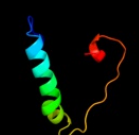
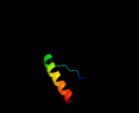
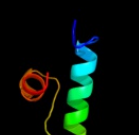
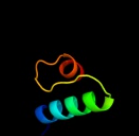
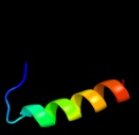
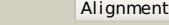


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1kqpa_	 Alignment		58.1	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
2	d1g5ha2	 Alignment		50.4	19	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
3	c2l5ya_	 Alignment		45.9	22	PDB header: signaling protein Chain: A: PDB Molecule: stromal interaction molecule 2; PDBTitle: nmr structure of calcium-loaded stim2 ef-sam.
4	d2ejna2	 Alignment		41.7	19	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
5	d2dnaa1	 Alignment		40.4	23	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
6	d2isya1	 Alignment		38.9	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
7	d1rioa_	 Alignment		38.7	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
8	d1llib_	 Alignment		38.4	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
9	d2oqoa1	 Alignment		37.5	20	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: PBP transglycosylase domain-like
10	d1g3wa1	 Alignment		35.9	35	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
11	d2g4ca2	 Alignment		35.0	24	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain

12	c1puoA_	 Alignment		34.8	10	PDB header: allergen Chain: A: PDB Molecule: major allergen i polypeptide, fused chain 2, PDBTitle: crystal structure of fel d 1- the major cat allergen
13	c3q4gA_	 Alignment		34.3	16	PDB header: ligase Chain: A: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad synthetase from vibrio cholerae
14	c2k60A_	 Alignment		29.9	15	PDB header: signaling protein Chain: A: PDB Molecule: protein (stromal interaction molecule 1); PDBTitle: nmr structure of calcium-loaded stim1 ef-sam
15	c2jqgA_	 Alignment		29.2	18	PDB header: protein transport Chain: A: PDB Molecule: conserved oligomeric golgi complex subunit 2; PDBTitle: solution structure of saccharomyces cerevisiae conserved2 oligomeric golgi subunit 2 protein (cog2p)
16	d2ev0a1	 Alignment		25.1	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
17	c2p14A_	 Alignment		21.7	17	PDB header: hydrolase Chain: A: PDB Molecule: heterodimeric restriction endonuclease r.bspd6i small PDBTitle: crystal structure of small subunit (r.bspd6i2) of the heterodimeric2 restriction endonuclease r.bspd6i
18	c3zqsB_	 Alignment		21.0	36	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase fanc1; PDBTitle: human fanc1 central domain
19	c2ejnB_	 Alignment		20.7	19	PDB header: allergen Chain: B: PDB Molecule: major allergen i polypeptide chain 1, chain 2; PDBTitle: structural characterization of the tetrameric form of the2 major cat allergen fel d 1
20	d1r57a_	 Alignment		20.5	18	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
21	d2hf5a1	 Alignment	not modelled	18.8	39	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
22	c3k1lA_	 Alignment	not modelled	18.0	18	PDB header: ligase Chain: A: PDB Molecule: fanc1; PDBTitle: crystal structure of fanc1
23	d2vqca1	 Alignment	not modelled	17.6	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: F112-like
24	c2vqcA_	 Alignment	not modelled	17.6	27	PDB header: dna-binding protein Chain: A: PDB Molecule: hypothetical 13.2 kda protein; PDBTitle: structure of a dna binding winged-helix protein, f-112,2 from sulfolobus spindle-shaped virus 1.
25	c3kk4B_	 Alignment	not modelled	16.7	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
26	c3olmA_	 Alignment	not modelled	16.4	12	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase rsp5; PDBTitle: structure and function of a ubiquitin binding site within the2 catalytic domain of a hect ubiquitin ligase
27	d2daha1	 Alignment	not modelled	16.2	15	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
28	c2dahA_	 Alignment	not modelled	16.2	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubiquilin-3; PDBTitle: solution structure of the c-terminal uba domain in the2 human ubiquilin 3
						PDB header: ligase

29	c3dpiA_	Alignment	not modelled	15.7	21	Chain: A: PDB Molecule: nad+ synthetase; PDBTitle: crystal structure of nad+ synthetase from burkholderia pseudomallei
30	c1g5hA_	Alignment	not modelled	15.4	19	PDB header: dna binding protein Chain: A: PDB Molecule: mitochondrial dna polymerase accessory subunit; PDBTitle: crystal structure of the accessory subunit of murine mitochondrial2 polymerase gamma
31	d1jdga_	Alignment	not modelled	15.4	56	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
32	c3fl2A_	Alignment	not modelled	14.6	20	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase uhrf1; PDBTitle: crystal structure of the ring domain of the e3 ubiquitin-2 protein ligase uhrf1
33	d1w55a2	Alignment	not modelled	14.2	15	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
34	c3h4sE_	Alignment	not modelled	14.2	17	PDB header: motor protein/calcium binding protein Chain: E: PDB Molecule: kcbp interacting ca2+-binding protein; PDBTitle: structure of the complex of a mitotic kinesin with its2 calcium binding regulator
35	c1wygA_	Alignment	not modelled	14.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
36	c2uzhB_	Alignment	not modelled	13.9	15	PDB header: lyase Chain: B: PDB Molecule: 2c-methyl-d-erythritol 2,4-cyclodiphosphate PDBTitle: mycobacterium smegmatis 2c-methyl-d-erythritol-2,4-2 cyclodiphosphate synthase (ispf)
37	c3li6G_	Alignment	not modelled	13.6	23	PDB header: metal binding protein Chain: G: PDB Molecule: calcium-binding protein; PDBTitle: crystal structure and trimer-monomer transition of n-terminal domain2 of ehcbp1 from entamoeba histolytica
38	c3li6J_	Alignment	not modelled	13.6	23	PDB header: metal binding protein Chain: J: PDB Molecule: calcium-binding protein; PDBTitle: crystal structure and trimer-monomer transition of n-terminal domain2 of ehcbp1 from entamoeba histolytica
39	c3li6A_	Alignment	not modelled	13.5	23	PDB header: metal binding protein Chain: A: PDB Molecule: calcium-binding protein; PDBTitle: crystal structure and trimer-monomer transition of n-terminal domain2 of ehcbp1 from entamoeba histolytica
40	c3li6D_	Alignment	not modelled	13.4	20	PDB header: metal binding protein Chain: D: PDB Molecule: calcium-binding protein; PDBTitle: crystal structure and trimer-monomer transition of n-terminal domain2 of ehcbp1 from entamoeba histolytica
41	c3nuwC_	Alignment	not modelled	13.4	30	PDB header: transferase Chain: C: PDB Molecule: 2-oxo-3-deoxygalactonate kinase; PDBTitle: crystal structure of 2-oxo-3-deoxygalactonate kinase from klebsiella2 pneumoniae
42	d1gx1a_	Alignment	not modelled	13.4	15	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
43	d1t0aa_	Alignment	not modelled	13.2	18	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
44	c1ozsA_	Alignment	not modelled	12.9	14	PDB header: structural protein Chain: A: PDB Molecule: troponin c, slow skeletal and cardiac muscles; PDBTitle: c-domain of human cardiac troponin c in complex with the2 inhibitory region of human cardiac troponin i
45	c3g1nA_	Alignment	not modelled	12.8	12	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase huwe1; PDBTitle: catalytic domain of the human e3 ubiquitin-protein ligase2 huwe1
46	c3hzsA_	Alignment	not modelled	12.5	11	PDB header: transferase Chain: A: PDB Molecule: monofunctional glycosyltransferase; PDBTitle: s. aureus monofunctional glycosyltransferase (mtga)in complex with2 moenomycin
47	c2kzvA_	Alignment	not modelled	12.5	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of cv_0373(175-257) protein from2 chromobacterium violaceum, northeast structural genomics consortium3 target cvr118a
48	c2pmpA_	Alignment	not modelled	12.4	12	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana
49	c1no1C_	Alignment	not modelled	11.8	42	PDB header: replication Chain: C: PDB Molecule: replisome organizer; PDBTitle: structure of truncated variant of b.subtilis spp1 phage g39p helicase2 loader/inhibitor protein
50	d1b76a2	Alignment	not modelled	11.8	24	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
51	d1pava_	Alignment	not modelled	11.7	44	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
52	c3dr5A_	Alignment	not modelled	11.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative o-methyltransferase; PDBTitle: crystal structure of the q8nrd3_corgl protein from2 corynebacterium glutamicum. northeast structural genomics3 consortium target cgr117.
53	c2w2A_	Alignment	not modelled	11.5	75	PDB header: transcription Chain: A: PDB Molecule: protein leafy;

53	c2vy6A	Alignment	not modelled	11.3	73	PDBTitle: structure of leafy transcription factor from arabidopsis2 thaliana in complex with dna from ag-i promoter
54	d1veja1	Alignment	not modelled	11.5	21	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
55	c2oniA	Alignment	not modelled	11.3	19	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase nedd4-like protein; PDBTitle: catalytic domain of the human nedd4-like e3 ligase
56	c3f0gA	Alignment	not modelled	11.1	9	PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp
57	c3t69A	Alignment	not modelled	10.8	30	PDB header: transferase Chain: A: PDB Molecule: putative 2-dehydro-3-deoxygalactonokinase; PDBTitle: crystal structure of a putative 2-dehydro-3-deoxygalactonokinase2 protein from sinorhizobium meliloti
58	d1je3a	Alignment	not modelled	10.7	44	Fold: IF3-like Superfamily: SirA-like Family: SirA-like
59	c3fiuD	Alignment	not modelled	10.7	18	PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmh synthetase from francisella tularensis
60	d1zbpa1	Alignment	not modelled	10.7	33	Fold: ImpE-like Superfamily: ImpE-like Family: ImpE-like
61	d1k3xa2	Alignment	not modelled	10.4	17	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
62	c2aaoA	Alignment	not modelled	10.2	20	PDB header: transferase Chain: A: PDB Molecule: calcium-dependent protein kinase, isoform ak1; PDBTitle: regulatory apparatus of calcium dependent protein kinase from2 arabidopsis thaliana
63	d1c4za	Alignment	not modelled	10.2	25	Fold: Hect, E3 ligase catalytic domain Superfamily: Hect, E3 ligase catalytic domain Family: Hect, E3 ligase catalytic domain
64	d1iv3a	Alignment	not modelled	10.0	18	Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
65	d1s6ja	Alignment	not modelled	9.8	17	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
66	d1b8la	Alignment	not modelled	9.8	23	Fold: EF Hand-like Superfamily: EF-hand Family: Parvalbumin
67	d1atia2	Alignment	not modelled	9.7	24	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
68	c2dnaA	Alignment	not modelled	9.7	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: unnamed protein product; PDBTitle: solution structure of rsgi ruh-056, a uba domain from mouse2 cdna
69	c1zvdA	Alignment	not modelled	9.5	29	PDB header: ligase Chain: A: PDB Molecule: smad ubiquitination regulatory factor 2; PDBTitle: regulation of smurf2 ubiquitin ligase activity by anchoring the e2 to2 the hect domain
70	c1npqA	Alignment	not modelled	9.2	21	PDB header: structural protein Chain: A: PDB Molecule: troponin c; PDBTitle: structure of a rhodamine-labeled n-domain troponin c mutant2 (ca2+ saturated) in complex with skeletal troponin i 115-3 131
71	c2b1uA	Alignment	not modelled	8.9	21	PDB header: metal binding protein Chain: A: PDB Molecule: calmodulin-like protein 5; PDBTitle: solution structure of calmodulin-like skin protein c2 terminal domain
72	d2bnma1	Alignment	not modelled	8.7	63	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
73	c3hz7A	Alignment	not modelled	8.7	44	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the sirA-like protein (dsy4693) from2 desulfotobacterium hafniense, northeast structural genomics3 consortium target dhr2a
74	c1bmxA	Alignment	not modelled	8.6	28	PDB header: viral protein Chain: A: PDB Molecule: human immunodeficiency virus type 1 capsid; PDBTitle: hiv-1 capsid protein major homology region peptide analog,2 nmr, 8 structures
75	d1sl8a	Alignment	not modelled	8.6	13	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
76	c1yfnG	Alignment	not modelled	8.6	57	PDB header: protein binding Chain: G: PDB Molecule: sigma-e factor negative regulatory protein; PDBTitle: versatile modes of peptide recognition by the aaa+ adaptor2 protein ssbp- the crystal structure of a ssbp-rsea complex
77	d1lmb3	Alignment	not modelled	8.5	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
						Fold: Homing endonuclease-like

78	d1jvaa2	Alignment	not modelled	8.5	21	Superfamily: Homing endonucleases Family: Intein endonuclease
79	c2novD	Alignment	not modelled	7.9	24	PDB header: isomerase Chain: D: PDB Molecule: dna topoisomerase 4 subunit a; PDBTitle: breakage-reunion domain of s.pneumoniae topo iv: crystal2 structure of a gram-positive quinolone target
80	c2hncC	Alignment	not modelled	7.7	7	PDB header: transferase Chain: C: PDB Molecule: sam-dependent o-methyltransferase; PDBTitle: crystal structure of sam-dependent o-methyltransferase from2 pathogenic bacterium leptospira interrogans
81	c2kp7A	Alignment	not modelled	7.7	16	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
82	d2fxta1	Alignment	not modelled	7.6	11	Fold: Cystatin-like Superfamily: NTF2-like Family: TIM44-like
83	c30aaO	Alignment	not modelled	7.6	28	PDB header: hydrolase/transport protein Chain: O: PDB Molecule: atp synthase gamma chain; PDBTitle: structure of the e.coli f1-atp synthase inhibited by subunit epsilon
84	d1fs0g	Alignment	not modelled	7.5	28	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit
85	d1fmta2	Alignment	not modelled	7.4	18	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
86	c3b85A	Alignment	not modelled	7.4	20	PDB header: hydrolase Chain: A: PDB Molecule: phosphate starvation-inducible protein; PDBTitle: crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
87	d1jfja	Alignment	not modelled	7.4	23	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
88	c2ev5B	Alignment	not modelled	7.3	20	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator mntr; PDBTitle: bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
89	d2j0sc1	Alignment	not modelled	7.1	14	Fold: Mago nashi protein Superfamily: Mago nashi protein Family: Mago nashi protein
90	c2kvvA	Alignment	not modelled	7.1	14	PDB header: hydrolase Chain: A: PDB Molecule: putative excisionase; PDBTitle: solution nmr of putative excisionase from klebsiella pneumoniae,2 northeast structural genomics consortium target kpr49
91	c1fmtA	Alignment	not modelled	7.1	18	PDB header: formyltransferase Chain: A: PDB Molecule: methionyl-trna fmet formyltransferase; PDBTitle: methionyl-trnafmet formyltransferase from escherichia coli
92	d2gxba1	Alignment	not modelled	7.1	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
93	d1sw8a	Alignment	not modelled	7.0	17	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
94	d1pprm1	Alignment	not modelled	6.9	19	Fold: Peridinin-chlorophyll protein Superfamily: Peridinin-chlorophyll protein Family: Peridinin-chlorophyll protein
95	c3i3IA	Alignment	not modelled	6.9	29	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
96	d1rk8b	Alignment	not modelled	6.8	14	Fold: Mago nashi protein Superfamily: Mago nashi protein Family: Mago nashi protein
97	d1sl7a	Alignment	not modelled	6.8	10	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
98	d1v97a1	Alignment	not modelled	6.8	22	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
99	c2d3kA	Alignment	not modelled	6.7	25	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: structural study on project id ph1539 from pyrococcus2 horikoshii ot3