



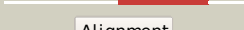

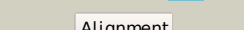
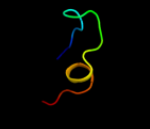

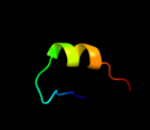

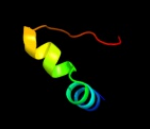

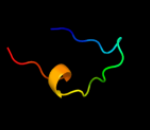
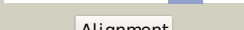
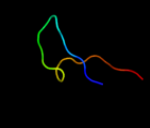





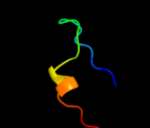

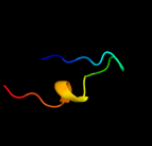
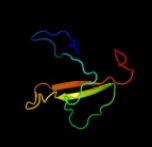

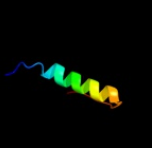
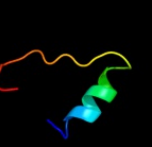

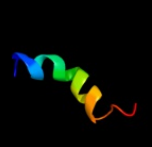
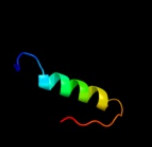

























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2o18A_	 Alignment		100.0	97	PDB header: lipid binding protein Chain: A: PDB Molecule: thiamine biosynthesis lipoprotein apbe; PDBTitle: crystal structure of a thiamine biosynthesis lipoprotein2 apbe, northeast strcutural genomics target er559
2	d1vrma1	 Alignment		100.0	26	Fold: T-fold Superfamily: ApbE-like Family: ApbE-like
3	d2o34a1	 Alignment		98.5	21	Fold: T-fold Superfamily: ApbE-like Family: DVU1097-like
4	c2gpzC_	 Alignment		35.7	42	PDB header: hydrolase Chain: C: PDB Molecule: transthyretin-like protein; PDBTitle: transthyretin-like protein from salmonella dublin
5	c3qvaB_	 Alignment		30.9	42	PDB header: hydrolase Chain: B: PDB Molecule: transthyretin-like protein; PDBTitle: structure of klebsiella pneumoniae 5-hydroxyisourate hydrolase
6	d1udxa3	 Alignment		30.4	30	Fold: Obg GTP-binding protein C-terminal domain Superfamily: Obg GTP-binding protein C-terminal domain Family: Obg GTP-binding protein C-terminal domain
7	d1f86a_	 Alignment		27.9	42	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
8	d1kgia_	 Alignment		27.6	37	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
9	d1tfpa_	 Alignment		26.5	42	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
10	c2h0eA_	 Alignment		26.1	33	PDB header: hydrolase Chain: A: PDB Molecule: transthyretin-like protein pucm; PDBTitle: crystal structure of pucm in the absence of substrate
11	c2h1xB_	 Alignment		25.9	26	PDB header: hydrolase Chain: B: PDB Molecule: 5-hydroxyisourate hydrolase (formerly known as PDBTitle: crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)

12	d2vo1a1	Alignment		25.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
13	d1ttaa_	Alignment		21.8	42	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
14	c3gehA_	Alignment		20.8	14	PDB header: hydrolase Chain: A: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
15	dis1ma2	Alignment		20.8	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
16	d1vcoa2	Alignment		20.3	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
17	c2xw7A_	Alignment		17.3	24	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrofolate reductase; PDBTitle: structure of mycobacterium smegmatis putative reductase ms0308
18	d1t95a1	Alignment		16.5	50	Fold: RuvA C-terminal domain-like Superfamily: Hypothetical protein AF0491, middle domain Family: Hypothetical protein AF0491, middle domain
19	c2k10A_	Alignment		16.0	30	PDB header: antimicrobial protein Chain: A: PDB Molecule: ranatuerin-2csa; PDBTitle: conformational analysis of the broad-spectrum antibacterial2 peptide, rantuerin-2csa: identification of a full length3 helix-turn-helix motif
20	c3nvaB_	Alignment		14.9	30	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
21	c2o7pA_	Alignment	not modelled	14.4	21	PDB header: hydrolase, oxidoreductase Chain: A: PDB Molecule: riboflavin biosynthesis protein ribd; PDBTitle: the crystal structure of ribd from escherichia coli in complex with2 the oxidised nadp+ cofactor in the active site of the reductase3 domain
22	c2ad5B_	Alignment	not modelled	14.3	33	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
23	d2azna1	Alignment	not modelled	14.2	29	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: RibD C-terminal domain-like
24	c3l51B_	Alignment	not modelled	14.0	15	PDB header: cell cycle Chain: B: PDB Molecule: structural maintenance of chromosomes protein 4; PDBTitle: crystal structure of the mouse condensin hinge domain
25	c1vcnA_	Alignment	not modelled	13.9	22	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
26	c2d5nB_	Alignment	not modelled	13.7	25	PDB header: hydrolase, oxidoreductase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribd; PDBTitle: crystal structure of a bifunctional deaminase and reductase2 involved in riboflavin biosynthesis
27	d2gxfa1	Alignment	not modelled	13.6	19	Fold: Cystatin-like Superfamily: NTF2-like Family: YybH-like
28	d1gxja_	Alignment	not modelled	13.3	15	Fold: Smc hinge domain Superfamily: Smc hinge domain Family: Smc hinge domain

29	c2jppB_	 Alignment	not modelled	13.3	21	PDB header: translation/rna Chain: B: PDB Molecule: translational repressor; PDBTitle: structural basis of rsma/csra rna recognition: structure of2 rsme bound to the shine-dalgarno sequence of hcna mrna
30	d1v97a5	 Alignment	not modelled	13.2	18	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
31	c1vraA_	 Alignment	not modelled	12.4	15	PDB header: transferase Chain: A: PDB Molecule: arginine biosynthesis bifunctional protein argj; PDBTitle: crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
32	d1cm3a_	 Alignment	not modelled	12.3	31	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
33	d2cyga1	 Alignment	not modelled	12.2	8	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
34	d2afhe1	 Alignment	not modelled	11.6	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
35	d1ffvb2	 Alignment	not modelled	11.0	15	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
36	d1g3qa_	 Alignment	not modelled	10.8	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
37	c2hxA_	 Alignment	not modelled	10.5	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: diaminohydroxyphosphoribosylaminopyrimidine deaminase/ 5- PDBTitle: crystal structure of a diaminohydroxyphosphoribosylaminopyrimidine2 deaminase/ 5-amino-6-(5-phosphoribosylamino)uracil reductase (tm1828)3 from thermotoga maritima at 1.80 a resolution
38	c2an1D_	 Alignment	not modelled	10.4	30	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
39	c1vpzB_	 Alignment	not modelled	10.1	18	PDB header: rna binding protein Chain: B: PDB Molecule: carbon storage regulator homolog; PDBTitle: crystal structure of a putative carbon storage regulator protein2 (csra, pa0905) from pseudomonas aeruginosa at 2.05 a resolution
40	d1vpza_	 Alignment	not modelled	10.0	18	Fold: CsrA-like Superfamily: CsrA-like Family: CsrA-like
41	d2di9a1	 Alignment	not modelled	9.7	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
42	c3mwdA_	 Alignment	not modelled	9.7	11	PDB header: transferase Chain: A: PDB Molecule: atp-citrate synthase; PDBTitle: truncated human atp-citrate lyase with citrate bound
43	d2b3za1	 Alignment	not modelled	9.7	25	Fold: Dihydrofolate reductase-like Superfamily: Dihydrofolate reductase-like Family: RibD C-terminal domain-like
44	c3l51A_	 Alignment	not modelled	9.4	20	PDB header: cell cycle Chain: A: PDB Molecule: structural maintenance of chromosomes protein 2; PDBTitle: crystal structure of the mouse condensin hinge domain
45	c2qwuB_	 Alignment	not modelled	9.4	14	PDB header: cell invasion Chain: B: PDB Molecule: intracellular growth locus, subunit c; PDBTitle: crystal structure of f. tularensis pathogenicity island2 protein c
46	c2bekB_	 Alignment	not modelled	9.4	29	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein2 soj
47	d1a9xa3	 Alignment	not modelled	9.4	19	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
48	c2p4gA_	 Alignment	not modelled	9.3	5	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a pyrimidine reductase-like protein (dip1392)2 from corynebacterium diphtheriae nctc at 2.30 a resolution
49	d1n62b2	 Alignment	not modelled	8.8	16	Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
50	c2kdoA_	 Alignment	not modelled	8.8	40	PDB header: rna binding protein Chain: A: PDB Molecule: ribosome maturation protein sbds; PDBTitle: structure of the human shwachman-bodian-diamond syndrome protein, sbds
51	c2vy8A_	 Alignment	not modelled	8.6	25	PDB header: transcription Chain: A: PDB Molecule: polymerase basic protein 2; PDBTitle: the 627-domain from influenza a virus polymerase pb22 subunit with glu-627
52	c1t95A_	Alignment	not modelled	8.5	50	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein af0491; PDBTitle: crystal structure of the shwachman-bodian-diamond syndrome2 protein orthologue from archaeoglobus fulgidus
		Alignment				Fold: TIM beta/alpha-barrel

53	d1aq0a_	Alignment	not modelled	8.4	10	Superfamily: (Trans)glycosidases Family: beta-glycanases
54	d1zxoal	Alignment	not modelled	8.2	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
55	d1zbsa2	Alignment	not modelled	7.9	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
56	d1oo2a_	Alignment	not modelled	7.8	16	Fold: Prealbumin-like Superfamily: Transthyretin (synonym: prealbumin) Family: Transthyretin (synonym: prealbumin)
57	c2panF_	Alignment	not modelled	7.7	26	PDB header: lyase Chain: F: PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase
58	c3jswA_	Alignment	not modelled	7.6	14	PDB header: structural protein Chain: A: PDB Molecule: filamin-a; PDBTitle: crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cfr
59	d1cp2a_	Alignment	not modelled	7.4	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
60	d1g5ha2	Alignment	not modelled	7.3	8	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
61	d1ghsa_	Alignment	not modelled	7.3	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
62	c3htnA_	Alignment	not modelled	7.3	14	PDB header: metal binding protein Chain: A: PDB Molecule: putative dna binding protein; PDBTitle: crystal structure of a putative dna binding protein (bt_1116) from2 bacteroides thetaiotaomicron vpi-5482 at 1.50 a resolution
63	d1i78a_	Alignment	not modelled	7.3	11	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane protease OMPT
64	c2ojlB_	Alignment	not modelled	7.3	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of q7waf1 borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
65	c3endA_	Alignment	not modelled	7.2	11	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase PDBTitle: crystal structure of the l protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
66	c3f55A_	Alignment	not modelled	7.1	10	PDB header: hydrolase, allergen Chain: A: PDB Molecule: beta-1,3-glucanase; PDBTitle: crystal structure of the native endo beta-1,3-glucanase (hev b 2), a2 major allergen from hevea brasiliensis (space group p41)
67	c2obkE_	Alignment	not modelled	7.1	21	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: selt/selw/selh selenoprotein domain; PDBTitle: x-ray structure of the putative se binding protein from pseudomonas2 fluorescens. northeast structural genomics consortium target plr6.
68	d1g2914	Alignment	not modelled	7.0	44	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
69	d1dvka_	Alignment	not modelled	7.0	9	Fold: Functional domain of the splicing factor Prp18 Superfamily: Functional domain of the splicing factor Prp18 Family: Functional domain of the splicing factor Prp18
70	c2rc9A_	Alignment	not modelled	7.0	25	PDB header: membrane protein Chain: A: PDB Molecule: glutamate [nmda] receptor subunit 3a; PDBTitle: crystal structure of the nr3a ligand binding core complex with acpc at2 1.96 angstrom resolution
71	d1tteal	Alignment	not modelled	6.9	16	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
72	c2wd5A_	Alignment	not modelled	6.9	15	PDB header: cell cycle Chain: A: PDB Molecule: structural maintenance of chromosomes protein 1a; PDBTitle: smc hinge heterodimer (mouse)
73	d3e9la1	Alignment	not modelled	6.9	38	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Prp8 beta-finger domain-like
74	c2f7fa_	Alignment	not modelled	6.8	11	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase, putative; PDBTitle: crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
75	c2p0gB_	Alignment	not modelled	6.8	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: selenoprotein w-related protein; PDBTitle: crystal structure of selenoprotein w-related protein from2 vibrio cholerae. northeast structural genomics target vcr75
76	c3dexA_	Alignment	not modelled	6.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sav_2001; PDBTitle: crystal structure of sav_2001 protein from streptomyces2 avermitilis, northeast structural genomics consortium3 target svr107.
77	d2dcfa1	Alignment	not modelled	6.7	3	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like

					Family: beta-Lactamase/D-ala carboxypeptidase
78	c2jtqA	Alignment	not modelled	6.7	17 PDB header: transferase Chain: A: PDB Molecule: phage shock protein e; PDBTitle: rhodanese from e.coli
79	c2fs1A	Alignment	not modelled	6.7	24 PDB header: protein binding Chain: A: PDB Molecule: psd-1; PDBTitle: solution structure of psd-1
80	d3e9oa1	Alignment	not modelled	6.7	38 Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Prp8 beta-finger domain-like
81	c1t3oA	Alignment	not modelled	6.7	18 PDB header: rna binding protein Chain: A: PDB Molecule: carbon storage regulator; PDBTitle: solution structure of csra, a bacterial carbon storage2 regulatory protein
82	c3e66B	Alignment	not modelled	6.5	38 PDB header: splicing Chain: B: PDB Molecule: prp8; PDBTitle: crystal structure of the beta-finger domain of yeast prp8
83	d2i14a1	Alignment	not modelled	6.5	13 Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
84	d1g8fa3	Alignment	not modelled	6.4	10 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ATP sulfurylase C-terminal domain
85	d1tifa	Alignment	not modelled	6.3	15 Fold: beta-Grasp (ubiquitin-like) Superfamily: Translation initiation factor IF3, N-terminal domain Family: Translation initiation factor IF3, N-terminal domain
86	d1p42a1	Alignment	not modelled	6.2	18 Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase LpxC
87	c3kjqB	Alignment	not modelled	6.1	25 PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
88	d3enba1	Alignment	not modelled	6.1	38 Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Prp8 beta-finger domain-like
89	c3jtwB	Alignment	not modelled	6.1	13 PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrofolate reductase; PDBTitle: crystal structure of putative dihydrofolate reductase (yp_805003.1)2 from pediococcus pentosaceus atcc 25745 at 1.90 a resolution
90	c2jyaA	Alignment	not modelled	6.0	22 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1810; PDBTitle: nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
91	d2isba1	Alignment	not modelled	6.0	19 Fold: The "swivelling" beta/beta/alpha domain Superfamily: FumA C-terminal domain-like Family: FumA C-terminal domain-like
92	c3fg8B	Alignment	not modelled	5.9	7 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein rha05790; PDBTitle: crystal structure of pas domain of rha05790
93	d1t3qb2	Alignment	not modelled	5.9	11 Fold: Molybdenum cofactor-binding domain Superfamily: Molybdenum cofactor-binding domain Family: Molybdenum cofactor-binding domain
94	c2lc2A	Alignment	not modelled	5.8	14 PDB header: protein binding Chain: A: PDB Molecule: avr3a4; PDBTitle: solution structure of the rxlr effector p. capsici avr3a4
95	c2nqcA	Alignment	not modelled	5.8	23 PDB header: immune system Chain: A: PDB Molecule: filamin-c; PDBTitle: crystal structure of ig-like domain 23 from human filamin c
96	d2nqca1	Alignment	not modelled	5.8	23 Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Filamin repeat (rod domain)
97	d1a9xa4	Alignment	not modelled	5.7	19 Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
98	d2fa8a1	Alignment	not modelled	5.7	21 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Selenoprotein W-related
99	c3kgvA	Alignment	not modelled	5.7	25 PDB header: oxidoreductase Chain: A: PDB Molecule: bifunctional deaminase-reductase domain protein; PDBTitle: crystal structure of putative dihydrofolate reductase (yp_001636057.1)2 from chloroflexus aurantiacus j-10-fl at 1.50 a resolution