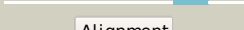
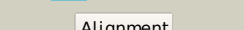
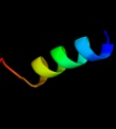
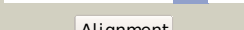
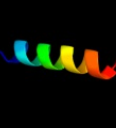
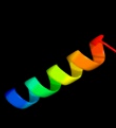
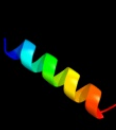
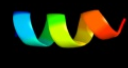


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kb4D_	 Alignment		100.0	19	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr8543 protein; PDBTitle: crystal structure of the alr8543 protein in complex with 2 geranylgeranyl monophosphate and magnesium ion from nostoc sp. pcc3 7120, northeast structural genomics consortium target nsr141
2	c3msqC_	 Alignment		100.0	18	PDB header: biosynthetic protein Chain: C: PDB Molecule: putative ubiquinone biosynthesis protein; PDBTitle: crystal structure of a putative ubiquinone biosynthesis protein2 (npun02000094) from nostoc punctiforme pcc 73102 at 2.85 a resolution
3	d1eexg_	 Alignment		37.4	19	Fold: Open three-helical up-and-down bundle Superfamily: Diol dehydratase, gamma subunit Family: Diol dehydratase, gamma subunit
4	c2l6gA_	 Alignment		36.1	41	PDB header: transferase, cell adhesion Chain: A: PDB Molecule: focal adhesion kinase 1, linker, paxillin; PDBTitle: fat-1d2 double labeled construct with free 1d4 peptide
5	c1uc5M_	 Alignment		33.9	19	PDB header: lyase Chain: M: PDB Molecule: diol dehydrase gamma subunit; PDBTitle: structure of diol dehydratase complexed with (r)-1,2-2 propanediol
6	d1iwpq_	 Alignment		30.3	19	Fold: Open three-helical up-and-down bundle Superfamily: Diol dehydratase, gamma subunit Family: Diol dehydratase, gamma subunit
7	c2lnaA_	 Alignment		28.9	26	PDB header: hydrolase Chain: A: PDB Molecule: afg3-like protein 2; PDBTitle: solution nmr structure of the mitochondrial inner membrane domain2 (residues 164-251), ftsh_ext, from the paraplegin-like protein afg3l23 from homo sapiens, northeast structural genomics consortium target4 hr6741a
8	c3r4hD_	 Alignment		26.4	39	PDB header: de novo protein Chain: D: PDB Molecule: coiled coil helix cc-tet-phi22; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet-phi22
9	c3r4aA_	 Alignment		25.7	39	PDB header: de novo protein Chain: A: PDB Molecule: coiled coil helix cc-tet; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet
10	c3r4aC_	 Alignment		25.5	39	PDB header: de novo protein Chain: C: PDB Molecule: coiled coil helix cc-tet; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet
11	c3r4aD_	 Alignment		25.4	39	PDB header: de novo protein Chain: D: PDB Molecule: coiled coil helix cc-tet; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet

12	c2uv1B_	Alignment		25.3	75	PDB header: inhibitor Chain: B: PDB Molecule: host-nuclease inhibitor protein gam; PDBTitle: hexagonal crystal form of gams from bacteriophage lambda.
13	c3r4hF_	Alignment		25.2	39	PDB header: de novo protein Chain: F: PDB Molecule: coiled coil helix cc-tet-phi22; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet-phi22
14	c3r4aB_	Alignment		25.0	39	PDB header: de novo protein Chain: B: PDB Molecule: coiled coil helix cc-tet; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet
15	c3r4hB_	Alignment		24.8	39	PDB header: de novo protein Chain: B: PDB Molecule: coiled coil helix cc-tet-phi22; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet-phi22
16	c3r4hC_	Alignment		24.8	39	PDB header: de novo protein Chain: C: PDB Molecule: coiled coil helix cc-tet-phi22; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet-phi22
17	c3r4hA_	Alignment		24.8	39	PDB header: de novo protein Chain: A: PDB Molecule: coiled coil helix cc-tet-phi22; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet-phi22
18	c3r4hE_	Alignment		23.6	40	PDB header: de novo protein Chain: E: PDB Molecule: coiled coil helix cc-tet-phi22; PDBTitle: crystal structure of the 4-helix coiled coil cc-tet-phi22
19	c3dkaA_	Alignment		18.9	19	PDB header: unknown function Chain: A: PDB Molecule: dinb-like protein; PDBTitle: crystal structure of a dinb-like protein (yjoa, bsu12410) from2 bacillus subtilis at 2.30 a resolution
20	d1a9xa1	Alignment		16.9	18	Fold: Carbamoyl phosphate synthetase, large subunit connection domain Superfamily: Carbamoyl phosphate synthetase, large subunit connection domain Family: Carbamoyl phosphate synthetase, large subunit connection domain
21	c2k7rA_	Alignment	not modelled	15.5	18	PDB header: replication Chain: A: PDB Molecule: primosomal protein dnaI; PDBTitle: n-terminal domain of the bacillus subtilis helicase-loading2 protein dnaI
22	c1or7A_	Alignment	not modelled	15.4	6	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma-e factor; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
23	c1ykuB_	Alignment	not modelled	15.2	18	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein pxo2-61; PDBTitle: crystal structure of a sensor domain homolog
24	d2f23a1	Alignment	not modelled	15.0	30	Fold: Long alpha-hairpin Superfamily: GreA transcript cleavage protein, N-terminal domain Family: GreA transcript cleavage protein, N-terminal domain
25	d2pjqa1	Alignment	not modelled	14.2	7	Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
26	c2vcba_	Alignment	not modelled	13.7	27	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylglucosaminidase; PDBTitle: family 89 glycoside hydrolase from clostridium perfringens2 in complex with pugnac
27	c3gw7A_	Alignment	not modelled	13.5	16	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein yedj; PDBTitle: crystal structure of a metal-dependent phosphohydrolase2 with conserved hd domain (yedj) from escherichia coli in3 complex with nickel ions. northeast structural genomics4 consortium target er63
28	c2ff4B_	Alignment	not modelled	13.3	20	PDB header: transcription Chain: B: PDB Molecule: probable regulatory protein embr; PDBTitle: mycobacterium tuberculosis embr in complex with low

					affinity2 phosphopeptide
29	c3pmdA_	Alignment	not modelled	12.3	19 PDB header: lipid binding protein Chain: A: PDB Molecule: conserved domain protein; PDBTitle: crystal structure of the sporulation inhibitor pxo1-118 from bacillus2 anthracis
30	d1yfnal	Alignment	not modelled	12.1	29 Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
31	c3d5pB_	Alignment	not modelled	11.9	23 PDB header: gene regulation Chain: B: PDB Molecule: putative glucan synthesis regulator of smi1/knr4 family; PDBTitle: crystal structure of a putative glucan synthesis regulator of2 smi1/knr4 family (bf1740) from bacteroides fragilis nctc 9343 at 1.453 a resolution
32	c3zs9C_	Alignment	not modelled	11.8	38 PDB header: hydrolase/transport protein Chain: C: PDB Molecule: golgi to er traffic protein 2; PDBTitle: s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
33	d1ou9a_	Alignment	not modelled	11.4	36 Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
34	d1ou8a_	Alignment	not modelled	11.3	36 Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
35	c3zs9D_	Alignment	not modelled	11.2	38 PDB header: hydrolase/transport protein Chain: D: PDB Molecule: golgi to er traffic protein 2; PDBTitle: s. cerevisiae get3-adp-alf4- complex with a cytosolic get2 fragment
36	d3dtoal	Alignment	not modelled	10.8	9 Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
37	dlzszc1	Alignment	not modelled	10.7	29 Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
38	d1ufia_	Alignment	not modelled	10.4	24 Fold: ROP-like Superfamily: Dimerisation domain of CENP-B Family: Dimerisation domain of CENP-B
39	d1b76a2	Alignment	not modelled	10.2	27 Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
40	d2prva1	Alignment	not modelled	10.2	14 Fold: SMI1/KNR4-like Superfamily: SMI1/KNR4-like Family: SMI1/KNR4-like
41	d3proc1	Alignment	not modelled	9.5	21 Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
42	c3hugA_	Alignment	not modelled	9.4	14 PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rslal2 in complex with -35 promoter binding domain of sigl
43	d1or7a1	Alignment	not modelled	9.1	6 Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
44	d1ka8a_	Alignment	not modelled	8.5	5 Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: P4 origin-binding domain-like
45	d1xu2r_	Alignment	not modelled	8.1	55 Fold: TNF receptor-like Superfamily: TNF receptor-like Family: BAFF receptor-like
46	c1xu2R_	Alignment	not modelled	8.1	55 PDB header: cytokine, hormone/growth factor receptor Chain: R: PDB Molecule: tumor necrosis factor receptor superfamily member 17; PDBTitle: the crystal structure of april bound to bcma
47	d1m9fd_	Alignment	not modelled	7.9	22 Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
48	d1aisb1	Alignment	not modelled	7.9	14 Fold: Cyclin-like Superfamily: Cyclin-like Family: Transcription factor IIB (TFIIB), core domain
49	d1k1xa1	Alignment	not modelled	7.9	25 Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: 4-alpha-glucanotransferase, domain 2
50	c3sjdE_	Alignment	not modelled	7.8	33 PDB header: hydrolase/transport protein Chain: E: PDB Molecule: golgi to er traffic protein 2; PDBTitle: crystal structure of s. cerevisiae get3 with bound adp-mg2+ in complex2 with get2 cytosolic domain
51	d2g4ca2	Alignment	not modelled	7.8	32 Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
52	d2pq7a1	Alignment	not modelled	7.7	14 Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain
53	d2paga1	Alignment	not modelled	7.6	19 Fold: SMI1/KNR4-like Superfamily: SMI1/KNR4-like Family: SMI1/KNR4-like
54	d3djba1	Alignment	not modelled	7.6	6 Fold: HD-domain/PDEase-like Superfamily: HD-domain/PDEase-like Family: HD domain

55	d2icga1	Alignment	not modelled	7.6	10	Fold: SMI1/KNR4-like Superfamily: SMI1/KNR4-like Family: SMI1/KNR4-like
56	d1y0ua_	Alignment	not modelled	7.5	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
57	c2auaB_	Alignment	not modelled	7.5	36	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: structure of bc2332: a protein of unknown function from bacillus2 cereus
58	c1ufiD_	Alignment	not modelled	7.5	23	PDB header: dna binding protein Chain: D: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of the dimerization domain of human cenp-b
59	c2jo8B_	Alignment	not modelled	7.4	30	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase 4; PDBTitle: solution structure of c-terminal domain of human mammalian2 sterile 20-like kinase 1 (mst1)
60	c3ikmC_	Alignment	not modelled	7.3	32	PDB header: transferase Chain: C: PDB Molecule: dna polymerase subunit gamma-2; PDBTitle: crystal structure of human mitochondrial dna polymerase2 holoenzyme
61	d2r7ca2	Alignment	not modelled	6.9	30	Fold: Rotavirus NSP2 fragment, N-terminal domain Superfamily: Rotavirus NSP2 fragment, N-terminal domain Family: Rotavirus NSP2 fragment, N-terminal domain
62	d2ff4a2	Alignment	not modelled	6.9	30	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: BTAD-like
63	c2a3dA_	Alignment	not modelled	6.6	47	PDB header: three-helix bundle Chain: A: PDB Molecule: protein (de novo three-helix bundle); PDBTitle: solution structure of a de novo designed single chain three-2 helix bundle (a3d)
64	c3nr7A_	Alignment	not modelled	6.6	17	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein h-ns; PDBTitle: crystal structure of s. typhimurium h-ns 1-83
65	c2rq5A_	Alignment	not modelled	6.4	16	PDB header: transcription Chain: A: PDB Molecule: protein jumonji; PDBTitle: solution structure of the at-rich interaction domain (arid)2 of jumonji/jarid2
66	c2lfwA_	Alignment	not modelled	6.4	9	PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
67	d1yira2	Alignment	not modelled	6.3	13	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
68	d2bpa1_	Alignment	not modelled	6.3	22	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP
69	c2b6gA_	Alignment	not modelled	6.3	15	PDB header: rna binding protein Chain: A: PDB Molecule: vts1p; PDBTitle: rna recognition by the vts1 sam domain
70	c2fmmE_	Alignment	not modelled	6.3	20	PDB header: transcription Chain: E: PDB Molecule: protein emsy; PDBTitle: crystal structure of emsy-hp1 complex
71	d1xl3c1	Alignment	not modelled	6.1	25	Fold: Type III secretion system domain Superfamily: Type III secretion system domain Family: TyeA-like
72	d1vaja1	Alignment	not modelled	6.1	13	Fold: AMMECR1-like Superfamily: AMMECR1-like Family: AMMECR1-like
73	c2ylaA_	Alignment	not modelled	6.1	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
74	d1kvpa_	Alignment	not modelled	5.9	36	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: ssDNA viruses Family: Microviridae-like VP
75	d2ivda2	Alignment	not modelled	5.7	13	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: L-aminoacid/polyamine oxidase
76	d1mtyg_	Alignment	not modelled	5.7	19	Fold: Open three-helical up-and-down bundle Superfamily: Methane monooxygenase hydrolase, gamma subunit Family: Methane monooxygenase hydrolase, gamma subunit
77	c3mzyA_	Alignment	not modelled	5.7	16	PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
78	c2l6fA_	Alignment	not modelled	5.5	21	PDB header: transferase,cell adhesion Chain: A: PDB Molecule: focal adhesion kinase 1, linker1, paxillin, linker2, PDBTitle: nmr solution structure of fat domain of fak complexed with ld2 and ld42 motifs of paxillin
79	d1atia2	Alignment	not modelled	5.4	27	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
80	d1seza2	Alignment	not modelled	5.4	18	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: L-aminoacid/polyamine oxidase
						Fold: Class II aaRS and biotin synthetases

81	d1g5ha2	Alignment	not modelled	5.3	23	Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
82	d1ybea2	Alignment	not modelled	5.3	17	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolate PRTase N-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like