignment	not modelled	6.4	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ATP sulfurylase C-terminal domain
60	c3gwiE_	Alignment	not modelled	6.3	33	PDB header: oxygen transport Chain: E: PDB Molecule: arylphorin; PDBTitle: crystal structure of antheraea pernyi arylphorin
61	d1vj5a2	Alignment	not modelled	6.0	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
62	d1p3da2	Alignment	not modelled	5.9	26	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
63	c1wsuA_	Alignment	not modelled	5.9	15	PDB header: translation/rna Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: c-terminal domain of elongation factor selb complexed with2 secis rna
64	d2zdra2	Alignment	not modelled	5.8	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
65	c1yrlD_	Alignment	not modelled	5.7	9	PDB header: oxidoreductase Chain: D: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: escherichia coli ketol-acid reductoisomerase
66	c2xkyl_	Alignment	not modelled	5.6	30	PDB header: metal transport Chain: I: PDB Molecule: inward rectifier potassium channel 2; PDBTitle: single particle analysis of kir2.1nc_4 in negative stain
67	d1k6ma1	Alignment	not modelled	5.6	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain
68	d2o97b1	Alignment	not modelled	5.5	27	Fold: IHF-like DNA-binding proteins Superfamily: IHF-like DNA-binding proteins Family: Prokaryotic DNA-bending protein
69	c2ov2O_	Alignment	not modelled	5.5	22	PDB header: protein binding/transferase Chain: O: PDB Molecule: serine/threonine-protein kinase pak 4; PDBTitle: the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4)
70	d1bifa1	Alignment	not modelled	5.4	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain
71	c2odbB_	Alignment	not modelled	5.3	33	PDB header: protein binding Chain: B: PDB Molecule: serine/threonine-protein kinase pak 6; PDBTitle: the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6)